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Baker et al.(10) **Pub. No.: US 2003/0036123 A1**(43) **Pub. Date: Feb. 20, 2003**(54) **SECRETED AND TRANSMEMBRANE
POLYPEPTIDES AND NUCLEIC ACIDS
ENCODING THE SAME**(75) **Inventors: Kevin P. Baker**, Darnestown, MD
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(73) **Assignee: Genentech, Inc.**(21) **Appl. No.: 10/180,551**(22) **Filed: Jun. 25, 2002****Related U.S. Application Data**

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(57) **ABSTRACT**

The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCAC
CAATGTTCTGTTGCTGCTCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCTCTTCAACCT
CCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTGGAGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCT
GTTAAAAATCTTTGCGTGGGCTACCTTGAGAAATGGAGCGAGGAGCAAGGAGAAGAACCCAGCTTTACAAGCC
CTACACCAACGGATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGGTAG
TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGGAAAGGAATGGAGAC
CAATTATGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCTCTGGAACCTGCTGAGCAGAACCA
TTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCTGTGGGGTTAGGAGTGTGATTCCGTACTGCTTTCT
GCTGCCGCTCAGGATAGCACTGGCTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACTGTGGTGGGATAGT
GCCAAATGGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGCAGCGCT
GACAGCCATCATCACCTACCATGACAGGGAAACAGACCAAGAAATGGTGGCATCTGTGTGGCAATCATACCTC
ACCGATCGATGTGATCATCTTGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGGGGGACTCATGGG
TGTGATTGAGAGCCATGGTGAAGGCTGCCACACGTCTGGTTGAGCGCTCGGAAGTGAAGGATCGCCACCT
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAGCAAGCTGCCTATCCTCATCTTCCAGAAAGGAACCTG
CATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTGAATTTGAGGCCACAGTTTACCCTGTTGCTAT
CAAGTATGACCTCAATTTGGCGATGCCCTTCTGGAACAGCAGCAAAATACGGGATGGTGACGTACCTGCTGCGAAT
GATGACCACTGGGCCATTTGCTGTCAGCGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
CCAGTTTGCGAATAGGTGAAATCTGCCATTGCCAGGAGGAGGACTGTGGACCTGCTGTGGGATGGGGGCT
GAAGAGGGAGAAAGTGAAGGACAGCTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
CAAGGACAGGAGCGCTCTGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
TGGAGTTGCCGCGCGCGCCCACTGCTGTGCTCTTTCCAGACTCCAGGGCTCCCGGGGCTGCTCTGGATCCCAG
GACTCCGCTTTTCCGCGAGCGCAGCGGGATCCCTGTGCACCCGCGCGAGCCTACCCTTGGTGGTCTAAACGGAT
CTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTCTTTTACAATAAGTGGTGGAGGAATGCCATTAAAG
TGAAGTCTCCCATCTTGCAAGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGTGG
CGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGCGGCCACCCGCTCTCCAGGAAAGGC
ACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGCCTTGGAGCTCTGCAGACATGATAGGAAG
GAAACTGTCTGCAAGGGCTTTCAGCAAAATGAAGGTTAGATTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
GGGAGGGGAAGAGGCCAGGTGGGCGCTGACTGGGCCATGGGAGAACGTGTGTTCTGCTACTCCAGGCTAACCTG
AACTCCCATGTGATGCGCGCTTGTGTAATGTGTGCTCGGTTTCCCATCTGTAATATGAGTGGGGGGAATG
GTGGTGAATTCCTACCTCACAGGCTGTGTGGGATTAAAGTGTGCTGGGGTGAAGTGAAGGACATACAGTTTCA
TGTTTCAAGTACAGGCCCAAAACGGGGCACGGCAGGCTGAGCTCAGAGCTGCTGCACTGGGCTTTGGATTTG
TTCTTGTGAGTAAATAAACTGGCTGGTGAATGA

Related U.S. Application Data

which is a continuation of application No. 09/380,138, filed on Aug. 25, 1999, now abandoned, and which is a continuation of application No. 09/380,139, filed on Aug. 25, 1999, now abandoned, and which is a continuation of application No. 09/380,142, filed on Aug. 25, 1999, now abandoned, and which is a continuation of application No. 09/403,297, filed on Oct. 18, 1999, now abandoned, and which is a continuation of application No. 09/423,844, filed on Nov. 12, 1999, now abandoned, and which is a continuation of application No. 09/644,848, filed on Aug. 22, 2000, and which is a continuation of application No. 09/664,610, filed on Sep. 18, 2000, now abandoned, and which is a continuation of application No. 09/665,350, filed on Sep. 18, 2000, and which is a continuation of application No. 09/709,238, filed on Nov. 8, 2000, now abandoned, and which is a continuation of application No. 09/747,259, filed on Dec. 20, 2000, and which is a continuation of application No. 09/816,744, filed on Mar. 22, 2001, and which is a continuation of application No. 09/854,208, filed on May 10, 2001, and which is a continuation of application No. 09/854,280, filed on May 10, 2001, and which is a continuation of application No. 09/866,028, filed on May 25, 2001, and which is a continuation of application No. 09/874,503, filed on Jun. 5, 2001, and which is a continuation of application No. 09/908,827, filed on Jul. 18, 2001, and which is a continuation of application No. 09/918,585, filed on Jul. 30, 2001, and which is a continuation of application No. 09/924,419, filed on Aug. 6, 2001, now abandoned, and which is a continuation of application No. 09/929,404, filed on Aug. 13, 2001, now abandoned, and which is a continuation of application No. 09/931,836, filed on Aug. 16, 2001, and which is a continuation of application No. 09/941,992, filed on Aug. 28, 2001, and which is a continuation of application No. 09/946,374, filed on Sep. 4, 2001.

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Sep. 1, 1999	(WO).....	PCT/US99/20111
Sep. 15, 1999	(WO).....	PCT/US99/21090
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Dec. 2, 1999	(WO).....	PCT/US99/28551
Dec. 30, 1999	(WO).....	PCT/US99/31274
Jan. 5, 2000	(WO).....	PCT/US00/00219
Feb. 18, 2000	(WO).....	PCT/US00/04341
Feb. 18, 2000	(WO).....	PCT/US00/04342
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Mar. 1, 2000	(WO).....	PCT/US00/05601
Mar. 2, 2000	(WO).....	PCT/US00/05841
Mar. 15, 2000	(WO).....	PCT/US00/06884
Mar. 30, 2000	(WO).....	PCT/US00/08439
May 17, 2000	(WO).....	PCT/US00/13705
May 22, 2000	(WO).....	PCT/US00/14042
May 30, 2000	(WO).....	PCT/US00/14941
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Jul. 28, 2000	(WO).....	PCT/US00/20710
Aug. 24, 2000	(WO).....	PCT/US00/23328
Nov. 8, 2000	(WO).....	PCT/US00/30952
Dec. 1, 2000	(WO).....	PCT/US00/32678
Dec. 20, 2000	(WO).....	PCT/US00/34956
Feb. 28, 2001	(WO).....	PCT/US01/06520
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Jun. 20, 2001	(WO).....	PCT/US01/19692
Jun. 29, 2001	(WO).....	PCT/US01/21066
Jul. 9, 2001	(WO).....	PCT/US01/21735
Aug. 29, 2001	(WO).....	PCT/US01/27099

FIGURE 1

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCCCGCTCTCCGCCCTTCTGCATCGCGGCTTCGGCG
GCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCGTCTGTGAGGGGGTCGGCACGGGGAGTCGGGCGGTCT
TGTGCATCTTGGCTACCTGTGGGTCTGAAGATGTCGGACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCACGC
GCTATTGGTTCGCCGCCACCGTCGCCGTGCCCTTGGTCCGCAAACTCGGCCCTCATCAGCCCGGCTACCTCTTCC
TCTGGCCCGAAGCCTTCCTTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTTATTTCCCTGTGGGTC
CAGGAACTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTTACGCGACTTGAAACAGGAGCTT
TTGATGGGAGGCCAGCAGACTATTTATTATGCTCCTCTTTAACTGGATTTGCATCGTGATTACTGGCTTAGCAA
TGGATATGCAGTTGCTGATGATTCTCTGATCATGTCTAGTACTTTATGTCTGGGCCAGCTGAACAGAGACATGA
TTGTATCATTTTGGTTTGAACACGATTTAAGGCTGCTATTTACCCTGGGTATCCTTGGATTCAACTATATCA
TCGGAGGCTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTCCTAATGTTGAGATACC
CAATGGACTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTTTTGTACCGCTGGCTGCCAGTAGGAGAGGAG
GAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGCTGCTGATCAGAATGGCGAGGCGGGAGACACA
ACTGGGGCCAGGGCTTTCGACTTGGAGACCAGTGAAGGGGCGGCCCTCGGGCAGCCGCTCTCTCAAGCCACATTT
CCTCCAGTGCTGGGTGCACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTC
TTTCAGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTCCACAAGTTTTCACGATTCTCATTCA
AGTCTTACTGCTGTGAAGAACAATAACCAACTGTGCAAAATGCAAACTGACTACATTTTTTGGTGTCTTCTCT
TCTCCCTTTTCCGTCTGAATAATGGGTTTTAGCGGGTCTTAATCTGCTGGCATTGAGCTGGGGCTGGGTACCAA
ACCTTCCCAAAGGACCTTATCTCTTTCTTGACACATGCCTCTCTCCACTTTTCCCAACCCACATTTGCA
ACTAGAAAAAGTTGCCATAAAATTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGT
CACAACAATCATATTCACGTTATTTTCCCTTTTGGTGGCAGAAC'TGTTACCAATAGGGGGAGAAGACAGCCACG
GATGAAGCGTTTCTCAGCTTTTGGAAATTGCTTCGACTGACATCCGTTGTTAACCGTTTGGCACTCTTCAGATATT
TTTTATAAAAAAAGTACCACTGAGTTTCATGAGGCCACAGATTGGTTATTAATGAGATACGAGGGTTGGTGTGG
GTGTTTGTCTCTGAGCTAAGTATCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGG
GGATGCACCCCTTTGCGTTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGTTA
GGAGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTGATTCCCATTTCAATC
TCATTCTGGATATGTGTTTATTGAGTAAAGGAGGAGAGACCCCTCATACGCTATTTAAATGTCACTTTTTTGCCTA
TCCCCCGTTTTTGGTTCATGTTTCAATTAATTGTGAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTA
AAGCTAATGTAAGCACATCTAAGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGAG
GTGTGTTATTTTGTGATCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTTTCGTA
GGTGGGCTTTTTCTATCAGAGCTTGGCTCATAACCAAATAAAGTTTTTTTGAAGGCCATGGCTTTTACACAGTTA
TTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGTATTGAGTGGCTGTACACTTTGAGGCAACTA
AAAAGGCTTCAAACGTTTTGATCAGTTTCTTTTCAGGAAACATTGTGCTTAACAGTATGACTATTCTTTCCCC
ACTCTTAAACAGTGTGATGTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTT
GTGTGTACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTATGTTTGT
TGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAATTTTAGAGGCCATTACTCCAATTATGTTGCACGTACAC
TCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATATTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGT
ACCCTCTTACCAGTCAGCTGCCTGCGAGCAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAATTTTCAGTT
CAGGGCAAAATGTTTCATGAAGTTATTCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGA
TTATGTTTTCTGGAATAATTTTACCAAAACAAGCTATTTGAGTTTTGACTTGACAAGGCAAAACATGACAGTGGAT
TCTCTTTACAAATGGAAAAAAAATCCTTATTTTGTATAAAGGACTTCCCTTTTGTAAACTAATCCTTTTTAT
TGGTAAAAATTGTAATTAATGTGCAACTTG

FIGURE 2

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGLISPAYLFLWPEAFLYRFQIWRPITATFYFPVGP GTGFLYLVN
LYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIPLIMSVLYVWAQLNRDMIVSFWFGTRF
KACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFLMFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPA
SMRRAADQNGGGGRHNWGQGFR LGDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 3

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTCAAATGCACGGATT
 CTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGAAGTCCTGAGCGCTCAAGTTTGTCCGT
 AGGTGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCC
 CCGAGTCTTTGCTGCCGAAGCTGTGACTGCCGATTCCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGT
 CCCAGAGCCCTATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAAT
 TTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAATACC
 AGCTTTTATTATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCATAACCGGTTTGATGCTGT
 GCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGCTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTT
 TGTGACTATATTCAACACAGTGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAAT
 TGCAGGAGCTGTACGGGAAGTCTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCATAATTGG
 AGCCTTGCTGGGCACTCCTGTAGGAGGCTGCTGATGGCATTTCAGAAGTACGCTGGTGAGACTGTTTCAAGAAAG
 AAAACAGAAGGATCGAAAGGCACCTCCATGAGCTAAAACTGGAAGAGTGGAAAGGCAGACTACAAGTTACTGAGCA
 CCTCCCTGAGAAAATTGAAAGTAGTTTACGGGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCT
 AAACCTTCCTAGAAACCCTTCAGTAATAGATAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTG
 GAGAGCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGCTGACAAATT
 TAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTCTTTTCTTTTAACTAAGAATGGGGCTGTT
 GTACTCTCACTTTACTTATCCTTAAATTTAAATACATACTTATGTTTGTATTAATCTATCAATATATGCATACAT
 GGATATATCCACCCACCTAGATTTTAAGCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELFGKDEQQRISKDLA
NICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAETIYHNRFDAVQSAHRAATRGFIRYGWRGWRTAVFVTIEN
TVNTSLNVYRNKDLSHFVIAGAVTGSLFRINVGLRGLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDR
KALHELKLEEWKGRLQVTEHLPEKIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD
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Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 5

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGCGCCTGAAGTCGGC
 GTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGCTTAAGAAGTAAAAATGGCAGGCTTCC
 TAGATAATTTTCGTTGGCCAGAATGTGAATGTATTGACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTG
 CAGGTATATTGTTTTTACAGGCTGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGA
 ACCATGCCTTTCACACATGTGGTGTATTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTCAGG
 TGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTTTTCATGCTTTCATGT
 TGATGTTTGGGTCACCTATTGCTTCCATGTGGATTCTTTTTGGTGCATATGTTACCCAAAATACTGATGTTTATC
 CGGGACTAGCTGTGTTTTTTTCAAAATGCACCTATATTTTTTAGCACCTCTGATCTACAAATTTGGAAGAACCGAAG
 AGCTATGGACCTGAGATCACTTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATC
 TCTCAGTACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTCTGAGTT
 TTGAAATAGTTTTATGAAATTTCTTTATTTTTTCATTGCATAGACTGTTAATATGTATATAATACAAGACTATATG
 AATTGGATAATGAGTATCAGTTTTTTATTCTGAGATTTAGAACTTGATCTACTCCCTGAGCCAGGGTTACATCA
 TCTTGTCATTTTAGAAGTAACCACTCTTGTCTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTT
 TGGGAGGCCGAGGCGGGCCGATTGCTTGAGGTCAAGTGTGTTGAGACCAGCCTGGCCAACATGGCGAAACCCATC
 TACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGCTGAGGCAGG
 AGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCACTGCACTCTAGCCTGGGGGAGAA
 AGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATCTCTGATTTCTGAAGATGTACAAAAAATATAGCTT
 CATATATCTGGAATGAGCACTGAGCCATAAAAGGTTTTTCAGCAAGTTGTAACCTTATTTTGGCCTAAAAATGAGGT
 TTTTTTGGTAAAGAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC
 CAAAGGACTAGTTTGAAAGCTCTTTTAAAAAGAATTCTCTAATATGACTTTATGTGAGAA

FIGURE 6

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWMIDAADVYPKPEQLNHAFHTCGVFSTLAFFMINAV
SNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQNTDVYPGLAVFFQNALIFFSTLIYKF
GRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 7

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTGTAGCTTCTCCACG
TATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAGGATGTGCGTTCTTC
CACTAGAAGCTCTTCTGAGGGAGGTAATTAAAAAACAGTGGAAATGGAAAAACAGTGCTGTAGTCATCCTGTAATA
TGCTCCTTGTCAACAATGTATACATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTA
GTGAAGTATTCTGCCAATGAAGAAAAACAAGTATGATTATCTTCCAACACTACTGTGAATGTGTGCTCAGAACTGGTG
AAGCTAGTTTTCTGTGTGCTTGTGTCAATTCGTGTATTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATATGCT
TCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCGCTTTCTTTATTTCTGGATAACTTGATTGTC
TTCTATGTCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTT
CTATTCAGGATAGTGCTGAAGAGGCGTCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATT
GTGGCCTTGACTGCCGGGACTAAAACTTTACAGCACAACCTTGGCAGGACGTGGATTTCATCACGATGCCTTTTTTC
AGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTGTACAGCAAAGGAATGGACT
TTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTCACATCCGTCTTGGCATGGGCCATGTTCTTATT
ATAGTCCAGTGTTTTATTTCTTCAATGGCTAATATCTATAATGAAAAGATACTGAAGGAGGGGAACAGCTCACT
GAAAGCATCTTCATACAGAACAGCAAACCTCTATTTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCCTTCAG
AGGAGTAACCGTGATCAGATTAAGAACTGTGGATTTTTTTATGGCCACAGTGCAATTTTCAGTAGCCCTTATTTTT
GTAAGTGCATTCCAGGGCCTTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAACATGTTCCATGTCTTGATGGCC
CAGGTTACCACTGTCTATTATCACAACAGTGTCTGTCTTGGTCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTG
GAAGCCCCATCAGTCCTTCTCTATATTTATTTATAATGCCAGCAAGCCTCAAGTTCCGGAATACGCACCTAGG
CAAGAAAGGATCCGAGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTT
ACCAAACCCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCAGCTCTCTTGAAC
CTTATTTTCACATTTTCAGTGTTTGTAAATTTATCTTTTCACTTTGATAAACCAGAAATGTTTCTAAATCCTAA
TATCTTTGTCATATATCTAGCTACTCCCTAAATGGTTCATCCAAAGGCTTAGAGTACCCAAAGGCTAAGAAATTC
TAAAGAAGTATACAGGAGTAACAATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATAT
GTGCAGATTATTTTCTTGGCCTTCAAGCTTCCAAAAAAGTTGTAATAATCATGTTAGCTATAGCTTGTATATAC
ACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGTCTTCCCTTTTTAACA
TTATAAAAGCTAGGTTGTCTCTTGAATTTTGAGGCCCTAGAGATAGTCATTTTGCAAGTAAAGAGCAACGGGACC
CTTTCTAAAAACGTTGGTTGAAGGACCTAAATACCTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAA
ATATTTTGCTGAAGAAGCAGTTTCTCAGACACAACATCTCAGAATTTTAATTTTAGAAATTCATGGGAAATTGG
ATTTTTGTAATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTTACCACCTGTATTTAAGTCA
TTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGATGTCTATTACTCCTGAATTA
TTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACTAATTCAAGCTGTGACTATTGTATATCTTTCC
AAGAGTTGAAATGCTGGCTTCAGAATCATACCAGATTGTGAGTGAAGCTGATGCCTAGGAACTTTTAAAGGGATC
CTTTCAAAGGATCACTTAGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAA
AGACCAGTAATATATAAGTCACTTTACAGTGCTACTTCAACATTAAGTGCATGGTATTTTCATGGTATTTTG
CATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAATAATTAGCAAAACAAAGTGAC
TTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGGCTTTAACTGGCAGGCCTGTATGTTTACAGACTAC
CATACTGTAAATATGAGCTTTATGGTGTCAATTCAGAAACTTATACATTTCTGCTCTCTTTCTCCTAAGTTTC
ATGCAGATGAATATAAGGTAATATACTATATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAAT
TGGTGGAAATTTGTAATTAATAATTAATTATTAACCT

FIGURE 8

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVKLVFCVLVSFCVIK
KDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLPAMAVIFS NFSIITTALLFRIVLKRRLNWIQ
WASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFFSPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNTTARVFS
HIRLGMGHVLIIVQCFISSMANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFY
GHSAFSVALIFVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNA
SKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293, 298-318,
328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 9

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATGAGCAGGTCTG
AAGACTAACATTTTGTGAAGTTGTAAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTC
CTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACTCCACCAT
ATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTA
AATATTGCGGCAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAG
AACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTTGGAATACTGAGTTGTTTAGGACTTCTATTTGTGGCA
AACTTCCAGAAAACAACCCCTTTTGTGCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATAT
ATGTTTGTTCAGACCATCCTTTCCTACCAAATGCAGCCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTG
TTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTCACAGTGGCAATTTT
GGGACTGATTTAGAACAGAACTCCATTGGAACCCGAGGACAAAGGTTATGTGCTTCACATGATCACTACTGCA
GCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCTGACTTACATTCGTGATTTTCAGAAAATTTCTTTA
CGGGTGAAGCCAATTTACATGGATTAACCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGG
CTACTTTCAGAGATATTTGATGAAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTCCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCT
GATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTATTAAAAACA
CCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

FIGURE 10

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRY
KQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMOPKI
HGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT
YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLLSRDI

FIGURE 11

CCCACGCGTCCGCCCCGCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGGCCGGGGTGCGGAG
CCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCACCTTCGCCTTGTAATTGCTGTGACGC
GACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGGAGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGG
CAGAGCTGCGGGAGCTCTCTGAGGTCTTCGAGAGTACCGGAAGGAGCACCAGGCCACGTGTTCTGCTCTTCT
GCGGCGCTACCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTTGAATGTTTTAGCTGGTGCCTTGT
TTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGCTGCTACCTGCTCTCCA
GTATTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGATAAAGTGGCCCTGCTGCAGAGAAAGGTGGAGGAGA
ACAGAAACAGCTTGT'TTTTTTTTCTTATTGTTTTTGGAGACTTTTCCCATGACACCAAACCTGGTTCTTGAACCTCT
CGGCCCCAATTCTGAACATTCCCATCGTGAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAAATTTCA
TCTGTGTGCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTTCTCCTGGGACACTGTCTTTA
AGCTGTTGGCCATTGCCATGGTGGCATTAATTCCTGGAACCCTCATTAAAAAATTTAGTCAGAAACATCTGCAAT
TGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGACACATGATCTGGATTTTCTGTTTGCCACATCC
CTGGACTCAGTTGCTTATTTGTGTAATGGATGTGGTCTCTAAAGCCCCTCATTGTTTTTGATTGCCTTCTATAG
GTGATGTGGACACTGTGCATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATC
AGTTTTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGTGGCCGGGCG
CGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTACAAAGGTCAGGAGTTCAAGACC
AGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAATACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGT
AATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGAT
CACACCACTGCACTCCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 12

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYRKEHQAYVFLFCG
AYLYKQGFALPGSSFLNVLGALFGPWLGLLLCCVLTSVGATCCYLLSSIFGKQLVVSYPDKVALLQRKVEENR
NSLFFFLFLRLFPMTPNWFLNLSAPILNIPVQFFSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKL
LAIAMVALIPGTLIKKFSQKHLQLNETSTANHIHSRKDT

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 13

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACCGTGTGAG
GGGGCCTGTGGCCCCAGCGTGCTGTGGCCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTCCTTACACTTCGCCA
TGAGTTTCCTCATCGACTCCAGCATCATGATTACCTCCAGATACTATTTTGGATTGGGTGGCTTTTCTTCA
TGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTT
CTTGACCATGTTTGGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACTGGA
AAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCA
ATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGA
AACTAGGAGATCCCTTTCCCATTTCTCAGCCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTG
GTGTGATTGGAGTGACTCTCATGGCTCTTCTTCTGGATTGGGTGCTGTCAACTGCCCATACACTTACATGTCTT
ACTTCCTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGATCA
TAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACAAACCATCAG
GTTTTCTGGGAATGATAAAAAGTGTACCACCTCAGCATCAGGAAGTGAAATCTTACTCTTATTCAACAGGAAG
TGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAG
AATACTCCAAACCTTCAAGGGGAAATATTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAA
TTTTTCATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCATTGAGATCA
CTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATTTCTTCTATTCTTGTGGAATAA
TCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCT
CCAATGTCATTGTCTGCTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGTCTGTGATCCGAATGA
GTATGCCTTTAGAATACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGT
TTGATGTGATCTTCTGGTCAGCGCTCTCTTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCAGAGA
AGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTAGATATAAGAGG
GGGGAAAATGGAACAGGGCCTGACATTTTATAACAAACAAAATGCTATGGTAGCATTTTTCACCTTCATAGC
ATACTCCTTCCCCGTCAGGTGATACTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGGAGAACTAACTCAA
GACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAAAG
GTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTA
AGGTTACATGGAAGGTTATAGCTTTGCCTTGAGATTGACTCATTAAAAATCAGAGACTGTAACAAAAA
AAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTG
CAGCTTATAATG

FIGURE 14

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGVLNSSSRYPFW
KMNLCVILLILVEMVFPYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFFWKLGDPPILSPKHGILSIEQLISRV
GVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPS
GFWGMIKSVTTSASGSENLTIIQQEVDAL EELSRQLFLETADLYATKERIEYSKTFKGKYNFLGYFFSIYCVWK
IFMATINIVFDRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKS
SNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPE
KQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

FIGURE 15

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCGGGACATGCGGCCCC
CAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTGCTGCTGCCGCCGCCCGTGCCTTGCC
CACAGCGCCACGCGCTTCGACCCACCTGGGAGTCCCTGGACGCCCGCCAGCTGCCCGCGTGGTTTTGACCAGGCC
AAGTTCGGCATCTTCATCCACTGGGGAGTGTTCCTGCGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGG
CAAAAGGAAAAGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTTCAAATATGAAGATTTT
GGACCACTATTTACAGCAAAATTTTTTAATGCCAACAGTGGGCAGATATTTTTTCAGGCCTCTGGTGCCAAATAC
ATTGCTCTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGTGAGAATATTCGTGGAACCTGGAATGCCATA
GATGAGGGGCCCCAAGAGGGACATTGTCAAGGAACCTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGA
CTGTACTATTTCCCTTTTTGAATGGTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAA
TTTCCAGTTTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGGTCCGAT
GGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTTATATAATGAAAGCCAGTT
CGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCATCTGTAAGCATGGTGGCTTCTATACCTGCAGT
GATCGTTATAACCCAGGACATCTTTTGCCACATAAATGGGAAAACCTGCATGACAATAGACAACTGTCTGGGGC
TATAGGAGGGAAGCTGGAATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCA
TGTGGAGGAAATCTTTTGATGAATATTGGGCCCCACACTAGATGGCACCATTCTGTAGTTTTTGAGGAGCGACTG
AGGCAAGTGGGGTCTCGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTATACCTGGCGATCCCAGAATGAC
ACTGTCACCCCAAGATGTGTGGTACACATCCAAGCCTAAAGAAAAATTAGTCTATGCCATTTTTCTTAAATGGCCC
ACATCAGGACAGCTGTTCTTGGCCATCCCAAAGCTATTTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGA
CAGCCACTTAACTGGATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATG
CCGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTGATGCTGCAAGTT
ATGCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGAAAGCAATGTAACTGGATAAGAAAA
TTATTTGGCAGTTTCAGCCCTTTCCCTTTTCCCACTAAATTTTTCTTAAATTACCCATGTAACCATTTTAACTCT
CCAGTGCACCTTTGCCATTAAAGTCTCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCA
CATTATAGTAGCAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATGAT
TATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAATTTTTTTTTTGTGCCAA
CATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACACACCTAATGTGTATGGTATAGACTGTTG
CTCCTAGGCTACAGACATATACAGCATGTTACTGAATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAA
ACATATGGAAACATAGAGAAGGTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCAC
GAATGGAGCTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTATTGAA
CACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAGTTTTTCTTTCTTCAATT
ATAAATTAACATAAGTGTACTGTAACCTTACAAACGTTTTAATTTTTTAAACCTTTTGGCTCTTTGTATAAAC
ACTTAGCTTAAACATAAATCATTTGTGCAATGTAA

FIGURE 16

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHGVSFVPSFGSEWFW
WYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQASGAKYIVLTSKHHEGFTLWGSEYSWNW
NAIDEGPKRDIVKELEVAIRNRTDLRFGLYSLFEWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVL
WSDGDGGAPDQYWNSTGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKL
SWGVRREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYTWRS
QNDTVPD VWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWISEQNGIMVELPQLTI
HQMPCKWGWALALTNI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 17

[illegible]

FIGURE 18

MKFLLDIILLLLPLLIIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKL
VLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVVYT
SDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYCSSK
FAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMHGILT
EQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:
amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.
amino acids 30-34, 283-287

Casein kinase II phosphorylation site.
amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.
amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 19

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCTAGAGAT
 GCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCCGCCAGCCCGCTCCACCGCCGTAG
 CGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGGCCG
 TGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCCTCGG
 ATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTATAAAG
 TCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCTGCAGGA
 GGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAAAAGTTCA
 TTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGAGGAGAAAC
 AAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGACTGATGGCAGCATATCACAATTTA
 GGAAGTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTTCATGTACCATCAGC
 CATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGACCGGTGCAACA
 TGAAGAACAATTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTTCTAGAGAAGCTG
 AAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAGGAAGAAGATGCCA
 AAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACATCCTAATCCCCAGCA
 TTCCCTTCTCCTCCTCCTTGTGGTCACACAGTTGTATGTTGGGTTTGGATCTGTAGAAAAA
 GAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATCTGGCCCTCTCCTCACC
 AGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACAAAGCGAAGCTGACTTAG
 CTGAGACCCCGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTTGCGGAGAAGCCACTCCCG
 ATGACATGTCTTGACTATGACAACATGGCTGTGAACCCATCAGAAAGTGGGTTTGTGACTC
 TGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGAGTTCTCCCAGACCAAATGG
 GGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATGGTTATTAGGACATATAAAAAA
 CTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATCCTCTTATTTTCTATAAGGAAAA
 TACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGTGGATGAGCATGTGGTCCCCACGA
 CCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTATCCCAGCCAGTCATCCAGCTCGACC
 TTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTAGAGTCTCAATAAATGCTACTTGGTT
 GGTGTATCTAACTTTTAAGGGACAGAGCTTTACCTGGCAGTGATAAAGATGGGCTGTGGAGC
 TTGGAAAACCACCTCTGTTTTCTTGCTCTATACAGCAGCATATTATCATAACAGACAGAAA
 ATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAGGTTGGCCTGTGCATCGGCAATTCTC
 ATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGAGCAGGAAAAAAA

FIGURE 20

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRLGGQPVCRRGTQRPCYKVIYFHDTSRRLN
FEEAKEACRRDGGQLVSI ESEDEQKLIKFIENLLPSDGDFWIGLRRREEKQSNSTACQDLYA
WTDGSISQFRNWWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWND DRCNMKNNFICKYSDE
KPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLVVTTV
VCWWVICRKRKREQPD PSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETR PDLKNISF
RVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENE
IYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 21

AGGCTCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
CGTGGAGCCTCCGGCGGAGGCCGGCCCCGACGCTGGGACTCCTGCTGCTGGTCTGCTTGGGCTTCCTGGTGTCTC
GCAGGCTGGACTGGAGCACCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCGTGTGGCTTGAACACCCTCACCACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGATGGCCGCAGAGATCG
GGCTGTGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAAGTGGACCTCGGGGGCTTGGCCAGCTGGCTAC
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACC
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG
GTTCCCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTTGTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT
ACTGGACGGGGTGGTTTGAAGTCTGCTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG
GAGCCATGCACCTTCATGACTACAAGTCAAGTGTCAACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTAACCTGTCTCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCCT
TCGGGTACATTTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGGAATCTCTATCTGAATGATTACCCCTGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTTTCAAGGTTTCGGCCTGGACAAATGGNGTTCCCTCCCAGAAACACCCACATTACCTGCTTTCTTCTTGG
GTAGCTTTGTCCATCAGCTCCACGCCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACGCTTTACCTCCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTATCGTTTGTGAGGAGACGATGGCGGGCCCTGCATTACAGTTACAGGAAACCCCCC
ACCTGGGCAGGAACCAAGTACATTAAGTGAAGCGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCCCTGTCTCAGCTCAAAACCCCTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC
TGGCTTTGTTGATGATGGCTTTCCTACAGCCCTGCTCTTGTGCCGAGGCTGTCCGGCTGTCTCTAGGGTGGGAGC
AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGCACCGGACGTACAGCCC
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTGTCTGGTTTCTGGGAGGCTTGGCCACATCCCTCATGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCAACAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTCAACCTTCTGAGCCTTCTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCTT
TCCCTTCCCACTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCCCAACAGCAGGGGCGAGCAGCCCTCCTTC
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCAAA

FIGURE 22

MTTWSLRRRPPARTLGLLLLLVVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFWI
FGGSIHYFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMMAE
IGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQYKR
GGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKGDLKSGIVQGVLATINLQ
STHELQLLTTFLFNVQGTQPKMVMEYWTGWFD SWGGPHNILDSSSEVLKTVSAIVDAGSSINLY
MFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSI SGIPLPPPPD
LLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYETSITSSG
ILSGHVHDRGQVFVNTVSI GFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGENIDDQRKGL
IGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSL SISSTPCDTFLK
LEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPALQFTETPHLG
RNQYIK

Signal sequence:
amino acids 1-27

Casein kinase II phosphorylation site.
amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.
amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 23

[illegible]

FIGURE 24

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPENF
TELSYCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDITISWALSLKNCSAMGAHLVVINSQEEQEF
LSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCAIMRDSSNPR
QNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 25

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACCC
TGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGGGG
AGCAAAGCCGGGCTCGGCCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATCCGA
CACGTGACGGTCTGTCCGCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCCAAGA
AGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCAGGCAG
ACACTCGGTCGTTTCGTAGTGGATAGGGGTCATGACCGGTTTCTCCTAGACGGGGCCCCGTTCC
GCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGACCGGCTTT
TGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTACCACGAGC
CACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTCGCTTTTCTGAATGAGGCAG
CTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAGTGGGAGATGG
GGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTCAGATCCAGACT
TCCTTGCCGCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATCCATGGCTTTATC
ACAATGGGGGCAACATCATTTAGCATTCAGGTGGAGAATGAATATGGTAGCTACAGAGCCTGTG
ACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCACTGCTAGGAGAAAAGATCTTGC
TCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGGGACTCTATACCACTG
TAGATTTTGGCCCAGCTGACAACATGACCAAAATCTTTACCCTGCTTCGGAAGTATGAACCCC
ATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTACTGGGGCCAGAATCACT
CCACACGGTCTGTGTGCTGTAACCAAAGGACTAGAGAACATGCTCAAGTTGGGAGCCAGTG
TGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGGAATGGTGCCGATAAGAAGG
GACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACCTATATCTGAAGCAGGGGACC
CCACACCTAAGCTTTTTGCTCTTCGAGATGTATCAGCAAGTTCAGGAAGTTCTTTGGGAC
CTTTACCTCCCCGAGCCCCAAGATGATGCTTGACCTGTGACTCTGCACCTGGTTGGGCATT
TACTGGCTTTTCTAGACTTGCTTTGCCCCCGTGGGCCCATTCATTCAATCTTGCCAATGACCT
TTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACCGAACCTATATGACCCATAACATTT
TTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTCCATGACCGTGCCTATGTGATGGTGG
ATGGGGTGTTCCAGGGTGTTGTGGAGCGAAATATGAGAGACAAACTATTTTTGACGGGGAAAC
TGGGGTCCAACTGGATATCTTGGTGGAGAACATGGGGAGGCTCAGCTTTGGGTCTAACAGCA
GTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTGGGGCAAACAATCCTTACCCAGTGGATGA
TGTTCCCTCTGAAAATTGATAACCTTGTGAAGTGGTGGTTTCCCCTCCAGTTGCCAAAATGGC
CATATCCTCAAGCTCCTTCTGGCCCCACATTCTACTCCAAAACATTTCCAATTTTAGGCTCAG
TTGGGGACACATTTCTATATCTACCTGGATGGACCAAGGGCCAAGTCTGGATCAATGGGTTTA
ACTTGGGCCGGTACTGGACAAAGCAGGGGCCACAACAGACCCCTCTACGTGCCAAGATTCTGC
TGTTTCCCTAGGGGAGCCCTCAACAAAATTACATTGCTGGAAGTGAAGATGTACCTCTCCAGC
CCCAAGTCCAATTTTTTGGATAAGCCTATCCTCAATAGCACTAGTACTTTGCACAGGACACATA
TCAATTCCCTTTCAGCTGATACACTGAGTGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAA
AGGTAGGCCCGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTG
GATTACCTGAGGTCAGGACTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTA
AAAATACAAAATTAGCCGGGCGTGATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTG
AGGGCAGGAGAATTGCTTGAATCCAGGAGGCAGAGCTTGCACTGAGTGAGGTTGTACCACTG
CACTCCAGCCTGGCTGACAGTGAGACACTCCATCTCAAAAAAAAAA

FIGURE 26

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRHDFLLDGAPFRYVSGSLHYFRVPRVLW
ADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICA
EWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEYGS
YRACDFSVMRHLAFLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIFTLLR
KYEPHGFLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNFGYWNG
ADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMLGPVTLH
LVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPNNGVHDRA
YVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKPPILGQTIL
TQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYLPGWTKGQVW
INGFNLGRYWTKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLDKPILNSTSTL
HRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 27

[illegible]

FIGURE 28

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQG
ASVILPCRYRYEPALVSPRRVRVKWWKLSNGAPEKDVLVAIGLRHRSFGDYQGRVHLRQDKE
HDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQVCA
EQAAVVASFQQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPRHRL
HRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDRCDAGW
LADGSVRYPVVHPPHPCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303,
307-313

FIGURE 29

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGACAGTTCCCCTGGCAGTCCTGGTGCTGTTG
 CTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTGCGGTCATCACGGACGAGAAC
 TGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCTTGT
 CAAAATCTTCAACCGGAATGGGAAAGTTTGTGCTGAATGGGGAGAAGATCTTGAGGTTAATATT
 GCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTTCCT
 ACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAGAAGGAC
 TTCATAAAGCTTTATAAGTGATAAAGAGTGAAGAGTATTGAGCCCGTTTCATCATGGTTTGGT
 CCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGATCAGGACG
 TGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACTGTTTTTGCT
 TTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGCAGATTGCCTT
 TGTCTTCAAAAAGGCGCAGACCACAGCCATAACCATAACCCTTCAAAAAAATTATTATCAGAA
 TCTGCACAACCTTTGAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAAGATGTTTCAGAA
 GAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGCCATAAGACAACGC
 TCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAGTTATCTTAATATTA
 TGATTTTGATAAAAACAGAAGATTGATCATTTTTGTTTGAAGTGAAGTGAAGTGAAGTGAAGT
 GAATATTGCAGGGTTCAGTCTAGATTGTCATTAAATGAAGAGTCTACATTGAGAACATAAAA
 GCCTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATGGTTTAAATAGTTCTCTA
 ATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGTTTAAATAACCTATTTT
 AAGTCTGAGTTTGAAGTTTACATTTCCCAAGTATGTCATTATTGAGGTATTTAAGAAGATT
 ATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTCTCTGTTTCACTGTGTGAAAAAAG
 AAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGCTCAAGAAATGTGTATTTTCACTGACAA
 TTTCTGTTGTTTGTAGAGGTATATTCCAAAATTTCTTGTATTTTGTAGTTATGCAACTAAT
 AAAAAGTACCTTACATTAATTAATTACAGTTTCTACACATGGTAATACAGGATATGCTACTG
 ATTTAGGAAGTTTTTAAGTTTATGTTTCTCTGATTTCCAAACAAAGTTTGATTTTCTCTTGT
 ATTTTCTTACTTACTATGGGTTACATTTTTTATTTTCAAATGGATGATAATTTCTTGGAA
 ACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTTGTTTCAAAGTGAAGTTTACTGAGAGA
 TCCATCAAATGAACAATCTGTTGTAATTTAAATTTTGGCCACTTTTTTTCAGATTTTACATC
 ATTCCTTGCTGAAGTTCAAGTTGAAATTTTCTTTTTTTTCTTTTTTGGATGTGAAGGTGAACATT
 CCTGATTTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTTGAAAAATCAAAGAAGCTT
 AATATAAAAGTTTGCATTTCTACTCAGGAAAAAGCATCTTCTTGTATATGTCTTAAATGTATTT
 TTGTCCTCATATACAGAAAGTTCTTAATTGATTTTACAGTCTGTAATGCTTGTATTTTTAAAA
 TAATAACATTTTTATATTTTTTAAAGACAACTTCATATTATCCTGTGTTCTTTCTGACTG
 GTAATATTGTGTGGGATTTTACAGGTAAAGTCAAGTATGGAACATTTTAGTGTATTTTTTA
 CTCCTTAAAGAGCTAGAATACATAGTTTTTACCTTAAAGAGGGGGGAAATCATAAATACAA
 TGAATCAACTGACCATACGTAGTAGACAATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGT
 TGCTGTGTGAATCCATTAGATTTACAGTATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCC
 TTTAGAATTTAAATATTGTACCATTAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAA
 AATATCCTAAGCACAAAATAAACCTTTCTAACCCTTCATTAAAGCTGAAAAAAAAAAAAAAA
 AAA

FIGURE 30

MAPSGSLAVPLAVLVLLLVWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNLQ
PEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFINF
ISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFALATL
FSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEAEDEEDVSEEEAE
SKEGTNKDFPQNAIRQPSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 31

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTCACGATGGC
TCGCCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCCTTCCTACTCGTGAGGAAAC
TGCCGCCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTGACT
GGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGATCCA
TCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAATTCTTT
TCTTCCGCTTGGATATTTCGCATGGGCCCTACTTTACATCACACTCTGCATAGTGTTCCTGATGA
CGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAAACCATTG
ATGAGGAAGTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCTTTGCCAATTGGTCTA
ATGACTGCCAATCATTTGCCCCCTATCTATGCTGACCTCTCCCTTAAATACAAGTGTACAGGGC
TAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTACAAAGTGAGCA
CATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAAGGAGGCAATGC
GGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTGAGGAGAATGTGA
TCCGAGAATTTAACTTAAATGAGCTATAACAGCGGGCCAAGAACTATCAAAGGCTGGAGACA
ATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGATGGGGAAAACAAGA
AGGATAAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATTCAGGCTCTTTCCAT
AACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGGCTGNGACTGGNTGGGG
CAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCCTACAGGAAGGC
CTGCCATGCTGTGGCCAAGTGTTCCTGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGA
AATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATCAGCTATTACAGACATCTCCA
TGGTTTCTCCATGAACTCTGTGGTTTCATCATTCCTTCTTAGTTGACCTGCACAGCTTGGTT
AGACCTAGATTTAAACCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTCCCCCAAG
GACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAAAGTATAAGCCTAA
CTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTTATCATTTGAAGACAATATT
GAACAACCCCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGACTTTCCTTTGT
GTGGTAGGACTTGAGAGAGAAATCCCCCTGGACTTTCATAACCCCTCTGACATACTCCCCACAC
CCAGTTGATGGCTTTCGGTAATAAAAAGATTGGGATTTTCCTTTTG

FIGURE 32

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVKLPPLCHGLPTQREDGNPCDFDW
REVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFLMT
CKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPYADLSLKYNCTGL
NFGKVDVGRYTDVSTRYKVSTSPGTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSEENVI
REFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 33

CGGACGCGTGCGGGTGCCCGACATGGCGAGTG TAGTGCTGCCGAGCGGATCCCAGTG TGCGGCG
GCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGGCA
CTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAAGACGTGACAGTGATCGAGGGAGAG
GTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATT CAGCTACTGAATCCC
AACAGGCAGACCATTTATTT CAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTT CAGTTGCTG
AATTTTTCTAGCAGTGA ACTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAAGGAAGA
TACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGTCTTGGTC
CCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGGAGATTGAA
GTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAAGGGAACACA
GAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGACCAGTCAGCTG
ATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGGAGCACCTGCG
GTCAGTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCTCAAGTGCACATT
CAGATGACTTATCCTCTACAAGGCTTAACCCGGAAGGGGACGCGCTTGAGTTAACATGTGAA
GCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATGATGAAATGCCTCAA
CACGCCGTACTGTCTGGGCCCAACCTGTT CATCAATAACCTAAACAAAACAGATAATGGTACA
TACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATAC
GATCCCCCACA ACTATCCCTCCTCCCACAACAACCACCACCACCACCACCACCACCACC
ACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGAT
CATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGCTCATCATT
CTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGAT
GACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGAACTCCGAAGAA
AAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTTCATGAGGTGTCCA ACTGGCCCTATT
TAGATGATAAAGAGACAGTGATATTGG

FIGURE 34

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQ
VNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSIISDEGRYFCQLYT
DPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSE
VEEWSDMYTVTSQMLKVKHEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPVHMQMTYPLQ
GLTREGDALELTCEAIGKPQPMVMTWVRVDEMPQHAVLSGPNLFINNLNKTNDNGTYRCEASN
IVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAIVGGV
VAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
```

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 35

GGTTGCCACAGCTGGTTTATAGGGCCCCGACCACTGGGGCCCCCTTGTGAGGAGGAGACAGCCTCCCCGGCCCCGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCCGTGAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCGCGTTTATCGGGAGG
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGAAAACCCATTTTGGAGCAGGAATTCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAAACTCCCAGGCAGGAACACCTTTTGCTGTG
ATGGCCGCGTCATGATGGCCCGGCAAAAGGGCATTTCCTACCTGACCCTTTTCCCTCATCCTGGGGACATGTACAC
TCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTGTTGAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGCGCTACCAGATG
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCAACCGCTCGTA
TCAAGAATTTCCAGATAAAACAACAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCCGGCCTCCCC
GGGCCTCCCATTCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGAATTGTG
TTGGAAAGAGGAACACCGCTACTTCTACCTCTTCACTCTTCTCTCTCCCTCCTCACAATCTATGCTTTCGCCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGAGACATTGAAAGAAAACCTCGGAAGCTG
TTCTAGAAGTCTCATTTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCACTTTCTCGTGG
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGT
TTTTGCCACTGGAGGAAAGTGAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTGTT
TAATTAGGGCTATGAGAGATTTAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTTCTTTGGTCTTTAGTCACCCAGTTGCACACTGGCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACT
CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAATAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGGTCCCCTTGACCCCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCAC
TGGTCTCATTCTGGGGCTAAAAGTTTTTGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCCCACAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTGTTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCCCTTTTGACTCCTGCTCCCATTAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCCCTCAGAGGAAGCCCAGTGCTCACTTAAAC
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCCGATGTACCCTCAAAAAAATAATGCTAACCAGTTCTTCCATTAAAGCCT
CGGCTGAGTGAGGGAAGCCAGCACTGCTGCCCTCTCGGGTAACCTCACCTAAGGCCTCGGCCCACCTCTGGCT
ATGGTAACCACACTGGGGGCTTCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCAGAGCCACTT
CACCTTGGGGGTGGGCTGTGGCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGGAGTGTAACCGGAACTTTTTCATCTATTTGAAGGCGATTAAACTGTGTCTAATGCA

FIGURE 36

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTFLILGTCTLFFAFECRYLAVQ
LSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPPRI
KNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNRYFYLFIL
SLSLLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLI CFFTLWSVGLTGFHTFLVAL
NQT TNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSRPPSTQ
ETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPEPPQEAAEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 37

GGCGGAGCAGCCCTAGCCGCCACCGTCTCGCAGCTCTCGTCGCCACTGCCACCGCCGCCCGCTCACTGCG
TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGGCCATGCGAGCCCCGCGCGCCAGGCGCCCGGTGCGCAGCTGC
TGCCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCCGAGGCAGCTCCCTGGCCAACCCGGTGCCCC
CCGCGCCCTTGTCTGCGCCCGGGCCGTGCGCCGCGCAGCCCTGCCGAATGGGGGTGTGTGCACCTCGCGCCCTG
AGCCGGACCCGCGAGCACCCGGCCCCCGCGCGGAGCCTGGCTACAGCTGCACCTGCCCGCCCGGGATCTCCGGCG
CCAACTGCCAGCTTGTGTCAGATCCTTGTGCCAGCAACCCCTTGTCAACATGGCAACTGCAGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGTATGAAGGTCCCAACTGTGAACAGGCACCTCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTCAGCCTGTTCCCTGCTACTCAGGAGCCTGACA
AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCTTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCAGATATTGCCCTGTGGGAATGCCAGTTCTAACAGCTCTGCGGGTGCC
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTCCGCAAGATGCCACTGCCTCACTGATTTTGC
TCTGGAAGGTACCGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT
CAGGGGACTGGTCTCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG
TGACTAAGTCTATTGTGGCTTTGCGCTTAACCTCTGGTGGTGAAGGTGAGCACCTGTGTGCCGGGGGAGAGTCACG
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCAGAAAGCCGTGAGAGGCAACTTTTTCTGTACCTGTG
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAACCGCAGCT
GTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTGCCTTCCTGGTTATACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT
GCCAGAACAACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA
CCTGTGCCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCGAGCGTGGGCACCGAGCT
ACAAATGCCCTCTGTGATCCAGGTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCCTGGCAGAATACAAAGGAACAC
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTGAGCTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA
ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCACATTGACATAAATGAATGTGACAGTAACC
CCTGCCACCAATGGTGGGAGCTGCCTGGACCGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG
CAAATGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC
TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTGCGCA
TCAGCCGATTTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACCTGCCGAGCATCGACAGCG
AGTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCCTGCAATGTATGATGTGA
GCCCCATCGCCTATGAAGATTACAGTCTGTGACAAACCCCTGGTCACTGATTAAAACTAAAGATTTGTAAT
CTTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCATTAAATATTTTTAAGAAAATAAAAGCTTAA
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTTCAGTAGAATATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG
GAAAAATATTTAAAAACAAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAACTGT
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAAATTTCTGTGGTTGTTACA
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGAGTGCCGGCTTTCTGAGTAGAGTTAGGAAAACAC
GTAACGTAGCATATGATGTATAATAGAGTATACCCGTTACTTAAAAAGAAGTCTGAAATGTTCTGTTTGTGGAAA
AGAACTAGTTAAATTTACTATTCTAACCCTGAATGAAATAGCCTTTGCCTTATTCTGTGCATGGGTAAAGTAAC
TTATTTCTGCACTGTTTTTGTGAACCTTTGTGGAAACATTCTTTTCAGTTTTGTTTTTGTGCTTTTTCGTAACAGTCTG
TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCTAGCGAGGCAAATTCGATTGATTTGAATCTATATTT
TTCTTTAAAAAGTCAAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGATTTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
AAGTCA

FIGURE 38

><subunit 1 of 1, 737 aa, 1 stop
><MW: 78475, pI: 5.09, NX(S/T): 11
MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSRP
EPDPQHPAPAGEPGYSCTCPAGISGANCLVADPCASNPCHHGNCSSSSSSSSSDGYLCICNEG
YEGPNCEQALPSLPATGWTESMAPRQLQPVPAEQEPDKILPRSQATVTLPTWQPKTGQKVEM
KWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQQCSL
IDGRSVTPLQASGGLVLLLEEMLALGNNHFIGFVND SVTKSIVALRLTLVVKVSTCVPGESHAN
DLECSGKGKCTTKPSEATFSC TCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQDGSNFTC
VCLPGYTGELCQSKIDY CILDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDP CASSPCQN
NGTCYVDGVHFTCNCS PGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPGYHGLYCEE
EYNECL SAPCLNAATCRDLVNGYECVCLAEYKGTHCELYKDPCANVSCLNGATCDSDGLNGTC
ICAPGFTGEECDIDINECD SNPCHHGGSCLDQPNGYNCHCPHGWVGANCEIHLQWKSGHMAES
LTNMPRHSLYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYNCRSIDSEFSNA
IASIRHARFGKKS RPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 39

[illegible]

FIGURE 40

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979
><subunit 1 of 1, 204 aa, 1 stop
><MW: 22147, pI: 8.37, NX(S/T): 3
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIAGVIFLFLIALVG
LIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLAALNQEQQGQLLEVGNNTASARNDIQRL
NCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVFGGIGLFFSFTEILGVWLTyr
YRNQKDPRANPSAFL
```

Signal Peptide:
amino acids 1-34

Transmembrane domains:
amino acids 47-63, 72-95 and 162-182

FIGURE 41

CAGTCACCA**AT**GAAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTGC
 TCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGTCT
 GCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCC
 AGGTCAAGGCCTACACTTTCAGTGAACCTTCCACCTGATTGTGTCTATGACTGGCTGATCC
 TCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGCCTGGC
 AAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGC
 CTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCACTGCAGTG
 GCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTGGCTATCACAGTCC
 AAGAACTGTTTTCCAGCGCCAATTCTCAGAGCTGTACCTCAGCTGAACCCCAAGCAGGAAGCC
 CCATGACCCTGAGTTGTGAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCCGCTCCTCTTCT
 CCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATTCCAGATCCCCA
 CAGCTTCAGAAGATCACTCCGGGTCACTAGGTGTGAGGCAGCCACTGAGGACAACCAAGTTT
 GGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCTGCTGCACCTCCCA
 CATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCTGAGGAGGCCCTGGGC
 CTCTGCCCTCCGCCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGGATGC
 CAGATCCTCATCTGTATCACAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCC
 TCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAA
 AGGCTACTGCTGAA**TAGA**AGTAAACAGTTCATCCATGATCTCACTTAACCAACCCCAATAAATC
 TGATTCTTTATTTTCTCTTCTTCTGTCCTGCACATATGCATAAGTACTTTTACAAGTTGTCCCAG
 TGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTTATATAAAGTGAGAATTAGAG
 TTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCCTGCTGTCTAGATCAGGAATTT
 CTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATAC
 AGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTT
 TGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGTGTGTCTACTGGCATCCAGTAAATA
 GAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAGGGCAGTACCCACAACGAAAAATAA
 TCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAACCCAGCCTAATGAAACCTAGGTGT
 TGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCTCATTGAGCTAT
 TCTTACTGACATAACAGTCTTTAGCTGGTGCTATGGTCTGTTCTTTAGTTCTAGTTTGTATCC
 CCTCAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAGAAGTGGGCCTTT
 GGGAAGTGATTAGATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTTAAAAA
 GGCCCCAGAGAGCTAACTCACCTTCCACCATATGAGGACGTGGCAAGAAGATGACATGTATG
 AGAACCAAAAAACAGCTGTGCGCAAACACCGACTCTGTGTTGCCTTGATCTTGAACCTCCAG
 CCTCCAGAACTATGAGAAATAAAATTTCTGGTTGTTTGTAGCCTAA

FIGURE 42

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQVK
AYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQAWQDWPLTQVTFYRDGSALGPPGPNR
EFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMT
LSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQ
SPQLEIRVQGASSSAAPPTLNPAPQKSAAPGTAPPEEAPGPLPPPPTPSSDPGFSSPLGMPDP
HLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE
```

Signal sequence:
amino acids 1-17

Leucine zipper pattern sequence:
amino acids 12-33

Protein kinase C phosphorylation site:
amino acids 353-355

FIGURE 43

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTTCGTAACTAATTCAACAAACGGGACCCCTTC
TGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGGAA
GGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACC**ATG**AAACTCTGGGTGTCTGCATT
GCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTGGGCA
CATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATCCTTGT
GGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGACTAGCAA
GTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGGTGAAGCG
GCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGTCAGGACTCAGCTGCAGGTTTTAT
CGCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGGAGCTGCCAA
AGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCAGAGGGGAACT
TCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGC
CTACAATGAAGGGGACTATTATCATACGGTGTTGTGGATGGAGCAGGTGCTAAAGCAGCTTGA
TGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCAGCTATGCTGTCTT
CCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTCTCCCTTGACCCAAG
CCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAGGAAGAGAGAGAAAA
AACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCATCTATGAGAGGCCTGT
GGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTTGGGGAGGGTGTCAAACCTGAC
ACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAACAGGGCCCCACAGCTGCT
CATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGGTACTACGATGT
CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAACTTGCACGAGCCAC
CGTTCTGTGATCCCAAGACAGGAGTCCTCACTGTGCGCAGCTACCGGGTTTCCAAAAGCTCCTG
GCTAGAGGAAGATGATGACCCTGTTGTGGCCCCGAGTAAATCGTCGGATGCAGCATATCACAGG
GTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAATTATGGAGTGGGAGGACAGTATGA
ACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGGCCTCAAACAGAGGGGAATAGGTT
AGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTGGTGGTGCCACCGTCTTCCCTGATCT
GGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTGTTCTGGTACAACCTCTTGCGGAGCGG
GGAAGGTGACTACCGAACAAGACATGCTGCCTGCCCTGTGCTTGTGGGCTGCAAGTGGGTCTC
CAATAAGTGGTTCCATGAACGAGGACAGGAGTTCTTGAGACCTTGTGGATCAACAGAAGTTGA
CTGACATCCTTTTCTGTCTTCCCCTTCCCTGGTCCTTCAGCCCATGTCAACGTGACAGACACC
TTTGTATGTTCCCTTGTATGTTCCCTATCAGGCTGATTTTGGAGAAATGAATGTTTGTCTGGA
GCAGAGGGAGACCATACTAGGGCGACTCCTGTGTGACTGAAGTCCCAGCCCTTCCATTCAGCC
TGTGCCATCCCTGGCCCCAAGGCTAGGATCAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGC
CTAGCAAGGTGCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTC
TGATACCTTGTTTACATGTTTGTTTTATGGCATTCTATCTATTGTGGCTTTACCAAAAAAT
AAAATGTCCCTACCAGAAAAA

FIGURE 44

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWAN
KMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFPTD
EDEIGAALKMRLQDQTYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTVLWM
EQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLRYFEQ
LLEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEVGLTPRRQKRLFCRYHH
GNRAPQLLIAPFKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTGVLTVAS
YRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDPSRRPFDSG
LKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEVDYRTRHAACPV
LVGCKWVSNKWFHERGQEFRLPCGSTVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 45

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGGG
CGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCCTGTGTCCTGTTTCTTTGTGCTCCCAGCC
TGTCTGTGTCGTGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTGCACACCGATCCTGGGC
TTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAGCGGG
TCGTCTGTGTCTCTCTCTCTCTGCGCCGCGCCCCGGGGATCCGAAGGGTGCGGGGCTCTGAGGA
GGTGACGCGCGGGGCCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCAGGTGTGA
GCAGCCTATCAGTCACCATGTCCGCGAGCCTGGATCCCGGCTCTCGGCCTCGGTGTGTGTCTGC
TGCTGTGTCGCCGGGGCCCCGGGCGAGCGAGGGAGCCGCTCCCATTGCTATCACATGTTTTACCA
GAGGCTTGACATCAGGAAAGAGAAAAGCAGATGTCCTCTGCCAGGGGGCTGCCCTCTTGAGG
AATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGCTGTCC
ACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTCGAGAAA
ACTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGATGGTCTGCTTCTT
TCACAGTAACTAAAGGCAAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACAGCAC
ATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGGCAATAAAGATTGTA
AAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGCGCCGATTTAATTTAC
AGAAGAATTTTGTGTTGGAAGAGTGGCTCTAATGTTGGGAATTGGAACAGAAGGACCACATGTGG
GCCTTGTTCAAGCCAGTGAACATCCCAAAATAGAAATTTTACTTGAAAAACTTTACATCAGCCA
AAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTAATTCCAATACAGGAAAAG
CCTTGGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGAGTAAGAAAAGGGATCCCCA
AAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACATCGAGGAAGCAGGCATTGTGG
CCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCAAGCCTATCCCTGAAGAAGCTGG
GGATGGTTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGTGCGAATAATGGCTTCTTCTCTT
ACCACATGCCCAACTGGTTTGGCACCAAAAATACGTAAAGCCTCTGGTACAGAAGCTGTGCA
CTCATGAACAAAATGATGTGCAGCAAGACCTGTTATAACTCAGTGAACATTGCCTTTCTAATTG
ATGGCTCCAGCAGTGTGTTGGAGATAGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAG
CCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATC
AGCGCACGGAGTTCAGTTTCACTGACTATAGCACCAAAGAGAATGTCCTAGCTGTCATCAGAA
ACATCCGCTATATGAGTGGTGGAAACAGCTACTGGTGATGCCATTTCCCTTCACTGTTAGAAATG
TGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAACTTCCTAGTAATTGTCACAGATGGGCAGT
CCTATGATGATGTCCAAGGCCCTGCAGCTGCTGCACATGATGCAGGAATCACTATCTTCTCTG
TTGGTGTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTC
ACGCTTTCTTCACAAGAGAGTTACAGGATTAGAACCAATTGTTTCTGATGTCATCAGAGGCA
TTTGTAGAGATTTCTTAGAATCCCAGCAATAATGGTAACATTTTGACAACCTGAAAGAAAAAGT
ACAAGGGGATCCAGTGTGTAAATTGTATTCTCATAATACTGAAATGCTTTAGCATACTAGAAT
CAGATACAAAACCTATTAAGTATGTCAACAGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCG
CTGCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAAACACTGCTGAGGCTTCATAATCAT
GGCTCTTAGAAAACCTCAGGAAAGAGGAGATAATGTGGATTAAAAACCTTAAGAGTTCTAACCATG
CCTACTAAATGTACAGATATGCAAATTCATAGCTCAATAAAAGAATCTGATACTTAGACCAA
AAAAAAA

FIGURE 46

MSAAWIPALGLGVCLLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEEF SVYG
NIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASF TVTKG
KSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKNFVG
KVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKALKHTA
QKFFTVDAGVRKGIPKV VVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELGMVQDV
TFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNI AFLIDGSSSV
GDSNFRMLLEFVSNI AKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVIRNIRYMS
GGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITIFSVGVAVA
PLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:
amino acids 1-24

N-glycosylation site.
amino acids 100-104, 221-225

Casein kinase II phosphorylation site.
amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.
amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.
amino acids 145-149

FIGURE 47

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGAG
 CCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCT
 GCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCCTCTTCCTGG
 GGGTGCTGGTGTCCATCATTATGCTGAGCCCGGGCGTGAGAGTCAGCTCTACAAGCTGCCCT
 GGGTGCTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGGCTCCC
 TGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTT
 TCACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAGAATGGGT
 TTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACATCCCTGACG
 GCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCTTCTTCATCCTCATCC
 AGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGCAAGGCCGAGG
 AGTGCGATTCCCGTGCCCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTTCTACTTGCTGT
 CGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCCAGCGGCTGCCACGAGGGCA
 AGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGCCCA
 AGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTTCATACCCTCTACACCA
 TGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTTGCCAA
 CCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATG
 CCCCAGCATTGTGGGCCTCATCATCTTCCCTCCTGTGCACCTCTTCATCAGTCTGCGCTCCT
 CAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCA
 CACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACG
 GCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCTGGCCTCACTGCACGTCATGA
 TGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGATGATCAGCACGTGGACCGCCG
 TGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTCTACCTGTGGACCTGGTAGCCC
 CACTCCTCCTGCGCAACCGCGACTTCAGCTGAGGGCAGCCTCACAGCCTGCCATCTGGTGCCTC
 CTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTCCCCACACCAATCAGCC
 AGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCCCTGAGCCGGGCCTTCTAGTCGT
 AGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCACACCCAC
 ACGGTGGAGCTGCCTCTTCTTCCCCCTCCTCCCTGTTGCCCATACTCAGCATCTCGGATGAAA
 GGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACCTCCACC
 ACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCCAGGGGACCCTGCC
 CCCTTCTGGACTTCGTGCCTTACTGAGTCTCTAAGACTTTTTCTAATAAACAAGCCAGTGCG
 TGTAAAAAAA

FIGURE 48

MGACLGACSLSCASCSCGSAPCILCSCCPASRNSTVSRLLFTFFLFLGVLVSIIMLSPGVES
QLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPR
AAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQR
WLGKAEECDSDRAWYAGLFFF'TLLFYLLSIAAVALMFMYYTEPSGCHGKVFISLNLTFVCVVS
IAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGY
ETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRA
FDNEQDGV'TYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICASWAGLLLY
LWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 49

[illegible]

FIGURE 50

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSS
SCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKSRR
KRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTOK
LRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYALLEL
KKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGA
SGSGVYVRMWKRQQQKWERKIIGIFS GHQWVDMNGSPQDFNVAVRITPLKYAQICYWIKGNYL
DCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 51

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCTCTGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCACCACCC
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCCAACATCGATTCTCTCTGGCGCTGGT
GCTGGTATCTCTGCTCTACCTGCAGGCGGCCGCGAGTTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTCTAGCC
TGTGTGCCAACCACGATGCAAAATGTTGAATGTATCGGGCCAAACAAGTGAAGTGTCTCTGGTTATGCTGG
AAAACTGTAAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGTCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTGCTCAAGTGCCTTGACCTG
CTCCATGGCAAACCTGTGATGCTGTTGTTAAAGGACAAATACGGTGCCAGTGCCTATCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTATAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCTGATGACATAGACGAATGCTCACTTGGTCACTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCTTACAAGTGCAAATGTAAAGAAGGATACAGGGGTGATGGACTGACTTGTGTGTATATCCCAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTAACAA
CAGGCTACTTCTAAGCCAAACAAGACCTACACCAAAGCCAACCAATTCCTACTCCACCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCACCGGACTGACAACTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGATTACAGTTGACAACAGGGTACAGACAGACCTCAGAAACCCAGAGG
AGATGTGTTTCACTGTTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTCCGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCAATTCAGGGGACCTGTGCCTGTCTTCAGGCA
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAACACAGATCACTTGCAGGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTTGGAAAAAAGATCTATGATGGAAAATTAAAGGAACCTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAACCAATTGATGGTTTTCAAGTATATGAAGGTTGGCACAGAGAGGGTGGCGACCACTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG
GGCCATTGTTAGAATACTTCATAAAAAAAGAGTGTGAAAATCTCAGTATCTCTCTCTCTTCTAAAAAATTAGA
TAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAAGTAACAAATTATAGAATTTCCCAA
AGATGTTTTGATCTTACTAGTAGTATGCACTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGATTGAAAGGGGAAGAGCCCAACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTTCAGATTTTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTTCAAGAG
ATTTTCATCGGGTGCAATCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTTCTTCACTCATCAGTATGATTGATTTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTTAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTTAATGGTTTATT
TCCTTTATGGTCAATAACTGCACAGCTGAAGATGAAAGGGGAAAAATAAATGAAAATTTTACTTTTCGATGCCAA
TGATACATTGCATAAAGTATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTTATTATTAAATGTTTTT
CTAAAAATAAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAAACAATATTGTAATAAAAAACACTGTTAGTAAT

FIGURE 52

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQPR
CKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGS
CSSALTCSMANCQYGCDVVKGQIRCQCPSPLHLAPDGRTCDVDVDECATGRASCPRFRQCVNT
FGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT
CVYIPKVMIEPSGPIHVPKGNGTILKGD TGNNNWI PDVGSTWWPPKTPYIPPIITNRPTSKPT
TRPTPKPTPIPTPPPPPLPTLRTPLPTTPTTGLTTIAPAASTPPGGITVDNRVQTD
QKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVL
PLGRLMHSGDLCLSFHVKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIK
SESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 53

CGGGCCGCCCCCGGCCCCCATTTCGGGCCGGGCCCTCGCTGCGGCGGGCGACTGAGCCAGGCTGGG
 CCGCGTCCCTGAGTCCCAGAGTCGGCGCGGGCGGGCAGGGGCAGCCTTCCACCACGGGGAGCC
 CAGCTGTCAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGTGCA
 TGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGGTCCC
 TGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCCCCTGA
 GCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATAACAAACAGCTGGT
 GCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCCTCTTCCC
 GGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGTGTGGCGGACGAGGG
 CAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTGAGCCTGCAGGTGGC
 CGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGCCAGGGGACAC
 GGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGGATGG
 GCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGAGCAGGGCTTGT
 TGATGTGCACAGCGTCTGCGGGTGGTGTGGGTGCGAATGGCACCTACAGCTGCCTGGTGGC
 CAACCCCGTGTGCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGGCAGCCTATGACATT
 CCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCATTTGCACTGGTGGC
 CCTGGCTTTCTGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAGCTGA
 GGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAG
 CAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGGGAGCTGTACCCCTCCCT
 ACAGCTCCTACCCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCCAACAGATGCATC
 CTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACACAGACCACTGTGCAGCCTTAT
 TTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTTTTTCTTATAGACACAATGAACA
 GACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCTGCCTTATTTACAGTACATACA
 TTTCTTAGGGACACAGTACACTGACCACATCACCACCCTCTTCTTCCAGTGCTGCGTGGACCA
 TCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTGAGACTGACTGACCCCTGCCTTATTTT
 ACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTCTCCAATGGCCGTGATACACTAGTGA
 TCATGTTTCCAGCCCTGCTTCCACCTGCATAGAATCTTTTCTTCTCAGACAGGGACAGTGCGGCC
 TCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTTCCCTTCTCCTCCCTGCCCCAAGTGAA
 GACAGGGCAGGGCCAGGAATGCTTTGGGGACACCGAGGGGACTGCCCCCACCACCATGG
 TGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGCTTGCTCTGGCCAGCTCCTGGCCTCTGGT
 AGAGTGAGACTTCAGACGTTCTGATGCCTTCCGGATGTCATCTCTCCCTGCCCCAGGAATGGA
 AGATGTGAGGACTTCTAATTTAAATGTGGGACTCGGAGGGATTTTGTAACTGGGGGTATATT
 TTGGGGAAAATAAATGTCTTTGTAAAAA

FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQL
NLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFVSI
RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGVPLTGN
VTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVNPNVLQQDAHXSVTITGQPMTFPPEALWVT
VGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKEDDGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 55

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGGAGCGCCAGGCGTCCGGCCGCCGTG
GCTATGTTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTT
CTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAG
TGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGCATTT
CTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTA
TTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGGCCAGTC
AATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAACAAGATGATGACCTT
GAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATTTCAGGAAAT
GACAGTGATGGGTTCAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATAGTGGAGCAA
ACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCTCTTTGACTAC
GAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGGCTTGATGCTG
TCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGACCAGTGGGTGCAA
GACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCGCCACGTTTCCCGC
CACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCACACGGATCTCCTTT
GAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGACAGCCTGTGCAACACC
AGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAAGCGGCTCCAGGAGTTC
CTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCAGGCCATGGACATCTCC
TTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAAATAAATTTGGGATGAAGGACATG
CGCGTGCAGACTTTCAGCATTCAATTTGGGTTCAAGCACAAAGTTTCTGGCCAGCGACGTGGTC
TTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCTCAGGGACAGATCACTTCATC
CAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTGTACCATGGCCTGGAACCTCGCC
AAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGCCTTTGCACCAACCTCGTCATC
TCCCAGGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCACTCCAGATGTCATGCTGTTCTCT
AGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCAAGTCCTTTGTGTGTTGACAAAG
AACCGGCGCTGCAAACTGCTGCCCCTGGTGATGGCTGCCCCCTGAGCATGGAGCATGGCACA
GTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTCGGACAGGAAGAAGCTTTTTTGGGAGG
GCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGATGCTGCACAACCATTTTGACCTCTCA
GTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTTCTGGACGCACTTATTTCCCTCCTGTCC
TAGGAATTTGATTCTTCCAGAATGACCTTCTTATTTATGTAAGTGGCTTTCATTTAGATTGTA
AGTTATGGACATGATTTGAGATGTAGAAGCCATTTTTTATTAAATAAAATGCTTATTTTAGGAAA

FIGURE 56

MFVSDFRKEFYEVVQSQRVLLFVASDVDA L CACKILQALFQCDHVQYTLVPVSGWQELET AFL
EHKEQFHYFILINCGANVDLLDILQPD E D T I F F V C D S H R P V N V N V Y N D T Q I K L L I K Q D D D L E
VPAYEDI FRDEEEDEEHSGNDS DGSEPSEK R T R L E E E I V E Q T M R R R Q R R E W E A R R R D I L F D Y E
QY E Y H G T S S A M V M F E L A W M L S K D L N D M L W W A I V G L T D Q W V Q D K I T Q M K Y V T D V G V L Q R H V S R H
N H R N E D E E N T L S V D C T R I S F E Y D L R L V L Y Q H W S L H D S L C N T S Y T A A R F K L W S V H G Q K R L Q E F L
A D M G L P L K Q V K Q K F Q A M D I S L K E N L R E M I E E S A N K F G M K D M R V Q T F S I H F G F K H K F L A S D V V F
A T M S L M E S P E K D G S G T D H F I Q A L D S L S R S N L D K L Y H G L E L A K K Q L R A T Q Q T I A S C L C T N L V I S
Q G P F L Y C S L M E G T P D V M L F S R P A S L S L L S K H L L K S F V C S T K N R R C K L L P L V M A A P L S M E H G T V
T V V G I P P E T D S S D R K N F F G R A F E K A A E S T S S R M L H N H F D L S V I E L K A E D R S K F L D A L I S L L S

FIGURE 57

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGGC
 CCGCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTGCGCTTGCTGACGGCGTCGAG
 CCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTG
 GCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACCCCT
 TCTGTGGGGCTCAATTTTGGAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTGCTCCT
 TCAAGTGGTTTTTGGAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCCTCTAGGAGGA
 ACAAATACAGGTGCCTTGACACCAAGAGGCCTCAAGTGGTCACCAAAATATGGAACCCCTGCAA
 GGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCTCCAGA
 CCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAAGGAATCAGA
 GATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCCAGGCTGGAGTGCAGTGGCA
 CGATCTCGGCTCACTGCAACCTCCGCTCCCGGTTCAAGCGAGTCTCCTGCCTCAGCCTCTG
 AGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCGATGTACGTACGC
 ACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCTGAACGTGTACCG
 CCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTC
 ATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCCGCGAGAAAGTGGTGCTG
 GTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGACGACAGCCACGCGCGC
 GGGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGGAGAACATCGCAGCC
 TTCGGGGGAGACCCAGGAAATGTGACCCTGTTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCA
 GGACTGATGATGTCACCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACC
 GCGTTATTACAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGGTTGCCACCTG
 GCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACC
 AAGGTGATGCGTGTGTCCAACAAGATGAGATTCCTCCAAGTGAACCTCCAGAGAGACCCGGAA
 GAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTGTATCCAGATGACCCTTTGGTG
 CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTC
 AATTGGCTCTTGCCTTATAATATCACCAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTG
 GACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGAT
 GCCACTTTCGTGTATGCCACACTGCAGACTGCTCACTACCACCGAGAAACCCCAATGATGGGA
 ATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAA
 GAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAGTCTGTACCAGTCTCAAA
 GACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGC
 CCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA
 CCCCAGTTTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGT
 TGTGTGGGACCTGCACTGCCCTTTCCAGCCTGACATCCCATGATGCCCTCTACTTCACTGTT
 GACATCCAGTTAGGCCAGGCCCTGTCAACACCACACTGTGCTCAGCTCTCCAGCCTCAGGACA
 ACCTCTTTTTTTTCCCTTCTTCAAATCCTCCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTA
 TGGGAGGTCGACCCAGACTGCCACTGCCCCTGTCACTGCACCCAGCTTGGCATTATACCATCCA
 TCCTGCTCAACCTTGTTCCTGTCTGTTCAATTGGCCTGGAGGCCTAGGGCAGGTTGTGACAT
 GGAGCAAACCTTTTGGTAGTTTGGGATCTTCTCTCCCACCACACTTATCTCCCCCAGGGCCAC
 TCCAAAGTCTATACACAGGGGTGGTCTCTTCAATAAAGAAGTGTTGATTAGAAAAAAAAAA

FIGURE 58

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSGF
GTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPPFSRPPLG
ILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLSVWG
YRCLQESWGQLASMYVSTRERYKWLRFSCLYLNQVYAPARAPGDPQLPVMVWFPGGAFIVGA
ASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGD
PGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLACN
HNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRPDPEEIIWSMSPVVDGVVIPPDDPLVLLTQ
GKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFV
YATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

FIGURE 60

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192
<subunit 1 of 1, 694 aa, 1 stop
<MW: 77400, pI: 9.54, NX(S/T): 6
MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLRKTPLMTEFSVKSTIISR
YAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKEKR
NKTTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLSVDV
NILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIIFKPTVVQQARIAQN
GILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASVMVGTKLRQTK
DALFTILHDLRPQDRFSIIGFSNRIKVWKDHLISVTPDSIRDGKVYIHHMSPTGGTDINGALQ
RAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKI LNNTREAARGQVCIFTIGIGND
VDFRLLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFP
NYFNGSEII IAGKLVDRLDHLHVEVTASNSKKFII LKTDVPVRPQKAGKDVTGSPRPGDGE
GDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRM
DGLLEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGRDGVFPLHHLGIR
```

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 61

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTCTAGTGAACC
ACGAAGGGACGATACCAGAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTGGC
TGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGGAAAGCTAAGTC
TTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAACAATTGAGT
AAAGTACGCTCCGGTCACCATGGGTGACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTCCTGCT
CTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGCCAGCGG
CTGCCAACGGTGCTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAGCCTCTTC
CTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATCCTGAAGGG
TGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGGTCCCCAAGG
GGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCGGCGCCCCGTG
CCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGCGGCGAGGACTT
CCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGACATGGCGACCGG
CCAGTTTGCTGCTCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGCACAGCTGGAATTA
CAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTATCCTGTACGCGCAGCC
CAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACCGCGT
CTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAACGCCATCTACAGCAACGACTTCGACACCTA
CATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACTGAGGGCCTCTGGGCCACCCCTC
CGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAGTTTGCACCTGTGTGAAGC
AGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTCTGGGGAGACCCTGCTTCTATCTTGGCT
GCCATCATCCCTCCAGCCTATTTCTGCTCCTCTCTTCTCTCTTGGACCTATTTTAAGAAGCT
TGCTAACCTAAATATTTCTAGAACTTTCCCAGCCTCGTAGCCAGCACTTCTCAAACCTTGAAA
TGCATGCGAATCACCCGGGGTTCGTGTTAAATGCAGATTCTGACTCAGCAGGTCTGAGTGGGT
CCAGGATTCTGTGTTTCTCATATGTTCTCCTGGGTGATGCTGATGGGGTCAGTCTATGAACACA
CTGGAGCAACAGGTTCTAGGACTTTCTCAATATTCTAGTACTTTCTGAACATTCTGGAATCC
TCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCTTGAGACAGAGTCTTGCTCTGTTGCC
CAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGCAACCTCTGCCTCCCGGGTTCAAGCGA
TTCTTCTGCCTCAGCCTCCCTAGTGGCTGGGATTACAGGCGCCTGCTACCATGCCTGGCTAAT
TTTTGTATTTTTAGTAGAGATGGGGTTTACCATATTGGCCAGGCTGGTCTTGAACCTCTGAC
TTCAGGTGACCCACCCGCTCGGCCTCTCAAAATGCTGGGATTACAGGTGTGAGCCACCGTGC
CTGGCCAATTCCAACATTCTTAAATTCTCTCATCCCTCCAGGGCTCCCCGTGCTATGTTCTCT
TTACCCCTTCCCCCTCTTCTCTTGCTCAGGCCTGCACCACTGCAGCCACCGTTCATTTTATTCA
TTCATTAAACACTGAGCACTCACTCTGTGCTGGGTCCCGGGAAGGGTGAGGGGGTCAGACACA
GGCCCTGCCCTGCCCTCAGTGAAGTGGCCAGTCCAGCCAGGCGGGGAGAGATGTGTACATAG
GTTTTAAAGCAGACCCAGAGCTCATGGGGGCTGTGTTCTGGGTGTTTCAAGGTGCTGCTGGTCC
TCCATTACCCACTGCTCCCCAAGGCTGGTGGGACGGGGTCCCGGTGGCAGGGGCAGGTATCTC
CTTCCCGTTCTCATCCACCTGCCAGTGCTCATCGTTACAGCAAACCCAGGGGGCCTTGGC
CAGGTCAAGGGTTCTGTGAGGAGAGGACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGC
CCCCGAAGAATGGAACCCACACCCATAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAG
ACCTGCCCTCCTCACTGGGATCCCTTCTGCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTC
AGTCCCTTCCACCAAAGTCACTGAACTTCCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACA
CTGATGTCTGTCCCCAGGTGCTCTTGCCCCCTCATGCCCCCTCTCACCGGGCCAGTGCCCCGAC
TCTCCAGGCTTTATCAAGGTGCTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTC
CGGCCTGGTGCTGCCTTTACAAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGA
GCCCTCAGCAGGTCTGGGGAGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTTCC
AGGGTGGGGTGGCCTGGTGTTCCTTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAG
AGGAGGCGGCCTCCGCCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGT
GATCTCTGGTGCTCACAGCCGAGGGAGCGGTGGCTCCATGGCCAGATGACGGAAACAGGGTCT
GACCAAGTGCCAGGAAGACCTGTGCTATAAACACCCCTGCCTGATCCTGCCCTGCCTGACCC
CGCCACGCCCTGCCGTCCAGCATGATTAAAGAATGCTGTCTCCTCTTGGAATAAAAAAAAAAAAAA

FIGURE 62

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPHA
LPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEFPGPQGSKGDKGEMGSPGAPCQKRFFA
FSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKETVH
IMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITFSGH
LIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 63

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGAC
TCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCACCA
TGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCCTTG
ATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTGTCAC
TGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGCACTGG
CCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCTTTAAGT
GTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGACGAGTACC
GCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTTACAGCTGCTTCGTGGAAGA
CCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAACTGGGTTTCC
CAAGCTATGTGAGTTTCAAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCGAGTTCCGGGAGGAGT
TTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCACTCAGTATATG
TGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCTGTGGTCATAGAA
GGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAGTGGCCCTGGCAGG
CCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCTATCACGCCCTGTGGATCA
TCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGACCATCCAGGTGGGTC
TAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACCTGGTGGAGAAGATTGTCTACCACAGCA
AGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCTGGCCGGGGCCACTCACGT
TCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGAACTTCCCCGATGGAAAAG
TGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGACGCCCTCCCTGTCTGAACC
ACGCGGCCCTCCCTTTTGATTTTCCAACAAGATCTGCAACCACAGGGACGTGTACGGTGGCATCA
TCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCGTGGACAGCTGCCAGGGGGACA
GCGGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAGCTTTG
GCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACACCCGTGTACCTCCTTCCTGGACT
GGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTTGAAGAGGAAGGGGACAAGTAGCCACCT
GAGTTCCCTGAGGTGATGAAGACAGCCCGATCCTCCCCTGGACTCCCGTGTAGGAACCTGCACA
CGAGCAGACACCCTTGAGGCTCTGAGTTCCGGCACCAAGTAGCAGGCCCGAAAGAGGCACCCTT
CCATCTGATTCCAGCACAACTTCAAGCTGCTTTTTTGTTTTTTTGTTTTTTTGAGGTGGAGTCT
CGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAATCCCTGCTCACTGCAGCCTCCGCTTCCC
TGTTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCAGTAGCTGGGACCACAGGTGCCCGCCACCA
CACCCAATAATTTTTGTATTTTTTAGTAGAGACAGGGTTTTACCATGTTGGCCAGGCTGCTCT
CAAACCCCTGACCTCAAATGATGTGCCTGCTTACAGCCTCCCACAGTGCTGGGATTACAGGCAT
GGGCCACCACGCCTAGCCTCACGCTCCTTTCTGATCTTCACTAAGAACAAAAGAAGCAGCAAC
TTGCAAGGGCGGCCTTTCCCACCTGGTCCATCTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCT
GACGAGATAAGCAGTTATGTGACCTCACGTGCAAAGCCACCAACAGCCACTCAGAAAAGACGC
ACCAGCCCAGAAGTGCAGAACTGCAGTCACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAA
CCCACCCTTTCTACTTCCAAGACTTATTTTACATGTGGGGAGGTTAATCTAGGAATGACTCG
TTTAAGGCCTATTTTCATGATTTCTTTGTAGCATTGGTGCTTGACGTATTATTGTCTTTGA
TTCAAATAATATGTTTCCCTCATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAAT
CAAAATCATCCACTGAAA

FIGURE 64

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILAL
AIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVLQVFTAASWK
TMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVTALHHSVY
VREGCASGHVVTLQCTACGHRRGYSSRIVGGMNLSLQWPWQASLQFQGYHLCGGSVITPLWI
ITAAHCVDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKLAGPLT
FNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPPLISNKICNHRDVYGGI
ISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSFQIGCAEVNKPQVYTRVTSFLD
WIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

FIGURE 65

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCAACCGTTAAGGTGTCTTCTCTTTAGGGATGGT
GAGGTTGGAAAAAGACTCCTGTAACCCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAG
AACGCTCTCACCGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCC
ACACAACCTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTC
AGGAGGACTTTCTGTTTGTGTTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATA
GAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTAC
TATTCTTCATATTTTGATATATTTCTTCTGGCAGTTTTTTCGATTTAAAGTGTTAATACTTGCA
TATGCTGTGTGCAGACTGCGCCATTGGTGCGCAATAGCGTTGACAACGGCAGTGACCAGTGCC
TTTTTACTAGCAAAAGTGATCCTTTTGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTG
CCCATCATTTTCATTCATCCTTGCCTGGATTGAGACGTGGTTTCTGGATTTCAAAGTGTTACCT
CAAGAAGCAGAAGAAGAAAACAGACTCCTGATAGTTTCAGGATGCTTCAGAGAGGGCAGCACTT
ATACCTGGTGGTCTTTCTGATGGTCAGTTTTATTCCCCTCCTGAATCCGAAGCAGGATCTGAA
GAAGCTGAAGAAAAACAGGACAGTGAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTA
AATGTGAAAAACCCCTCACAGAAAGTCATCGAGGCAAAAAGAGGCAGGCAGTGGAGTCTCCCTG
TCGACAGTAAAGTTGAAATGGTGACGTCCACTGCTGGCTTTATTGAACAGCTAATAAAGATTT
ATTTATTGTAATACCTCACAAACGTTGTACCATATCCATGCACATTTAGTTGCCTGCCTGTGG
CTGGTAAGGTAATGTCATGATTCATCCTCTCTTCAGTGAGACTGAGCCTGATGTGTTAACAAA
TAGGTGAAGAAAGTCTTGTGCTGTATTCCCTAATCAAAAGACTTAATATATTGAAGTAACACTT
TTTTAGTAAGCAAGATACCTTTTTTATTTCAATTCACAGAATGGAATTTTTTTGTTCATGTCT
CAGATTTATTTTGTATTTCTTTTTTAACACTCTACATTTCCCTTGTTTTTTAACTCATGCACA
TGTGCTCTTTGTACAGTTTTTAAAAAGTGTAATAAAATCTGACATGTCAATGTGGCTAGTTTTA
TTTTTCTTGTTTTGCATTATGTGTATGGCCTGAAGTGTTGGACTTGCAAAAGGGGAAGAAAGG
AATTGCGAATACATGTAAAATGTCACCAGACATTTGTATTATTTTTATCATGAAATCATGTTT
TTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAAATGACTTAAACC
ATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAAATGAACATAAATTAATAA

FIGURE 66

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDL
LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAI
ALTTAVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVL PQEAEENRLLIV
QDASERAALIPGGLSDGQFYSPPESEAGSEEAEEKQDSEKPLLEL

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

FIGURE 67

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCATC
CAACCATTCCTCCCTTGTAAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGACT
AACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCAC
GGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTACCTGC
CACCTCAACGTCCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGCTACAC
AGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGA
GATGTTCTCCTCCAGTTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTTCAAGACCGCGT
GGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTGCAGCCGGA
GGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGGCCATGGCAA
GATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGGCCGTGATTGT
GGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTCATCTTGGTGCTGATGGTGGTCAAGTGTGT
GAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGAGGAGGGCAAGAC
GGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCCCTGCAGCCTCCCG
TGTCCCGTCTCTCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCGCTCTTGGTGTGCTT
CCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCCGACTTCGTATCTCCCA
CCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCATGCTCTGGGACGTGTG
GGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGGGGGAGGCAGGAGGCAC
ATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGAGGAGGGGCGCTGTACCC
TGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGGGGAGGGAGGGCTTTCCTGT
GCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTGTGCTCCTCCCTGCTCCAG
CCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGAACTTGGAGGGGCATGTTAAA
GGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGGCTGCAGGCAAAGCTGGACATGT
GCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATTGCTAGTGGCCTCCTTGGGGCTCC
TGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAGACTGGAAGAGCAGCTCCAGGTAGG
GGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCCAGTTTCAAAGTCAGCTGAGGGGCTG
AGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAGGCTCTGCCTTCTCCATGGGGTAACCA
CCCTCGCCTGGGCAGGGGAGCCAAAGGCTGGGAAATGAGGAGGCCATGCACAGGGTGGGGCAG
CTTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTTGCCCTTGGTGGGGTTTCCACCTGGCTTT
TGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCGGCATAAGGGGAGGCCTTGAACCTGAGCT
GCCAATGCCAGCCCTGTCCATCTGCGGCCACGCTACTCGCTCCTCTCCCAACAACCTCCCTTC
GTGGGGACAAAAGTGACAAATTGTAGGCCAGGCACAGTGGCTCACGCCTGTAATCCAGCACTT
TGGGAGGCCAAGGCGGGTGGATTACCTCCATCTGTTTAGTAGAAATGGGCAAAACCCCATCTC
TACTAAAAATACAAGAATTAGCTGGGCGTGGTGGCGTGTGCCTGTAATCCAGCTATTTGGGA
GGCTGAGGCAGGAGAATCGCTTGAGCCCGGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGAT
AGTGCCACTGCAATTCAGCCTGGGTGACATAGAGAGACTCCATCTCAAAAAAAA

FIGURE 68

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415  
<subunit 1 of 1, 215 aa, 1 stop  
<MW: 24326, pI: 6.32, NX(S/T): 4  
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SLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGIYN  
CYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRKKEQ  
KLSTDDLKTEEEGKTDGEGNPDDGAK
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

FIGURE 69

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCCGCCAGCCTCCGCCGCCGAGCCTC
 GTTCGTGTCCCCGCCCTCGCTCCTGCAGTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA
 GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC
 CGCAGAGGCGGAGGCTCGCGTATTCTTGCAGTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC
 GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCT
 CACCTCTCCCAGGAACTTACACTGGAGAGCCAAAAGGAGTGGAAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
 ATCCTGAGGTCAATTCATTATGAAGTGTACC CGCGGGAGTGGCTCAGAGTAACCACAGTGCTGTTTATGGCTAGA
 GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
 GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
 AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
 TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
 TTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTAGGTGTTCTGGCCCTGTATGTACACATTATACA
 CAGGTGCTGTGGGCAACTAGTAACAGAATCGTTTGTGCCATTAATTTGTGTCTAACATGAACATCTGGGGGCAG
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTTACAAA
 CATGGGCGGCCCTGTTCTGCTTGGCCACCTAGTTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG
 TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
 CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTGTTTTCT
 TGTGAAGTAAGATTAAGAGATCAGTGCAAAGGAACAACCTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGAT
 AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
 ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTATCAAGTCCAATAGA
 AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTTCAAGCTGTG
 ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTCATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCT
 CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAATTGGAACCTCGAGTTTATTCTGATCTGTCCAGTATC
 TGCAGAGCAGCAGTACATGCTGGAGTGGTTCCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
 AAGACCTACATTGCTTCTTTTCAAGATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATT
 AGAGTGTTTGCTGTTGTGTGAAACTGAATACTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAACTTACTGTACAGAGTACATCAACTATTTTTCAGCCCCAAAAGGTGCCAAATGCATA
 TAAATCTTGATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
 TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
 GTTCTACGTTTCATATATTATATGGTGTCTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
 GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC
 AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTCT
 TGTTAATTTAGGCATATAGAATATTAAATTTCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC
 CAAATGAATCTGTTAAATGTTTGAATTCCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
 ATGAAAACATTCCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
 AAATGAGGTACATATTTTCTTTTGTATCCTGGCAAATACCTCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
 GAACAAAGATGAACAAATGTATTACATTACCATTGCCACTGATTTTTTTTTTAAATGGTAAATGACCTTGTATATAA
 ATATTGCCATATCATGGTACCTATAATGGTGATATTTTGTCTATGAAAAATGTATTGTGCTTTGATACTAAA
 AATCTGTAAATGTTAGTTTTTGGTAATTTTTTTTCTGCTGGTGGATTTACATATTAAATTTTTTCTGCTGGTGGG
 TAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAAA

FIGURE 70

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417
<subunit 1 of 1, 500 aa, 1 stop
<MW: 56888, pI: 8.53, NX(S/T): 2
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SILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHG PASLLPSIGQNLGAHWGR
YRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLCHNM
NIWGQIWP KAVYLV CNYSPKGNWWGHAPYKHGRPCSACPPSF GGGCRENLCYKEGSDRYYP PR
EEETNEIERQQSQVHDTHV RTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNRYECPA
GCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGVVDITRQGRKH YFIKSNRNGIQTIGKY
QSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIGTRVYSDL
SSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRVFAVV
```

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

FIGURE 71

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGGC
 TGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGCCT
 CTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCC
 CTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGGACCCCTGCC
 GAGCGCCACGCGGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCC
 GCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAG
 ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTT
 GCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA
 TACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTT
 GGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACT
 ATTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT
 TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA
 GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCT
 GGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATC
 TGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGA
 GGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGACAGTGGC
 ACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCA
 TCTCTGATTCCAGAATTTCTCTGATGGTTTCTGGACTGGGTCCAGCTGGCGTGCTGGACGAAT
 TCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGC
 AGGTCAATCCGTATCACAATCCTGCCTCAGCTTTACATTAGCCCATGATGGGGGCCGGCCTG
 AATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCACAAATGCGCTGGTGATCGGTGCCACG
 GTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC
 CCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTCTCAACAGAGGAT
 GTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCCTAT
 GCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTT
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 CGCTGGAAATGAATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCA
 CATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTTCTCCTGTGCCACCCGTCTTCAAT
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 CAAATCCTCCCTACTTCCAAGAAAAATAATTAATAAAAAAAAACTTCATTCTAA

FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
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DTYFDTERSSTYRSKGFDTVVKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFLLP
GIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLG
GIEPSLYKGDWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSTTLRLRPQKV
FDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISYLRDENSRSFRITILPQ
LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAV
SEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLIIVLLLLLPFRCQRRPRDPE
VVNDESSLVRHRWK
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 73

GCCGCGGCGAGAGCGCGCCAGCCCCGCGCGATGCCCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCGGC
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGCGGGCGCTGGGGCGCCCGGGCCAGG
AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACC
TGTACACGGCCGACATGTTTCACGCACGGGATCCAGAGCGCCGCGCACTTCGTTCATGTTCTTCGCGCCCTGGTGTG
GACACTGCCAGCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAAAGCATGGAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCCAGGGGGTGCGAGGATACCCACCTTAA
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTTCGGGACTTCCAGACACTGGAAAACCTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGAACCGCCAGTGCCCCCGAGCTCAAGCAAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCCGAAACTG
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGGAACAGGTTCTGGCTATCCCACTC
TTCTCTGGTTCCGAGATGGGAAAAGGTGGATCAGTACAAGGAAAAGCGGGATTTGGAGTCACTGAGGGAGTACG
TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCGGTGCTGGCAG
CTGAGCCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAAATTCGATGACACCATTGCAGAAGGAA
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA
AAAAGGAATTCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGACGAACCTT~~TAG~~GAAACACAGTTGGAGGTCAC
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ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTTCACTGGCGATA
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TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGCGCGCTGC
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CCTTCTGTTTCTCACGGGGTGAACATGTCTTTAGTTCCCTCATGTTAACACGAAGCCAGAGCCCATGAACTGT
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CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTGATCTCAAGAC
CAAAGACAGATGTCACTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
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GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATAATAACCACTTTGCATCCAACACTCTTACCCACCT
CCCATACGCAAGGGGATGTGATACTTGGCCCAAAGTAACCTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA
CTGCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCACG
TATGGTTTACAGATAATCTTTTTTTAAAAAAACCCCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA
CACAACTTCAGCTTTGCATCACGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTTACACTAT
GATACTTTCTAAATAAACTCTTTTTTTTTTAA

FIGURE 74

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VCSAQGVRGYPTLKLFPKPGQEAVKYQGPRDFQTLNWMQLTLNEEPVTPEPEVEPPSAPELKQ
GLYELASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCTQHYE
LCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEAPVLAA
EPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLAGVKIAE
VDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL
```

Signal sequence:

amino acids 1-32

FIGURE 75A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
 CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG
 TAGGGACCCCGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
 GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCCCGCTGCTGAGTGTGCGGGGAGATTGGCAAACGCCTAGG
 AAAGGACTGGGGAAAATAGCCCTGGGAAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG
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 TCCCGCCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGSCCACA
 AAAGTTCCTGTCCACTGTGATTCCTCAATTCCTTGCTTGGTTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA
 ACTTTTTCTTTTTTTTTTCTTCTGGTGAAGCTGCTCTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAAATGTGC
 TGGAGAAGAGCGAGCCCTCCTTGTTCTTCCGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
 CGGACATGGTGACAGCTGAGAGGAGAGGAGATTCTTCCAGGTGGAGAGTCTTACCCTGTGTGGGTGCATG
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 TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG
 GTGCCAGCCTACGGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
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 GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC
 AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTCAGCACTG
 GAAATGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACC
 GTGGCACAATGAACGGATCACCTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA
 GAGGTGGAACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCTACGAGGGCTCTCAGAGTTCAACAAAAC
 TGCAGTGCCGGTCAGGTATCCCCCAAGACCCCAAGGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG
 GTATAAAGAGGAAACCAAGAAAAAGAACCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAAGCAAAAAA
 GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
 GGCTTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCACACTGAAAACCTGCTGCTCAGTG
 CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG
 GTGAGTCTGAGTTCAGTGTGCTTCACTGACCACTGACCAACACTGCTTTGAATTATAGGAGGAGAACAATA
 ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC
 AGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTATATGA
 CACTTGGGTTTTTTAATTAAATCTATTTTATATATATAAATATATGTTTCTTTTCTGTGAAAAGCTGTTTTTCT
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 ATTTTATTTTCAATTTCTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
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 AATTATTAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAATCTTAGCTAAATTT
 GTATCATTTGGTCTTAAAAAATAAAATCTTTACTAATAGGCAATGAAGGAATGGTTTGCTAACCAACCACAGTAA
 TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAAGATTTCCCATATAATAAATACTAA
 TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT
 GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAACCCC
 ACATGCAAACGTGATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTGATCAATGAGCATA
 GATTGGTGTGATCCTGTAGACCCTGGTGTCTTTCTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTGAAGCTTAC

FIGURE 75B

[illegible]

FIGURE 76

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYSWQALEEEEEEGALLAQAGEKLEPSTTSTSQ
PHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVKLENYYVQPICTPSRSQFITGKYQIHTGLQHSIIRPTQP
NCLPLDNATLPQKLKEVGYSTHVMVGKWHLGFNKECMPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCGYDLYEN
DNAAWDYDNGIYSTQMYTQQRVQQILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCL
DEAINNVTLALKTYGFYNNIIIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCHEL
HITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPGQQAMGSGTLQSSQPSE
CSTGNCLQEILATATGSPLSLSATWDRTGCTMNGSPCQLAKVYGFSTSQPTHMRGWTYLTGIQES
```

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 77

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCTTTTGAAGAACAGTACTGTGGA
GCTATTTAAGAGATAAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
GCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGACACGCGCCTGAAGCACAAAGCAGAT
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT
GGGCGAAGGAACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT
TCCTGCGGACTGCACCGGACTACAAAGGGCTTGCTGCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG
ATGCACCCAGATACGCTATTAGTTCCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG
TCAATTAAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
CGACAATGCGCCTTACTTTCTGTGAAAGTGAATTAGAAATAAAAAATTAGTGAAATGCAGCCACTGAGATGCGGTT
CCCTCTACCCACGCCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCCAACACTCA
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCGAATTGGTGCTGAAACGCGCCCTGGACCG
CGAAGAAAAGGCTGCTCACCACCTGGTCCCTTACGGCCTCCGACGGGGGCGACCCGGTGCGCACAGGCACCGCGCG
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACCCAGCGTTTGCTCAGCCGAGTACCGCGCGAGCGTTCC
GGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT
GAGGTATTCCTTCCGGTATGTGGACGACAAGGCGGCCAAGTTTCAAACCTAGATTGTAATTCAGGGACAATATC
AACAAATAGGGGAGTTGGACCACGAGGAGTCAGGATTCTACAGATGGAAGTGCAAGCAATGGATAATGCAGGATA
TTCTGCGCGAGCCAAAGTCCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCT
CGCCAGCTCGGTTCCCGAAAATCTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA
TAGTTTAGTACAGACATAGTCTTGGATAGGGAACAGGTTCCCTAGCTACAACATCAGAGTGACCGCCACTGACCG
GGGAACCCCGCCCCCTATCCACGGAACCTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCCGGTCTT
CCCTCAGGCCTCCTATTCCGCTTATATCCAGAGAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCCA
CGACCCGACTGTGAAGAGAACGCCCAGATCACTTATTCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC
GTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA
CTTGCAAGTGAAAAGTGATGGCGCGGGACAACGGGCACCCGCCCTCAGCAGCAACGTGTGCTTGAGCCTGTTGCT
GCTGGACCAGAACGACAATGCGCCCCGAGATCCTGTACCCCGCCCTCCCAACGGACGGTTCCACTGGCGTGGAGCT
GGCTCCCGCTCCGACAGAGCCCGGTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC
CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG
CACGGCGGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCGTCCAGGACCACGGCCAGCC
CCCTCTCTCCGCCACTGTACGCTCACCCTGGCCGTGGCCGACAGCATCCCCAAGTCTTGGCGGACCTCGGCAG
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG
CGTCTTCTGGCCTTCGTATCTTGTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTGCTGCAGGC
TTCAGGAGGCGGCTTGACAGGAGCGCCGGCTCGCACTTTGTGGCGTGGACGGGGTGAGGCTTTCCTGCAGAC
CTATTCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACCTGATCTTCCCCAGCCCCAATATGCAGA
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCTTTTGCTGTGAGGTGATTCCGTATTTTCTAAAGA
CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTAAATTGCTCTGTCTCCCAAGC
TGGAGTGACGGGTACGATCATAGCTCACTGCGGCCTCAAACCTCTAGGCTCAAGCAATTATCCACCTTTGCCT
CCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTAT
CTATCTATCTATCTATCTATTACTTTCTTGTACAGACGGGAGTCTCACGCCTGTAATCCCACTACTTTGGGAGGC
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGAGACCAGCCTGACCAACATGGAGAAAACCCCGTCTATACTAA
AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCCACTACTTTGGGAGGCTGAGTCAGGAGAAAT
TGCTTTAACTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG
AAACTCTATCTCA

FIGURE 78

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pI: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPEELEKGSRVGDISRDLGLEPRELAERGVRRIIPRGRTQLF
ALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVRDINDNAPYFRESELEIKISENAATEM
RFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGADGSKYPELVLRALDREEKAAHHLVLTASDGGDPVRTGT
ARIRVMVLDANDNAPAFAPQPEYRASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGT
ISTIGELDHEESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVNDQD
SEENGQVICFIQGNLPFKLEKSYGNYSLVTDIVLDREQVPSYNITVTATDRGTPPLSTETHISLNVADTNDNPP
VFPQASYSAIIPENNPRGVSLSVTAHDPDCEENAQITYSLAENTIQGASLSSYVSINSDTGVLIALSSFDYEQF
RDLQVKVMARDNGHPPLSSNVLSLFLVDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVVAVDNRDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIQVLADL
GSLESPANSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLQLQASGGGLTGAPASHFVGVDGVQAFL
QTYSHVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGLIEVSLYQIFFLFFFNCSVS
QAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLSIYLSIYLSIYLSIYLLSCTDGSGLTPVIPVLW
EAEAGGSPEVGSRLPA
```

Signal sequence:
amino acids 1-30

Transmembrane domains:
amino acids 693-711, 809-823, 869-888

FIGURE 79

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCA**ATG**AGTCCCCGCTCGTGCCTGCGTTTCGCTGCGCCTCCTC
 GTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCAAGCTGTCTCGTGGTGGGAGCATCTCA
 GAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATCCAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTC
 ATGGACTCGGTGCGCCGCGGTGCCACGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGGAACCGGCGCTGGAAC
 TGCTCCACACTCGACTCCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCCTTCGTGTAC
 GCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGACAGTGGGGAGCTGGAGAAGTGCGGCTGT
 GACAGGACAGTGCATGGGGTCAGCCACAGGGCTTCCAGTGGTCAGGATGCTCTGACAACATCGCCTACGGTGTG
 GCCTTCTCACAGTTCGTTTGTGGATGTGCGGGAGAGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTC
 CACAACAATGAGGCCGGCAGGAAGGCCATCCTGACACACATGCGGGTGGAAATGCAAGTGCCACGGGGTGTGAGGC
 TCCTGTGAGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGCCAGGTGGGTACGCACCTGAAGGAGAAGTTT
 GATGGTGCCACTGAGGTGGAGCCACGCCGCTGGGCTCCTCCAGGGCACTGGTACCACGCAACGCACAGTTCAAG
 CCGCACACAGATGAGGACCTGGTGTAATTGGAGCCTAGCCCCGACTTCTGTGAGCAGGACATGCGCAGCGGCGTG
 CTGGGCACGAGGGGCGCACATGCAACAAGACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGC
 GGCTTCCACACGGCGCAGGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATTCCACTGGTGCTGCTTCGTCAAGTGC
 CGGCAGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGAT**G**ACCGCCTGCCTAGCCCTGCGCCGGCAACCACCTA
 GTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCACACCTACCCCAAGAGATACTGGTTGTATTTTTTTGTT
 CTGGTTTGGTTTTTGGGTCTCATGTTATTTATTGCCGAAACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGC
 CTCCCCAAAGCTGGGCCTTTGTGGCTGCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTG
 GCTGCCACTGACCACTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTA
 TTACCACCACATGGCTACTGACCGTGTGATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAAATAGGTACCGACTTG
 ATGGAAGTCAACCCCTCTGGAAAAAAGAACTCTTAACCTCTCCAGCACACATACATGGAATCCTGGCAGCTTGA
 GCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGGGAACAAGCAGATACCAGGTCAAGGGCACCAGGTTTCATT
 TCAGCCCTTACATGGACAGCTAGAGGTTGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAG
 AGACGACTGAAGTCCACCCCTAGAACCCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAACTTAACCACTCCCC
 AGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTTTGCAGTCATGCCCGA
 GTCACCTTTCACAGCGCTGTTCTCCATGAAACTGAAAAACACACACACACACACACACACACACACACACAC
 ACACACACACGGACACACACACACACCTGCGAGAGAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAG
 TCACCTTTCACAGCACTGTTCTCTC

FIGURE 80

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRLRLLVFAVFSAAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLAI
EECQYQFRNRWNCSTLDSLVPFGKVVTQGTREAAFVYAISSAGVAFVTRACSSGELEKCGCDRTVHGVSPQGF
QWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCWRAVP
PFRQVGHALKEKFDGATEVEPRRVGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTS
KAIDGCELLCCGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 81

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
CTGATGGTGGGTCTGTTAACCTCAGTGGGGACTCCAAGATTTCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT
TGGGGTCTGGCTCAGAAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTTCCGCAACCGCTTCT
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTGACGGAGCCCCCTGTGA
CAGACCCCGTTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCC
CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTCATTCGCCACGGAGACAGGTACCCACTGTATGTCAATCCCA
AAACAAAGCGACCAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTCGAAAGCCCCTTGAACCTCCTTGCTCTTTACCCAAATCACC
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA
TCTATCTAAAGAAACACAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA
GCCGGACCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA
GGCACCAGCCAAGTGCCTGTCTGCTCTGGAAGCTGCTATTGCCCGTAAGAAACAGTATCTGGAAAAGGAGC
AGCGTCGTGAGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAAGACCTACGGGGAGATGGCCAAGATCGTGG
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCTATAGACTCCATGCTCTGCCACTTCTGCCACAATGTGAGCT
TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
GGGAAAGACGGGAGAAGAAATTGTACTTCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAACCATCG
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT
CACCAGTTCTCAGTGCCTTGGGCCCTTTCAGAAGCCAGGTTCCCAAGGTTTGAGCCAGGTTGATCTTTGAGCTTT
GGCAAGACAGAGAAAAGCCAGTGAACATTCGTCGGATTCCTTACAATGGCGTCGATGTACATTCACACCT
CTTTCTGCCAAGACCACCACAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACTTGGTCCGCTTTGTGAAAA
GGGACATGTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTACAGGGAAGGATTTCTAAAGG
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTTAC
TAAGGGTAGAAGATTATTGCTTTTTAAAGGCTAAATATTGTTTGTGGGAACCACAGATGGTTGGGGTTGAACAGT
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
TCTTCTGGCCTGCCCATGTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTAATCTTAGACATT
TTTACCTTGTCTTGTAAAGAAATTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACTTTTTCTGTAAAGG
GCCAGATTGTAAATATTTAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTACATACTACTCAACTCTGT
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCAGGGCCAGACAAAACA
GATGGTGACCAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACATAAATTGC
ACTTCCAGCACTTTGAGAAGAGTTGAATACCAAGAATTATTCATGGTTTCTCCAGTAACTTCTGCTAGAAACA
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAATATT
TTCTAAGACCAGTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
GAGGCTAGAAGATGAATTCAGGCATTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA
ACTGGATTCATTTTTAAACCATTTTCATCAGTTCAAATGGTAAATCTGATTGATTTTTAAATGCGTTTTTGGA
AGAACTTGTCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
TGATTTCTGAACTAATGGTGCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTATCGGCATTCC
AACTTTTTCTCTTTGTTTTGTCCAGTGTGCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

FIGURE 82

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLLALALAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMDPVTEPPVTDPVYEALLYCNIPSAE
RSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKPYHPKLEAFISHMSKSGSGASFESPLNS
LPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLLKKHLLPNDWSADQLYLETTGKSRTLQSGLLALLYGFLPDF
DWKKIYFRHQPSALFCSGSCYCPVRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMC
HFCHNVSFPCTRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELFALY
SAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSFCQDHHKRSPPKMCPL
NLVRFVKRDMFVALGGSGTNYDACHREGF
```

Signal sequence:
amino acids 1-18

FIGURE 83

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGT
GACGTTGTGGAGATGGGGAGCGTCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGTCTATGCCGATGCTGTCTTAGTGGAAACAACTCCACTGTAAGTATGATCTATGCACCTTTCTTG
CTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAGTGAATAAGATTCCTGGATTT
TGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATTTTGGTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGT
TTGGCTATGTTCTATCTTCTTCTCTTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTG
CACAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGA
ACTTTTACAACCTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACCTAGTCTTACTT
ATTGATTTTGCACATTCATGGAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCA
GCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTCTGTTCTTTGTCTACTACACT
CATCCAGCCAGTTGTTTCAGAAAAAAGGGCGTTTACGTGTCAACATGCTCCCTGCGTTGGTGTCTCTGTAATG
TCTATACTGCCAAAAATCCAAGAATCACAACCAAGATCTGGTTTGTACAGTCTTCAGTAATTACAGTCTACACA
ATGTATTTGACATGGTCAGCTATGACCAATGAACCAGAAACAAATTGCAACCCAAGTCTACTAAGCATAATTGGC
TACAATACAACAAGCACTGTCCCAAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTA
ATTTCTTTTTTGTGTGTGTATTTTATCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAACTGACTCTA
ACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATCACTGGAGGATGGGGACGATGTT
CACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACAGTTATTCCTTCTTTCACTTCATGCTTTTCTGGCT
TCAGTTTATATCATGATGACCCTTACCAACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAAGTCAGTGGACA
GCTGTCTGGGTGAAAATCTCTTCCAGTTGGATTGGCATCGTGTCTGTATGTTTGGACACTCGTGGCACCCTTGT
CTTACAAATCGTGATTTTGAAGTGAAGTGTGATGTTTCTAGCATGAAAGTCCCACTTTGATTATTGCTTATTTGAAAC
AGTATTTCCCAACTTTTGTAAAGTTGTGTATGTTTTTGTCTCCATGTAACCTCTCCAGTGTCTGGCATGAATTA
GATTTTACTGCTTGTCAATTTTGTATTTTCTTACCAAGTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAA
AGTTTTATGAATATGGTGATGAGTTAGTAAAGTGGCCATTATTGGGCTTATTCTCTGCTCTATAGTTGTGAAAT
GAAGAGTAAAAACAATTTGTTTGAAGTATTTTAAATTTATATTAGACCTTAAGCTGTTTTAGCAAGCATTAAAGC
AAATGTATGGCTGCCTTTTGAATATTTGATGTGTTGCCTGGCAGGATAGTGCAGAAAGCATGGTTTATTTTAAA
ATTTATAAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATAAGGTTTTACCTTGATACGGAATTTACA
CAGGTAGGGAGTGTTTAGTGGACAATAGTGTAGTTTATGGATGGAGGTGTCGGTACTAAATGAATAACGAGTAA
ATAATCTTACTTGGGTAGAGATGGCTTTTGCCAACAAAGTGAAGTGTGTTTGGTTGTTTAACTCATGAAGTATG
GGTTCAGTGGAAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTAGAGGAA
GTGTTTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCCAGCAGGTAGCTCACCTTGGAATCCAGCACTTTG
GGAGCTTAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCAGCTTGGCACATGGTGAACCTGTTCTATAAAA
ATAATCTGGCTTTGAGCATATGCCTGTGGTCCAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAG
GTTGCAGTGAGCAAGTCACGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATATTGAAAT
CAAGGAGGCAAAATTTTGACAGGGAAGGAAGTAAGTGCAGAAACCACTAGGCTTTAGTAGGTACTTATATAAAATC
TAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATAGCTCAGATAGCTAATTAGGAA
ATTTCAAGTTGGCCAATAATAGCATTCCTCTGACATTTAAAAATAATTTCTATTCAAATACATGCATATTGAT
TTACACCTCATACTGTGATAATTAATGTGATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGA
ATGATGGAATGTTTTAGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAGATGTTTAAATGCTTTTGT
ATTTACTGCCATGTAATTGAAATATATAGATTATTGTAACTTTCAACCTGAAAATCAAGCAGTATGAGAGTTTA
GTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAAAATCTACAATTTCTCTTTAAAAATATTATTAAAT
GTGAATGGAATATAACAATTCAGCTTAATCCCCAACCTTATTCTGTGTGTAGACATTGTATCCACAATTTTGA
ATGGCTGTGTTTTACCTCTAAATAAATGAATTACAGAGAAAAA

FIGURE 84

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENE
KGVVPCNILVGKYKAVYRLCFGLAMFYLLLSLLMIKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTF
VWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKMEEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPAS
CSENKAFISVNMLLCVGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTT
STVPKEGQSVQWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVHRAV
DNERDGVTSYSFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVVKISSSWIGIVLYVWTLVAPLVLTNRDFD

FIGURE 85

AACAAAGTTCAGTGA CTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGAGCTGCTGGGCAGA
GAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCCTCGTGGGATGGATCACAGGTGCTGCT
GTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACCTGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGG
AACCGTACAGCTGCAGGGGGAAACCGAGTCCGCCGGGCCAGCCCTTGGCCCTTCCGGCGGGGGGCCACCTGGGA
ATCTTTTACCATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCACCC
CGCCACACCCCTCACCACCTCCACCACCACCACCACCCACCGCCACCATCCCCGCCACGCTCGCTGAGGCTGC
TGTCGCCGGTGCTGTGGACAGCAGCTGCCCCTGCCCTCCCATCTGTTCCCAGGACAAGTGGACCCCATGTTTCC
ATGTGGAAGGATGCATCTCTGGGGTGAACGAGGGGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGC
ATGCCCCAGTGTA CTATGGCAGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAG
AGCAAGGGTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATGACAAGC
GTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTCATCAGGCTGCTGCAGGCCCT
CTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCTTTTGGTTTGGAGAAGGCAGTGTGAGGCTGCACAGT
CAATTCATCGGTGCCTTAGTCCAAGAAAATAAAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 86

MLGLLGSTALVGWITGAAVAVLLLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRRRAQPWPFRRRGHLGIFHHHRH
PGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

FIGURE 87

CCCACGCGTCCGTCCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTATTGCAACGGTCAAGGCTGGCTTGT
 GCCAGAACGGCGCGCGCGCGCGCACGCACACACACGGGGGAACTTTTAAATAAGGCTAGAAGA
 GCTCAGCGCGCGCGCGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA
 CGCCCCGGCCCCGGCTCGGCGCCCCGCTGGGATGGTGCAGCGCTCGCCGCGGGCCCCGAGAGCTGCTGCACTGAAG
 GCCGGCGACGATGGCAGCGCGCCCCGCTGCCCGTGTCCCCGCGCCGCGCCCTCCTGCTCGCCCTGGCCGGTGTCT
 GCTCGCGCCCTGCGAGGCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCACTGCCTCTGT
 TCGGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAAATCATCCAGAAGTGTGAATATTGCACT
 ACAACGGGAAAGCAAAGAACTGATCATAAATCTGGAAAGAAATGAAGGTCTCATTTGCCAGCAGTTTCACGGAAC
 CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT
 ACGGGGATATTCTGATTTCAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAATAATGA
 AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCACGCGAAGAAGCTGAAAAGCGT
 CCGGGGATCATGTGGATCACATCACAACACACCAACCTCGCTGCAAAGAATGTGTTTCCACCACCCTCTCAGAC
 ATGGGCAAGAAGGCATAAAAAGAGAGACCTCAAGGCAACTAAGTATGTGGAGCTGGTGTGTCGAGCAACAACCG
 AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAA
 GTTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAAAGTGTGGAATGACATGGACAAATGCTCTGT
 AAGTCAGGACCCATTACACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA
 TGACAATGCGCAGCTTGTCACTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG
 CACGGCAGACCAGTCTGGGGGAATTGTATGGACCATTCAGACAATCCCCCTGGGTGCAGCCGTGACCCCTGGCACA
 TGAGCTGGGCCACAATTTGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
 GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTAACTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCA
 GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
 CTGCAATGCCACCACCTGTACCCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
 GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC
 TCACCTGCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
 CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAAGTGTCTAAACCTGCCCCCTGGGATCTGCTTTGA
 GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTTCTTTGCCAAATGCGAGAT
 GAGAGATGCTAAATGTGGAATAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC
 CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTACTTGGGCGATGA
 CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
 AAATATTAGTGTCTTTGGGGTTCACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA
 CTGCCACTGCGAGGGCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC
 CATCCGGCAAGCAGAAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG
 ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCACTG
 CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
 TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA
 CAGTGCAGGAAGGGCAGCGACTTCTGGTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGCTGCTCCTGAG
 AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAGTCTGGCCTTTC
 ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCCAAGTGTCCCTTTCCCACTGACACCTCAGCCT
 TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAT
 AGCAGGGTTTGTAGTTTAAATTTATCAGAGACCTGCCACCCATTCCATCTCCATCCAAGCAAACCTGAATGGCAA
 TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACCTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC
 AGTACTCAGGTTTGGAGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCCCTTCATTTAACAAGTAAGAA
 TGTTAAAAAGTGAAACAATGTAAGAGCCTAATCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
 GAAAT

FIGURE 88

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVVSASVRSGDLWIPVKSFDSKNHPEVLNIRLQRE
SKELIINLERNEGLIASSFTTETHYLQDGTDVSLARNYTGHCYYHGHVVRGYSDSAVSLSTCSGLRGLIVFENESYV
LEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTNPLAAKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQ
RQKDLKVKQRLIEIANHVDFYRPLNIRIVLVGVEVWVNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNA
QLVSGVYFQGTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEKGGC
IMNASTGYPFPMVFSSCSRKDLETSLEKGMGVCLFNLEVRRESFQQKCGNRVFVEEGEEDCDGEPEECMNRCNA
TTCTLKPDVCAHGLCCEDCQLKPAGTACRDSNSCDLPEFCTGASPHCPANVYLHDGHSCQDVGVCYNGICQT
HEQQCVTLWGPAGKAPAGICFERVNSAGDPYGNCGKVSKESSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIET
NIPLQQGGRILCRGTHVYLGDDMPDPGLVLVAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVCNNRKNCHC
EAHWAPPFCDFGFGGSTDSGPIRQAEARQEAESNRERGGQEPVGSQEHASTASLTLI
```

Signal peptide:
amino acids 1-28

FIGURE 89

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAGTGAGGCGGGCCGG
CGCGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGCTCTGGATTTCTA
GAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTA
CTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCA
TACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGT
GATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTTCATGTTGGCCTTT
GGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCTGGA
ATTGCTGTATTTTTCCAGAATGCCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTA
TGGCAGTGAACACATCTGATTTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTTTACTGCTCACTCC
CAACCTTTTTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACTAAAATC
ACGAGAACACCTAAACAACAACCAAAAATCTATTGTGGTATGCACTTGATTAACCTTATAAAATGTTAGAGGAAAC
TTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATTTGTAAAAATAAAAAGAAATTACAAAAGAAATT
ATGGATTTGTCAATGTAAGTATTTGTCAATCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGT
GTTTATTCAAATGTGGTCTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTTAGTTTTTAAAATATTCC
GTGGTCAAATTTCTTCCTCACTATAATTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAATGTAAGTGGC
TTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCATGGTCCAGCCACCAGGCTCCCTG
TGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATTCCAAGGGCAGGAAGATGTGACTCAGCCATGACACG
TGGTTCTGGTGGGATGCACAGTCACTCCACATCCACCACTG

FIGURE 90

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDAAVIYPTMKDFNHSYHACGVIATIAFLMINAVSN
GQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEKDIVYPGIAVFFQNAFIFFGGLVFKFG
RTEDLWQ

FIGURE 91

CGACGCCGGCGTGAATGTGGCTTCCGCTGGTGTGCTCCTGGCTGTGCTGCTGCTGGCCGTCTCTGCAAAGTTTA
CTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTCAAACGGCCCCCAGCGCCCTGGTAAC
TGACAAGGAGGCCAGGAAGAAGGTTCTCAAAACAAGCTTTTTTCAGCCAACCAAGTGCCGGAGAAGCTGGATGTGGT
GGTAATTGGCAGTGGCTTTTGGGGGCTGGCTGCAGCTGCAATTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGCT
GGAACAACATACCAAGGCAGGGGGCTGCTGTACATCCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAATCCA
TTACATTGGGCGTATGGAAGAGGGCAGCATTGGCCGTTTATCTTGGACCAGATCACTGAAGGGCAGCTGGACTG
GGCTCCCCTGTCTCTCCTTTTGACATCATGGTACTGGAAGGGCCCAATGGCCGAAAGGAGTACCCCATGTACAG
TGGAGAGAAAGCCTACATTCAAGGCCTCAAGGAGAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAA
GCTGGTTAAGGTGGTATCCAGTGGAGCCCCCTCATGCCATCCTGTTGAAATTCCTCCCATTTGCCGTGGTTTCAGCT
CCTCGACAGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCCCTTCAAGCATCCACCCAGAGCCTGGCTGAGGTCTCT
GCAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCACTTACGGTGTACCCCCAA
CCACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTACATGAAAGGAGGCTTTTATCCCCGAGGGGGTTC
CAGTGAATTTGCCCTTCCACACCATCCCTGTGATTACAGCGGGCTGGGGGCGCTGTCTCTACAAAGGCCACTGTGCA
GAGTGTGTTGCTGGACTCAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTA
TTGCCCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGCCCGCTGCCT
GCCAGGTGTGAAGCAGCAACTGGGGACGGTGCAGGCCCGGCTTAGGCATGACCTCTGTTTTTCATCTGCTGCGAGG
CACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTATGTTTACTATGACACGGACATGGACCAGGCGATGGA
GCGTACGTCTCCATGCCCAGGGAAGAGGCTGCGGAACACATCCCTCTTCTTCTTCCGCTTTCCCATCAGCCAA
AGATCCGACCTGGGAGGACCGATTCCAGGCCCGGTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTT
TGAGGAGTGGCAGGCGGAGCTGAAGGGAAGCGGGGCGAGTACTATGAGACCTTCAAAAACCTCCTTTGTGGAAGC
CTCTATGTGAGTGGTCTGAAACTGTTCCACAGCTGGAGGGGAAGGTGGAGAGTGTGACTGCAGGATCCCCACT
CACCAACCAGTTCTATCTGGCTGCTCCCCGAGGTGCCGTGTACGGGGCTGACCATGACCTGGGCCGCTGCACCC
TTGTGTGATGGCCTCCTTGAGGGCCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTG
TGGACTGGTCCGGGGCCCTGCAAGGTGCCCTGTGTGTCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGACCT
TAAGAATCTTGATTCTAGGATCCGGGACAGAAAGAAAAGAATTAGTTCCATCAGGGAGGAGTCAGAGGAATTTG
CCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTGCATTAGTTCCCTGACAGTATAAAGCACT
CTAATTTGGTTCTGATGCTGAAGAGAGGCCTAGTTTAAATCACAATCCGAATCTGGGGCAATGGAATCACTGC
TTCCAGCTGGGGCAGGTGAGATCTTTACGCCCTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATA
GCTTGATGTCTCATGACGAGCGGCGCTCTGCATCCCTCACCCATGCCCTCCTAACTCAGTGATCAAAGCGAATATT
CCATCTGTGGATAGAACCCTGGCAGTGTGTGTCAGCTCAACCTGGTGGGTTTCAGTTCTGTCTGAGGCTTCTGCT
CTCATTCAATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGGGAAGGGAGACTAATGAGGCTTAACTCAAA
ACCTGGGCGTGGTTTGGTTGCCATTCCATAGGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGCTTCAGTGGCT
CTTCAGGGGACAGGAAATGCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGT
TAGTAGGGTGCATGTGATGATCATATCCAATTCATATGGAAGTCCCGGGTCTGTCTTCTTATCATCGGGGTG
GCAGCTGGTTCTCAATGTGCCAGCAGGACTCAGTACCTGAGCCTCAATCAAGCCTTATCCACCAAATACACAGG
GAAGGGTGTATGCAGGGAAGGGTGACATCAGGAGTCAGGGCATGGACTGGTAAGATGAATACTTTGCTGGGCTGAA
GCAGGCTGCAGGGCATTCCAGCCAAGGGCACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAGTC
ACATCAGAAAAGGGAAAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTCAGTTAATTAGCATGTGAG
GGTTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTGGTATCAGACAT
ACGAAAGGTCTCTTTGTAGTTTCGTGTTAATGTAACATTAATAAATTTATTGATTCCATTGCTTTAAAAA

FIGURE 92

MWLPLVLLLLAVLLLLAVLCKVYLGLFSGSSPNPFSEDVKRPPAPLVTDKEARKKVLKQAFSANQVPEKLDVVVIGS
GFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLFDTGIHYIGRMEEGSIGRFILDQITEGQLDWAPLS
SPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQEEAIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRC
GLLTRFSPFLQASTQSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIA
FHTIPVIQRAGGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLPGVK
QQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTMDQAMERYVSMPREEAAEHIPLLFFAFPSAKDPTW
EDRFPGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEASMSVVLKLFQLEGKVESVTAGSPLTNQF
YLAAPRGACYGADHDLGRLHPCVMASLRAQSPINLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLD
SRIRAQKKKN

FIGURE 93

GGGAAAGATGCGGCGACTCTGGGACCCCTTGGGTCTGGCAGCAGTGGCGGCGATGTTTGTGCGCTCGGGATGG
 GTCCAGGATGTTACTCCTTCTTTGTTGGGGTCTGGGCAGGGGCCACAGCAAGTCGGGGCGGGTCAAACGTT
 CGAGTACTTGAAACGGGAGCACTCGCTGTGCAAGCCCTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAA
 TCTGATGGGCAATGCCATGGTGATGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCCT
 GTGGAACCGGGTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAAGAA
 GAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGCCTGTGTTTGAAACAT
 GGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAATGAGGAGAAGCAGCAAGAGCGGGTATTCCC
 CTACATCTCAGCCATGGTGAACAACGGCTCCCTCAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGG
 AGGCTGCACAGCCATTGTCCGCAATCTTCATTACGACACCTTCTGGTGATTGCTACGTCAAGAGGCATTTGAC
 GATAATGATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCCCGCGG
 CTACTACTTCCGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCATTTCTTGAAGTTGTTGA
 ACTGACAGTGGAGAGAACCCAGAGAGGAAAAGCTCCATCGAGATGTGTTCTTGCCCTCAGTGGACAATATGAA
 GCTGCCTGAGATGACAGCTCCACTGCCGCCCCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGT
 GTTTTCTGTATTTGCCATAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTA
 CTGAGCCCTCCTGCTGCCACCACTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCCTGGCCTGAGCA
 TGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTGTCACTGGAGTTTGAATGCAGG
 GACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACTCTGGTCTGGGAAGCCACCCACCCAGGGCAATGCT
 GCTGTGATGTGCCTTTCCCTGCAGTCCTTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGC
 CAAAATCACAGAACAGAATTTATAGCCCAAGGCTGCCGTGTTGTTTGAAGTCAAGAGGCCCTTCTACTTCAGTTT
 GAATCCACAAAGAATTAATAAAGTGGTAACACACAGGCTTTCTGACCATCCATTCTGTTGGGTTTTGCATTTGACC
 CAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACAGGATGGAAACTTCTTCCCTGCCTTACCTTCCCTTCA
 CTCCATTCAATTGTCTCTCTGTGTGCAACCTGAGCTGGGAAAGGCATTTGGATGCCTCTCTGTTGGGGCTGGGG
 CTGCAGAACACACCTGCGTTTCACTGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTG
 TTCCCTAGCATGGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTGAA
 GTTTGGCTAAAGTTGGTGTAATAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATGGATTAGCTGTGCAAC
 TGACCAGCTCCAGGTTTGTATCAAACCAAAAGCAACATTTGTGATGTGGTCTGACCATGTGGAGATGTTTCTGGAC
 TTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGTTACGATTTTTTGAATCCCACTTTGAGTGCTGAAAGTGTAAAG
 GAAGCTTTCTTCTTACACCTTGGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTTTCTTAATGGACAA
 GAGACAGTTGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCCTCATCATCTGTGCCTGGAAGAGTTCAGTG
 TCATTGAGCAGCACAGCCTGAGTGTGGCCTCTGTCAACCTTATTCCACTGCCTTATTTGACAAGGGGTACAT
 GCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAGAGTCTCCTTGGAGGGCTGGAACCTGAGTCT
 CTCCTATGAACCTCTGTAGCCTAAATGAAATCTTAAATCACCAGTGAACCAAAAAAAAAAAAAAAAAAGGGCG
 GCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

FIGURE 94

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLM
GNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKEIHGQGGKKNLHGDGLAIWYTKDRMQPGPVFGNMDK
FVGLGVFVDTPNEEKQQERVFPYISAMVNNGSLSYDHERDGRPTLGGCTAIVRNLYHYDTFLVIRYVKRHLTIM
MDIDGKHEWRDCIEVPGVRLPRGYFFGTSSITGDLSDNHDVISLKL FELTVERTPEEEKLHRDVFLPSVDNMKLP
EMTAPLPPLSGLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY
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Signal sequence:
amino acids 1-38

Transmembrane domain:
amino acids 310-329

FIGURE 95

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACACACATCCCCAAGA
ACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTCGCTTGTCATCTCCCTCCCGGGGAG
CCGGCGCGCGCTCCCACCTTTGCCGCACACTCCGGCGAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGA
ACTCGGATTGCAGCTCTGAACCCCCATGGTGGTTTTTTTAAACACTTCTTTTCCTTCTCTTCCCTCGTTTTGATTGC
ACCGTTTTCCATCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTGTGGCTTGCCATCGTCCA
TCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGGCTGCGAGAAGGGGTG
ACGCTGGGCGAGCGGCGAGGAGCGCGCCGCTGCTCTGGCGGGCTTTTCGGCTTGAGGGGCAAGGTGAAGAGCGCAC
CGGCCGTGGGGTTTACCGAGCTGGATTGTATGTTGCACCATGGCTTCTTGGATCGGGGCTGTGATTCTTCCCCT
CTTGGGGCTGTGCTCTCCCTCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTA
CGGTGCCAAGGGATTACAGCTTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTGTCTCTCA
GGAATATACATGCTGCACCAACAGAAATGGAAGACAAAGTTAAGCCAACAAAGCAAACCTCGAATTTGAAAACCTTGT
GGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGGCATAAGAAATTTGACGAATTTTTCGAGAGCT
CCTGGAGAATGCAGAAAAGTCACTAAATGATATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGA
AGTCTTCCAGGACCTCTTACAGAGCTGAAAAGGTACTACACTGGGGGTAAATGTGAATCTGGAGGAAATGCTCAA
TGACTTTTGGGCTCGGCTCCTGGAACGGATGTTTCACTGATAAACCTCAGTATCACTTCAGTGAAGACTACCT
GGAATGTGTGAGCAAATACACTGACCACTCAAGCCATTTGGAGACGTGCCCCGGAACCTGAAGATTCAAGTTAC
CCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTGACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAA
GGTCAGCCCAACCCCGGGTGTATCCGTGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCAC
TGTGAGGCCTGCAACAACCTACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGA
GTGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACATTGAGTCGGTCA
GGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAAACAGCATGCAGGTGTCTGCAAGGT
CTTTCAAGGATGTGGTCAGCCCAAACCTGCTCCAGCCCTCAGATCTGCCGCTCAGCTCCTGAAAATTTTAATAC
ACGTTTCAAGGCCCTACAATCCTGAGGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGA
CATAAAGAGAAATTGAAGCTCTTAAAAAGGTCTGGTCAGCATTACCTTACACTATCTGCAAGGACGAGAGCGT
GACAGCGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTTGCCTGAGATCATGAA
TGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACATCACTCGGCCTGACACTTTTCATCAGACA
GCAGATTATGGCTCTCCGTGTGATGACCAACAACTAAAAAACGCCCTACAATGGCAATGATGTCAATTTCCAGGA
CACAAGTGATGAATCCAGTGGCTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCACGGAGTTTGAGTT
TGTCAACACAGAGGCCCGCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCAGCGTGGCCACTC
CCTGCTCTCCTGGTCTCTCACCTGCATTGTCTGGCACTGCAGAGACTGTGCAGATAAATCTTGGGTTTTTGGTCA
GATGAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTTTTCTTACACTCTTGGACAATGGACCATGCCA
CAAAAACCTTACCGTTTTCTATGAGAAGAGAGCAGTAATGCAATCTGCCTCCCTTTTGTTTTCCCAAAGAGTACC
GGGTGCCAGACTGAACTGCTTCCTCTTCCCTTCAGCTATCTGTGGGACCTTGTTTATTCTAGAGAGAATTTCTTA
CTCAAATTTTTTCGTACCAGGAGATTTTCTTACCTTCATTGCTTTTATGCTGCAGAAGTAAAGGAATCTCACGTT
GTGAGGGTTTTTTTTTTCTCATTTAAAT

FIGURE 96

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADVKAQSCGEVRQAYGAKGFSADIPYQEIAGEHLRIPCQEYTCCTTEMEDKL
SQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEKSLNDMFVRTYGMLYMQNSEVFQDLFTELKRY
TGGNVNLEEMLNDFWARLLERMFQLINPQYHFSELYECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGL
TVGREVANRVSKVSPTPGCIRALMKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFDAMLLVAE
RLEGPFNIESVMDPIDVKISEAIMNQENSMQVSAKVFQCGGQPKPAPALRSARSAPENFNTRFRPYNPEERPTT
AAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSGKARYLPEIMNDGLTNQINNPEVD
VDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSGSGSGCMDDVCPTFEFEFVTTEAPAVDPDRR
EVDSSAAQRGHSLLSWSLTCIVLALQRLCR
```

Signal peptide:
amino acids 1-23

FIGURE 97

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGATATTGACAAACTG
AAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGACAGCTTTAGTGGCCGGCCGGCCGCTC
TCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGACCAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAA
TGGGAAGGTTTTATTGAAAACCTACAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTG
CAGAAATTTTATCCAACCTTTGTTTGGGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTTCAT
AGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGCCATTCAAAGATGAATT
TCATTACCGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCAAATGCTGGTTCTCATGATAATGGCAGCCA
GTTTTTCTTCACACTGGGTCGAGCAGATGAACCTTAACAATAAGCATAACCATCTTTGGAAAGGTTACAGGGGATAC
AGTATATAACATGTTGCGACTGTGAGAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAA
AAGCTGTGAGGTTTTGTTTAAATCCTTTTGATGACATCATTTCAAGGGAAATTAAAAGGCTGAAAAAAGAGAAACC
AGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTAGTTTACTTTTATTGGAGAGGAAGCTGA
GGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAGGGCAAAAGCAAAAGTAGTCATGACTTGCTTAA
GGATGATCCACATCTCAGTTCTGTTCCAGTTGTAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGG
AGAAGATGAAAGTGACAGAGCATGATGAATATATTGATGGTGTGATGAAAAGAACCCTGATGAGAGAAAGAATTGCCAA
AAAATTAAGAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATCAGTCAGCCG
CAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAACCGGGAACCTCTTAGCAGCAAAACAAAAAAGTAGAAAA
TGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAAGCCCTCCAGATGGTGTGTTGCCGAATACAGAAG
AGAAAAGCAAAAGTATGAAGCTTTGAGGAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGC
ACTGCTGAACCAAGTTTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGA
AGTAGAAGATGATGAAGGATGGATGTACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGTGAAAGATGCAAG
CATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGAATAAAGAAGGAGGGAAGAAAGCAA
AAAGCTGATGAGAGAGAAAAAAGAAAGAAGATAAATGAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCT
ACAATGGCCTTGTAACAGCCATTGTTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTT
GTCTGGTTTTGAAAAACAATTATCTTGTGTTTGCAAATGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGGTA
CATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCTTCCACAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYDNTIFHRVVPGFIVQGGDPTGTGSGG
ESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELNKHTIFGKVTGDTVYNMLRLSEVDID
DDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEKPBEVVKLKPKGTKNFSLLSFGEEAEVEVNRVSQSM
KGKSKSSHDLKDDPHLSSVPVVESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKDTSANVKS
A
GEGEVEKKSVSRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAVA EYRREKQKY EALRKQQS
KKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVKDASMQDSDTFEIYDPR
NPVNKRREESKKLMREKKERR
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 99

CTTTTCTGAGGAACCCACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTATCCTCCTGGTACTA
TTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCTTACCGCTGAAGTCTGTGCCACACACACA
ATTTACCAGGACCCAAAGGAGATGATGGTGAAAAAGGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGA
CGCATGGGGCCGAAAGGAATTAAAGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCC
ATTGGGAAGAAGGGTGACAAAGGGGAAAAAGTTTGCTTGAATACCTGGAGAAAAAGGCAAAGCAGGTACTGTC
TGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCTCAAGACATCTATGAAG
TTTGTCAAGAAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAATTCTACTACATCGTGCAGGAAGAGAAGAAC
TACAGGGAATCCCTAACCCTGCAGGATTGGGGTGAATGCTAGCCATGCCCAGGATGAAGCTGCCAACACA
CTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTTGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGA
CAGTACATGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAAACCCAGCGACCCCTAT
GGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTT
GTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCTACGTATTTGCTATTTTCCTGTGACCGTCATTA
CAGTTATTGTTATCCATCCTTTTTTTCCTGATTGTACTACATTGATCTGAGTCAACATAGCTAGAAAATGCTAA
ACTGAGGTATGGAGCCTCCATCATCAAAAAAAAAAAAAAAAAA

FIGURE 100

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDGPGEKGKHGKVGRMGPKGI
KGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDCCGRYRKFBVGQLDISIARLKTSMKFVKNVIA
GIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDN
TPLQNYSNWNEGEPSDPYGHEDCVEMLSGRWNDTECHLTMYFVCEFIKKKK
```

Signal peptide:
amino acids 1-25

FIGURE 101

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGCGCCCGGGCGCGGACCCCAACCCCGACCCAGAGCTTCTCC
 AGCGGCGGCGCAGCGAGCAGGGCTCCCCGCTTAACTTCCTCCGCGGGGCCAGCCACCTTCGGGAGTCCGGGTT
 GCCCACCTGCAAACTCTCCGCTTCTGCACCTGCCACCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCA**TGGCCA**
 ACGCGGGGCTGCAGCTGTTGGGCTTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGC
 CCCAGTGGAGGATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGATGT
 CCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGC
 AAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
 AGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAGATGAGGATGGCTGTCA**T**TGGGGTGCGATATTTCTTC
 TTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT**T**CTATGACCC**T**ATGA
 CCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGG
 GAGGTGCCCTACTTTGCTGTTCCCTGTCCCGAAAAACAACCTCTTACCCAACACCAAGGCCCTATCCAAAACCTG
 CACCTTCCAGCGGGAAAGACTACGTGT**GAC**ACAGAGGCAAAAGGAGAAAATCATGTTGAAACAAACCGAAAATGG
 ACATTGAGATACTATCATTAAACATTAGGACCTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAAC
 AAACAAACAAACAAAAACCCATGTGTAA**AA**ATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTTC
 CTCAATATAGGAGGGAAGATTTTCCATTGTATTACTGCTTCCCAT**T**GAGTAATCATACTCAAATGGGGGAAGG
 GGTGCTCCTTAAATATATATAGATATGTATATACATGTTTTCTATTA**AA**ATAGACAGTAA**AA**ATACTATTCT
 CATTATGTTGATACTAGCATACTTAA**AA**ATATCTCTAA**AA**ATAGGTAAATGTATTTAATCCATATTGATGAAGATG
 TTTATTGGTATATTTTCTTTTTCGTCCTTATATACATATGTAACAGTCAAATATCATT**T**TACTCTTCTTCATTAGC
 TTTGGGTGCCTTTGCCACAAGACCTAGCCTAATTTACCAAGGATGAATTTCTTCAATCTT**C**ATGCGTGCCCTTT
 TCATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTG**C**ATCGTTATTAAGCCCTTATTTGTTTTGTGTT
 TCATTGGTCTCTATCTCCTGAATCTAACACATTT**C**ATAGCCTACATTTTAGTTTCTAAAGCCAAGAAGAA**TT**TAT
 TACAAATCAGAACTTTGGAGGCAAATCTTCTGCATGACCAAAGTGATA**AA**ATTCCTGTTGACCTTCCACACAAT
 CCCTGTACTCTGACCCATAGCACTCTTGTTTGCTTTGAA**AA**ATATTTGTCCAAT**T**GAGTAGCTGCATGCTGTTCCC
 CCAGGTGTTGTAACACAACCTTTATTGATTGAATTTTAA**AG**CTACTTATT**C**ATAGTTTTATATCCCCCTAAACTAC
 CTTTTTGTTC**CC**CAATCCTTAATTTGTATTGTTTTCCCAAGTGTAAT**T**ATCATGCGTTTTATATCTTCTTAATAAG
 GTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATAATCTGGTGACAAATATCTCTCTGTAGC
 TGTAAGCAAGTCACTTAATCTTTCTACCTCTTTTCTATCTGCCAAAT**T**GAGATAATGATACTTAACCA**GT**TAG
 AAGAGGTAGTGTAATATTAATTAGTTTATATTACTCTTATTCTTTGAACATGAAC**T**ATGCCTATGTAGTGTCTT
 TATTTGCTCAGCTGGCTGAGACACTGAAGAAGTCACTGAACAA**AA**ACCTACACACGTACCTTCATGTGATTCACTG
 CCTTCCTCTCTTACCAGTCTATTTCCACTGAACAA**AA**ACCTACACACATACCTTCATGTGGTTCAGTGCCTTCCT
 CTCTCTACCAGTCTATTTCCACTGAACAA**AA**ACCTACGCACATACCTTCATGTGGCTCAGTGCCTTCCTCTCTTA
 CCAGTCTATTTCCATTCTTT**C**AGCTGTGCTGACATGTTTGTGCTCTGTTCCATTTTAACA**ACT**GCCTTACTTTT
 TCCAGTCTGTACAGAATGCTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAG
 ACCTGGATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGAAGCTTATTG
 CTT**C**ATCTGTAAGCGGTGGTTTGTAA**TT**CCTGATCTTCCACCTCAGAGTATGTTGTGGGGATCCAGTGAGATA
 GAATACATGTAAGTGGT**TT**TGTAATTTAA**AA**AGTGCTATACTAAGGGAAAGAA**TT**GAGGAATTA**ACT**GCATAC
 GTTTTGGTGTGCTTTTCAA**TT**GTTTGAA**AA**ATA**AA**AAATGTTAAG

FIGURE 102

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAFLGWIGAI VSTALPQWRIYSYAGDNIVTAQAMY EGLWMSCVSQSTGQIQCKVFDSLLNLSS
TLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDEDEVQKMRMAVIGGAIFLLAGLAILVATAWYGNRIVQEFYD
PMTFVNARYEFGQALFTGWAAASLCLLGALLCCSCPRKTTSYPTPRPYPKPAPSSGKDYY
```

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

FIGURE 103

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCCAGGTCTGGAGCGAATTCCAGCCTGCAGGGCTGATAAGCGAGG
CATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGCGCGCAGTAGAGCAGCAGCACAGGGCGC
GGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATGTGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACC
GCGCGCCGCGCGCTGGCTGTGCGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTCTC
GGGTGGTTTATAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGATGAA
TTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTACACAGATACCACATTTAGCAGGAACAGAACAAAAC
TTTCAGCTTGCAAAGCAAATCAATCCCAGTGGAAAGAATTTGGCCTGGATTCTGTTGAGCTAGCTCATTATGAT
GTCTGTGTGCTACCCAAATAAGACTCATCCCACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTC
AACACATCATTATTTGAACCACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTC
TCTCCTCAAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAATTTGGAA
CGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGTTTTCAGAGGAAATAAGGTT
AAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCAATCTCTACTCCGACCTGCTGACTACTTTGCTCTGGGGTG
AAGTCTTATCCAGACGGTTGGAATCTTCTGGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCA
GGAGACCTCTCACACCAGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAAATTCAGAGGCTGTTGGTCTT
CCAAGTATTCCTGTTTCAATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAGACCA
CCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTACTGGAAACTTTTCTACA
CAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTACTCTCAGAGGA
GCAGTGAACCCAGACAGATATGTCATTCTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCTCAG
AGTGGAGCAGCTGTTGTTTCAAGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGA
ACAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTCTTACTGAGTGGGCAGAGGAGAATTCA
AGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAGAAGGAACTACACTCTGAGAGTT
GATTGTACACCGCTGATGTACAGCTTGGTACACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAA
GGCAAATCTCTTTATGAAAGTTGGACTAAAAAAGTCTTCCCCAGAGTTCAAGTGGCATGCCCAGGATAAGCAAA
TTGGGATCTGGAATGATTTTGAGGTGTTCTTCCAACGACTTGGAAATGCTTCAGGCAGAGCACGGTATACTAAA
AATTGGGAAACAAAACAATTTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATATGAGTTGGTGGAAAAG
TTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTCCAGGAGGGATGGTGTGTTGAGCTAGCCAAT
TCCATAGTGTCTCTTTTGTATTGTGAGATTATGCTGTAGTTTAAAGAAAGTATGCTGACAAAATCTACAGTATT
TCTATGAAACATCCACAGGAAATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTT
ACAGAAATTGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAATGATG
AATGATCAACTCATGTTTCTGGAAGAGCATTATTTGATCCATTAGGGTTACCAGACAGGCCTTTTATAGGCAT
GTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCAGGAATTTATGATGCTCTGTTTGAT
ATTGAAAGCAAAGTGGACCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTG
CAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTA
TGTCACCTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTTGAAATAAAGTTGAATATT
ATATATAA

FIGURE 104

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLLHETDSAVATARRPRWLCAGALVLAGGFLLGFLFGWFIKSSNEATNITPKHNMKAFLDELKAENIKKFLH
NFTQIPHLAGTEQNFQOLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTHPNYISIIINEDGNEIFNTSLFEP PPPG
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKIVVIARYGKVFRGNKVKNQLAGAKGV
ILYSDPADYFAPGVKSYPDGWNLPGGGVQORGNILNLNGAGDPLTPGYPANAYAYRRGIAEAVGLPSIPVHPIGYY
DAQKLLKMGGSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPD RYVILG
GHRDSWVFEGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLQLQERG VAYI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGND FEVFF
QRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGCMVFELANSI VLPFDCRDY
AVVLRKYADKIYSISMKHPQEMKTYSVSFDSLFSVAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQ LMFLERAF
IDPLGLPDRPFYRHVIYAPSSHKNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAETLSEVA
```

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340, 459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341, 360-366, 427-433, 529-535, 707-713

FIGURE 105

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTTTATGTTGGGAATT
CCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGAAAGTCAAGCAGCCAGTGCATCTCAT
TTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTTTTTGTACCAGAGGAAATGAATACGACTAGTCATCACATC
GGCCAGCTAAGATCTGATTTAGACAATGGAACAATCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGT
ACTTTTATCATTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTCTAC
ATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTTCATCAAAGTT
TCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATGAGGCCATGTACCAGAGATGTCTCCAGAA
GGAACATTAGTTATCCAGGTGACAGCAAGTGATGCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTAC
AGCTTACTTCAAGGCCAGCCATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGAT
AGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTGTCTGGA
ACAACAAGTGTATTAATTAACCTTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAAAGTTTATACCGCTTG
ACTGTCTCTGAATCTGACCCCACTGGGACTTCTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAAT
GCAGAAATGGATTACAGCATTGAAGAGGATGATTTCGCAACATTTGACATTATTACTAATCATGAACTCAAGAA
GGAATAGTTATATTAATAAAGAAAGTGGATTTTGGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAAC
CATCATGTTTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAAGATCCAGGTGGAAGAT
GTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGAAGAAACCCACAGGGATCATTT
GTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAATCTCCTATCAGGTATCTATTACTAGGAGCAAAGTG
TTCAATATCAATGATAATGGTACAATCACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTA
AGTATTACAGCCACAGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATC
AATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCTGGTCAGGTAATT
CAGACTATCAGTGAGTGGATAGAGATGAATCCATAGAAGAGCACCATTTTACTTTAATCTATCTGTAGAAGAC
ACTAACAATTCAAGTTTTACAATCATAGATAATCAAGATAACACAGCTGTCATTTTGACTAATAGAAGTGGTTTT
AACCTTCAAGAAGAACCTGTCTTCTACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACA
AACACCCCTTACCATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTGTG
CTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTCATTATGATCATATTTGGGTTTATTTTTT
TTGACTTTGGGTTTTAAAACAACGGAGAAAAACAGATTCTATTTCTGAGAAAAGTGAAGATTTAGAGAGAAATATA
TTCCAATATGATGATGAAGGGGTGGAGAAGAAGATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACC
ATAATGCGGGAACGCAAGACTCGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT
GGCCCCGACAGTGCCATATTCAGGAAATTCATTCTGGAAGGCTCGAAGAAGCTAATACTGATCCGTGTGCCCCCT
CCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCCCTGAGCTCCTTAGAATCA
GCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTTGGGACCTCGCTTTAAAGATTAGCATGCATG
TTTGGTTCTGCAGTGAGTCAAATAATTAGGGCTTTTACCATCAAAATTTTAAAAGTGCTAATGTGTATTCTGA
ACCCAATGGTAGTCTTAAAGAGTTTTGTGCCCTGGCTCTATGGCGGGAAAGCCCTAGTCTATGGAGTTTTCTGA
TTTCCCTGGAGTAAATACTCCATGGTTATTTAAGCTACCTACATGCTGTCTATTGAACAGAGATGTGGGGAGAAA
TGTAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAAATAATGTAGGAAGATATTAAGTAGA
TGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATATCATTATTTACTTAGGAAAGAGTAAAATAACCAA
CGAGAAAATTTAAAGGAGCAAAAATTTGCAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTAT
CATATTGACATGAAAATGAAAATGTATAGTCAGAGAAAATTTTCATGAATTATTCATGAAGTATTGTTTCTTT
ATTTAAA

FIGURE 106

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKRGWVWNQFFVPEEMNTTSHHIGQLRSDLDNGNN
SFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSINDNEPKFLD
EPYEAIVPEMSPEGLTVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVIIRISSKMDRELQDEYWVIIQ
AKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDS
QTFDIITNHETQEGIVILKKKVD FEHQNHYGIRAKVKNNHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPYY
VFEVFEETPQGSFVGVVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISAWYNLSITATEKYNIEQ
ISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDRDESIEEHFFYFNLSVEDTNNSSFTIIDNQ
DNTAVILTNRTGFNLQEEPVFYISILIADNGIPSLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIA
ILICIMIIFGFIFLTLGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTT
AEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGLAGSLSSLESASVSDQDESYDYL
NELGPRFKRLACMFGSAVQSN
```

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

FIGURE 107

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCCACATGATTTGACTCAGAGATT
 CTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCCCAAATGCTATATCTATTTCAGGGGCTC
 TCAAGAACAATGGAATATCATCTGATTTAGAAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCT
 CAAAGCAATACCAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCT
 GTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCCAGC
 CCTTGTCTCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCTACTAAATTCCTGGGATGGA
 AGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCTAAAGATAGACAGCTCAAATGAATTGGGATTTATAGTA
 AAACAAGTGTCTTCCCAACCTGATAATTCATTTTGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTC
 TGGGAGGATGGATCAACATTCTCTTAACCTATTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCA
 AATTGTGTATGGATTACGTTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGTGAGAAG
 AAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTAAGGAGGACAGAAAACAGAA
 CAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATGTTTAGAGAGCTTGSCCAACTGTAATCTTAACC
 AAGAAATGAAGGGAGAGGCTGTGATTTCTGTATTTGTGACCTACAGGTAGGCTAGTATTATTTTCTAGTTAG
 TAGATCCCTAGACATGGAATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTTTATTTATTTTTTTGAGATAGG
 GTCTCACTTTGTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGCCTCAGCCCC
 TCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTGGTGTTTTTTGTAGAGACTGGGTTTT
 GCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAGTGATCTGCCCGCCTTGCCCTCCCAAAGTGCTGGGA
 TTACAGATGTGAGCCACCACACCTGGCCCCAAGCTTGAATTTTCTATTCTGCCATTGACTTTGGCATTACCTTGGG
 TAAGCCATAAGCGAATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGG
 TGTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAAGTGAGGGTGAAATATATTTCTGAAT
 AGCTAAATGAAGAAATGGGAAAAATCTTCACCACAGTCAGAGCAATTTTATTATTTTCATCAGTATGATCATAA
 TTATGATTATCATCTTAGTAAAAAGCAGGAACCTCTACTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATC
 TGCCATATCTCTAATAGAATCTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTGCCCAGGCTG
 GAGTGCAACGGCACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCC
 CAAGTAGCTGGGATTACAGTCAGGCACCACCACCCCGCTAATTTTGTATTTTTTTAGTAGAGACAGGGTTTCT
 CCATGTCCGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGCCTGCCTCGGCTCCCAAGTGCTGGGATT
 ACAGGCGTGAGCCACTGCACCCAGCCTAGAATCTTGATAATATGTAATTGTAGGGAACCTGCTCTCATAGGAAA
 GTTTTCTGCTTTTTTAAATACAAAAATACATAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACC
 TCATTGGAACAAGTATTAACATTTTGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTACCAT
 TTTTTTCAGTAATTACTGTAAATGGTATTATTGGAATGAAACTATATTTCTCATGTGCTGATTTGTCTTATTT
 TTTTCATACTTTCCCACTGGTGTATTTTTATTTCCAATGGATATTTCTGTATTACTAGGGAGGCATTTACAGTC
 CTCTAATGTTGATTAATATGTGAAAAGAAATGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTT
 ATGTTATGTGATTTCAATTAATAAAAAAACTCTTATCAAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTT

FIGURE 108

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGS CAASPPWRLIAVILGILCLVILVIAVVLGTMGVLSSPCP
PNWIIYEKSCYLFMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQVSSQPDNSFWIGLSRPQTEVPWLWED
GSTFSSNLFQIRTTATQENPSPNCVWIIHVSVIYDQLCSVPSYSICEKKFSM
```

Important features:

Type II transmembrane domain:

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

FIGURE 109

CTGCAAGTTGTTAAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCACA
ATATCTTAACCTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAGAC
CTACCTACCCGTACGCATACATACATATGTGTATATATATGTAACTAGACAAAGATCGCAGATCATAAAGCAAG
CTCTGCTTTAGTTTCCAAGAAGATTACAAAGAATTTAGAGATGTATTTGTCAAGATCCCTGTCGATTCTATGCCCT
TTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCTTTGGTTTTGGGGACATTATGATTTGTGTAAAGACTCAGAT
TTACACGGAAGAAGGGAAAGTTTGGGATTACATGGCCTGCCAGCCGGAATCCACGGACATGACAAAATATCTGAA
AGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCTCCTGAGACGTTCTGTGCAATGGGCAATCCCTACAT
GTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCCCTGAGCTGATGTTTGAATTTGAAGGAAG
ACATCCCTCCACATTTTGGCAGTCTGCCACTTGGGAAGGAGTATCCCAAGCCTCTCCAGGTTAACATCACTCTGTCT
TTGGAGCAAAACCATTTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACCAAATGATCCT
GGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTAGATGCTTTTCA
CATGGATCCTAAATCCGTGAAGGATTTATCACAGCATACGGTCTTAGAAATCATTTCACAGAGAAGAGTACTCAAC
AGGGTATACACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTTCGCGCTTTTGTCTGGACCTCGCCT
ACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAAACTCAGAGATTTCTTTACAGTCACAGACCT
GAGGATAAGGCTGTTAAGACCAGCCGTTGGGGAAATATTTGTAGATGAGCTACACTTGGCAGCTACTTTTACGC
GATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTGTGTATGACAACAGCAA
ATTGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAGAATTATCAGGGCCGACC
TTGGAGTCCAGGCTCCTATCTCCCCATCCCCAAAGGCACGCAAAATACCTGTATCCCGAGTATTTCCAGTATTGG
TACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACAACAACGTGCGCTCGCTGTG
CCCGGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGCTCCGACTCTGG
CCAGGGCGCGCCCCCGCACGGCACCCCGAGCGTGTCTGCTGACCACGCTGCTGGGAACCGCCAGCCCCCTGGT
GTTCTAGGTGTACCTCCAGCCACACCGGACGGGCTGTGCCGTGGGGAAGCAGACACAACCCAAACATTTGCTA
CTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAACTAAGAAGGCCTAACTGAACTAA
GCCATATTTATACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGCAGCTG
TTGATATTATCACTGCAAAATCAATTGCCAGCTGCAGAGCATATTGTGGATTGGAAAGGCTGCGACAGCCCCCA
AACAGGAAAGACAAAAAACAACAAATCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGCGCCCTAGTAC
GACTCCGCCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAGGTGCATTGTGGGCATAAGGAAATCTGT
TACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCCAACCTGTGCTTTAGTGAACGTTGCTCTGTAA
CCCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGTATGCATGTGTAAACAGCCCCCTCTAAAAGCGCAAG
CCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGAGCACACCCACTATACAAGAGTGGCTATA
GGAAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTTATTTTCTTGAACACTGTAAATATGTAGATT
TTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAATGTATCTAATTGCAATCAGCAAAGACTGACATT
TTATTTTGTCTCTTTCTGTTCTGTTTTGTTTCACTGTGCAGAGATTTCTCTGTAAGGGCAACGAACGTGCTGGCA
TCAAAGAATATCAGTTTACATATATAACAAGTGTAAATAAGATTCCACCAAAGGACATTCTAAATGTTTCTTGT
GCTTTAACACTGGAAGATTTAAAGAATAAAAACCTCCTGCATAAACGATTTTCAGGAATTTGTATTGCAATTTCTTA
AGATGAAAGGAACAGCCACCAAGCAGTTTCACACTCACTTTACTGATTTCTGTGTGGACTGAGTACATTGAGCTG
ACGAATTTAGTTCCCAGGAAGATGGATTGATGTTCACTAGCTTGGACAACTTCTGCAAAATATGAGACTATTTCC
ACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 110

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLKVCLDPPDITCGDP
PETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI
TFESGRPDQMILEKSLDYGRWQPYQYYATDCLDAFHMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEI
KDRFALFAGPRLRNMASLYGQLDTTKLRDFFTVTDLRIRLLRPVGEIFVDELHLARYFYAISDIKVRGRCKCN
LHATVCVYDNSKLTCECEHNTTGPDGKCKKNYQGRPWSPGSLPIPKGTANTCIPSISSIGTNVCDNELLHCQN
GGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLTLLGTASPLVF

FIGURE 111

GCGTGCCGTGAGCTCGCCGGGCACCGCGCCTCGCCCTCGCCCTCGCCCTGCGCCTGCACCGCGTAGACCGAC
 CCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCCGACCGGTCCCCGCCTTTTGTAAAACT
 TAAAGCGGGCGCAGCATTAAAGCTTCCCGCCCCGGTGACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCGCGCGC
 TAAGGAACATGCGGAAGGTGGAGCAGGTCTGAGCCTCGAGCCGCAGCACGAGCTCAAATCCGAGGTCCCTTCA
 CCGATGTTGTCAACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTACAG
 CACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATTAATGTATCTGTGATGT
 TACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTTTATGGTTTCAGTCTATGTTTGTCTCAACTG
 ACACCTCAGATATGGAAGCAGTATGGAAGGAGGCAAAACCGGAAGACCTTATGGATTCAAAACCTTAGATGTGTGT
 TTGAATTGCCAGCAGAGAATGATAAACCATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGA
 CAGAAACACCAATAGTGTCTAAGTCTCTGAGTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGGAAGAAT
 GTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAAACAAGCAGTTCAAGGAAGAAGATGGACTGCGGA
 TGAGGAAGACAGTGCAGAGCAACAGCCCCATTTAGCATTAGCCCCAACTGGGAAGGAAGAAGGCCTTAGCACCC
 GGCTCTTGCTCTGGTGGTTTTGTCTTTATCGTTGGTGTAATTATTGGGAAGATTGCCTTGTTAGAGGTAGCATG
 CACAGGATGGTAAATTGGATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGA
 AATTAATGTATGATGACATCTCACAGGTCTTGCTTTAAATTACCCCTCCCTGCACACACATACACAGATACACA
 CACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTGATTGAGGGGGAAAAAGAATGAT
 CTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAATGGCATATTGTAAATGTCAATTTAAACATTGGTAGG
 CCTTGCTACATGATGCTGGATTACCTCTCTTAAATGACACCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAG
 CTGGAGCCAGCATGCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCT
 GCTTTCCTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAA
 TTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGA
 AATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACTG
 TTATTCAGAGATGTTTAAATGCATATTTAACTTATTTAATGTATTTTATCTCATGTTTTCTTATTGTCACAAGAGT
 ACAGTTAATGCTGCGTGCTGCTGAACCTGTGTTGGGTGAACCTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCTGT
 CTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCAGGAAGTGTTTTTTCT
 GGGTCAGTAAATAACAACCTGTATAGGGAGGAAATTTCTCAGTAGTGACAGTCAACTCTAGGTTACCTTTTTTAA
 TGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATACCACCTCTCAACCATTACTCACACTCCAGCGCCAGGTCC
 AAGTCTGAGCCTGACCTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAA
 GCGAGGGCACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTACTAGTT
 GAGAGTTTGAAGTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAA
 AGAAAAATTATAATAAAGCCCCAAAATTAAGAAA

FIGURE 112

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFTDVVTNLKLGNPDRNVCFKVKTAPRRYCVRPNSGIIDAGASINVSVMQLQ
FDYDPNEKSKHKFMVQSMFAPDTSDMEAVWKEAKPEDLMDSKLRVCFELPAENDKPHDVEINKIISTASKTET
PIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREENKQFKEEDGLMRKTVQSNSPISALAPTGKEEGLSTRLL
ALVVLLFFIVGVIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

FIGURE 113

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGGCGGCGGGTAGCTGGCA
GGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTTCTCTGTGGACCATGTCCGTGATCTT
TTTTGCCCTGCGTGGTACGGGTAAAGGATGGACTGCCCCCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTT
TTTGGAATGGAGGAGACGGCTCAAGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGG
TTGTGACTTTAGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCCAGC
AGCCATGGCCTTCTGCTTCCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCCTATGACACTACCTGCATTGGCCT
AGCCTCCAGGCCATACGCTTTTTCTTGAGTTTGACAGCATCATTAGAAAAGTGAAGTGGCATTTTAACTATGTAAG
TTCTCTCAGATGGAGTGCAGCTTGGAATAATTCAGGAGGAGCTCAAGTGCAGCCTCCAGCGGTTCTCACTCT
GGAGGACACAGATGTGGCAAATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCG
AATGGAACCAAGTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCTCATTCTG
AGGAGTTCACCTTGACAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGTTGGACCAAACCTCGTGAGC
CAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCATCCGGGAGCAGTGATGTCAAACCTCTGCTGCTG
GGGAAATCTCATCAGCAGGGAGCCTGTGGAAAAGGCATGTGAGTGAATCTGGGAATGGCTGGATTCCGAAACA
TCTGCCCATGTGTATTGATGGCAGAGCTGTTGCCACAAGCGCCTTTTATTTAGGGTAAAATTAACAAATCCATT
CTATTCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTTACATTTATATGATTCTGGGGTTGCTTCAGAA
GTGTTATTTTCATGAATCATTTCATATGATTGATCCCCCAGGATTCTATTTTGTGTTAATGGGCTTTTCTACTAAA
GCATAAAATACTGAGGCTGATTTAGTCAGGGCAAAACCATTTACTTTACATATTCGTTTTCAATACTTGCTGTTT
ATGTTACACAAGCTTCTTACGGTTTTCTTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAAAC
TCAGTAGTACAACCTAACTTGTATAAAAGTGTGTAATAATGTATAGCCATTTATATCCTATGTATAAATTAAT
GAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTATAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 114

MSVIFFACVVRVRDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHFSSFGDVACMAICS
CQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKWHFNYVSSSQMECSLEKIQEELKLQPP
AVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPV TALGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

FIGURE 115

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTCGATTGAAACGTGAGCGCGACCCGACCTTAAAG
 AGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAAAACGAGGCGGGTGGTGCCCGCCCTTTAAGGGCGGGGCGTCC
 GGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTG
 TGGGTGCTTGGCGGCGGCGGCTTCCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCT
 GAGCAGAGTATGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAG
 TGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTCAAGAAGCCT
 GCTGAGTTACACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGCGCTCGAGCTGTGCACCTTTACCCCTG
 GCAATTGCCCCGGGTGCTGTCTGCTCCTGCCCCCTTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCTCG
 AACTACTACATCCAGTGGCTCAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTG
 TCCCTCATCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAGGGTGT
 CTGGGCCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCTAGGTATGGTGTGGGTGGCA
 TCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCTATGACTTTTGGGAGTACTATCTCCCTACCTC
 TACTCATGCATCTCCTTCTTGGGGTCTGCTGCTCCTGGTGCTACTCCACTGGGTCTCGCCCGCATGTTCTCC
 GTCAGTGGGAAGCTGCTAGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAG
 GAGGCAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTGCTACACAGA
 CAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGCTTCAGCCTGGCAACGGAACCTG
 GGCTACCCCTGGCTATGCTGTGCTTGTGCTGGTGCTGACGGGCTGTCTGTGCTCATTGTGGCCATCCACATCCTG
 GAGCTGCTCATCGATGAGGCTGCCATGCCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAG
 CTGGGCTCCTTTGGTGCCGTCATTGAGGTGTACTCATCTTTTACCTAATGGTGCTCCTCAGTTGTGGGCTTCTAT
 AGCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCACGACACTGCCATGACGCAGATAATTGGGAACGTGTGTC
 TGTCTCCTGGTCCCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCTGGGGCTCACTCGCTTTGACCTGCTGGGT
 GACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACATTGTGTCTCTTCTACAACGCAGCCTTTGCAGGCCTCACC
 AACTCTGTCTGGTGAAGACCTTCACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCCTTTGGGCTGGACAGACTG
 CCGCTGCCCCGTCTCCGGTTTCCCCCAGGCATCTAGGAAGACCCAGCACCAGTGAACCTCCAGCTGGGGGTGGGAAG
 GAAAAAAGTGGACACTGCCATCTGCTGCCCTAGGCTGGAGGGAAGCCCAAGGCTACTTGGACCTCAGGACCTGGA
 ATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATTGCATAATCTGAGCCAGAGTTTGGGACCA
 GGACCTCCTGCTTTTCCATACTTAACTGTGGCCTCAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGAT
 CCCAAATCTGTTTACACATCAATCTGCCCTCACTGCTGTTCTGGGCCATCCCATAGCCATGTTTACATGATTTGA
 TGTGCAATAGGGTGGGGTAGGGGCAGGGAAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCCCTTGC
 CTCTGGCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGCTTTGGACCACCTGAAAGACCAAGGGGATAGG
 GAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGAAAAAA

FIGURE 116

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNKIALELCTFTLAIA
LGAVLLLPFSIISNEVLLSLPRNYIQLNGSLIHGLWNLVFLFPNLSLIFLMPFAYFFTESEGFAGSRKGVLR
VYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYPYLYSCISFLGVLLLLLVCTPLGLARMFSVTG
KLLVKPRILLEDLEEQLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQQRVLLKRRKASAWQRNLGYP
LAMLCLLVLTGLSVLIVAIHILELLIDEAAMPQGMQTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGFYSSP
LFRSLRPRWHDAMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLC
LVKTFTAAVRAELIRAFGLDRLLPLPVSGFPQASRKTQHQ

FIGURE 117

[illegible]

FIGURE 118

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1 stop
><MW: 60268, pI: 9.53, NX(S/T): 3
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NHQSREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGSYVTYNFMNDGFFLKVTVLSFTPRPQD
HNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPP
ATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV
LENLNGTSLPVLLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGS
QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPT
AGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR
PEARMPKGTQADYAEVKFQ
```

Important features:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

FIGURE 119

CTCGCGCAGGGATCGTCCCATGGCCGGGGCTCGGAGCCGCGACCCCTGGGGGGCCTCCGGGATTGCTACCTTTT
 TGGCTCCCTGCTCGTGAAGTCTCTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCCTTGCACAA
 GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
 GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTG
 CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
 GGAGAACCAGTGGTTGGGAGTCACTGTTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA
 TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTTCGCTGCTTTGTGCTCAGCCAGGA
 CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT
 TGGGTTCTGCCAGCAGGGCACAGCTGCCGCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
 CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGCTCAGCGGACCTGGCACACCTGGACGACGG
 TCCCTACGAGGCGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCCTGCCAACAGCTACTTTGGCTT
 CTCTATTGACTCGGGGAAAGGTCTGGTGGCTGCGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCAACCA
 CAAGGTGCTGTGGTCTATCTGCGCAAGGACAGCGCCAGTGCCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCG
 CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTATGGCTGGCCAGACCTGATAGTGGG
 TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTCTGTATGTGTACTTGAACCAGGGGGGTCACTG
 GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCCGGGATCAGCCTGGCTGTCTGGGGGA
 CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCCCTTTGATGGTGTATGGGAAAGTCTTCATCTACCA
 TGGGAGCAGCTGGGGGTTGTGCGCAAACTTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
 CTACTCCCTGTGAGGCAGCTTGGATATGGATGGGAACCAATACCTTGACCTGCTGGTGGGCTCCCTGGCTGACAC
 CGCAGTGTCTTTCAGGGCCAGACCCATCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT
 GGAGCAGCCCCAAGTGTGTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTCAGTCCC
 CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCCGAGGCTCCGGGGCCAGGT
 TCCCCGTGTGACGTTTCTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCTCGGGCACCCTGTGGCTGAAGCA
 CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAATGTCAAAGACAAGCTTCGGGCCATTGT
 AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC
 CCCCATCCTCAATGCCACCAGCCAGCACCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA
 CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCAGCCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACC
 TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTGTGGCAGCCAGTCACTGGCTGGAGCTGAT
 GGTCAACCACTGCCATCGGACCCAGCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTCCTGGT
 CATGCTTCTGACTCACTGACTCACTCAGGGGTCCGGGCCCTGGACCTGCGGAGAAGCCACTCTGCCTGTCCAA
 TGAGAATGCCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCCAGGTCACTTCTACCTCAT
 CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAAGTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA
 GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC
 CCAGCAACTCTTCTTCTCTGGTGTGGTGGAGGGCGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT
 CAAGTATGAGCTGACGGTTTCCAACCAAGGCCAGTCTGCTCAGAACCCCTGGGCTCTGCCCTTCTCAACATCATGTG
 GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCTGG
 GCAGAAAGGGCTTTGCTCTCCAGGCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGCGGGCGGA
 GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGC
 TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCACGGCCAACCTGTGTGGTGTTCAGCTGCCCCACTCTA
 CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
 TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA
 TGCCTCCACAGTGATCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCTGGTGGGT
 CATCTCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTT
 CAAACGGGCGAAGCACCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCA
 GTTCAAGGAGGAGAAGACGGGCACCATCTGAGGAACAACCTGGGGCAGCCCCCGGGGAGGGGCCGGATGCACA
 CCCCATCCTGGCTGCTGACGGGCATCCGAGCTGGGCCCGATGGGCATCCAGGGCCAGGCACCGCTAGGTTCC
 CATGTCCAGCCTGGCTGTGGCTGCCCTCCATCCCTTCCCGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
 GGGCTGCTGGTGTGCGCATCAAGATTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAAC
 TCCTCCCACCCAACCTCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG
 TGAGAAGGGCAGGGGTGTCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT
 GTAACAGGACCCCAAGGACCTGCCCTCCCCGAAGTGCCTTAACCTAGAGGGTCCGGGAGGAGGTTGTGTCACTGA
 CTCAGGCTGTCTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGTGCCATCAGTCTAGTGGTTTCGTGGT
 TTCGTCTATTATTATAAAAAATATTGAGAACAAAAA

FIGURE 120

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQLQPRPQSWLLVGAP
QALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWLGVSVRSQGPQGGKIVTCAHRYEARQRV
DQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFCGRPQGHEQFGFCQQTAAAFSPDSHYLLFGAPGTYNWKGT
ARVELCAQGSADLAHLDDGPYEAGGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVT
LRKDSASRLVPEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGISPL
RLCGSPDSMFGISLAVLGDNLQDGFDPDIAGAPFDGDGKVFIYHGSSLGVVAKPSQVLEGEAVGIKSGYSLSGS
LDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVSIAPRSIDLEQPN CAGHSCVCDLRVCFSYIAPVSSYSPT
VALDYVLDADTDRLRGQVPRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTL SYS
LQTPRLRRQAPGQGLPPVAPILNAHQ PSTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVD
GTTALFALSGQP VIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSNENASHV
ECELGNPMKRGAQVTFYLILSTSGISIE TTELEVELL LATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFS
GVVRGERAMQSERDVGSKVKYEVTVSNQGSRLRTLGS AFLNIMWPHEIANGKWLLYPMQVELEGGQGPQKGLCS
PRPNILHLDVDSRDRRRRRELEPPEQQEPGERQE PSMWWPVSSAEKKKNITLDCARGTANCVVFSCLYSFDRAA
VLHVWGRLWNSTFLEEYSAVKSLEVIVRANITVKSS IKNLMLRDASTVIPVMVYLDPMAVVAEGVPWWVILLAVL
AGLLVLALLVLLWKMGGFFKRAKHPEATVPQYH AVKIPREDRQQFKEEKTGTILRNNWGS PRREGPD AHPILAAD
GHPELGPDGHPGPGTA
```

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 121

GGCACGAGGCGGCGGGGAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGTCTCTGCAGGTGTC
GTGGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTTGCCACTTCAGCAGCTTTAGCCCATGAGGAGGATGT
GACCGGGACTGAGTCAGGAGCCCTCTGGAAGCATGGGAGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCA
TCTTCTGGCTTCGTTTGCAGCCTTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGC
GCTATGATTCTAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAGTGG
ACGATGTGCTTATCACCAACCCCAATTGAGGCCATTCTGGAGAATGAAGACTGGATCGAAGATGCCTCGGGTC
TCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACTCTGACAGAGAAGCTTGTGGCCATGACAATGGGCT
CTGGGGCCAAGATGAAGACTTCAGCCAGTGTGAGCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGG
ATGATGTTGTGAAGTCGATGTACCTCCGTTGGACCCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGT
CTGTCACTCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACCAGTCTC
TGTCGGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAGCCAGATAAAGGCCTCCAG
GCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTTAGTGCCCTACAGGCCAGCAGCTAGCCATGAAGGCCCTGC
CGCCATCCCTGGATGGCTCAGCTTAGCCTTCTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTT
CAGCTGTGTGTGCATAGTAAAGCAGGAGATCCCCGTCACTTTATGCCTCTTTTGCAGTTGCAAACCTGTGGCTGGT
GAGTGGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAACCTGGTGGAC
TGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCTAAGAAATCAAGAGGTTTCACAT
TAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATGTGTGGCAATTCTGATCTGCATTTTCAGAAGAGGAC
AATCAATTGAACTAAGTAGGGGTTTCTTCTTTTGGCAAGACTTGTAATCTCTCACCTGGCCTGTTTCATTTATT
TGTATTATCTGCCTGGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAGGTTTGGGTTTGAAGCTGAGGAAC
TACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTGGATAGTAAATTT
ATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 122

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSELELDDVVITNPHIE
AILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
DPKLLDARTTALLLSVSHLVLVTRNACHLTGGLDWIDQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

FIGURE 123

CCCTTACATCCTCCTAGGACCCGGTCGGTAGTCGTGCCCCAGCCCGCCGGGGGCGCAGCGCCCCGAGCCGCGGCC
CTCGAGACGGGACCGAGAGCATCATGGGCAGCACTGTCCCGCGCTCCGCCTCCGTGCTGCTTCTGCTGCTGCTCC
TGCGCCGGGGCCGAGCAGCCCTGCGGGGCCGAGCTCACCTTCGAGCTGCCGGACAACGCCAAGCAGTGCTTCCACG
AGGAGGTGGAGCAGGGCGTGAAGTTCTCCCTGGATTACCAGGTCACTACTGGAGGCCACTACGATGTTGACTGCT
ATGTAGAGGACCCCCAGGGGAACACCATCTACAGAGAAACGAAGAAGCAGTACGACAGCTTCACGTACCGGGCTG
AAGTCAAGGGCGTTTATCAGTTTTGCTTCAGTAATGAGTTTTCCACCTTCTCTCACAAGACCGTCTACTTTGACT
TTCAAGTGGGCGATGAGCCTCCCATTTCTCCAGACATGGGGAACAGGGTCACAGCTCTCACCCAGATGGAGTCCG
CCTGCGTGACCATCCATGAGGCTCTGAAAACGGTGATTGACTCCAGACGCATTACCGGCTGCGGGAGGGCCAGG
ACCGGGCCCGAGCGGAAGACCTTAATAGCCGAGTCTCTTACTGGTCTGTTGGCGAGACGATTGCCCTGTTGCTGG
TCAGCTTCAGTCAGGTGCTACTGTTGAAAAGCTTCTTCACAGAAAAACGACCCATCAGCAGGGCAGTCCACTCCT
AGCCCCGGCATCCTGCTCTAGGGCCCCCTCATGCCCCAGGCTGGAGCAGCTCTCCTAGGTCACAGCCTGCTGGGCT
GGGTGCGGTAGCCCGAGGTGGAGGCAGAACGATGCTGCTGTGGTAGCCCTTTGCCTTTTCATGCCCATGCTTGATT
CTTGACCTCAGCAGCTGAAGGTCTCAGAGACCAGTAATCAGAAGGCATCCGACTGCATTAAGTGTGCAGCGCTG
AAAAGACATTTACAAC TAGGCCAGGGATTAGCCACTGTGGGAGGGTGGACAGGCAATGGTT CAGTGGCCTGGCTG
TTGGCAGGAAC TCCAAGTGCCAGGCCTCTTGGGCAGCTTAGGGCCCTGCCTCTGTTTCATGATGCATGGGT CAT
TTGCTCTGGGTGTCCTATCCCATATGGAGAAGAAAGGGGCTCTAAGTTCTGGCTCTTCTTTCTTTGGGGTTCTCT
GTACCTGAGGAAACCAGGCCCTGGGTGACTTTGCAGATCTGCTCACCCCTCGGTGAGCAACAGTGT CAGCCATGCA
AGCAGGACAGAAATGGTGACTGGGTGCCCTTGGTGAGCTGTGTATTTCTAGGAGGTAGAAAAC TGTGGGAAACTG
TGGCTAATAAAAACTAAGTGTGAGCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 124

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56052
<subunit 1 of 1, 217 aa, 1 stop
<MW: 24777, pI: 5.55, NX(S/T): 0
MGSTVPRSASVLLLLLLLLRRAEQPCGAELTFELPDNAKQCFHEEVEQGVKFSLDYQVITG
GHYDVDCYVEDPQGNTIYRETKKQYDSFTYRAEVKGVYQFCFSNEFSTFSHKTVYFDFQV
GDEPPILPDMGNRVLTALTQMESACVTIHEALKTVIDSQTHYRLREAQDRARAEDLNSRVS
YWSVGETIALFVVSFSQVLLLLKSFFTEKRPISRVAHS

Important features:

Signal peptide:

amino acids: 1-23

Transmembrane domain:

amino acids: 187-201

N-myristoylation sites:

amino acids: 26-32, 48-54, 131-137

Tyrosine kinase phosphorylation site:

amino acids: 82-91

Glycosyl hydrolases family 25 proteins:

amino acids: 53-61

FIGURE 125

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTGAGCCCATTTGGCCCCGACGCCTCTGT
TCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTGCAAGATGGAGGAAGGCGGGAACCTAG
GAGGCCTGATTAAAGATGGTCCATCTACTGGTCTTGTCAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCT
CAGGCTTCCTGCTTTTCCGAAGCCTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTTCCCCTTCTACT
TCCACATCTCCATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCACAT
TCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTTGAGCCTTACGCTGGCCACTGTCAACGCCCGCTGGCTGGAAC
CCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGAGCGAGGCCTGGGTGGGAGGTACCAGGCA
GCCACCAGGTCCCGATCCCTACCGCCAGCTGCGAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCT
TCCGCTACCATGGGCTGTCCTCTCTTTGCAATCTGGGCTGCGTCTGAGCAATGGGCTCTGTCTCGCTGGCCTTG
CCCTGGAAATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAAAAAAAA
AAAAAA

FIGURE 126

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKMVHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISMGC AFINLCILASQ
HAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKERGLGGEVPGSHQGPD PYRQLREKDPKY
SALRQNFFRYHGLSSL CNLGCVL SNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 127

GCTTCATTTCTCCCGACTCAGCTTCCCACCCCTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGC
CATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGATTTGGAGTGTTTTCTGTTCTTTGG
AATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAT
TGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGT
ATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTGTTTCAGGGG
CTTCTTTCTGTGCTTGTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAATTTACCTGGAATTAG
ATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATAACAACAAGTGAATTTGAAGACTCATTTAAAATA
TTGTGTTATTTATAAAGTCATTTGAAGAATATTCAGCACAAAATTAAATTACATGAAATAGCTTGTAAATGTTCTT
TACAGGAGTTTAAAACGTATAGCCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAACACAGGCTTCTA
CTCAAGTGAAC TAAGAAGAAGTCAGCAAGCAAAGTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAACTC
TTGAAGGCTATTTGTGTTGTTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAACTGTGGTGCCTGTTTCT
TTTCTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCTTTT TAGAAGTGTCCACTGCAATGGCAAAAA
TATTTCCAGTTGCACTGTATCTCTGGAAGTGATGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAC
CAAGGAAACCCCAATTTTGATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

FIGURE 128

MISLTDQKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQKHMKATGFFLGGV
FVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGIRSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 129

AATTCAGATTTTAAGCCCATCTGTCAGTGGAATTTTCATGAAGTAGCAAGAGGACACCATCTTCTTGATTATACA
AGAAAGGAGTGACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGGCCCTCCTAATCCTCTGTGGTT
TTCTGTGGACTCGTAAAGGAAAATAAGATTGAAGACATCACTGATAAGTACATTTTATCACTGGATGTGACT
CGGGCTTTGGAACTTGGCAGCCAGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAAT
CAGGATCAACAGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGA
ATGTCAGAGGAGTGGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTG
GTGTTCCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAACCTGT
TTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCA
GTGTTGGAGGTCGCCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACA
GCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAAACAACTTGG
CAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCAGACATCAAAACAACATATG
GAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGG
TGGTAGAGTGCATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGG
CTAATCCCAAGGCAGTGTGACTCAGCTAACCAAAATGTCTCCTCCAGGCTATGAAATTGGCCGATTTCAAGAAC
ACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGATCGTGCTTATTTGGATTGCAA
AGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTGCTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGT
ACATCACATAGGCAAGTCCTGCCCTGTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTT
GCCCATTCAAAATGATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCAGCATTTACAGTAACTTGTGAATGT
TAAGTATCATCTCTTATCTAAATATTAAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGILLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESGSTALKAETSE
RLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDYREPIEVNLFGLISVTLNMLP
LVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMKAFGVHVSCEPGLFKTNLADPVKVIKKLA
IWEQLSPDIKQQYGEQYIEKSLDKLKGKSYVNMDLSPVVECMDHALTSLEPKTHYAAGKDAKIFWIPLSHMPAA
LQDFLLLKQKAELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 131

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAAGCCATGAACATCA
 TCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAGTCGTTGGTGAAGTTTTTCATTCCCTC
 AGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCATTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTT
 ATGAATTTGCAAAACGACAGAGCATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTG
 AGTGCCGAAAAC TAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCTCTC
 TAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACAGTATATCCAGCCGATC
 TTCTCAGCACCAGGATGAAGAGATTACCAAGACATTTGAGGTCAACATCCTAGGACATTTTTGGATCACAAAAG
 CACTTCTTCCATCGATGATGGAGAGAAAATCATGGCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGA
 TTCCTTACCTCATCCCATATTGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTC
 AGGCCTTGGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCCACAAAAATC
 CAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATAGATGGAATACTTACCAATA
 AGAAAATGATTTTTGTTCATCGTATATCAATATCTTCTGAGACTACAGAAGTTTCTTCTGAAACGCGCCTCAG
 CGATTTTAAATCGTATGCAGAATATTCAATTTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATA
 AGCTCCAGCCAGAGATGTATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTTCACAT
 TTTTTTCAGTCCTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTAATTACCTGT
 CTTCTGTTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCTTTTCATGCCTCTTAAAAACTTCTG
 TGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATATTTTATTTTTCCATTTAAAGGTGGACAAAAGCTACC
 TCCCTAAAAGTAAATACAAAGAGAACTTATTTACACAGGGAAGGTTTAAAGACTGTTCAAGTAGCATTTCCAATCTG
 TAGCCATGCCACAGAATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTT
 TATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTTTTCATTAGCCCAA
 AACGGTGCAACTCTATTCTGGACTTTATTAATTGATTCTGTCTTCTGTATAACTCTGAAGTCCACCAAAGTGGA
 CCCTCTATATTTCTCCCTTTTTATAGTCTTATAAGATACATTATGAAAGGTGACCGACTCTATTTTAAATCTCA
 GAATTTTAAGTTCTAGCCCCATGATAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGAT
 GTTTAGACAATTTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAACA
 ATGGACCCAAGAGAAGAA

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

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TAAECRKLGVTAHAYVVDSCNREEIYRSLNQVKKEVGDTVIVVNNAGTVYPADLLSTKDEEITKTFEVNILGHFW
ITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYCSSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFNVTGF
TKNPSTRLWPVLETDEVVRSLIDGILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

FIGURE 133

CTGAGGCGGCGGTAGCATGGAGGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCGGCGCACTCGCTTT
 CCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTTGGGGAAGTAAAAGGTGAAGCCAAGAACAGCAT
 TACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGACATTGAGAAATATATCCATGCTATCAGCT
 TTTTAGCTTTTATAAATCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAA
 TGTGGTAGGTTGGTACAAATTCGGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAAA
 CTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACACCAAGTATAATAACAGAAAGCTGCTC
 TACTCATCGACTGGAACATTCCCTTATATAAACCTCAAAAAGGACTTTTTTCACAGGGTACCTTTAGTGGTTGCCAA
 TCTGGGCATGTCTGAACAACCTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGT
 ACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGC
 TTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACTAGTAAA
 GGATGTAAACAGATTAAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGGCAGCAAGAGAGAAGAAT
 CCAAAAAGACCCTCAGGAGAACATTTTCTTTGTCAGGCATTACGGACCTTTTTTCCAAATTTCTGAATTTCTTCA
 TTCATGTGTTATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACACCAACCACCTCTCGATGTAGT
 AGACAATCTGACCTTAATGGTAGAACACACTGACATTCTGAAAGCTAGTCCAGCTAGTACACCACAAATCATTAA
 GCATAAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGACAAACGATC
 TAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAATGAGCAGCCCAGAAACAGATGAAGAAATTGA
 AAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACATTTGATCCTTTTAACTTACAAGGAGATTTTTTT
 ATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTTGAGCTACTTGACAGTAAGTTCAATTTGTT
 TTTACTATGTTACCTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTTCAA
 CATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAGACACA
 TTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACTTAGGGAAGACAAGTC
 AGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATTGAGACCATGTCTATAAAAAATAAA
 ATGGAAAAGCAAGAATAGCCTTATTTTCAAAATATGGAAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAA
 TTCTCCTTAAGTGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAAT
 AAATTTGCAAAACATCATCTAAATTTAAAAA

FIGURE 134

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYTIDIQKYIPCYQLFSFYN
SSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLLHKNLQEHFSNQDLVFLLLTPSIITESCSTHRLE
HSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEE
LKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS
LKNRHVSKSSCNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDDRWFKRSRLDTPQDKRSKANTG
SSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTF

FIGURE 135

GGCACAGCCGCGCGGCGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCC
 CAAGCAGCGCGCAGCGAACGCCCCGCGCCGCCACACCCCTCTGCGGTCCCCGCGGCGCCTGCCACCCCTCCCTCC
 TTCCCCGCGTCCCCGCTCGCCGCGCCAGTCAGCTTGCCGGGTTCGCTGCCCCGCGAAACCCCGAGGTACCCAGCC
 CGCGCCTCTGCTTCCCTGGGCGCGCGCCGCTCCACGCCCTCCTTCTCCCTGGCCCGGCGCCTGGCACCCGGGG
 ACCGTTGCTTGACGCGAGGCCCAGCTCTACTTTTCGCCCCGCGTCTCTCCGCTGCTCGCCTCTTCCACCAACT
 CCAACTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCCGCTGCCGTAGCGCCGC
 TTCCCGTCCGGTCCCAAAGGTGGGAACGCGTCCGCCCGGCCCGCACC**ATGG**CACGGTTCCGGCTTGCCCGCGCTT
 CTCTGCACCCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGA
 CGTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTGAGATC
 TGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAA
 AGTGTGGTCAGCGAACAGTGCAATCATTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATTCCTC
 AAAGAAGTACTTGAAAATGCAGAGAAAATCCCTGAATGATATGTTTGTGAAGACATATGGCATTATACATGC
 AATCTGAGCTATTTAAAGATCTCTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAA
 ATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCCCTGGTGAACCTCCAGTACCCTTTACAGAT
 GAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCTCGCAAATGAAGCTC
 CAGGTTACTCGTGCTTTTGTAGCAGCCCGTACTTTTCGCTCAAGGCTTAGCGGTTGCGGGAGATGTCGTGAGCAAG
 GTCTCCGTGGTAAACCCACAGCCCAAGTGTACCCATGCCCTGTTGAAGATGATCTACTGCTCCACTGCCGGGGT
 CTCGTGACTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGCTGTTTGGCCAACCAAGGGGATCTC
 GATTTTGAATGGAACAATTTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGAGGGTCTTTCAACATTGAA
 TCGGTTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGATAATAGTGTTCAGTGTCT
 CAGAAGGTTTTCCAGGGATGTGGACCCCCCAAGCCCTCCAGCTGGACGAATTTCTCGTTCCATCTCTGAAAGT
 GCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGCAGCTGGCACTAGTTTGGACCGA
 CTGGTTACTGATGTCAAGGAGAACTGAAAACAGGCCAAGAAATCTGGTCTCCTTCCGAGCAACGTTTGCAAC
 GATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTACCTGTTT
 GCAGTGACAGGAAATGGATTAGCCAACCGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAAACAGACATA
 CTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
 GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAAGTGAAGTGGCTGTGAGTATCAGCAGTGCCCTTCA
 GAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCTC
 GGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTTCTGGTTATGCAGAGAGAGTGGAGAT**TA**ATTCTCA
 AACTCTGAGAAAAAGTGTTCATCAAAAAGTTAAAAGGCACCAGTTATCACTTTTCTACCATCCTAGTGACTTTGC
 TTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAAGTGCTGACTTTGTTTTT
 TCATTGAGTTTTGGGAGGAAAAGGGACTGTGCATTGAGTTGGTTTCTGCTCCCCCAACCATGTTAAACGTGGCT
 AACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTTT
 TTCTCATTTTCTGTTTGTGGGTTTTTTTTTCCAAGTGTGATCTCGCCTTGTTTCTTACAAGCAAACAGGGTCCCTT
 CTTGGCACGTAACATGTACGTATTTCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTATCATGTATATC
 TTATTAAGAAAAAGGCCAAAAAGC

FIGURE 136

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGSTCCSQEMEKEY
SLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGHLYMQNSELFKDLFVELKRY
VVGNNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGL
AVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAE
RLEGPFNIESVMDPIDVKISDAIMNQDNSVQVSQKVFGCGPPKPLPAGRISRSISESAFSARFRPHHPEERPT
TAAGTSLDRLVTDVKEKLKQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEV
QVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAGKSANE
KADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 137

GCGGGCTGTTGACGGCGCTGCGATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTTCTCTCAGTCGGA
CTTCTCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCCGTCGCCACCACTGTAGTCATGTACCCACCGCCGCCGCC
GCCGCTCATCGGGACTTCATCTCGGTGACGCTGAGCTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGGCG
GCGCTCGTGCTGGAGGAAATGGAAGCAACTGTGAGATTGCAGCGGAATATGATTCTCTTCTCTTGCCTTTCT
GCTTTTCTGTGGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAGCTCTGGCTTTTCTAGGCTAGAGGAAGA
GCAGAAGATGAGGCCAGAAATTGCTGGGTAAACCAGCAAATCCACCCGTCTTACCAGCTCCTCAGAAGGCCGA
CACCGACCTGAGAACTTACCTGAGATTTTCGTACAGAAGACACAAAGACACATCCAGCGGGGACCACCTCACCT
GCAGATTAGACCCCCAAGCCAGACCTGAAGGATGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCGTGT
GGATCCCCCGCCGGAAGGAGATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGG
CACCGAGCTCCCTTCAAGAAGAGCAGAAGTGCCCAACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGGCACACC
AGTGCACTGAACTATCGCCAGAAGGGCGTGATTGACGTCTTCTGTCATGCATGGAAAGGATACCGCAAGTTTGC
ATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGTGAGTGGTTTGGCCTCGGTCTCACACTGATCGA
CGCGCTGGACACCATGTGGATCTTGGGTCTGAGGAAAGAAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTT
ACACTTTGAAAAGGACGTGGACGTCAACCTGTTTTCAGAGCACGATCCGCATCTCTGGGGGGGCTCCTGAGTGCCTA
CCACCTGTCTGGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGCCTTCAGAAC
ACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCCGCCACGGTGGACCTCCGACAG
CACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGGGAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCA
GGAGGCAGTGGAGAAGGTGACACAGCACATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGGCCATGTTTCAT
CAATACCCACAGTGGCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTA
CCTGCTGAAGCAGTGGATCCAGGGCGGGAGCAGGAGACACAGCTGCTGGAAGACTACGTGGAAGCCATCGAGGG
TGTCAGAACGCACCTGCTGCGGCACCTCCGAGCCCAGTAAGCTCACCTTTGTGGGGGAGCTTGCCCCACGGCCGCTT
CAGTGCCAAGATGGACCACCTGGTGTGCTTCTGTCAGGGACGCTGGCTCTGGGCGTCTACACGGCCTGCCCGC
CAGCCACATGGAGCTGGCCAGGAGCTCATGGAGACTTGTATACCAGATGAACCGGCAGATGGAGACGGGGCTGAG
TCCCGAGATCGTGCACTTCAACCTTTACCCCCAGCCGGGCGTCGGGACGTGGAGGTCAAGCCAGCAGACAGGCA
CAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCTCACAGGGGACCGCAAATACCAGGA
CTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTCACACGGGTCCCCTCGGGTGGCTATTCTTCCATCAACAA
TGTCCAGGATCCTCAGAAGCCCCGAGCCTAGGGACAAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCT
GTTCTTGCTCTTCTCCGATGACCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCACCTCT
GCCTATCTGGACCCCTGCCTAGGGTGGATGGCTGCTGGTGTGGGGACTTTCGGGTGGGCAGAGGCACCTTGCTGGG
TCTGTGGCATTTCCTAAGGGCCACGTAGCACCGGCAACCGCCAAGTGGCCCAGGCTCTGAACTGGCTCTGGGCT
CCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGAGGCCGTGAGTCTTGGTGTGATGCGGGGTGGG
CTGGGCCGCTGGAGCCTCCGCTGCTTCTCCAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAG
GTCTCTGTGGGCCGACCAGAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGT
GCAGCTCTGCCCCGGGCTCGTGAAGCCTCAGATGTCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGACTCCAGAG
GCCTGAGGCTCCAGGGCTGGCTCTGGTGTTCACAAGCTGGACTCAGGGATCCTCCTGGCCGCCCGCAGGGGGCT
TGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCCCTCCAGTGAATGGGTCTTTTCGGTGGAGATAAAAG
TTGATTTGCTCTAACCGCAA

FIGURE 138

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGCAPWAVATTVMYPPPPPPPHRDFISVTLSEGESYDNSKSWRRRSCWRKW
KQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLEEEQKMRPEIAGLKPANPPVLPAQKADTDPENLP
EISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEATKRQEAPVDPPEGDPQRTVISWRGAVIEPEQGTLPSSR
AEVPTKPPLPPARTQGTPVHLNRYRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWI
LGLRKEFEEARKWVSKKLHFEKDVDVNLFESTITRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPYS
DVNIGTGAHPPRWTSdstVAEVTsiQLEFRELSRLTGDKKFQEAVEKVTQHihGLSGKKDGLVPMFINTHSGLF
THLGVFTLGARADSYEYLLQWiqGGKQETQLLEDYVEAIEGVrTHLLRHSEPSKLTfVGELAHGRFSakMDHL
VCFLPGTLALGVYHGLPASHMELAQELMETCYQMNRMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLRPET
VESLFYLYRVTGDRKYQDWGWEILQSFSRfTRVPSSGGYSSinnVQDPQKPEPRDKMESFFLGETLKYLFLLFSD
PNLLSLDAYVFNTeahPLPIWTPA
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Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 139

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGACCTGAGTCATC
CCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTG
CGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGA
ATCCAGGGGTCGCCAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAAT
GTGAGTGCAAAGATTGGTTCCCTGAGAGCCCCGAGAAGAAAATTGATGACAGTGTCTGGGCTGCCAAAGAAGCAGT
GCCCCGTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCATT
CCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGC
CCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTC
ACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGT
TGCTCTCTCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTAC
CTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTCAATTTAACCTTAAATGCAATCAGGAAAGTAGCAAAC
AGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 140

MKVLISL L L L L L L P L M L M S M V S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R K F M T V S G L P K K Q C
P C D H F K G N V K K T R H Q R H H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L

FIGURE 141

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCTGCTATGCAGACGA
CAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCAAAGCCAGACTTCCCCAAATTCCTAAG
CCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGAGTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTAT
GGAATTTGATGATAATGAAGGAAAACATTCATCAAAGTGAATCCTCAGGACACACCCATGTGGCTCCTGGACAA
TCCAAGAGCAGCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAACTCC
CAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACCCTGACTGCATTTTTCG
TTTTAGAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTGATGGAGAGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 142

MAVLVLRRLTVVLGLLVLFITCYADDKPKDPDDKPDDSGKDPKPDFPKFLSLLGTEI IENAVEFILRSMRSTGFM
EFDDNEGKHSSK

FIGURE 143

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG
CC**ATG**GACATCCTGGTCCCACTCCTGCAGCTGCTGGTGCTGCTTCTTACCCCTGCCCTGCACCTCATGGCTCTGC
TGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCA
AGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTAC
TGGAGCTGGGCTGCGGAACCGGAGCCAACTTTAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAA
ATCCCCACTTTGAGAAAGTTCTTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGG
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGCTGTGCTCTG
TGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGC
ATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTTCGAGCCACCTGGAAACACATTGGGG
ATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGGAACGAC
AGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCT
CCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGA
GAGGGACCT**AG**CAGAATGAGAGAAGACATTATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGG
ACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTCCCTTTTCCTT
CGTTCCCATGGTAAAGCTCCTCTCGCTTTTCCTCCTGAGGCTACACCCATGCGTCTCTAGGAACTGGTCACAAAAG
TCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCTCTCCCCACTACCACCTTCTTCCCTGAGCTGGGGCA
CCAGGGAGAATCAGAGATGCTGGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTCTCAAATATTTTT
TAATAAATAGACGAAACCACG

FIGURE 144

MDILVPLLQLLVLLLTLPPLHLMALLGCWQPLCKSYFPYLMVLTPKSNRKMESKKRELFSSQIKGLTGASGKVALL
ELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLYERFVVAPGEDMRQLADGSMDVVVCTLVLCV
QSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFEPWTKHIGDGCCLTRETWKDLENAQFSEIQMERQ
PPPLKWLVPVGPHIMGKAVKQSFPSKALICSFPSLQLEQATHQPIYLPLRGT

FIGURE 145

GTGGGATTTATTTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGGCAGATGTTGGGGC
TTTGTCCGAACAGCTCCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAAAA
AGATGTCATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATA
ACTTCCTCAGCTTGAGCAGTTTTGTTAAGGAATGAGGTTACAGATTCAGGAATGTAGGGCCTCAACCTATAGACT
TTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATCTGAAG
ACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTG
TTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAA
TTGTCAATTTTGACCCTAAACTTTTGGGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGGAATCCATGAAACCTT
TAACCTTTGCAAGGTTCTACTTGCCCAATTCTGGTTCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAA
TTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTTCAGAAGATT
GTGATTCAGCCTCTACTAAAGTTGTTCATCCGTGGAGCAGGAAACAGTACAATTACATTGGCTATCTTGACTATA
AAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAACC
TGACGGAATGGAAACGACAGAATATAACTAACCCTGGAAGGAAATGGATGAACTCAATGTAGAAGAGGGACTGT
ATAGCAGAACCCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCG
ATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCA
AGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGT
ATATTCAGACCCCAACAGGCAAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAAGTGAAACAGAA
TTTGAAGTGAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTC
AATGCCATATCGGTAGCAAGCCATGGAAAAAGATGTGTGAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGT
CAGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTG
AATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTTA
ATTTTGTAACTGTGGCCTGATCTGTAAATAAACTTACATTTTTC

FIGURE 146

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGRQEEIPVVIAASED
RLGGAIAAINSIQHNTRSNVIFYIVTLNNTADHLRSWLNSDSLKSIRYKIVNFDPKLLEGKVKEDPDQGESMKPL
TFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKVVRGAGNQYNYIGYLDYK
KERIRKLSMKASTCSFNPGVFVANLTEWKRQNITNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTID
PMWNVRLHGSSAGKRYSPQFVKAACKLLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

FIGURE 147

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTTCCTCCAAGCA
 AGTCATTTCCCTTATTTAACCAGTGTGTCCCTCAAACACCTGAGTGCTACTCCCTATTTGCATCTGTTTTGATAA
 ATGATGTTGACACCCCTCCACCGAATTCCTAAGTGGAATCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCC
 TCGCATTAGCCTTGTCTTTGGCCATGATGTTTACCTTCAGATTCATCACCACCCTTCTGGTTCACATTTTCATTT
 CATTGGTTATTTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCA
 GCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGG
 CAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCACAAATA
 AAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCATTTTTCTTCTGGGTCC
 TCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAATATA
 AGCCCCCTTCGGGCATTTCGGTACATGTGGTTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTG
 CGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTCAACAGAAGTAAAAATGATCCTCCTGATC
 ATCCCATCCTTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCT
 CTGTGGTGAGGATTCCGAGAATCATTGTTCATGTACATGCAAAACGCACCTGAAAGAACAGCAGCATGGTGCATTGT
 CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATG
 CATATACTACAACCTGCTATTAAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCTTGTCCAAGA
 ACTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTAGGAAAGGTGTTAGTGGTGTGTT
 TCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGG
 TAGCTTTTTTTGCTTACTTAGTAGCCCATAGTTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGT
 GTTTTGCTGTTGATCTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTT
 TCGTAAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAGGAATGAGGAGGGAA
 CAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATTTCTTCTAAGAGCCA
 TTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTTTTTAAAGACCTAATAAACCTATTCT
 TTCCTCAAAA

FIGURE 148

MSGRDTILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYDTNDLSIELDTERENMKC
VLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFAILIFFWVLWVAVLLSLGTAG
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFY
HQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFC
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAHSFL
SVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

FIGURE 149

[illegible]

FIGURE 150

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVG
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWRESFIVLESKPKKGVITYPSAL
TYSSSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSQE
MDLWSTATYTSSQNRPRADPGIQRQDPSGAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRA
ISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENEKQYVVEPNFANKAV
CRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDRLACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKF
EISDTRIGAVQYTYEQRLFEFGFDKYSSKPDILNAIKRVGYWSSGTSTGAAINFALEQLFKKSKPNKRKLMILI
TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELVIATHPARHSSFVDEFNLHQYVPRIIQNICTEFNSQPRN

FIGURE 151

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCTATGCCTTTCCGGCT
GCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGTGCGCCAGGTCCCGACGGCTCCGCGCC
AGATCCCGCCCACTACAGTTTTTCTCTGACTCTAATTGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTC
AGAATTCCAAAGAGTGGTTGAAGTGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGA
AACAAACATTGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGGAAGTAGAGGC
TGGATGGCCCTGTTCCGGGGCTCTCCTGAGAATGGCTGAGGAGGCGGCCCGAAAACTCCTCCAGCCTTTCAGAC
CCCCACTGGCATGCCATATGGAACAGTGAACCTTACTTCATGGCGTGAACCCAGGAGAGACCCCTGTCACCTGTAC
GGCAGGGATTGGGACCTTCATTGTTGAATTTGCCACCCTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGT
GGCCAGAGTGGCTTTGATGCGCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCT
CACTGGCAAGTGGGTGGCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGTGAAAGG
AGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTTCTAGAGTATAACAAAGCCATCCGGAACACACCCG
CTTCGATGACTGGTACCTGTGGGTTCAGATGTACAAGGGGACTGTGTCCATGCCAGTCTTCCAGTCCTTGGAGGC
CTACTGGCCTGGTCTTCAGAGCCTCATTGGAGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGT
ATGGAAGCAGTTTGGGGGGCTCCCGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTA
CCCACTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCACCCCTCCTAGAACT
CGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGC GGATTTGCAACAATCAAAGATCTGCG
AGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTGGCCGAGACTGTGAAATACCTCTACCTCCTGTTTGA
CCCAACCAACTTCATCCACAACAATGGGTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGG
GGCTGGGGGGTACATCTTCAACACAGAAGCTCACCCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAA
GGAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTGGAATTTTCAAG
AAACACTGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACACTCTTCTCACCAGAAAACCATGACCA
GGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCACTTCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTT
GGCATTACTGGGACAGGTTTTCTAGACTCCTCATAACCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCT
AAACTATAATAAATTGCTTTTGGCTATCATAAAA

FIGURE 152

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVEVLQDSVDFDIDVN
ASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPAFQTPTGMPYGTVNLLHGVNPGET
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFE
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLWVQMYKGTVSMFVQSLEAYWPGLQSLIGDIDNAMRTFL
NYYTVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMLYRATGDPTLLELGRDAVESIEKISKVECGFAT
IKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC
CQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGLFSPENHDQARERKPAKQKVPLLSCPSQP
FTSKLALLGQVFLDSS

FIGURE 153

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAAAGTGAAGAAAACA
GAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCCCTTCGT
CACTCACCTGTTCTTGCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACG
CCTATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGAT
GCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGGGGC
CCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTCATCTGCTGTGAATAT
GCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTCATGGTGAGCTAAGGAGAGGGTGGTGGCAG
TGTCTCTGAAGGTCCATAAAAGAAAAAGAGAAGTGTGGTAAGGGAATGGTCTGTGTGGAGGGGTCAAGGAGT
TAAAAACCCTAGAAAGCAAAAGGTAGGTAATGTGAGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTTC
TGAGGGTGCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCCCTCTCTGGTCTCGTGCT
TGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGAAGCCTGGCA
CCCCTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTTCCCAAGGAGATACTGGGTGGGAAAAAGATG
GGGCAAAGCGGTATGATGCCTGGCAAAGGGCCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCT
CCATGTTTCCTAACAGATTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCAGCACTTTGGGAGGC
CAAGGTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACTCCATCTCTACTAA
AAAAAAAAAAATACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTCATCTACTCGGGAGGCTAAGACA
GGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTGAGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTG
ACAGAGTAAGCGAGACTCCATCTCAAAAATAATAATAATAATAATTGAGACTCCTTATCAGGAGTCCATGATCTG
GCCTGGCACAGTAACTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGA
GGTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTAAAAAT

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPGDRRGDVYR
CPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS
```

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

FIGURE 155

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGAGGCTCCCAGCTGC
 AGCGTCCCCCGCCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCCCTCGGGGACCAAACAAGCCTGGCAGG
 GTCTCACTTTGTTGCCCAGGCTGGAGTTCAGTGCCATGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAA
 GCGATCCTGCTGAGTAGCTGGGACTACAGGACAAAATTAGAAGATCAAAATGGAAAATATGCTGCTTTGGTTGAT
 ATTTTTACCCCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAAGGT
 ACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATGCTAAGATGATGGTAAA
 TACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGCCTTTCTGAATTGGAGGATTATCTTTCCTA
 TGAGACTGTCTTTGAGAATGGCACCCGAACCTTAACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCA
 AAATATCACCAAAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTACGATCTT
 GGACAAAAGGTTCTTAACCAATTTCCCTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCATTCTCAT
 TTCCCCCTCAGCATGTTCTAACTGCTGCCCCTGTGTTTATGATGGAAAGGACTATGTCAAAGGGAGTAAAAAGCT
 AAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAGAAACGTCGAGGTTCTAAGAGGAGCAGGAGAGA
 AGCTAGTGGTGGTGACCAAGAGAGGGTACCAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAGAAAGAAA
 AAAATCTGGCCGGGGTTCAGAGGATTGCCGAAGGGAGGCCTTCCTTTTCAGTGGACCCGGGTCAAGAAATCCACAT
 TCCGAAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGAGCTGAAGCG
 TGCTCACAAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAATGCCTGGTGGAAATGATCCACTT
 CTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTATCGGTTTTCAGTGTGTCCGACGAATCCAATGATCT
 CCTTTACCAATACTGCGATGCTGAGTCGGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAA
 AAAGAATTGGGAAGCGCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGA
 CTACAACGTTGCTGTTCGCATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTTCACGGGAACGATGCCAA
 TTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAATCACAGAGAAAACCAGCTCTGCTTA
 CCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTTGAACCTCTGTCAATAGCATTTCAACATTTTCAAAATCA
 GGAGATTTTCGTCCATTTAAAAAATGTATAGGTGCAGATATTGAAACTAGGTGGGCATTCAATGCCAAGTATAT
 ACTCTTCTTTACATGGTGATGAGTTTCATTGTAGAAAAATTTGTTGCCCTTCTTAAAAATTAGACACACTTTAA
 ACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCTTACTCTAAGAAGAAT
 CTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAAGGTAGATGGTAAAGCAATTAGTATCAGA
 ATAGAGACAGAAAGTTACAACACAGTTTGTACTACTCTGAGATGGATCCATTACAGCTCATGCCCTCAATGTTTAT
 ATTGTGTATCTGTTGGGTCTGGGACATTTAGTTTAGTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGC
 ATTATAAAACAAAACATAAATGTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAATGGGA
 GAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTTTAAGATCTCAAGTTTTTA
 TTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGGAAGACACTTCACAAATTATGAATGATCATGT
 GTTGAAAGCCACATTATTTTATGCTATACATTCTATGTATGAGGTGCTACATTTTTAGGACAAAGAATTCTGTAA
 TCTTTTTCAAGAAAGAGTCTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTG
 ATTAGTAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

FIGURE 156

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVCGIECQKELPTPSL
SELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSRRKRQVYGTDSRFSILDKRFLTTFPFSTAVKL
STGCSGILISPQHVLTAHCVHDGKDYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQE
RAKGRRRRKSGRGQRIAEGRPSFQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIK
KMPGGMIHFSGFDNDRADQLVYRFCSVDESNDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKI IAVYSGHQW
VDVHGVQKDYNAVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 157

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAGGAGCATGTCCGCG
 CCGGGGAAGGCCCGTCTCCGGCCGCCATAAGGCTCCGGTCGCCGCTGGGCCCGCGCCGCGCTCCTGCCCGCCCC
 GGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCGCTCGCCCCGAGGCCCGGCCCGCAGC**ATGG**AGCCACCC
 GGACGCCGGCGGGGCCGCGCGCAGCCGCCGCTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGA
 GGCGGCGGGCGGGCGCGCGCGCGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGGCTGGCAGG
 GCGGCGGGCGGCCCGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACTCGCGCAGGTCTGCCCCAGATACTCTG
 CCCAACCGCACGGTCACCCTGATTCTGAGTAACAATAAGATATCCGAGCTGAAGAATGGCTCATTTTCTGGGTTA
 AGTCTCCTTGAAAGATTGGACCTCCGAAACAATCTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCA
 TCTCTAAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCGAATGCAGACATATTTGAGGACTCACCAAT
 CTGGTTTCGGCTAAACCTTTTCGGGGAATTTGTTTTCTTCATTATCTCAAGGAACTTTGATTATCTTGCCTCATTA
 CGGTCTTTGGAATTCAGACTGAGTATCTTTTGTGTGACTGTAACTACTGTGGATGCATCGCTGGGTAAAGGAG
 AAGAACATCACGGTACGGGATACAGGTGTGTTTTATCCTAAGTCACTGCAGGCCCAACAGTCACAGGCGTGAAG
 CAGGAGCTGTTGACATGCGACCCCTCCGCTTGAATTGCCGCTCTTTCTACATGACTCCATCTCATCGCCAAGTTGTG
 TTTGAAGGAGACAGCCTTCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAG
 GATGGGAGAATAGTTGAAACCGATGAATCGCAAGGTATTTTGTGAAAAGAACATGATTCACAACTGCTCCTTG
 ATTGCAAGTGCCTTAACCATTTCTAATATTCAGGCTGGATCTACTGGAAATTGGGGCTGTCTGTCCAGACCAA
 CGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAGAGAGTTCTGCACAGTACTGTCTCCAGAGAGGGTG
 GTAAACAACAAAGGTGACTTCAGATGGCCCAGAACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAAC
 ACCCATGGCAGTGGGATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGSC
 TTTTGGGCAGATGATGATTATTCTCGCTGTCAGTATGCAATGATGTCACTAGAGTTCTTTATATGTTTAAATCAG
 ATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGCTTACACTGTGGGAGCAGCCAACTTT
 TCTGACAAAATGGATGTTATATTTGTGGCAGAAATGATTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCA
 AAAGAGCTAGGTGACGTGATGGTTGACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCG
 CAGAGGGAAGCTAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTGGG
 GCTCACGTTTATTCAACATATTCACCAATATTGCTCTGGAAGCTTATGTCAAGTCTACTGGCTTCACGGGG
 ATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGGACTTTCGGATTATGGGAGGCGGGATCCA
 GAGGGAACCTGGATAAGCAGCTGAGCTTTAAGTGCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTA
 TGTTACATTTCTGCAATCATTTAAGACTATTTACAGTT**AAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAA
 CCTATTAAAGATTTTTTTTTTGCAGGAAGATAGGTATTATGCTTTTGTACTGTTTTAAAGAAAACTAACCAG
 GAAGAACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTCCTTTGATTCCCTTTCTTCACATAAAAAATATCA
 GAAATTACATTTTATAACTGCAGTGGTATAAATGCAATATACTATTGTTACATGTGAAAAAATTTTATTGACT
 TAAAAGTTTATTATTGTTTTTTTTTGCCTGATTTTAAAGACAATAAGATGTTTTTCATGGGCCCTTAAAGTATC
 ATGAGCCTTTGGCACTGCGCCTGCCAAGCCTAGTGGAGAAGTCAACCCTGAGACCAGGTGTTTAAATCAAGCAAGC
 TGTATATCAAAATTTTTTGGCAGAAAAACAAATATGTCATATATCTTTTTTTAAAAAAGTATTTTATTGAAGCA
 AGCAAAATGAAAGCATTTTTTACTGATTTTAAATTTGGTGTCTTTAGATATATTTGACTACACTGTATTGAAGCAA
 ATAGAGGAGGCACAACTCCAGCACCCCTAATGGAACACATTTTTTTCACTTAGCTTTCTGTGGGCATGTGTAATT
 GTATTCTCTGCGGTTTTTAAATCTCACAGTACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTC
 AGTCATTTTAAATGGCTGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAA
 TATTGAATGAATGAACGAAAAAAAAAAAAAAAAA

FIGURE 158

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGKVVCSSLELAQVLP
PDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGAFWGLSSSLKRLDLTNNRIGCLNADIFR
GLTNLVRLNLSGNLFSSLSQGTFDYLASLSLEFQTEYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPV
TGVKQELLTCDPPELELPSFYMTPSHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIH
NCSLIASALTISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGD FRWPRTL AGITAYLQ
CTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLNTNAVATARQLLAYTVE
AANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLADERVLWLAQREAKACSRIVQCLQRIATYR
LAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCTVFQKVAASDR TGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSL
ALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437,
453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105,
123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

FIGURE 159

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTT
 CTCTGCCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGAAAGTATTTATTGACCAAATTAACAGG
 TCTTTGGAGAATTACGAACCATGTTCAAGTCAAACTGCAGCTGCTACCATGGTGTGCATAGAAGAGGATCTAACT
 CCTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATC
 ACTAAGAACAGACTGTACCGGAAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATTTTG
 GAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGTACATGTACGAGATTATCCTCAGGTTCTAAATGGATG
 GAGCCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATGTATCCTGCTTGGACATTT
 TGGGAAGGGGACCTGCTGTTTGGCCAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTG
 GTAAGGTCAGCAGCACAGTGGCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCA
 GAACGAGATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAACAGGCC
 TGGAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAG
 TATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCTGTGTGGCTCACTTGTTTTT
 CATGTTGGTGATGAGTGGCTAGAATTCTTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACA
 GATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGG
 GGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCCTCTTGAGTGAATAC
 TCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTATTCCCAAAATGTTGAAAACCTGAA
 CTATAGTAGTCATCATAGGACCATAGTCCTCTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAAGCTTACC
 ATAAGCTTGGCTCCTATACCTTGAATATCTGCTATCAAGCCAAATACCTGGTTTTCTTTATCATGCTGCACCCAG
 AGCAACTCTTGAGAAAGATTTAAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGG
 ACCAGAAATCGTGAGATGTGGATTTTGAACCCAACCTACCTTTTCAATTTCTTAAGACCAATCACAGCTTGTGCC
 TCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCATGTGATGATGCCCTTTGTCCCATT
 TTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAACCTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATC
 TCTGTCACTTTATTTTAAATGTAGGAAACCTATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTC
 TAAGGAAGCGGTAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAAACCATAACTCTGTTACTCAGGA
 GGTTCCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATTTCAGGTTCCCTTTTT
 GTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 160

MEWWASSPLRLWLLLFLPSAQGRQKESGSKWKVFIDQINRSLENYEPSSQNCSCYHGVIEEDLTPFRGGISRK
MMAEVVRRKLGTHYQITKNRLYREND CMFPSRCSGVEHFILEVIGRLPDMEMVINVRDYPQVPKWMEPAIPVFSF
SKTSEYHDIMYPAWTFWEGGPAVWPIYPTGLGRWDLFREDLVRSAQWPWKKKNSTAYFRGSRTSPERDPLILLS
RKNPKLVDAEYTKNQAWKSMKDTLGKPAAKDVHLVDHCKYKYLENFRGVAA SFRFKHLFLCGSLVFHVGDEWLEF
FYPQLKPWWHYIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSYNVT
RRKGYDQIIPKMLKTEL

FIGURE 161

CCGAGCACAGGAGATTGCCTGCGTTT TAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAA
 CCATGTCTTTTTTCTGTTTTTCAGAGTAGTT CACAACAGATCTGAGTGTTTTAATTAAGCATGGAATACAGAAAA
 CAACAAAAAAGCTTAAGCTTTAATTT CATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTT
 GGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGTCTCCGACTACTCACCCTGAGTGTAAGAACCCTTCGGGCTCG
 CGTGCTTCTGAGCTGCTGTGGATGGCTCGGCTCTCTGGACTGTCCCTCCGAGTAGGATGTCACTGAGATCCCTC
 AAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTG
 ATAGAACGCGTGAACTGGATGTACTTCTATGAGTATGAGCCGATTTACAGACAAGACTTTCACTTCACACTTCGA
 GAGCATTCAAACTGCTCTCATCAAAATCCATTTCTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCC
 AGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTA
 GGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATA
 ATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGCATTTCAGGTGGGTAACTGAG
 TTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTAT
 CTTTAAACCTAAACCACTCAGAGAAGTTTTTACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTT
 TACCAAAAAACCCATATTTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTAT
 ATAATGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTACGTAACCCATCAAGTTTGAAGATGTT
 TATGTCCGGGATCTGTTTGAATTTATTAAGTGAACATTTCATATCCAGAAGACACAAATCTTTCTTTCTATAT
 AGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACT
 TTTTGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACTTCACATTCTACAAAAGCCTAGAAGGACAGG
 ATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAAGTGTGCTGGCTTACACT
 GAACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGGCCCTTCAAA
 GATGATATGTGGAGGAATTAATATAAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGGACCAAACAAATTTG
 GACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAA
 AACAAATGTAGAGTTTTATTTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAAT
 TTAATAATATATGTAGTTCTGTGTCAAAAAAAGTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTTTG
 GTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTACTTCAACTTTGTGTT
 TTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAATCATTCTTTACATGCAAACATTTTCCAGT
 TACTTAACTGATCAGTTTATTATTGATACATCACTCCATTAATGTAAAGTCATAGGTCATTATTGCATATCAGTA
 ATCTCTTGGACTTTGTAAATATTTTACTGTGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAAA

FIGURE 162

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQDFHFTLREHSNCSH
QNPFLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEAEKEDKMLALSLEDEHLLYGDIIRQDFLD
TYNNLTCLKTIMAFRWVTEFCPNAKYVMKTDTDVFINTGNLVKYLNLNLHSEKFFTGYPLIDNYSYRGFYQKTHIS
YQEYPFKVFPYCSGLGYIMSRDLVPRIYEMMGHVKPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVC
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

FIGURE 163

CATTTCTGAACTAATCGTGTGAGAAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATATTAACTTTTAGG
AGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCGCTCATATATAGGAAAATCGCATATGG
TCCTAGTATTAAATTCCTTATTGCTTACTGATTTTTTTTGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTG
AATATAAATAAGAGAAGAAAAAGAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTT
TGTTTTACATGCAAGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTCGAACCAATGTGTTTG
TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTTCAGATTCGGTTGCCAA
CTCGTCCCCATTGGTTTCTTTTTTGGTACTACAGAAGAGGAAATCCAGGAAATCTGCATAGAAACACTTAGGC
TTTATACCAGAAAAAGCCAACTATGAATTACTGGAAGAAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAG
CCAAATTAAAAGCAAAGGGATTGAATCCGGATGGAATCCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCT
CCAAGCCATCATCACCAGAGAAGTAAAAGCTGAAGAGAAATCACCATCTCCATTAATGTGAAGACAGTCAAAA
AAGAACC TGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAAAGACAGCAAGAGAAGTAGAA
ATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACGTTCTAGATCACATACTCCAAGAAGACACTATA
ATAATAGGCGGAGTCGATCTGGAACATACAGCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTC
GAAGACATCATAATCATGGTTCTCCTCACCTTAAGGCCAAGCATAACCAGAGATGATTTAAAAAGTTCAAACAGAC
ATGGTCATAAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAGCCAAGAAAC
ACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTTGAGAGGTCCCATAAAAGCAAGC
ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACTTTCTCTTCCCTTGAGCCTGCATCAGTTCT
TGGTTTTGCCTATCTACAGTGTGATGTATGGACTCAATCAAAAACATTAAACGCAAAGTATTAGGATTTGATTT
CTTGAAACCCTCTAGGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTGCACAT
TAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGTTGTGTATTGTTT
ATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTATACAGATAAAATGCAGACACTGT
TCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAATACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATT
TTTACAAGGAAATAAAATACAAATCTTGTTTTTCTAAAAAAGAAAAAAGT

FIGURE 164

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLFLFGTTEEEIQEICIETLRRLYTRKKPNYELLEKE
VEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEKSPISINVKTVKKEPEDRQQASKSPYN
GVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYNNRRSRSGTYSSRSRSRSHSESRRHHNHGSPHLKAKH
TRDDLKSNRHGHKRKKSRSRSQSKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHRR

FIGURE 165

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTA
 ATCTGAAGGTTCTCAGTCAAATTCCTTTGTGATCTACTGATTGTGGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTT
 GGCTGGTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGGAGAATGCAGCACACTGCTCGGAGAAATGAAGGCGC
 TTCTGTTGCTGGTCTTGCCCTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACCTTCTGTATT
 CAGAACTCTGTAAAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAG
 ACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCTTAATGACAG
 ACGAGCCTGGCCTAGACAACCTGCCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACT
 CTGGCCGGAGCAACCGAAGTGGGACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA
 ATCGAGCTTTGAGTGTCTTCGAAGGACAAAGAGCGGGAGTGCAAGTTGCCAACCATGCCGACAGGGCAGGGAAA
 ATTCTGAAAACACCCTGCCCCGAAGTCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCA
 TCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCC
 ATATCATTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTC
 TAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGG
 TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCAGCAGGAACAATGGACAGGCCCCGGATGCCTACAGAC
 CCGGAGATGACAGCTTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAATAAAACTGGTGCGCA
 AGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG
 AGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAGTGCAGGCTCATCTGATTC
 AGGCCAGTGAAAGACGTGTTACCTCGTCGTCTCCGCCAGGTTCCGGCAGCGGAGCCCTGACATCTTTCAGGAAG
 CCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACTCCCAAGCCCCCTCCATCCTA
 CAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCGGCATGACCGTCGAGGGG
 GAGCATCACATAGAGAATGGGATTTGCCTATCTATGTGATCAGTGTGAGCCCGGAGGAGTCATAAGCAGAGATG
 GAAGAATAAAACAGGTGACATTTTGTGTAATGTGGATGGGGTCGAACTGACAGAGGTGAGCCGGAGTGAGGCAG
 TGGCATTATTGAAAAGAACATCATCCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGCCCCAGGAAG
 ACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCTGGGTCA
 TGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG
 GCTTCTGCATTGTAGGAGGTTATGAAGAATAACAATGGAAACAAACCTTTTTTTCATCAATCCATTGTTGAAGGAA
 CACCAGCATAACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAA
 TGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAATATTGTTTCTTGGCCTG
 GCACTTTTTTATAGAATCAATGATGGGTGAGGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACT
 ATATTTATCTTGTGCTGATTTTATATTTAAAGAAAGAAATACATTGTAAAAATGTGAGGAAAGTATGATCATCTAA
 TGAAAGCCAGTTACACCTCAGAAAAATATGATTCAAAAAAATTAATACTACTAGTTTTTTTTCAGTGTGGAGGAT
 TTCTCATTACTCTACAACATTTGTTTATATTTTTTCTATTCAATAAAAAGCCCTAAAACAACATAAATGATTGATT
 TGTATACCCCACTGAATTCAAGCTGATTTAAATTTAAAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTAT
 GGCCATTTTTTAATTTACAGCTAAAATATTTTTTAAATGCATTGCTGAGAAACGTTGCTTTCATCAACAAGAAT
 AAATATTTTTTCAGAAGTTAAA

FIGURE 166

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPDGCASLTATAPSPEVSAAATIS
LMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQ
GRESENTTAPFVFPRLYHLIPDGEITSIKINRVDPSSELSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLPG
DIILKVNGMDISNVPHNYAVRLLRQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIK
LVRKVDEPGVFI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVSRQVRQRSPDI
FQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPIYVISVEPGGVI
SRDGRIKTGDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSP
SWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPFFIKSIVEGTPAYNDGRIRC GDILLAVNGRS
TSGMIHACLARLLKELKGRITLTIVSWPGTFL

FIGURE 167

GGGAAAGCCATTTTCGAAAACCCATCTATACAAACTATATATTTTCATTTCTGCTGCTAGCTGCCTTGGGCCTCAC
AATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAGTTGATCCCAACCATAACATCGTGGAG
GGTTTTAAATTTTGGTGGTAGCCCTCACCCAATTCTGGTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAAATCA
TGAACCTCTGGCTGTTGATCAAAAGAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCT
AGCAGAAGACTCAACCTGGCCTCCCATAAACAGGACAGATTATTCAAGGTGATGGCAAAATGGATTCTACATCAA
CGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACTCAAATTGGGAGGCCAACCCACAGAACAGCATTT
CTGGGCCAGGCTGTAATCAGAATTGTCGTGTCGTACATGCTCAACAGCATTGCTTTTTTCCCCAAAATTAACACATT
GTGGAGAAGTGATGATACTCTCCCTTACCTTTCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATT
AAACCTTGCAGCAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAAATGCATTT
CCTGTATCATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 168

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLAEDSTWPPINRTDY
SGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

FIGURE 169

[illegible]

FIGURE 170

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGYYTIPCCRNEENE
CDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGDCMRCGQVLRAPKGQILLESYPLNAHC
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKN
FDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDFGGPVNGYQKITGGPGLI
NGRHAKIGTVVSFFCNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMPQVQSRETPLHQLY
SAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIE
NITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLG
KFYRDDRDEKTIQSLQISAILHPNYDPILLDADIAILKLLDKARISTRVQPICLAASRDLSTSFAQESHITVAG
WNVLADVRSPGFKNDTLRSGVSVVDSLLCEEQHEDHGI PVSVDNMFCASWEPTAPSDICTAETGGIAAVSFPG
RASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 171

CTGTCGTCTTTGCTTCAGCCGCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCCAAGTGTGGCTTA
 ATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCTCTGCTAAGACCGCTGCCATGCCAGTGACGGTAACCCG
 CACCACCATCACAACCACCACGACGTATCTTCGGGCGCTGGGGTCCCCATGATCGTGGGGTCCCCCTGGGGCCCT
 GACACAGCCCCCTGGGTCTCCTTCGCCTGCTGCAGCTGGTGTCTACCTGCGTGCGCCTTCTCGCTGGTGGCTAGCGT
 GGGCGCCTGGACGGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGGCTTCTGCTTCTCCGTGACCCGTATCAT
 CCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCCATCACCTTCGCCTG
 CTATGCGGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCACCTATGTCCAGTTCCCTGTCCACGGCCG
 TTCGCGGGACCAACGCCATCGCCGCCACCTTCTTCTCCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTG
 GACCCGGGGCCCGCCGGCGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTT
 CGTTGCCTGCATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGTGCCT
 GCGCGTGTACGCCATCTGCTTCATCCTAGCGGCCATCGCCATCCTGCTGAACCTGGGGGAGTGCACCAACGTGCT
 ACCATCCCCCTTCCCCAGCTTCCGTGTCGGGGCTGGCCTTGCTGTCTGTCTCTCTATGCCACCGCCCTTGTTCT
 CTGGCCCCCTTACCAGTTCGATGAGAAGTATGGCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGCAG
 CCATGCCTACTACGTGTGTGCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTA
 TGTGGCTGACCTGGTGCCTCTGCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCCCGTTCCC
 TCTCCAACCTCTTTGTTCTTCTTGCCCCGAGTTTTCTTTATGGAGTACTTCTTCTCCTCCGCTTTCCTCTGTTTTC
 CTCTTCTGTCTCCCCCTCCCTCCACCTTTTTCTTCTTCCCAATTCTTGCCTCTAACCAGTTCTTGGATGC
 ATCTTCTTCTTCCCTTCCCTCTTGCTGTTTCTTCTGCTGTGTTTTGTTGTTGCCACATCCTGTTTTACCCCTG
 AGCTGTTTTCTTTTTCTTTTTCTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTG
 GAGTGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTCCTGGGTTCAAGCGATTCTCCTCCCCCAGCCTCC
 CAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTTTCCACTCTTCTTTTTTCTCATC
 TCTTTTCTGGGTGCTGCTCGGCTTCTTATCTGCCTGTTTTGCAAGCACCTTCTCCTGTGCTTGGGAGCCCT
 GAGACTTCTTCTCTCTTGCCTCCACCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTGCAGCCGTCC
 ATGCCACAGCCCCCAAGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCTCCCACTGGAGGAA
 GGTGTGCAGTGTACTTCCCCTTTAAATTAAAAACATATATATATATATTTGGAGGTCAATAATTCCAATGG
 GCGGGAGGCATTAAGCACCGACCTGGGTCCCTAGGCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAG
 AATTTTTGCCAGGCTTACAGAACCCCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCAT
 CCAACTATTCTCTGTGGTATGAAAAAG

FIGURE 172

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727

<subunit 1 of 1, 322 aa, 1 stop

<MW: 35274, pI: 8.57, NX(S/T): 1

MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTGSMGNWSMFTWCFC
FSVTLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTYVQFLSHGRSRDHAIATFFSCIACVA
YATEVAWTRARPGEITGYMATVPGLLKVLETFVACIIFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNL
GECTNVLPPIPFPSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILT
AINLLAYVADLVHSAHLVFVKV

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 173

[illegible]

FIGURE 174

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLCSLAWSFTRLLHPPL
SPGISQVVVDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSYSDLSEGEQEARFAAGVAEQFAIAEAK
LRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLGPHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSS
LCSLEDGLLGSPARLASQLLGDELLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPL
CPPLTGSWERQRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,
324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 175

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTGGCACCCCTCCTGC
TCAGTGCGACATTGTCACTTAACCCATCTGTTTTCTCTAATGCACGACAGATTCCTTTCAGACAGGACAACCTG
TGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAGCCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTT
CTTCATCTGCAAAATGGGCATAATACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACC
AATACCAAAGAAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCACGTTGTTTTATTCACTTCTATC
GGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTTTTAAACAATGGAAAA
TAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAAACTCAGATAAAGAAAATATAACCACCTCAAATCTCAAGGC
GAGTCATTCCCCCTCCTTTGAATCTACCCAACAACAGCCACGGAATAACAGATTCTCCAGTAACCTCATCAGCAGA
GCATTCTTTGGGCAGTCTAAACCCACATCTACCATTTCACACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAA
AGTGCCTTGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACCTGCTCT
GTCTTCAGAAAACCTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATAACAGTTCATTACAGTTAG
CATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTGATAGTGGAACCAAGTGGATGGCTTACCACAAA
CAGTGATAGCTTCACTGGGTTTACCCCTTATCAAGAAAAACAACCTCTACAGCCTACCTTAAATTCACCAATAA
TTCAAACTCTTTCCAAATACGTCAAGTCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTT
AGGTGCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGTACTTGTGTGTGGAAAAAGGAAAACGGATTTCATT
TTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCGCGATTAGACAATGCACCGGAACCTTATGATGT
GAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAATGATTTCAGCCATGCCAGAAAGTGAAGAAAATGCACG
TGATGGCATTCCTATGGATGACATACCTCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACA
GCAAGTGTCATCTACATCCTAGCCTTTTGACAAATTCATCTTTCAAAAGGTTACACAAAATTACTGTCACGTGGA
TTTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCATCAAAGGTTTTCT
TTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATTTGTATTTTAGTAGTATTTTCTTAGT
AGAAAAATATTTGTGGAATCAGATAAACTAAAAGATTTCAACATTACAGCCCTGCCTCATACTAAATAATAAAA
ATTATTCACCAAAAAATTCTAAAACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATT
CAAGATTGCATTTTCTTAAATGAAAATTGAAAGGGTGCTTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAGGA
CATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT
TTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGACAATGACTGCATTCAACGGGGCCATGGC
AGGAAAGCTGACCCTACCCAGGAAAGTAATAGCTTCTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGTC
TTAATATATCTTAGGCTTCAATTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNI AEVFKTMENKPISLESEANLNSDKENITTSNLKASHSPPL
NLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNAPIADEDLLPISAHPNATPALSSENFT
WSLVNDTVKTPDNSSITVSI LSSEPTSPSVTPLIVEPSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLFNP
TSDPQKENRNTGIVFGAILGAILGVSLTLVGYLLCGKRKTD SFSHRRLYDDRNEPVLRLDNAPEPYDV SFGNSS
YYNPTLND SAMP ESEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,
225-229, 298-302, 307-311

FIGURE 177

ACCAGGCATTGTATCTTCAGTTGTTCATCAAGTTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTTCTTGCCT
GCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGCTTCAACCTGACTTTCCACCTTTCTTA
CAAATTCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGG
TGCCATTCAAGAGATTCTTAAAGCAAAGGAGTTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGGAAA
AACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCCTTCTGTGTCTCCTTACCTCAGAGG
CCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGG
CCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATCCTCGTTCCCCACCGGAACAGAGAGAAACA
CCTGATGTACCTGCTGGAACATCTGCATCCCTTCCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCA
CCAGGCTGAAGGTAAAAAGTTTAATCGAGCCAAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAAA
TTGGGACTGCTTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAGCA
TCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGGGGGTGTTAC
TGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACACTACTGGGGATGGGGAGGCGAAGACGA
TGACCTCAGACTCAGGGTTGAGCTCCAAAGAATGAAAATTTCCCGCCCCCTGCCTGAAGTGGGTAAATATACAAT
GGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGT
CTGGAGAACAGATGGGTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATATATCAACAT
CACAGTGGATTTCTGGTTTGGTGCA~~TGA~~CCCTGGATCTTTTGGTGATGTTTGAAGAAGTGAATCTTTGTTTGCA
ATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTT
TCCTTTTTGTATTTTCTTAGCAGAGCTCCTGCTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAG
TCATTTTGATCATGAGGCTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGA
TAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGATAAAA
GGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAAAGGTACGAAGA
TACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAA
GAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGTTGAGTGTCCGC
TGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCCAGGTATGCCTTC
CAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAATGATTTTGTACAAGTAGG
ATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAAATATGTCTATCAAATACCTCTGTAGTAAAAT
GTGAAAAGCAAAA

FIGURE 178

MGFNLT FHLSYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTNEASTKKVELD
NCPSVSPYLRGQSKLIFKPDLTLEEVAENPKVSRGRYPQECKALQRVAILVPHRNREKHLMYLLEHLHPFLQR
QQLDYGIYVIHQAEKKFNRAKLLNVGYLEALKEENWDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYR
LRYSGYFGGVTALSREQFFKVNGFSNNYWGWGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAE
RMKLLHQVSRVWRTDGLSSCSYKLVSVEHNPLYINITVDFWFGA

Important features:

Signal peptide:

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

FIGURE 179

CGTGGGCGGGGTCGCGCAGCGGGCTGTGGGCGGCCCCGGAGGAGCGACCGCCGAGTTCTCGAGCTCCAGCTGC
ATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCCGCAATGGCCCCAGGCAGTGTGGTCGCGCCTCGG
CCGCATCCTCTGGCTTGCCTGCCTCCTGCCCTGGGCCCCGGCAGGGGTGGCCGCAGGCCTGTATGAACTCAATCT
CACCACCGATAGCCCTGCCACCACGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAG
CCTGGCCCTGCCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGTCTACTGGCAAGAT
GGAGAAGGCTCTCAGCTCCACCATCCGTGTGGTTCGGCCACGTGCCCGGGGAATTCCTGGTCTCTGTCTGGGTAC
TGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTGGTCTCCCCATCACAGAGTTCTCGTGGG
GGACCTTGTGTACCCAGAACACTTCCCTACCTGGCCAGCTCCTATCTCACTAAGACCGTCTCGAAAGTCTC
CTTCTCTCTCCACGACCCGAGCAACTTCTCAAGACCGCTTGTCTCTACAGCTGGGACTTCGGGGACGGGAC
CCAGATGGTGACTGAAGACTCCGTGGTCTATTATACTATTCCATCATCGGGACCTTACCCTGAAGCTCAAAGT
GGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGACCGGGGACTTCTCCGCCTC
GCTGAAGCTGCAGGAAACCTTTCGAGGCATCCAAGTGTGGGGCCACCTAATTCAGACCTTCCAAAAGATGAC
CGTGACCTTGAACCTTCTGGGGAGCCCTCCTCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCTCCCGCTGGA
GGAAGGGGAGTGCCACCCTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCTTGGGGA
CTACTGCTTCAGCATCCGGGCGGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGTGTGGCCCTC
CAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGATGTTGGCCTTCATCATGTACAT
GACCTTGCAGAAATGCCACTCAGCAAAAGGACATGGTGGAGAACCCGGAGCCACCTCTGGGGTCAGGTGCTGCTG
CCAGATGTGCTGTGGGCTTTCTTGCTGGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACCACGGGCT
GCTCCCGCCCTCTATAAGTCTGTCAAAACTTACACCGTGTGAGCACTCCCCCTCCCCACCCCATCTCAGTGTTA
ACTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGTTTCATTTCGCTGGGGCTG
TTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCCCTCCCTCTCTGTACCCCTGACCC
CAGCCATTACCCATCTGTACAGTCCAGCCACTGACATAAGCCCCACTCGGTTACCACCCCTTGACCCCTACC
TTTGAAGAGGCTTCGTGCAGGACTTTGATGCTTGGGGTGTTCGGTGTGACTCCTAGGTGGGCTGGCTGCCAC
TGCCCATTCCTCTCATATTGGCACATCTGCTGTCCATTGGGGTTCCTCAGTTTCCTCCCCCAGACAGCCCTACCT
GTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGTTGTACACATAGATGGGCACA
CTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACACACAGAAATATAAACACATG
CGTCACATGGGCATTTAGATGATCAGCTCTGTATCTGGTTAAGTCGGTTGCTGGGATGCACCCTGCACTAGAGC
TGAAAGGAAATTTGACCTCCAAGCAGCCCTGACAGGTTCTGGGCCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCA
GTTCTTGCGCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACTAATAC
TGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTGAAACTTTCACTGAGGAAA
AGGCCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGG
AGGCCGAGGCGGGTGGATCACGAGATCAGGAGATCGAGACCACCTGGCTAACACGGTGAAACCCCGTCTCTACT
AAAAAATACAAAAGTTAGCCGGGCTGGTGGTGGTGGCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGA
GAATGGTGCAGAACCCGGGAGGCGGAGCTTGCACTGAGCCAGATGGCGCCACTGCCTCAGCCTGAGTGACAGA
GCGAGACTCTGTCTCCA

FIGURE 180

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLALPADAHLRFRHWI
HTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVVTAADCWMCQPVARGFVVLPITEFLVGDLVVTQNTSLPWSS
YLTKTVLKVSFLLHDPSNFLKTALFLYSWDFGDTQMVTEDSVVYYNYSIIIGTFTVKLVVAEWEEVEPDATRAV
KQKTGDFSASLKLQETLRGIQVLGPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYN
LTHTFRDPGDYCFsIRAENIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQKDMVENP
EPPSGVRCCCMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 181

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGCTGGGCCCTCGGGCCTGACAGATGGCAGTGGC
CACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCGGCCCGCCGGTTCGTGGGGCCAGGGT
CCAGCGGCTGCGCAGAGGCGGGACCCGGGCCTCATGCACGGAAGACTGTGCTGATCACCGGGCGAACAGCGG
CCTGGGCGCGCCACGGCCCGGAGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCG
CGCCGAGGAGGCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGTCAG
CGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCGCCTTCTGCCAGGAAAT
GCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGGATCTTCCAGTGCCCTTACATGAAGACTGA
AGATGGGTTTGAGATGCAGTTCGGAGTGAACCATCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGAATCCT
CAAAAGTTTCACTCCCAGCAGGATTGTGGTAGTTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGA
CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTTGTTATAGCCGAGCAAACCTGGCTAACATTCTTTTTACCAG
GGAAGTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTGTCATCCTGGTATTGTACGGACAAATCT
GGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTCAATTTGGTGTGTCATGGGCTTTTTTCAAACTCC
AGTAGAAGGTGCCCAGACTTCCATTTATTTGGCCTCTTCACTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGG
GGATTGTAAAGAGGAAGAAGTGTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGA
AGTGATGGTTGGCCTGCTAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAGTTATATCTG
TGATCAGGAATGGTGTGGATTGAGAAGTTGTTACTTGAAGAAAAAGAATTTTGATATTGGAATAGCCTGCTAAGA
GGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAAGCAAGATGTTTAAAT
ATATATAGTAAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAATTTATAACTGGGCAAGCA
TGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGT
TTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAATTATCTGCCTGGTGTGTGCA
CACAAGTCTTACTTGAATAAATTTACTGGTAC

FIGURE 182

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCR
DRARAEAAAGQLRRELQAAECGPEPGVSGVGELIVRELDLASLRSVRAFCQEMLQEEPRLDVLINNAGIFQCPY
MKTEDGFEMQFGVNLGHFLLTNLLGLLKSSAPSRIVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANI
LFTRELARRLEGTVNVTNVLHHPGIVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSG
RYFGDCKEEELLPKAMDESVARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 183

AACAGGATCTCCTCTTGCACTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGCAGCCCGAAGATTCT
ACTATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGGAGGCGCGGCAAGACGTGGAGGCCCTC
CTGAGCCGACGGTCAGAACTCAGATACTGACCGGCAAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCC
TCTGGGAGATGTATGCTTACTCTCTTAGGCCTTTCAATCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATT
TACAAGTACTTTCATGCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCAAAT
TCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGAGGATGACAACATTGCA
ATCATTGATGTGCCGTGTCCTCAGTTTCTCTGATAGTGACCTGCAGCAATTATTCATGACTTTGAAAAGGGAATG
ACTGCTTACCTGGACTTGTGCTGGGGAACCTGCTATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAA
AATCTGGTAGAGCTCTTTGGCAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTA
GTTGCTGTGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGAAAGTCC
TTCCGCCCTTCGTGCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAAATGCTGGAAGATTAGACAC
TTCCCAACGAATTTATGTTGAGACCAAGATCTGTCAAGAGTAAGAGGCAACAGATAGAGTGTCTTGGTAATA
AGAAGTCAGAGATTTACAATATGACTTTAACATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTAC
TCTATTGCTTATGCTTTAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGG
TAATTGGCATTGCTTGT'TTTTGAAGTGAATTTACATGAGTTTCAATTTTCTTTGCATTTATAGGGTTTAGAT
TTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCCGTTGTTTTTTTTTGTGTTTGT
TTTTTCTTTTCTTTTAAAGTAAGCTCTTTATTCATCTTATGGTGGAGCAATTTTAAATTTGAAATATTTAAAT
GTTTTGAAGTTTTTGTGTAATAATATATCAGATCTCAACATTGTTGGTTTCTTTTGT'TTTTCAATTTGTACAAC
TTCTTGAATTTAGAAATTACATCTTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAT
TTTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTTCTCACTACTATCTGTATTGTGGAATGCACAAAAT
TGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATCTACAACCCTATAATAAATTTTACTCTATAC
AAAAAAAAAAAAAAAAAAAA

FIGURE 184

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVVRTQILTGKELRVATQEKESSSGRCLTLLGLSFILAGLIVGGACIY
KYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDNIAIIDVPVPSFSDSDPAIIHDFEKGMT
AYLDLLLGNCYLMPLNTSIVMPPKNLVELFGKLASGRYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSF
RLRRRDLLLGFNKRAIDKCWKIRHFPNEFIVETKICQE
```

Type II transmembrane domain:
amino acids 53-75

N-glycosylation site.
amino acids 166-170

Casein kinase II phosphorylation site.
amino acids 35-39, 132-136, 134-138

N-myristoylation site.
amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 63-74

FIGURE 185

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGGCCGCTTGCCT
CCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCAACAGACGGGACAACTTGCAGAGCT
GCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCA
CTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCT
ACCTGCCCTGCCCCCGTCCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGG
CTGGTTCTTTTGTTCCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 186

MALSSQIWAACLLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPICIFCCGCCHR
SKCGMCCKT

FIGURE 187

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCAC
CATGTTCCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCCTCTTCACCCT
CCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGGAGTCTCCTTTGGTATCCGCAAACCTACATGAAAAGTCT
GTTAAAAATCTTTGCGTGGGCTACCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCC
CTACACCAACGGAATCATTGCAAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGTCGAAGTGGTAG
TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGAAAGGAATGGAGAC
CATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCCTGGAACCTGCTGAGCAGAACCAA
TTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCTGTGGGGGTAGGAGTGTGATTCTCGGTACTGCTTTCT
GCTGCCGCTCAGGATAGCACTGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTT
GCCAAATGGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGCAGCGCT
GACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCTGTGTGGCCAATCATACCTC
ACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGGGGGACTCATGGG
TGTGATTGAGAGGCCATGCTGAAGGCTGCCACACGTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCT
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAAGCAAGCTGCCTATCCTCATCTTCCAGAAAGGAACCTG
CATCAATAATACGATCGGTGATGATGTTCAAAAAGGGAAGTTTGAAATTGGAGCCACAGTTTACCCTGTTGCTAT
CAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAAATACGGGATGGTGACGTACCTGCTGCGAAT
GATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCTCCCATGACTAGAGAGGCAGATGAAGATGCTGT
CCAGTTTGCGAATAGGGTGAAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCT
GAAGAGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAACA
CAAGGACAGGAGCCGCTCCT**TGAG**CCCTGCCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAACGGGCTCAGAGC
TGGAGTTGCCGCCGCCGCCCTTCTGCTGTGCTTTCAGACTCCAGGGCTCCCCGGGCTGCTCTGGATCCCAG
GACTCCGGCTTTTCGCCGAGCCGAGCGGGATCCCTGTGCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGAT
GCTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAAG
TGAACCTCCACCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGATGG
CGGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGCGGCCACCCGCTCTCCAGGAAAGGC
ACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGCCTTGAGCTCTGCAGACATGATAGGAAG
GAACTGTCTCTGCAGGGGCTTTCAGCAAAATGAAGGGTAGATTTTATGCTGCTGCTGATGGGGTTACTAAA
GGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTGTAATCCAGGCTAACCTG
AACTCCCATGTGATGCGCGCTTTGTTGAATGTGTGTCTCGGTTTCCCATCTGTAATATGAGTCGGGGGAATG
GTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGTGCGGGTGAGTGAAGGACACATCACGTTTCA
TGTTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAGCTCAGAGCTGCTGCACTGGGCTTTGGATTTG
TTCTTGTGAGTAAATAAACTGGCTGGTGAATGA

FIGURE 188

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIIVPAIFGVSGIRKLYMKSLKIFAWATLRMERGAKEKNHQLYKP
YTNGIIAKDPTSLEEEIKEIRRSKGSSKALDNTPEFELSDIFYFCRKGMETIMDDEVTKRFSAAEELESWNLLSRTN
YNFQYISLRLTVLWGLGVLIRYCFLPLRLIALAFTGISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRAL
TAIITYHDRENRPNGGICVANHTSPIDVIIILASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHL
VAKRLTEHVQDKSKLPILIFPEGTCINNTSMMMFKKGSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMVTYLLRM
MTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTFKEEQKLYSKMIVGNH
KDRSR

FIGURE 189

GCCCCTCGAAAACAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCACGTCTCCTCCAGG
GATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCACACCTGGCAGGCCAGGCTGTTCCAC
CATCCTGCCCCCTGGGCTGGCTCCAGACACCTTTGACGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAA
GGCAGCCCCCTGCTAAAGGAGGAAATGGCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGAC
CTGGGAGGACAAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGTCTA
CACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAGGCTCCCGGGAGCTCTA
CATGAGGCACTTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGGGCCCTGCAGCTGCTGCGAGGCAGTGGGGG
CTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGAGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGA
CTCTGTCCGCTTGGGCCAGTTTGCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCG
GGGCTGTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTGGAAGAC
TCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCCTGAAAGTCCAACATCTGCCACTTAGGAGC
CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAACATGGTTCCGGAC
CCAGCCCTAGCAGCCTTCTCCCAACCAGGATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTA
TGTGATGGGGACTTCCTGGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGA
GACATGGAGTTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGGA

FIGURE 190

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHHALLRESWEAAQET
WEDKRRGLTLPPGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSRELYMRHFPPKALHFYLIRALQLLRGSGG
CSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPPWKT
LLLAPGEFQLSGVGP

FIGURE 191

GTGGCTTCATTTAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCCCTCATCTATAT
CCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCCGTTCCGTTGGTGGGGCCGTGAC
TTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCAT
ACAGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTA
CTCCCTGAAGCTCAGCAAACTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCA
GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCA
GAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATAC
CTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGA
AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAA
GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCTCCTGCT
CAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAA
GAGAGTGGACATTTGTGCGGAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCC
TCACACTAATAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAATCCCCACTCACTGCTCACGATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGC
AGTGCACTCCCCTAAGTCTCTGCTCA

FIGURE 192

MAGSPTCLTLIYILWQLTGSAASGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIIVTON
RNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLT
CCMEHGEEDEVITYWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVS RNFS SPILARKLCEGAADDPDSS
MVLLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENT EYDTIPHTNRTILKEDPA
NTVYSTVEIPKKMENPHSLLTMPDTPRLFAYENVI

FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852

><subunit 1 of 1, 283 aa, 1 stop

><MW: 29191, pI: 4.52, NX(S/T): 0

MVSAAPSLILLILLILLGSPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTPALSPTSMGPQPTTLG
GPSPTNFDLGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKASAYYPSSFPKKKYVDQSDRAGGPRAF
SEVPDRAPDSRP EEALDSSRQLQADILAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVP
VETPEAQEEPCSGVLEGA VAGEGQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,
242-248

FIGURE 195

GAAAGACGTGGTCCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCTGCTGCTGTTTGGGA
CTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACTTTAATGTAGAAAAGATTAATGGG
GAATGGCATACTATTATCCTGGCCTCTGACAAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTG
GAGCAAATCCATGTCTTGGAGAATTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTA
TCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACTATA
CCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGAAACCTTCCAGCTGATG
GGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAAGGTTTGCACAACCTATGTGAGGAGCATGGA
ATCCTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAATGAAGAATGGCCTGA
GCCTCCAGTGTTGAGTGGACACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCCAGTA
TAAATTCTGTGATCTGCATTCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACCTAGGAT
ACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTTTTGATACACCCTTGACAATTTTTTCATGAAATTATTCTT
CTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

FIGURE 196

MKMLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQIHVLENSLVLKVH
TVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE
RFAQLCEEHGILRENIIDLSNANRCLQARE

FIGURE 197

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGATTTCAGCCTG
CTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAGTTGAGGAAGACCAATTT
TCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCA
ACAACAATGTCTTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTC
AGTGTGATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTCATG
TGTAATTTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTTCATCCAGAATCC
TTCAACTTGCACTGGTTTTTCAATGACTCTTGTCACCTCCTACTGGTTTTCAATAAACCCACCAGTAACGACACC
ATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCA
GTATTTTTTAGGTCTATTGCTTGTGGAATTCTGGAGGTCCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT
GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTATCAGTA
GTTTGAAAAAAAAAAAA

FIGURE 198

MTCCEGWTSCNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR
ACCNRTGMFLSSFFSVITVIGALYCMLISIQALLKGPLMCNSPSNSNANCEFSLKNISDIHPESFNLQWFFNDS
CAPPTGFNKPTSNDTMASGWRASSFHFDFSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR
SQIV

FIGURE 199

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG
AGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCC
CGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGACATGGAGAGAGTGACCCTGGCCCTTCTCCT
ACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAA
AAACCTGCAGCTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAA
ATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACATCACTCCAGGCTC
TGCCACTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACCTCCTC
CCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTTCTGATCAGGAGGC
TTCTTTATGAATTAACTCGCCCCACCACCCCTCA

FIGURE 200

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCKYKSSQKQHSPVPE
KAIP LITPGSATT C

FIGURE 201

[illegible]

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212

><subunit 1 of 1, 440 aa, 1 stop

><MW: 42208, pI: 6.36, NX(S/T): 1

MKFQGPLACLLALLCLGSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGAAGSKVSEALGQGT
REAVGTGVRQVPFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHGADAVRGSWQGVPGHSGAWETSGGHGI
FGSQGGLGGQGGNPGGLGTPWVHGYPGNSAGSFGMNPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQ
NEGCTNPPPSGSGSGSSNSGGGSGSQSGSSGSGSNGDNNNGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGSSSGS
RGDSGSESSWGSSTGSSSGNHGGSGGNGHKPGCEKPGNEARGSGESGIQGFRRQGVSSNMREISKEGNRLLGGS
GDNYRGQSSWGSGGDAVGGVNTVNSETPGMFNFDTFWKNFKSKLGFINWDAINKDQRSSRIP

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96,
96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169,
178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245,
240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276,
271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297,
292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,
323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389,
387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 203

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGAATGTCGCTGCTGAGCCTGCCCTGGCTGGGCCTCA
GACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCTACTCGCCCGCATCCTGGCTT
GGACCTATGCCTTCTATAACAAGTCCCGCCGGCTCCAGTGTTTCCCACAGCCCCAAAACGGAAGTGGTTTTGGG
GTCACCTGGGCCTGATCACTCCTACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGCGCCACCTATTCCCAGG
GCTTTACGGTATGGCTGGGTCCCATCATCCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATACCA
ATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCCCTGAAGCCCTGGCTGGGAGAAGGGATAC
TGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCCTTCATTTCACATCCTGAAGT
CCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCA
GTCGTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACA
GCCATTGTCAGGAGAGGCCCAGTGAATATATTGCCACCATCTTGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCC
AGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCC
TGGTGCATGACTTCACAGACGCTGTCATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTT
TCAAAGACAAAGCCAAGTCCAAGACTTTGGATTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTCAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGAGAGCCATGACACCACGGCCAGTGGCC
TCTCCTGGGTCCCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGCAAGAGCTTC
TGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCCCTTCTGACCATGTGCGTGAAGG
AGAGCCTGAGGTTACATCCCCCAGCTCCCTTCATCTCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCC
GAGTCATCCCCAAAGGCATTACCTGCCTCATCGATATTATAGGGTCCATCACAACCCAACCTGTGTGGCCGGATC
CTGAGGTCTACGACCCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTCTTCT
CCGCAGGGCCCAGGAACTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCCTGGCGTTGATGCTGC
TGCACTTCCGGTTCTGCCAGACCACACTGAGCCCCGCAGGAAGCTGGAATTGATCATGCGCGCCGAGGGCGGGC
TTTGGCTGCGGGTGGAGCCCCTGAATGTAGGCTTGCAGTGACTTTCTGACCCATCCACCTGTTTTTTTGCAGATT
GTCATGAATAAAACGGTGCTGTCAA

FIGURE 204

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPPKRNWFWGHLGLITPTEGLK
DSTQMSATYSQGFTVWLGPIIPFIVLCHPDITRSITNASAAIAPKDNLFIRFLKPWLGEGILLSGGDKWSRHRM
LTPAFHFNIKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHISLMTLDSLQKCI FSFDSHCQERPSEYIATI
LELSALVEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFD TAVIRERRRTLPTQGI DDFFKDKAKSKTLD FID
VLLLSKDEDGKALSDEDIRAEADTFMFGGHD TTASGLSWVLYNLARHPEYQERC RQEVQELLKDRDPKEIEWDDL
AQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENS
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLNVGLQ

FIGURE 205

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTGAAGACTCTCTGCT
 TTTGCCACAGCAGTTCCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCCTGCCCCCAGGGCCACCTGCAGGACGC
 CGACACCTACCCCTCAGCAGACGCCGAGAGAAATGAGTAGCAACAAAGAGCAGCGGTGAGCAGTGTTCGTGATC
 CTCTTTGCCCTCATCACCATCCTCATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTG
 CGGGGCGTAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGCAAC
 AAGACACTGCCCCCTCGGTGCCACCAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCTGGGCACCAAGCTGGGC
 CCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCACCCACCCTGGCTACTCAGCTGATGTGGGC
 AACAAAGACCACCTACCGCGTCGTGGGCCATTCCAGTGTGTTCCGCGTGCTGAGGAGGCCCCAGGAGTTGTCAAC
 CGGACCCCTGAAACCGTGTTCATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGT
 GTGATCCAGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGGCCGATGCGGCAATTT
 GACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTTGAGCACAGGCTGGTTTACC
 ATGGTGATCGCGGTGGAGTTGTGTGACCACGTGCATGTCTATGGCATGGTCCCCCCCCAACTACTGCAGCCAGCGG
 CCCCCCTCCAGCGCATGCCCTACCACTACTACGAGCCCAAGGGCCGGACGAATGTGTACCTACATCCAGAAT
 GAGCACAGTCGCAAGGGCAACCACCACCGCTTCATCACCGAGAAAAGGGTCTTCTCATCGTGGGCCAGCTGTAT
 GGCATCACCTTCTCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAGAGGAGAAGC
 AGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTGCTGGAGTGTCTCCAGCCAATC
 AGGGCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCCTGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGT
 CTATGTGGTTAATCAGGGGTGTCTTTCTTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATT
 TCTGAGTCAATCTGAGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTTCAAGCCCCCAGGAATGGACCCCC
 AATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAACTTGGTGTGGCCCCCTCAATTT
 CCAGCACAGAAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCCCGGCCAGAGAATTTGTGGGGTGTGG
 AGGTTGTGGGGGCGGTGGGGAGGTCCCAGAGGTGGGAGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTG
 GACAAACCCCTCCCCCTCTCTGGGCACCCCTCTGCCACACCAAGTTTCCAGTGCGGAGTCTGAGACCCCTTCCAC
 CTCCCCACAAAGTGCCCTCGGGTCTGTCTCCCCGTCTGGACCTCCAGCCACTATCCCTTGCTGGAAGGCTCA
 GCTCTTTGGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTAGGGTATTTTTCGCAAACTCCTTCAGG
 GTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCTTAGCCCTCAGCCAGCTGCCATTAGCTT
 GGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCTCTAGCAGGGAGGTTTTCCAACCTGTTGGAGGCGCCTTTGGGG
 CTGCCCTTTGTCTGGAGTCACTGGGGGCTTCCGAGGTCTCCCTCGACCCTCTGTCGTCTGGGATGGCTGTCTG
 GGAGCTGTATCACCTGGGTTCTGTCCCTGGCTCTGTATCAGGCACTTTATTAAAGCTGGGCCTCAGTGGGGTGT
 GTTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGAGGCTGGAGGGACCAGATG
 GAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGGGGCGGTGACTGCCCCAGACTTGGTTTGTGTA
 ATGATTTGTACAGGAATAAACACACCTACGCTCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 206

MSSNKEQRSVAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPILGNKTLPSRCHQCV
IVSSSSHLLGTKLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRVLRRPQEFVNRTPETVFIFWG
PPSKMQKPKQGSLVRVVIQRAGLVFPNMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHV
HVGGMVPPNYCSQRRLQRMPIHYEYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 207

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCAC
CGCC**AT**GGCAGGCATCAAAGCTTTGATTAGTTTGTCTTTTGGAGGAGCAATCGGACTGATGTTTTTGATGCTTGG
ATGTGCCCTTCCAATATACAACAAATACTGGCCCCCTCTTTGTTCTATTTTTTACATCCTTTCACCTATTCATA
CTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAAGTTGCCATCTTTCTTAC
AACGGGCATTGTTCGTGTACGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGAGCTTG
TGCACTTGTTCTCACAGGAAACACAGTCATCTTTGCAACTATACTAGGCTTTTTCTTGGTCTTTGGAAGCAATGA
CGACTTCAGCTGGCAGCAGTGGT**G**AAAAGAAATTACTGAACTATTGTCAAATGGACTTCCTGTCATTTGTTGGCC
ATTACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTAGGTGCTCC
CTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGCTGAAGGATTTAAAGGATTTTCTCTTTTGGAA
AAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTGTGGTGTCTCTGCTGAATTTAAATATTTATGTGTTT
TTCCTGTTAGGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCATTTGCATTGGT
TAGGAATTCAGAAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAAGTATTTTAGCCTCCATTA
TTACAAAAAATTATAAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATGCAGACATACAGAC
GGTTGGCATACTGTTATAGACTGTATACTCAGTGCAATATAGCTGCATTTATACCTCAGAGGGGCCAAGTGTTAA
TGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTGAAAATTATTTTATGG
AATTGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAATTTATGTTAAACTTTAAGGTAAGGGTGTA
ACATTTTGTAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGTGGGAAGAAATGACATTG
AAATTCAGTTTTTGAATCCTGTTTCTATTTATAAGTGAAATTTGTGATCTCCTATCAACCTTTCATGTTTTACC
CTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTTGCATCATATATGCCAGAAAAC
CTTCTCTGCTTCTCTCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAAAAATTTTCAAATATAGTTT
AATAACACTTAGAAGTGTTTACTTACCTGGAAAATAATTGCTATGCCGTACATTCAGAGTGCCCCCTCCCCTGCA
AGGCCTTGCCATGATTAAACAAGTAACTTGTTAGTCTTACAGATAAATTCATGCATTAAACAGTTTAAGATTTAGACC
ATGGTAATAGTAGTTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAGTATTTTAAAGACAAAGTTTCTGT
ATACCTCTGAAGTGTTTGATTTTGAAGTTTCATCATGATAGATCTGCTGTTTCTTATAAAAGGCATTTGTTGTGT
GAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACATACCTGACCAAAAAATTCAGTAAC
CAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTATCAGGACTTTTTCAGGAGTGGGTTATAAAAA
CATTCAGTTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTTGTATGTTTATTCAGTATACTTACATAAAAAAT
ATTTGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGTTTATGAAGTTTATTTCTCAAGAAAATG
GGAATAAATTTGGGATTTGTTTCAGCTTTTTTACTAAAGATGCCTAAAGCCACAGGTTTTATTGCCTAACTTAAGC
CATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGGCGTGTGGCTGGAGCCTTCCCCTGGAGGC
TGAAAGTGGCTTGTGGTATTATAATGTTTCAGATTTCAAGAGGAAGGTGCAGGTACACATGAGTTAGAGAGCTGGT
GAGACAGTTGGGAACCTTTGTGCTTGTGATCTACTGGACTTTTTTTTTTGCAGGAAGTGCATTCTCTGGTCTTCT
CCTATTTTCTGTTCTGGATGTCAGTGCACTGCTACTGTTTTTATCCACTTGGCCACAGACTTTTTCTAACA
GCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATTGTGTCTTTGACCTTGTATACTAGCTTGACATAGT
GCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAATTTTCCATAGAATATGCACTGATACAACATTACCAT
TCTTCTATGGAAGAAAACCTTTTGATGATGAAACAATAAAGATTTTAAATATCTATTTTAAAAA

FIGURE 208

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSNACKELAIFLT
T
GIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSNDDFSWQQW

FIGURE 209

CTTGCAGAGAAAGAGTCTTTTGTGCAGCACCCCTTTAAAGGGTGACTCGTCCCCTTGTGTTCTCTCTCCTGGTGC
AGAGTTGCAAGCAAGTTTATCAGAGTATCGCCATGAAGTTCGTCCCCTGCCTCCTGCTGGTGACCTTGTCTTGCC
TGGGGACTTTGGGTGAGGCCCCGAGGCAAAAGCAAGGAAGCACTGGGGAGGAATTCCATTTCCAGACTGGAGGGA
GAGATTCTGCACTATGCGTCCCAGCAGCTTGGGGCAAGGTGCTGGAGAAGTCTGGCTTCGCGTCGACTGCCGCA
ACACAGACCAGACCTACTGGTGTGAGTACAGGGGGCAGCCCAGCATGTGCCAGGCTTTTGTGCTGACCCCAAAC
CTTACTGGAATCAAGCCCTGCAGGAGCTGAGGCGCCTTCACCATGCGTGCCAGGGGGCCCCGGTGCTTAGGCCAT
CCGTGTGCAGGGAGGCTGGACCCCAGGCCCATATGCAGCAGGTGACTTCCAGCCTCAAGGGCAGCCCAGAGCCCA
ACCAGCAGCCTGAGGCTGGGACGCCATCTCTGAGGCCCAAGGCCACAGTGAAACTCACAGAAGCAACACAGCTGG
GAAAGGACTCGATGGAAGAGCTGGGAAAAGCCAAACCCACACCCGACCCACAGCCAAACCTACCCAGCCTGGAC
CCAGGCCCCGAGGGAATGAGGAAGCAAAGAAGAAGGCCTGGGAACATTGTTGGAAACCCCTCCAGGCCCTGTGCG
CCTTTCTCATCAGCTTCTTCCGAGGGTGAAGGTGAAAGACCCCTACAGATCTGACCTCTCCCTGACAGACAACC
ATCTCTTTTTATATTATGCGCTTTCAATCCAACGTTCTCACACTGGAAGAAGAGAGTTTCTAATCAGATGCAAC
GGCCCAAATTCTTGATCTGCAGCTTCTCTGAAGTTTGGAAAAGAAACCTTCTTTCTGGAGTTTGAGAGTTTCAG
CAATATGATAGGGAACAGGTGCTGATGGGCCCCAAGAGTGACAAGCATAACAACCTACTTATTATCTGTAGAAGTT
TTGCTTTGTTGATCTGAGCCTTCTATGAAAGTTTAAATATGTAACGCATTTCATGAATTTCCAGTGTTCAGTAAAT
AGCAGCTATGTGTGTGCAAAATAAAAGAATGATTTTCAGAAAAA

FIGURE 210

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602
<subunit 1 of 1, 223 aa, 1 stop
<MW: 24581, pI: 9.28, NX(S/T): 0
MKFVPCLLLVTLSCGLTLGQAPRQKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLR
VDCRNTDQTYWCEYRGQPSMCQAFADPKPYWNQALQELRRLHHACQGAPVLRPSVCREA
GPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKATVKLTEATQLGKDSMEELGKAKPTTR
PTAKPTQPGPRPGGNEEAKKKAWEHCKWKPQALCAFLISFFRG

Important features:

Signal peptide:

Amino acids: 1-19

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

DNA photolyases class 1 proteins:

Amino acids: 58-69

Tyrosine kinase phosphorylation site:

Amino acids: 64-71

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids: 4-15

FIGURE 211

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGCGCACTGACCCAGGCG
GTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAACTGGAGCCAGAACCGGACCCCGTGCGCC
GGCGGCGCCGTTGAGTTCCCGGCGGACAAGATGGTGTCTGCTGCAAGAAGGTACGCGCTCTCAGACATG
CTCCTGCGCTGGATGGGGAACCTCGTCCTGGCTTCAGGAGCCGGATTGGGCGTCTCAGACGTGGGCTCGCACCTG
GACTGTGGCGCGGGCGAACCCTGCCGTCTTCGCGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGTGGCGCT
CTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGCCACGACGACGTCTTCTTTC
CGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAGCCCCGTGCGTGTCCGCAGCATCTCGGCTCTGG
GCCGACGTTTACGCGCGACGAGGACCTGGCTGTTTTCTGCGTCCCGCGCGGGCCGCCTACGCTTCCACGGGC
CGGGCGCGCTGAGCGTGGGCCCGAGGACTGCGCGGACCCGTGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGC
CGTGGATCTGCGCGGCCCTGCTCCAGCCCCCT

FIGURE 212

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59603
<subunit 1 of 1, 197 aa, 1 stop
<MW: 20832, pI: 8.74, NX(S/T): 2
MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLV
QEGHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDRTCGAL
GTRHLASSSWTPSACPAATTTSSFRLVPPSAWGSALALAPCVSAASRLWAGRSRATRTWL
FSWRPARAAYASTGRAR
```

Important features:

Signal peptide:

Amino acids 1-19

N-glycosylation site:

Amino acids 35-39

Glycosaminoglycan attachment site:

Amino acids 81-85

N-myristoylation sites:

Amino acids 82-88;118-124;153-159

C-type lectin domain proteins:

Amino acids 108-118

FIGURE 213

[illegible]

FIGURE 214

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFARDAVKKCFVCLA

FIGURE 215

GGATTTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAAGTGCAGGGAGGCCAGGACAGGCCCACCC
TGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGCAGAGAGGCCAAGCCCCCTGCCTTGGG
TCACACAGCCAAAGGAGGCAGAGCCAGAACTCACAACCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACG
AAAAGGCAGTCACCCGCAGGGCCAAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCATTCACGGTCG
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGC
AGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCCCCCTGCCCCCG
CAGCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAAACTGTTTCAGCTCCACAGGTTTCAGGTCATCATCA
TCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGCTTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACA
AGAATAACTATGCTGCCATGGTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCT
TTAAATTATTTGTCTTCCGCTGAGTTCTTTCACCACAAGTTTGAGATCCTGGATGCCCGTCGTGGTGGTGGTCT
CATTCATCCTGGACATTGTCCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGCCTGCTGATTCTGCTCCGGC
TGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTTCAGAACGGCAACTCTTAAGGT
TAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACT
GATGAGTTTGCTGTATCAACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAATCCGACTTCTA
CTCTCACACAGCCACCGTGAAAGTCTTGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAGCAGGCTGGC
ATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA
CAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACCAAATCTATAAAGATATTCTGAAAATATGACAGAA
TTTGACAAATAAAAGCATAAACGTGTAAAAA

FIGURE 216

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEEEEEEEQPPPTPVSGEEGRAAPDVA
PAPGPAPRAPLDFRGMLRKLFSSHRFQVIIICLVVLDALLVLAELILDKIIQPDKNNYAAMVFHYMSITILVFF
MMEIIFKLFVFRLLSFTTSLRSWMPVVVVVSFILDIVLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSE
RQLRLKQMNVLAAKIQHLEFSCSEKPLD

FIGURE 217

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGCTTCCCTGGGG
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAGCAATTGCACTCATCATTTGGCTTTGGT
ATTTTCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC
TGCACTTTTGAACCTGACATCAAACCTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTC
CATGAGTTCAAAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTGAGAGGCCGGACAGCAGTGTGCT
GATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT
TATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG
AATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCACAGTGGTC
TGGGCATCCCAAGTTGACCAGGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAAT
GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAATGAC
ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAAC
TCAAAGGCTTCTCTGTGTGTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATG
CTAAAATAATGTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTTAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAAACAAG
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA
GAAGTTGGGAAAATAATTCAATGTGAACTAGACAAGTGTGTTAAGAGTGATAAGTAAAATGCACGTGGAGACAAGT
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTG
TCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCCCTGGAAAGTCTATCCCAACATATCCA
CATCTTATATTCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG
GGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTC
CCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGGGACACCGATTT
TATAAATAAACTGAGCACCTTCTTTTTAAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

FIGURE 218

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASRLKKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
SMPEVNVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSFELNSENVTMKVVSVLNVNTINNTYSC
MIENDIAKATGDIKVTESI KRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

FIGURE 219

[illegible]

FIGURE 220

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCGSLLYYLTL
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISP EWVRTRPFPILP
FPLQLFCFLVAIRVFPFWTVWRKTEAGVWD

FIGURE 221

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTGGAAGATGACAGCA
ATTATAGCAGGACCCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAAACTTTGCCAGTGGGAAGTACCTAGTGAAA
CGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCTTGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTC
CAGCACCATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGT
GCAGTGTAATTCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAGCTG
TATCAGCTCCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGTTCTGCTCAGCGGAGAA
CTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCTGCTGAAGAACACTTTTCATTTTGTAAGCCA
GTGCTGCCAAGGAAAGGAATGCAGCAACACCAGCGATGCCCTGGACCCTCCCCCTGAAGAACGTGTCCAGCAACGC
AGAGTGCCCTGCTTGTATGAATCTAATGGAACCTTCTGTCTGTTGGGAAGCCCTGGAAATGCTATGAAGAAGAACA
GTGTGTCTTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTCCAACGT
CAGTAACGCCACCTGTCAGTTCCCTGTCTGGTGAAAAACAAGACTCTTGGAGGAGTCATCTTTCGAAAGTTTGAGTG
TGCAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACTTCCCACAACGTGGGCTCCAAAGCTTCCCTCTA
CCTCTTGGCCCTTGCCAGCCTCCTTCTTCGGGGACTGCTGCCCTTGAGGTCTGGGGCTGCACTTTGCCCAGCACC
CCATTTCTGCTTCTCTGAGGTCCAGAGCACCCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAA
CTGCCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTAAAGCACTGG
TTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 222

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSLETPVRLYQNMFCSAENC
EETHITAFTVHVSAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAECPACYESNGTSCRGKPKCYEEEQCV
FLVAELKNDIESKSLVLKGCNSVSNATCQFLSGENKTLGGVIFRKFEKANVNSLTPTSAPTTSNHNVGSKASLYLL
ALASLLLRGLLP

FIGURE 223

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGCTTGCCTCAC
TGGCCACCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCGCGCTGCTGTGGGTCTCTGCTGCTG
AATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTGACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGC
TTTGGGGGCCCCATGACCCGAGCTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTA
GAGGACGAGAATGATGCCATGGCCGACGCGGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCCACG
GTGTCCACCGGCTTTAGCCGGTCCGTCCGCCATTAAACGAGGAGGATGGGTCTTCAGAAGAGGGGGTTGTGATTAAT
GCCGGAAGGATAGCACCCAGCAGAGAGCTTCCCAGTGCAGCTCCCAATACAGCGGGGAGTTCCAGCACGAGGTTT
ATAGCCAATAGTCAGGAGCCTGAAATCAGGCTGACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGAC
CTGCCAGGCTCGCAGGCCACCCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCAACCTCA
CCCACAGCCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCACTGCAAG
TCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTCCGGGCGCCTTCGAGTTGGGGCGCTGAGC
CAGCTCCGCACGGAGCACAAGCCTTGACCTATCAACAATGTCCCTGCAACCGACTTCGGGAAGAGTGCCCCCTG
GACACAAGTCTCTGTACTGACACCAACTGTGCCTCTCAGAGCACCACCAGTACCAGGACCACCACTACCCCTTC
CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCCAGCCCCTGCCAGCCCTGGCTTTTGGAAACGG
GTCAGGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATAGACAGAAAC
CAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCTCTTGCCCTTTCAATCCTAGCAC
CCACTAGATATTTTGTAGTACAGAAAAACAAAACCTGGAAAAACAAA

FIGURE 224

MVPAAGALLWVLLLNLGPRAAGAOGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRIILEDENDAMADAD
RLAGPAAAELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSRELPSATPNTAGSSSTRFIANSQEPEIRL
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWPSPTSPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGK
LHGLSGRLRVGALSQLRTEHKPCTYQQCPNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSL
PPASPCPALAFWKVRVIGLEDIWNSLSSVFTEMQPIDRNQR

FIGURE 225

CCGGGTCGACCCACGCGTCCGGGGAGAAAGGATGGCCGGCCTGGCGGCGCGGTTGGTCCTGCTAGCTGGGGCAG
 CGGCGCTGGCGAGCGGCTCCCAGGGCGACCGTGAGCCGGTGTACCGCGACTGCGTACTGCAGTGCGAAGAGCAGA
 ACTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCAGCCAATCTACATGAGTCTAGCAGGCTGGACCTGTC
 GGGACGACTGTAAGTATGAGTGTATGTGGGTACCGTTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCTCAGT
 TCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCTCAATG
 GCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACACCTGTG
 TGGCCTTCGCCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGACCTCACAG
 AGAAAATGGACTACTTCTGTGCCTCCACTGTCTACCTACACTCAATCTACCTGTGCTGCGTCAGGACCGTGGGGC
 TGCAGCAGCCAGCTGTGGTCAGTGCCTTCCGGGCTCTCTGCTGCTCATGCTGACCGTGACGCTCTCTACCTGA
 GCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTGGTGTGGTGGC
 TGGCCTGGTGCCTGTGGAACAGCGGCGGCTGCCTCACGTGCGCAAGTGCGTGGTGGTGGTCTTGCTGCTGCAGG
 GGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCATGCCATCTGGCACATCA
 GCACATCCCTGTCCACGTCCTCTTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTGAAGGAATCAGAGG
 ACAAGTTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCCGCCTGCTGGCCTC
 CCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGAAGGATGTGGGGCCAG
 AATCATGTGGCCAGCCACCCCTGTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGGAAGGCCTCCAGCATC
 TGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAACTGGGGTGGAACTGAGTGTGTTCTTAGCTCTA
 CCGGGAGGACAGCTGCCTGTTTCTCCCCACAGCCTCCTCCCCACATCCCAGCTGCCCTGGCTGGGTCTCTGAAG
 CCCTCTGTCTACCTGGGAGACCAGGGACCACAGCCTTAGGGATACAGGGGGTCCCTTCTGTACCACCCCCCA
 CCTCCTCCAGGACACCACTAGGTGGTGCTGGATGCTTGTCTTTGGCCAGCCAAGGTTACGCGGATTCTCCCC
 ATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCACCTGACCGTTGCCCTAGCCAGGTTCCCA
 GGAGGCCCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCAAGGATCCTGTGCTGCTGTCTGG
 TTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGATAGGTGACAGGGCCGTGAGCATGGGCC
 TGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTTGTGCGGGAAGAGGTGTGGCTTCAAAG
 TGTGTGTGTGCAGGGGGTGGGTGTGTTAGCGTGGGTTAGGGGAACGTGTGTGCGCGTGTGGTGGGCATGTGAGA
 TGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGATGAGGGAATCCTGTCAACATCAATAAT
 CACTTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGGCGGACAGCCAGGAGCTCTCCATGGCCAGGCTGCCT
 GTGTGCATGTTCCCTGTCTGGTGGCCCTTTGCCCGCCTCCTGCAAACCTCACAGGGTCCCCACACAACAGTGCCC
 TCCAGAAGCAGCCCTCGGAGGCAGAGGAAGGAAAATGGGGATGGCTGGGGCTCTCTCCATCCTCCTTTTCTCCT
 TGCCTTCGCATGGCTGGCCTTCCCTCCAAAACCTCCATTCCTGCTGCCAGCCCTTTGCCATAGCCTGATTT
 TGGGGAGGAGGAAGGGGCGATTTGAGGGGAGAAGGGGAGAAAGCTTATGGCTGGGTCTGGTTTCTTCCCTTCCAG
 AGGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCCACACTATGCCTGTGCCCTGGTAAAGGTGACCC
 CTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGGAATAGAATGGAGGGAGCTCCAGAACTTTCCAT
 CCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTGTCTGTGCCCTGACCCCTTGTCCCTCTTTGAGGGA
 GGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTGGCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTT
 AAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAATTCGAAGCCTCAAAAAAAAAAAAAAAAAA

FIGURE 226

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV
TVGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCRYRTFVPASSPMYHTCVAFAWVSLNAW
FWSTVFHTRDSDLTEKMDYFCASTVILHSIYLCCVRTVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNL
VANVAIGLVNVVWWLAWCLWNQRRLPVVRKCVVVVLLQGLSLLELLDFPPLFWVLDAHAIWHISTIPVHVLFFS
FLEDDSLYLLKESEDKFKLD

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 227

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTTGGGGTTTCGGTTCCCCCCTTCCCCTTCCCCGGGGTC
 TGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTTCGGTTGCCACCCACGCGGACTCCCCAGCTGGCGCGCCCC
 TCCCATTTGCTGTCTGGTCAGGCCCCACCCCCCTTCCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTCG
 GCTGCACTTTTCGTGCGTTTCGGCCCCGCTTTCGGCTTTTCTTGATCACTGTGGCTGGGACCCGCTTCGCGTTA
 TCATCCTGGTCGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCC
 ATGTGACCGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTTGGTGTCTGTCTCTGTCCTTCTAC
 AGGAGGTGTTCCGCTTTGCTACTACAAGCTGCTTAAGAAGGCAGATGAAGGGTTAGCATCGCTGAGTGAGGACG
 GAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCT
 CTGTTATCAATATTTTTGGCTGATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCCATTACTTCC
 TGACTTCAGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATGCCTGTG
 AGAGGAGACGGTACTGGGCTTTGGGCCCTGGTGGTTGGGAGTCACCTACTGACATCGGGACTGACATTCCTGAACC
 CCTGGTATGAGGCCAGCTGCTGCCCCATCTATGCAGTCACTGTTTCCATGGGGCTCTGGGCCCTTCATCACAGCTG
 GAGGGTCCCTCCGAAGTATTCAGCGCAGCCTCTTGTGTAAGGACTGACTACCTGGACTGATCGCCTGACAGATCC
 CACCTGCCTGTCCACTGCCCATGACTGAGCCCAGCCCCAGCCGGGTCCATTGCCACATTTCTGTCTCCTTCT
 CGTCGGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTTTACCAGGAG
 CAGCCTGGGTTGAGCCAGTCAGTGAAGTGGTGGTTTGAATCTGCACTTATCCCCACCACCTGGGGACCCCTTGT
 TGTGTCCAGGACTCCCCCTGTGTGCTGCTCTGCTCTCACCTGCCCAAGACTCACCTCCCTTCCCTCTGCAGG
 CCGACGGCAGGAGGACAGTCGGGTGATGGTGTATTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACCTAGG
 GGGGACCCCTGGGCCTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCA
 GGTGGCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAAGGATAGATGAGC
 TCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTCTCAGGCCTGAGGGGGAACCATTTTTGG
 TGTGATAAATACCTTAACTGCC'TTTTTTCTTTTTTGGAGGTGGGGGAGGGAGGAGGTATATTGGAACCTTCT
 AACCTCCTTGGGCTATATTTCTCTCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCCGTCCCTTTCTCCTTGG
 TCCCAGACCTTGGGGGAAAGGAAGGAAGTGCATGTTTGGGAACCTGGCATTACTGGAACATAATGGTTTAACTCC
 TTAACCACAGCATCCCTCCTCTCCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGCCACTCCAGAGCTGCA
 GTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGGGAGATTTTTTTGTAGTTTAAATTGGGG
 TGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGTATCATTTTCTGCTGAGGGTGGAGTGTCCCATCCTTTTAATC
 AAGGTGATTGTGATTTTGAATAAATAAAGAAATTTGTAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 228

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDRSDARLQYGLLI FG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEDRSPISIRQMAYVSGLSFGTIISGVFSVINILADALGPGVVGIIH
GDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSLCKD

FIGURE 229

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTGGGCTCTGCCCATCGCCTGCTCCTCCCAGGCTCCCGCG
 GCGGACCCCGCGCAACATGCAGCCCACGGGCCGCGAGGGTTCCCGCGCGCTCAGCCGGCGGTATCTGCGGCGTC
 TGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGCCCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAG
 CCTCTCCACGCTGGGCTCCCCAGCCTCTTCACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCTCA
 CTACGCCAGGCACCCCCAAAACCTGGACCTTCGGGGTTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCGTGG
 ACGGCCACAATGACCTGCCCCAGGTCTTGAGACAGCGTTACAAGAAATGTGCTTCAGGATGTTAACCTGCGAAATT
 TCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT
 CATGCCAGTCCCAGGACCAGACTGCCGTGCGCCTCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCT
 CCTACTCTGAACCTCGAGCTTGTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTTGGCG
 TGNAGGGTGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCTACCTGA
 CACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACACCACATGTACACCAACGTCA
 GCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAACCGCTGGGCATGATGATAGATTGTCTCTATG
 CATCGGACACCTTGATAAGAAGGGTCTTGAAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAG
 CTGTGTGTGACAATTTGTTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGA
 CACTGTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTGACCACATCA
 GGGCAGTCATTGGATCTGAGTTCACTCGGGATTGGTGAAATTATGACGGGACTGGCCGGTTCCCTCAGGGGCTGG
 AGGATGTGTCCACATACCCAGTCTTGATAGAGGAGTTGCTGAGTCTGTASCTGGAGCGAGGAAGAGCTTCAAGGTG
 TCCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCG
 TGGAGGCTGAGTTTCCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCCTCAGAATGGACACCAGG
 CTACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCTCCCCATACCTTG
 TTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTCTGCTTGACACAGTCGGTCCCCGCAGA
 GGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCTAGTTTCATTACAAGCATATGCTGAGAATAAACATGTTA
 CACATGGAAAA

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLRQPVTAEETPGAPRALSTLGSPSLFTTPGVPSALTTPGLTTPGTP
KTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQTSLDRLRDGLVGAQFWSASVSCQSQD
QTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSSQKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTC
STPWAESSTKFRHHMYTNVSGLTSGFEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL
LNVPPDILQLLKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDVSTY
PVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYGQLSTSCHSHLVPQNGHQATHLEV
TKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
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Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 231

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGATTGGCAAGCGCTGG
CCACCTCCCCACACCCCTTGCGAACGCTCCCTTAGTGGAGAAAAGGAGTAGCTATTAGCCAATTCGGCAGGGCCC
GCTTTT TAGAAGCTTGATTTCCTTTGAAGATGAAAGACTAGCGGAAGCTCTGCCTCTTTCCCAGTGGGCGAGGG
AACTCGGGGCGATTGGCTGGGAAGTGTATCCACCCAAATGTCACCGATTCTTCTCTATGCAGGAAATGAGCAGAC
CCATCAATAAGAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAAGTGGAGGCAAAGAGG
GTTGCTCAACGCCCCGCCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTGGCGGAGGCGGGGCGAT
GATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCTTTCCCGCCCCCTGAGACCTGCAGCACCA
TCTGTCAATGGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCG
GCGCCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCC
CCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCCAGACTCC
CATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATC
CTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAG
AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAAGTCTTCGACCCAGCAAGATCCAG
CTGCCAGAGGATGAGTGAACAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCT
TGACCTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

FIGURE 232

MAAGLFGLSARRLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEPTTPWQEDPEPEDENLYEKNPDSHG
YDKDPVLDVWNNMRLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE

FIGURE 233

GCGGCGGCTATGCCGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCGCGGCTGGTGCTTGCAGAACCCCCA
CGCGACAGCCTGCGGGAGGAACCTTGTCATCACCCCGCTGCCTTCCGGGGACGTAGCCGCCACATTCCAGTTCCGC
ACGCGCTGGGATTTCGGAGCTTCAGCGGGAGGAGTGTCCATTACAGGCTCTTCCCAAAGCCCTGGGGCAGCTG
ATCTCCAAGTATTCTCTACGGGAGCTGCACCTGTCTTACACAAGGCTTTTGGAGGACCCGATACTGGGGGCA
CCCTTCCTGCAGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAACTCT
TGGAAGGAGCTCAGTAATGTCCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGACTCCACCAACACAGTC
ACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTGACCACTACTTTCTGCGCTATGCTGTGCTG
CCGCGGGAGGTGGTCTGCACCGAAAACCTCACCCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTC
TCTGTGCTGCTGAAGGCAGATCGCTTGTTCCACACCAGCTACCACTCCCAGGCAGTGATATCCGCCCTGTTTGC
AGAAATGCACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTGAGTTGTATTTGATGCCCTTCATCAG
GGGCAGGAAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCTCACGGAGCCCTGCCCCCTGGCTTCA
GAGAGCCGAGTCTATGTGGACATCACCACTACAACCAGGACAACGAGACATTAGAGGTGCACCCACCCCGACC
ACTACATATCAGGACGTATCCTAGGCACTCGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATC
AACAACTCTCGAAACCTCAACATCCAGCTCAAGTGGAAGAGACCCCAAGAGAATGAGGCCCCCAGTGCCCTTC
CTGCATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTACAACACCCAC
CCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCGGCTGTATGTGCACACCCCTCAC
ATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCCACTACCAGCCTGCCAGGACCGGCTGCAACCCAC
CTCCTGGAGATGCTGATTGAGCTGCCGGCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTG
AAGTGAGCCGAGTACAGCCAGATCCTAACCATGGCTTCTATGTGAGCCCATCTGTCTCAGCGCCCTTGTGCCC
AGCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCTCTTCAACAGCCTGTTCCAGTCTCTGATGGC
TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC
AACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGTGCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTC
CACATCGAGGAGCCCCGCACAGGTGGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCC
CCACTCTGATTCTTGCCCTTTCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGGAGGGGAGCCCAAGGGCTGTTTC
TGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTGAGGGCCTACAGCTGTGTTGT
CCAGTACAGGAGCCACGAGCCAAATGTGGCATTGTAATTTGAATTAAGTATGAAATTCATTTCTCCTCACCCTGTAGT
GGCCACCTCTATATTGAGGTGCTCAATAAGCAAAAGTGGTGGTGGCTGCTGTATTGGACAGCACAGAAAAAGAT
TTCCATCACACAGAAAGTCCGGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGT
GTAGTGCATCGAGTTTACTGTTTGTGGAATAAAAAACGGCTGTTTCCGTGGAATAAAAAA

FIGURE 234

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWSELQREGVSHYRLFPAKALGQLISK
YSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDSWKELSNVLSGIFCASLNFIDSTNTVTPT
ASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWKKLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNA
RCTSISWELRQTLSSVFDAFITGQGKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTY
QDVILGTRKTYAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTHPYR
AFPVLLLDTPWPYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANSVTKVSIQFERALLKWT
EYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSDGSNYFVRLYTEPLLVLNLPDPFSMPYNVI
CLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLAKRLANLIRRARGVPPL

FIGURE 235

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAGCACCAGGAGC
 CCCTCCGGGTAGCTACTACCCCTGGACCCCCCAATAGTGGAGGGCAGTATGGTAGTGGGCTACCCCCTGGTGGTGG
 TTATGGGGGTCTGCCCCCTGGAGGGCCCTTATGGACCACCAGCTGGTGGAGGGCCCTATGGACACCCCAATCCTGG
 GATGTTCCCTCTGGAATCCAGGAGGACCATATGGCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCC
 AAGTTCCCTACGGTGCCAGCAGCCTGGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTA
 CTCCTGGTTCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAA
 CTGCAATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCAGGCCG
 CATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGAAGAACCTCTTCAGCAGTATGACCG
 GGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCCAAATGGGCTACAACCTGAGCCCCCA
 GTTCACCCAGCTTCTGGTCTCCCGCTACTGCCCACGCTCTGCCAATCCTGCCATGCAGCTTGACCGCTTCATCCA
 GGTGTGCACCCAGCTGCAGGTGCTGACAGAGGCCCTTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCT
 CAGCTTCGAGGACTTCGTACCATGACAGCTTCTCGGATGCTATTGACCCAACCATCTGTGGAGAGTGGAGTGCAC
 CAGGGACCTTTCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
 ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCTGCATCATAGCCACCAATAGTGAGG
 ACCGGGGCTGAGGCCACACAGATAGGGGCCTGATGGAGGAGAGGATAGAAGTTGAATGTCTGATGGCCATGAGC
 AGTTGAGTGGCACAGCCTGGCACCAGGAGCAGGTCTTGTAAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCACCC
 TGATGCCAGTGGTGAGTGTTCATCGGCCTGTTACCGTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAAC
 GAGCCCATTTTCTCCAAAGTGGAATCTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCT
 GCCACACCCATAAATCCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTG
 GGCATCTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCCTGCCATGCTCTGCTCGGCTTCAGT
 CTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTTAATTTGCATTTTTTTTCATTTGGGGCCAAAAG
 TCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

FIGURE 236

MASYFYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG
TPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSHSGYISMKELKQALVNCNWSS
FNDETCLMMINMFDKTKSGRIDVYGFSALWKFIQQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL
VSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREKDTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:

Signal peptide:

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

FIGURE 237

CAGGATGCAGGGCCGCGTGGCAGGGAGCTGCGCTCCTCTGGGCCTGCTCCTGGTCTGTCTTCATCTCCCAGGCCT
CTTTGCCCGGAGCATCGGTGTTGTGGAGGAGAAAGTTTCCCAAACTTCGGGACCAACTTGCCTCAGCTCGGACA
ACCTTCCTCCACTGGCCCCCTCTAACTCTGAACATCCGCAGCCCGCTCTGGACCCTAGGTCTAATGACTTGGCAAG
GGTTCCTCTGAAGCTCAGCGTGCCTCCATCAGATGGCTTCCCACCTGCAGGAGGTTCTGCAGTGCAGAGGTGGCC
TCCATCGTGGGGGCTGCCTGCCATGGATTCTTGGCCCCCTGAGGATCCTTGGCAGATGATGGCTGCTGCGGCTGA
GGACCGCCTGGGGGAAGCGCTGCCTGAAGAACTCTCTTACCTCTCCAGTGCTGCGGCCCTCGCTCCGGGCAGTGG
CCCTTTGCCTGGGGAGTCTTCTCCCGATGCCACAGGCCTCTCACCTGAGGCTTCACTCCTCCACCAGGACTCGGA
GTCCAGACGACTGCCCCGTTCTAATTCAGTGGGAGCCGGGGGAAAAATCCTTTCCCAACGCCCTCCCTGGTCTCT
CATCCACAGGGTTCTGCCTGATCACCCCTGGGGTACCCTGAATCCCAGTGTCTCCTGGGGAGGTGGAGGCCCTGG
GACTGGTTGGGGAACGAGGCCCATGCCACACCCTGAGGGGAATCTGGGGTATCAATAATCAACCCCAGGTACCAG
CTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGAAATATTAATCGGTATCCAGGAGGCAGCTGGGGGAA
TATTAATCGGTATCCAGGAGGCAGCTGGGGGAATATTCATCTATACCCAGGTATCAATAACCCATTTCTCCTGG
AGTTCTCCGCCCTCCTGGCTCTTCTTGAACATCCAGCTGGCTTCCCTAATCCTCCAAGCCCTAGGTTGCAGTG
GGGC**TAG**AGCACGATAGAGGGAAACCAACATTGGGAGTTAGAGTCCTGCTCCCGCCCCTTGCTGTGTGGGCTCA
ATCCAGGCCCTGTTAACATGTTTCCAGCACTATCCCCAC'TTTCAGTGCCTCCCCTGCTCATCTCCAATAAAATA
AAAGCACTTATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 238

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFQTNLPQLGQPSSTGPSNSEHPQPALDPRSNDLARV
PLKLSVPPSDGFPPAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAEDRLGEALPEELSYLSSAAALAPGSGP
LPGESSPDATGLSPEASLLHQDSESRRRLPRSNSLGAGGKILSQRPPWSLIHRVLPDHPWGTNLNPSVSWGGGGPGT
GWGTRPMPHPGEGIWGINNQPPGTSGWGNINRYPGGSGWGNINRYPGGSGWGNINRYPGGSGWGNIHLYPGINNPFPFPGV
LRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:

Signal peptide:

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-
274, 270-275, 280-285, 281-286, 305-310

FIGURE 239

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCCCGCGCTGTGCGCCG
 CTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCGGAGAGCTCAAGCGCCC
 AGCTCTGCCCCAGGAGCCCAGGCTGCCCGTGAGTCCCATAGTTGCTGCAGGAGTGAGGCCATGAGCTGCGTCCCT
 GGGTGGTGTGATCCCCTTGGGGCTGCTGTTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCT
 CTTAGAGGAGCTGCTCAGCAAATACCAGCACAACGAGTCTCACTCCCGGGTCCGCAGAGCCATCCCCAGGGAGGA
 CAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT
 GGTGAGCGCCGGCTCCGGCCGCAGAGGCTGGCACCGGGGGTGGGGCTGGGGCCACCAGCCTGCTCTGTTCCCCAG
 CCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGGCTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCCGGCTCTG
 TTCTGTTTTGTTTTGTTTTGTTTTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCA
 TGCCCTGAAACCTTAGACTCCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACCTACAGGCATGC
 ACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGTTGCCAGGCTGGTCTTGAA
 CTCCTAGGCTCAAGCAATCCTCCTGCCCTCAGCCTCTCAAAGTGCTAGGATTATAGGCATGAGTCACCCCTGTCTGG
 CTCTGGCTCTGTTCTTAACATTCTGCCAAAACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTC
 ATGTCACTCTTGGTAGCTCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCC
 AGGGCTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCCTGACTTCTCCTTAGCCCCG
 TGTGAGCCTCACTTTCCACTTGGAGAGTCTTCTCCTCGCGTGGTTGCCATGACTGTGAGATAAGTCGAGGCTGTGA
 AGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGGCTTTGCTAACCGGGAAAGGAGCTAACGGTGACAGA
 AGACAGCCAAGGTCAACCCTCCCGGGTGATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGAC
 CCCAAGCTCCAGTGTGGAACCTTCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAG
 GGTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTTTTTAAACAAACC
 CACGTCCAGCCTGGGTAAACATGGTAAAGCCCCGTCTCTACAAAAAATCCAAGTTAGCCGGGCATGGTGGTGCG
 CACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAGGTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGC
 TTGAGCCTGGGAAGTCGAGGCTGCAGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGAC
 CCTGTCTCAAAA

FIGURE 240

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILMLHNKLRGQVQPQAS
NMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGRGGSRLCSVLFVCFETGSHSATDAGVQ
WHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 241

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCC
CTTGTCCTCCTCTTGACCCTCCTTGGCAGCTCACATGGAAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG
GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCAT
CTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATGAAGCCA
TTGAAGCCTGTGTCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAG
CAGGCCCCCACCCTCCTGAGTGGCAATAAAATAAAATTCGGTATGCTG

FIGURE 242

MGSGLEPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSTSVTLHHARSQHHVVCNT

FIGURE 243

GGCAAGTGGAACTGGCTTGGTGGATTTTGCTAGATTTTCTGATTTTAACTCCTGAAAAATATCCCAGAT
AACTGTCCATGAAGCTGGTAACTATCTTCCTGCTGGTGACCATCAGCCTTTGTAGTTACTCTGCTACTGCCTTCCT
CATCAACAAAGTGCCCCCTTCCTGTTGACAAGTTGGCACCTTTACCTCTGGACAACATTCTTCCCTTTATGGATCC
ATTAAAGCTTCTTCTGAAAACTCTGGGCATTTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAAATGA
GCTGGGACCAGAGGCTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCTATCACACTTGGTGTGACATCAAGATAA
AGAGCGGAGGTGGATGGGGATGGAAGATGATGCTCCTATCCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT
CAAATGCCCTAAAAATGTAGTGACCCGTGAAAAGGACAAATAAAGCAATGAATACATTA

FIGURE 244

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59855  
<subunit 1 of 1, 93 aa, 1 stop  
<MW: 10161, pI: 7.39, NX(S/T): 0  
MKLVTIFLLVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLLKTLGISV  
EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV
```

Important features:

Signal peptide:

Amino acids 1-18

FIGURE 245

TGCTAGGCTCTGTCCCAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTCTATGACT
GCAATGTGAGGTGTCCGGCTTTGCTGGCCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGGCTGTGGT
CGGGTGTGTGCTGGTGCCCCCAGCTGAAGCCAACAAGAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACC
TTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCGAGAAGGACTGCAACTGCCTGCACGTGGTGGA
GCCCCATGCCAGTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCAC
CACCACCATCAAGGTCATCATTGTCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCTACATGGCCTTCCTGAT
GCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCACAATGAGGAGGAGAATGAGGATGC
TCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGC
CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGAT
GGGCTGGTGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGGCTACTT
CTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTCCTCCTTCTCCCTAACTTTAGAAATG
TTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTCTTGGGTCTTTGGGGTT
GAAGGGAGGGGGAAGGCAGGCCAGAAGGGAATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTC
TCCTGGCTCCACTCTTGCCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGGAAGATAAAGCTGGGTC
TTCAGGAACTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTGAGCATGTGTTCCCTTCTGCAGTGGTTCTTATC
ACCACCTCCCTCCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC
TGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACCTGGAAGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCA
CTGGGGCATGGAGTGCCCATGCATACTCTGCTGCCGGTCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTC
CTCTCCCCAGTGTCCACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCCAGGCTGAGCGTGGATCTGA
ACACCACAGCCCTGTACTTGGGTGCCTCTTGTCCCTGAACTTCGTTGTACCAGTGCATGGAGAGAAAATTTG
TCCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTTGTTTTATTTCTCTCA

FIGURE 246

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLL
CECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 247

AATTGTATCTGTGTAATGTTAAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTTCAAAAAACAACAGA
CTAGTACTCTAAAGAACTCTTTAAAAACAATTAACTGTTAGGATTGCAGTTATGATTGGATATTATTTAATTCTGT
TTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGCTATTAATATTTACCATTGCAGAAGCTTCATTTCAGTGTTG
AAAAATGAATGCTTAGTGGATCTGTGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAG
TTCCCCCTCCCCCTCCGATTGTTCTAAATAATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTGTAT
GATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTTTTTTCTTGGCACTAAT
CAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTAGTAAAAATAGAAACCTGTGTTTATTCTCAG
GTATTTTAGAAACAACAGCCATCATTTTATTTTATGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGG
GCTATCAAATATTACTTCATTCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCA
TTTTCTCAGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTATCTTCA
GATTACTTGATTCAAATAAACCAATTATGTTTGTAAATTGATATTAATAAAACCAGAATAAAAGTTCATATCTACCC

FIGURE 248

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLPSDCSK

Important features:

Signal peptide:

amino acids 1-29

FIGURE 249

AGCGGGTCTCGCTTGGGTTCCGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTTCATAGGGTCTGGGTCCCCGA
ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGGACCCAAGTGAGGGGCCCCGTGTTGGGGTCCCTCCC
TCCCTTTGCATTCCCAACCCCTCCGGGCTTTGCGTCTTCTGCGGACCCCTCGCCGGGAGATGGCCGCGTTGATG
CGGAGCAAGGATTCTGCTCTGCTGCTCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGCGGCGGGGAGACGCCTGGTCAGGCCGCCAATCGATCTGCG
GGCATGTACCAAGGACTGGCATTCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGTAGCAGT
GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA
AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCAGTT
ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAGGGCATGAAGGA
GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
CCAGTGCTCCATCAGGGGGAAGTCTGTACCAAAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT
TGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
TGTCAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGTATTTAATGCATTATAG
CATGGTGGAAAAATAAGGTTTCAGATGCAGAAGAATGGCTAAAAATAAGAAACGTGATAAGAATATAGATGATCACA
AAAGGGAGAAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
CAACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAATT
ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC
TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTA
GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTAATTTCTTAAAGATTGGCCATAACCTATATTTT
GATAGAATTAGATTGGTAAATACATGTATTTCATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
CACTGGAGTAAGCAAGAAAATTGGGAAAACCTTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG
AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCCTGTGTCGGTACTATCCTCAAATTATTTATTTTATAG
TGCTGAGATCCTCAAATAATCTCAATTTCAAGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
TTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAACCTCTGCAGCATCTG
CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTAAA
ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATCTTTGAAACCACTTTACTACTTTTTTTAACTT
AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAGGTTATCTTATAGTCGTGACTTTAAACTTTTG
TAGACCACAATTCACCTTTTGTATTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
AGATTGAGTTTGAGCCTGTATATCTATTAATAATTTCAACTTCCACATATATTTACTAAGATGATTAAAGACTTA
CATTTTCTGCACAGGTCTGCAAAAACAAAAATTATAAACTAGTCCATCCAAGAACCAGTTTGTATAAACAGGT
TGCTATAAGCTTGTGAATGAAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTATATTTACAAT
TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTATTTTGAAGTAATTTATTTACAGGAAATG
TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC
TTTGTAAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTTCTCTCTAAAAACTGAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 250

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA
YPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCRDMCCPSTRCNGICIPVTESILTPHIPALDGTRHRDR
NHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL
EIFQRCDCAKGLSCKVWKDATYSSKARLHVCQKI

Signal peptide:
amino acids 1-25

FIGURE 251

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAAGTGTTGGGATTAC
 AGGCGTGAGCCACCGCGCCCCGCCAACATCACGTTTTTAAAAATTGATTTCTTCAAATTCATGGCAAATATTTCC
 CTTCCCTTTAACTTCTTATGTCAGAAATGAGGAAGGATAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAAT
 ATTTTCATGTAGTATTTTCTAAGTTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTG
 AAAATACTTGATGTGTTTTTAAAGCCTTGGGCAGAAATCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCTTTT
 AAAGTCATCCGCTCCTTGGCTCAGGATTTGGAGAGCTTGACACCACCAAAAATGGCAAACATCACCAGCTCCCAGAT
 TTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACCCCAAGTACACAGCAGAATAGTACAAGTCA
 CCTTACAACCTACTACTTCTTGGGACCTCAAGCCCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAA
 ATCTCAACCTGAGCCATCCCCAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGT
 TCCTCCTCCTGGTTTGGAGTCTTTTCTTCCCAGGCCAAAATTCGAGAATCAACACCTGGAGACAGTCCCTCCAC
 TGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTTGAAAATATCTCTGTGTCTGTCCACCAGCCACAGCCCAA
 ACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAGATCCCAGCTTCTGCAGTGGAAATGCCTGGTTC
 AGCAGATGTACAGGATTAATGTGCAGTTTGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGG
 ATCAGCTCCAAGCAGTGAAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAA
 TACATCTTTATCAATGACCAGTGCAGTACAGAACTCCACATATACAACCTCCGTCATTACCTCCTGCAGTCTGAC
 AAGCTCATCACTGAATTCGTAGTCCAGTAGCAATGTCTTCTCTTATGACCAGAGTTCTGTGCATAACAGGAT
 CCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCTGAAG
 TCAGCAGACACTAGACAGTAAGTATAGCAGCAAGCTACTCTTGTGTCATGGCTGGTGCCAACCAACAGAGGAAGAG
 GATAGCTCACGTGATGTGGAAAACACCAGTTGGTCAATGGCTCATTTCGT~~TAA~~AAAGCAGCCCTTTTGCTTTTTTG
 TTTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGTGGTGGTCTCATA
 TTCTTCTGCCCTAATCAGACTGCACCACAAGTGACAGCATAAGTATGCATTTTAAAGATGCTTGGGCCAGGCGGG
 GTGGCTGATGCCCATATCCCAGTGCTTTGGGGGGCCAAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACC
 ACCCTGGGCAACATGGTGAAACTCTGTCTCTACTAAAAATACGAAAAACTAGCCGGGTGTGGTGGCGGCGGTGCC
 TGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCCGT
 CTGAAAAGA

FIGURE 252

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQNSTSHPTT
TTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAVTVPPPGLESFPSQAKLRESTPGDSPSTVNK
LLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAP
SSENSNQIPISLYSKSLSEPLNTSLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRI PYQ
SPVSSSESAPGTIMNGHGGGRSQQTLD SKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

Signal peptide:
amino acids 1-24

FIGURE 253

GGGCGCCCGCGTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAACATGGAGCTCTCGCAGATGTGCGAGCTCAT
GGGGCTGTGCGGTGTTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGGCGGTAGCGCGGGGTGGCTGCGCGCGGG
GGAGGAGAGGAGCGGCCCGCCCGCTGCCAAAAAGCAAATGGATTTCCACCTGACAAATCTTCGGGATCCAAGAA
GCAGAAACAATATCAGCGGATTTCGGAAGGAGAAGCCTCAACAACAACCTTACCCACCGCCTCCTGGCTGCAGC
TCTGAAGAGCCACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGCAGA
TGATCGCACCATCCGACTCTGGAGACCAAGGACTTCTTGCAGCGAGAGACCCGACAGTGAAGACCAAGTGGG
GCTGACCAACGCCACCCTGGTGCCTTCAGCCCTGACTGCAGAGCCTTCATCGTCTGGCTGGCCAACGGGGACAC
CCTCCGTGTCTTCAAGATGACCAAGCGGGAGGATGGGGGCTACACCTTACAGCCACCCAGAGGACTTCCCTAA
AAAGCACAAAGGCGCCTGTCTATCGACATTGGCATTGCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACAC
CACTGTCTCTCATCTGGAGCCTGAAGGGTCAAGTGCTGTCTACCATCAACACCAACCAGATGAACAACACACAGCT
TGCTGTATCTCCCTGTGGCAGATTGTAGGCTCGTGTGGCTTCACCCCAGATGTGAAGGTTTGGGAAGTCTGCTT
TGAAAGAAAGGGGAGTTCCAGGAGGTGTGCGAGCCTTCAAGTAAAGGGCCACTCCGCGGCTGTCAGTCTGCTT
TCTTTCTTCCAACGACTCACGGAGGATGGCTTCTGTCTCCAAGGATGGTACATGGAAACTGTGGGACACAGATGT
GGAATACAAGAAGAAGCAGGACCCCTACTTGCTGAAGACAGGCGCCTTTGAAGAGGCGGGCGGGTGC CGCGCCGTG
CCGCTTGGCCCTCTCCCCAACGCCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTTCATCTCTACAATACCCG
CGGGGGCGAGAAGGAGGAGTGCTTTGAGCGGGTCCATGGCGAGTGTATCGCAACTTGTCTCTTTGACATCACTGG
CCGCTTTCTGGCCTCCTGTGGGGACCGGGCGGGTGC GGCTGTTCACAACACTCTTGCCACCGAGCCATCTGTGA
GGAGATGACGGGCCACTGAAGCGGGCTTCAACGAGAGACCCCGCAGAGGCTTCGAGCAGCAGCTGACCCAGGC
CCAAGAGACCTTGAAGAGCTTGGGTGCCCTGAAGAAGTGACTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGA
GGGATCTGGCCTCCTCATGGCACTGCTGCCATCTTCTCTCCAGGTGGAAGCCTTTCAGAAGGAGTCTCCTGGTT
TCTTTACTGGTGGCCCTGCTTCTTCCATTGAACTACTCTTGTCTACTTAGTCTCTCTCTTCTTGCTGGCTGT
GACTCTCCCTGACTAGTGGCCAAGGTGCTTTTCTTCTCCAGGCCAGTGGGTGGAATCTGTCCCCACCTTGGC
ACTGAGGAGAATGGTAGAGAGGAGAGGAGAGAGAGAGAATGTGATTTTTTGGCCTTGTGGCAGCACACTCTCAC
ACCAAGAAGAGTTTGTAAATGTTCCAGAACAACCTAGAGAACACTGAGTACTAAGCAGCAGTTTTCGAAGGATG
GGAGACTGGGATAGCTTCCCATCACAGAAGCTGTGTTCCATCAAAAAGACACTAAGGGATTTCCTTCTGGGCCTCA
GTTCTATTGTGAAGATGGAGAATAATCCTCTCTGTGAAGTCTTGC AAAAGATGATATGAGGCTAAGAGAATATCA
AGTCCCAGGTCTGGAAGAAAAGTAGAAAAGAGTAGTACTATTGTCCAATGTCTATGAAAGTGGTAAAAGTGGGAA
CCAGTGTGCTTTGAAACCAAATTAGAAGACATTCTTGGGAAGGCAAAGTTTTCTGGGACTTGATCATACTTT
TATATGGTTGGGACTTCTCTCTCTGGGAGATGATATCTTGTTTAAAGGAGACCTCTTTTCAGTTCATCAAGTTCAT
CAGATATTTGAGTGCCCACTCTGTGCCCAATAAATATGAGCTGGGATTAAAAAAA

FIGURE 254

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQKQYQIRIRKEKPQQH
NFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQREHRSMRANVELDHATLVRFSPPDCRA
FIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKKHKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTI
NTNQMNNTHAAVSPCGRFVASCFTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD
GTWKLWDTDVEYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVHGEC
IANLSFDITGRFLASCGRDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQLQQQLTQAQETLKSLGALKK

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 255

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCGGGCCAGGTGCCCC
GTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGAAGCCCCCTTCCTCGGCGCTGCCAACCC
GCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTGCTTCTGGCGCTGGGCCTGCCGTTCTTGCTGGCCCGCTGG
GGCCGAGCCTGGGGGCAAATACAGACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACCAGCTCC
AGCTCCGATGGCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCCTGCTC
CTGGCTGTGGGGCTGGCACTGTGGGTGCGGAAGCTTCGGGAGAGAAGCGGCAGACGGAGGGCACCTACCGGCCAGT
AGCGAGGAGCAGTTCCTCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCTGCCTG
CCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCT
GGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCCTGAGGTCAAGAGA
GGATGGGGCTATTCACCTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAAA

FIGURE 256

MANPGLGLLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIVVFSLLAALLAVG
LALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 257

[illegible]

FIGURE 258

MGLFRGFVFLVLCLLHQSNTSFIKLNNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTYLFEATEKRFFFKN
VSILIPENWKENPQYKRPKHENHKKHADVIVAPPTLPGRDEPYTKQFTECGEKGEYIHFTPDLLLGGKKQNEYGPPG
KLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCISAGISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQF
FPDKVQTEKASIMFMQSIDSVEFCNEKTHNQEAPSLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPPVFSL
KISQRIVCLVLDKSGSMGGKDRNLNRMNQAAKHFLLOTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGL
PTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVHFIALGRAADEAVIEMS
KITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNS
LPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSRAANSVPPITVNAKM
NKDVNSFPSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNMGVYSRYFTAYTENGRYS
LKVRAHGGANTARLKLRPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTTLEDFSRTASGGAFVVSQVPSLPLP
DQYPPSQITDLATVHEDKIIILWTAPGDNFDVGKVQRYIIIRISASILDLRDSFDDALQVNTTDLSPKEANSKES
FAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPDKSHNSGVNISTL
VLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,
811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 259

CGCCGGAGGCAGCGGGCGCGTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTTTCAGCACAGTTCAA
 ACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGCACTGCTTGAGAAGCTGCTGGACCGCC
 CGCCCCCTGGCCTGCAGAGGCCCGAGGACCGCTTCTGTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCA
 GTCTACTGCCATGGAACCTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCCAG
 CCACCGGGGAGGACCCCTGAGGGCTCAGACATCCTGAACTACTTTGAGAGCTACCTTGCCGTTGCCCTCCACCGTGC
 CCTCCATGCTGTGCCTGGTGGCCAACTTCCCTGCTTGTCAACAGGGTTGCAGTCCACATCCGTTGCTTGGCCTCAC
 TGACGGTCACTCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAAGGTGGACACTTCCCTCGGACCCGTTGGTT
 TTTTTGCGGTCAACATTGTCTGCATGGTGATCCTCAGCGGTGCCCTCACTGTCTTCAGCAGCAGCATCTACGGCA
 TGACCGGCTCCTTTCTATGAGGAACCTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCG
 TGGCCTCATTTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGGCCACCA
 TCTTCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCCAGGTACTACATGAGGCTG
 TTCTTGCGGCCCATGTGTTTCTGGTGAAGAGGAGCTTCCCCAGGACTCCCTCAGTGCCCCCTTCGGTGGCCTCCA
 GATTCAATTGATTCCACACACCCCCCTCTCCGCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCT
 ACGTCTTCTTCATCACCAGCCTCATCTACCCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT
 CACTGTGGACCACCAAGTTTTTTCATCCCCCTCACTACCTTCTCTGTACAACTTTGCTGACCTATGTGGCCGGC
 AGCTCACCAGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCGCTCCAGGGTTCTGTGCTCTCCGGACCTGCC
 TCATCCCCCTCTTCTGTGCTCTGTAACACCAGCCCCGCGTCCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGT
 ACCCCGCACTCCTCAGCTCCCTGCTGGGGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCCTA
 AGATTGTGCCAGGGAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTGCTTGGGCTTAACACTGG
 GCTCAGCCTGCTCTACCTCCTGGTGACCTCATCTAGAAGGGAGGACACAAGGACATTGGTGCTTCAGAGCCTT
 TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCCTAAAGTTTCACTTGGGGACAGAGAG
 CAGAGCACACTCGGGCTCATCCCTCCCAAGATGCCAGTGAGCCACGTCCATGCCCATTCCTGTCAAGGCAGATA
 TTCCAGTCAATTAACAGAACACTCCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTCACA
 GCTGATGGTTAAACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTTCGCCCTAGAGTTATTACAAA
 GCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCAGCTGACAGCGAGATGCAA
 GCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGAAGTCCCTGGCATGGTCAGTCTTCAGGC
 CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACCTGCCCACTAACAGACTGGAAAACCCAG
 AAAGATGGGCTTCCATGAATGCTTCATTCCAGAGGGACCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCT
 GGCCTGGGTTTTCAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTCTTTCA
 GTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGCGTATTCAAAAA

FIGURE 260

MAVSEDDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYIIFSLGIGSLLPWNFFITAK
EYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPMSMLCLVANFLLVNRVAVHIRVLASLTVILAIFMVIT
ALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSD
VRNSALAFFLTATIFLVLCMGLYLLLSRLEYARYYMRPVLAAHVFSGEEELPQDSLSAPSVASRFIDSHTPPLRP
ILKKTASLGFCVTYVFFITS LIYPAVCTNIESLNKGSGLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVPGPN
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLALLYGPKIVPRELAEATG
VMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,
448-472

FIGURE 261

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACCACACCTGTTTA
AAGAACCCTAAGCACCATTTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATAAAGGAGGGCAGAAAT
GGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTACGTGGCCGGAATCATTCCCTT
GGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGGGTGCTGGCCTTCTCTGTGGAACGTCTCT
GGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTTATGAAGATATTCTTGAGGGAAAAACACCACCAAGCAAGTGA
AACACATAATGTGATTGCATCAGACAAAGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCA
CACACAGCTGCATGCCATATTTGGTGTTCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGG
TAACCTCCCATGTGCATTCTACTGACGATCCAGAAGCAGCAAGGTCCTAGCAATTCAAAATCACCACCACGCTGGG
TCTGGTTGTCCATGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTT
AATTGTGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCTTCTTGATGCATGCTGG
CTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCAATTGGCAGCACCAGTTATGTCCATGGTGACATA
CTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGGCCATGCTTTTCTCTGC
CGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGAATAGGGGCACAGCCACAAGCCCGA
TGCCACGGGAGGGAGAGGCCTCAGCCGCCCTGGAAGTGGCAGCCCTGGTTCTGGGTGCCTCATCCCTCTCATCCT
GTCAGTAGGACACCAGCATTAATGTTCAAGGTCCAGCCTTGGTCCAGGGCCGTTTGGCCATCCAGTGAGAACAGC
CGGCACGTGACAGCTACTCACTTCCTCAGTCTCTTGTCTCACCTTGCGCATCTCTACATGTATTCTTAGAGTCCA
GAGGGGAGGTGAGGTTAAAACTGAGTAATGGAAGGCTTTTAGAGTAGAAAACACATTTACGTTGCAGTTAGCTA
TAGACATCCCATGTGTATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAAATTTCTCTTAACCCTATTCTC
AGGGAAGATGGAATTTAGTTTAAAGGAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAATAC
AGTGTCTGTAATTAAGCTATGTCTCTTCTCTTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTAAACA
TGGTTCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTCATAGCACCCACTCA
CTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAATGATAGCAAGACACATTGAAAGCTC
TCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATTAAACAGCTCCTTTGGCACGTGCCT
CTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATT
TTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAAATACCTGTCTCCACATTCCCTAGAGAGGAGCCAAGTTCTAGT
AGTTTCAGTTCTAGGCTTTCCTTCAAGAACAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAAATTT
TAAGTGATTTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAATGTATGGTTGTCC
TTTTTTTTTGTTTTTTTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGG
TCAGCTTTGGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTCGCT
ATTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCTTTTCTTTGCTTTTCTTCTAACTTTTCCCTC
TAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATTTCTATCAGGACAA
CCACTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATTTCTTTATCCCCCTTCAAAGAAATACCTTTGTG
TCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCCTCATGTGTAAATGACACAATCACTAATCTGGTAAT
TTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATAATTTTTTTTTTCATATTTGCCAAAATTTTTGTAA
ACCCTGTCTTGTCAAATAAGTGTATAATATTGTATTATTAATTTATTTTTTACTTTCTATACCATTTCAAAACACA
TTACACTAAGGGGGAACCAAGACTAGTTTCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGAC
GCATAAGCTAGCATGCCTATGATTTATTTCTTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATAAGCTT
GTGAGCCCTCTGCTGGCCACAGTGAGGAAAGTAGCACAATAGGATACAGTTGTATGTAGTCATTGGCAACAATT
GCATACAATTTTACTACCAAGAGAAGGTATAGTATGGAAGTCCAAATGACTTCCTTGATTGGATGTTAACAGCT
GACTGGTGTGAGACTTGAGGTTTCATCTAGTCTTCAAACATATAGGTTGCCTAGATTCTCTCTGGAACCTGAC
TTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAA

FIGURE 262

MDDFISISLLSLAMLVGCVVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS
ETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQIGNSHVHSTDDPEAARSSNSKITTTL
GLVVHAAADGVALGAAASTSQTSVQLIVFVAIMLHKAPAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMT
YLGLSKSSKEALSEVNATGVAMLFSAFTFLYVATVHVLPVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI
LSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 264

MMVRRGLLAWISRVVVLVLCCATISVLYMLACTPKGDEEQALALPRANSPTGKEGYQAVLQEWEEQHRNYVSSL
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDS
FTLQKVYQLETGLTRHPPEKPVRKDKRDELVEAIESALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTYE
LTFKGDHKHEFKRLILFRPFSPIMKVNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNLCRLNT
QPGKKVFYPVLF SQYNPGIIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKWGGED
VHLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDELTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQ
KTSSKKT

FIGURE 265

GGATGCAGAAAGCCTCAGTGTGCTCTTCTGGCCTGGGTCTGCTTCTCTCTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCA
TGCCATGGGGGAGCCAAGGGAAACCTGGGGCTGCTGGATGGCTTCCCGATTTTCGCGGGTGTGTGGTGCTGA
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTACACGTGCTAGAGAGCCTCCTGTCTCCCTACCTT
TCCTGGGCAAACCTAAGCTCCTTGACAGAGGATCCTGGAGATTAGCCCCACCATGCCCGGCTCTACCGATCTCAGG
TTGACCTCTTACCACCACCATGCAGCGCCTCAAGGCCCTCACCCTGGCTCACTGCCTACCTTTATTGATGCTG
GTAGTAACCTCGCCAGCCACGCCATAGTGAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGCGGTAG
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGCTTTCTCAAAGCTTTCTTCTCCCATCTTCA
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA
AGAACTTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAAGTGGAGGTCTCAGCTGCTCTCTTTC
TGTATAGCCCCACAGCAGTCTTCCCCAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCCCTGCCCATCCCATTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
GGGGTGAAGACTCCAGCCCCACTCCTCTGCTTTAGCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
CCCCATTTCTTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
TCTCCAAGGCCTCTGCTGACTACAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
TTGCTGAGCTGCAGCAGTTCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC
GCATGGCGGGGGTACTGCTCTCTTGGCTGCTTCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC
CAGGCTTTCCATTCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCTGGTGGGGCCATAGCGTATGCTGGAC
TCCTGGGAACCTATTGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATCTCCCTT
TTCTGTGGAAGCCTGGGCTGGCTGGGGGTCCAAGAGGCCCTGGCAACCTGTTTCCCATCCCTGGGCCGTCC
TGTTACTCCTGCTGTTTCGCTTGGCTGTGTTCTTCTGATAGTTTGTGTAGCTGAGGCCAGGGCCACCCCT
TCCTTTTGGGCTCATTCTCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
TCACAATGCCCCGCTTGGCACTTCAGCCACAACAACCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG
GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTTGGCACT
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTTCGAGCCAGAATTTATGGTATGGAGCTTGTGTGG
CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCCGCTATGGTAATCTCAAGAGCCCCGAGCCAC
CCATGCTCTTTGTGCGCTGGGGACTGCCCCAATGGCATTGGGTACTGCTGCCTACTGGGCATTGGCGTCGGGG
CAGATGAGGCTCCCCCGCTCTCCGGGTCTGGTCTCTGGGSCATCCATGGTGTGCTCGGGCTGTAGCAGGGC
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCAA
GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA
TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGTTAGAGAGGACCAAAATCTCAGGGTCCCCTGACTGTGGCTG
CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTACAGCCCTCACCCTGTTGGCCTTCCCCTTCTGCTGT
TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCTTCTCCTACATCTGCTTGGCTG
CTGGGATACCCGTCACCAACCCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA
CACAGACCTTCTACTCCACAGGCCACAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCGTGGGATTCC
CAGAGGGTCATGGTCTCTGACTTGGCTGCTGCTTGTGCTAGTGGGAGCCAAACCTTTGCCTCCCACTCTCT
TTGCAGTAGGTTGCCCACTGCTCTGCTCTGGCCTTCTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG
ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGCCCTCAAGTACCTCTTATCCTTGGTATTAGATTCT
TGGCCTGTGCTTGGCAGCCTCCATCCTTTCGAGGCATCTCATGGTCTGGAAAGTGTTCCTTCAAGTTTCAATAT
TTGAGGCTGTGGGCTTCAATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGTGAGAGTGGATGGTG
CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTAGGACCACAGTGGAGTA
TGATCCCTAACTCCTGATTGGATGCATCTGAGGGACAAGGGGGCGGTCTCCGAAGTGAATAAAATAGGCCGG
GCGTGGTGAATTGCACCTATAATCCCAGCACTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
AGACCAGCCTGTGGAACATAACAAGACCCCGTCTCTACTATTTAAAAAAAGTGAATAAAATGATAATAT

FIGURE 266

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPFPGPSLPWGSQKPGACWMASRFSRVVLVLI
DALRFDFAQPQHSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQVDPPTTMMQRLKALTGSLPTFIDAG
SNFASHAIVEDNLIKQLTSAGRRVVFMDGDDTWKDLFPGAFSKAFFFPSEFNVRDLDTVDNGILEHLYPTMDSGEWD
VLIAHFLGVDHCGHKHGHPEMAKKLSQMDQVIQGLVERLENDTLLVVAGDHGMMTNGDHGGDSELEVSAAFL
YSPTAVFPSTPPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAELEFSGGEDSQPHSSALAQASALHLNAQQVS
RFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRGARAMCIESWARFSLVR
MAGGTALLAASCFICLLASQWAI SPGF PFCPLLLTPVAGLVGAIYAGLLGTIELKLDLVLLGAVAAVSSFLPF
LWKAWAGWGSKRPLATLFPPIPGPVLLLLLFR LAVFFSDSFVVAEARATPFLG SFILLLVVQLHWEGQLLPKLL
TMPRLGTSATTNPPRHNGAYALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVA
ALVALLAAVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLPRAVAGL
AASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQEEFRGLERTKSQGPLTVAA
YQLGSVYSAAMVTALTLLAFPLLLHAERISLVFLLLFLQS FLLLHLLAAGIPVTTPGPFTVPWQAVSAWALMAT
QTFYSTGHQPVFPAIHWHAFAVGFPEGHGSCTWLPALLVGANTFASHLLFAVGCPLLLLWPF LCESQGLRKRQQP
PGNEADARVRPEEEEEPLMEMRLRDAPQH FYAALLQLGLKYLFI LGIQILACALAA SILRRHLMVWKVFAPKFIF
EAVGFIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR
```

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034, 1052-1070

Leucine zipper pattern.

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 267

[illegible]

FIGURE 268

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHPASYPECGNNAQSPIDIQTDSVTFDPDLPALQPHGYDQPGTE
PLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSV
LWTVFYRRSQISMEQLEKLQGTLEFSTEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 269

GTGGCGCTGGCGGTTGCTGTCAGCTGATTCCCGGGGTTGGTGGCAGCGGCGGTAGCAGCAATGGACTTTCTCCTG
GGGAACCCGTTTCAGCTCTCCAGTGGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG
GCCCTCAACATGGAGATCTGCGACATCATCAACGAGACGGAGGAAGGTCCCAAAGATGCCCTCCGAGCAGTAAAG
AAGAGAATCGTGGGGAATAAGAACTTCCACGAGGTGATGCTGGCTCTCACAGTCTTAGAAACCTGTGTCAAGAAC
TGCGGGCACCCTTCCACGTGCTGGTGGCCAGCCAGGACTTCGTGGAGAGTGTGCTGGTGAGGACCATCCTGCCC
AAGAACAACCCACCCACCATCGTGCATGACAAAGTGCTCAACCTCATCCAGTCTGGGCTGACGCGTTCCGCAGC
TCGCCCCGATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGAGGAAAGGCCTGGAGTTCCCCATGACTGAC
CTGGACATGCTGTCAACCATCCACACACCCAGAGGACCGTGTCAACTCAGAGACACAATCAGGACAGGATTCTG
TGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGCTGCCCCCTCTGCCCCCCCCGCCATACTCTCCG
GTGACACGCCCCATAGCACCAACCCCGGAACAGATTGGGAAGCTGCGCAGTGAGCTGGAGATGGTGAGTGGGAACG
TGAGGGTGATGTGCGAGATGCTGACGGAGCTGGTGCCACCCAGGCCGAGCCCGCAGACCTGGAGCTGCTGCAGG
AGCTCAACCGCACGTGCCGAGCCATGCAGCAGCGGGTCTTGAGTGATACCTGCTCCGGGGCCCATGCCCCAAGGA
GCCCTTCAGAGCCACACTGCCAGTCGAGGCCTGGCTGGAGGCTGGCCACAGTGGAAATTCTGCCGAGCCTATTG
TCCCTACCTTGCTCTGCTGCATGGGGCCCCATGGCTTTGGCTGGCCACTGAGGGTAGGGTGTGGAGGTGTGGAGG
CCCCCTGAGGAGCTGCGGCGGCCAGGTACGAGCTGCAACTCTGCGCGCAGTGGGCGAGATCTCATCAGCCCCA
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCTCCGCTGCCTTGCCCTCCATCCTTCCTCTGT
TCCTTCTGGCCGGGCACCACAGCACTGGGGCTCACCTCTTGGTTGATCCTCTTGTAAGGAGAGGTGCCTTTTG
TATCCCCAATTAAAGGTAGAAAACC

FIGURE 270

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSPVGQRIEKATDGSLSQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLE
TCVKNCGRHFRFHLVASQDFVESVLVRTILPKNNPPTIVHDKVILNLIQSWADAFRSSPDLTGCVVTIYEDLRRKGLE
FPMTDLDMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTLASMLPLCPPRPYSPVTRP
```

Important features of the protein:

Signal peptide:

Amino acids 1-15

N-glycosylation site:

Amino acids 41-45

N-myristoylation sites:

Amino acids 6-12;23-29

FIGURE 271

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCGTCTGCCATGGGGC
TCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCCCTGAAGCCCCCGCAG
GCTCCTGGGGGGGCCAGATCATCGGGGGCCACGAGGTGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCT
TCGGGGGGCCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCC
ACAGAGACCTCCGCACTGGCCTGGTGGTGTCTGGGCGCCACGTCTGAGTACTGCGGAGCCCACCCAGCAGGTGT
TTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGACATCTGCCTGCTGCCGC
TGAACGGCTCTGCTGTCTTGGGCCCTGCAGTGGGGCTGCTGAGGCTGCCAGGGAGAAGGGCCAGGCCCCCCACAG
CGGGGACACGGTGCCGGGTGGCTGGCTGGGGCTTCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGG
CCAAGGTCCGAGTGTCTGGACCCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCA
CCCGCAGTGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCCCTGGTGTGCAGGAACCGGG
CTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGACGTGTACACGCAGGTGTCCG
CCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCCCCAGCCCGGCCCCCTGCCTGGGACCACCAGGC
CCCCAGGAGAAGCCGCCTGAGCCACAACCTTGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCG
TGGCTGGGCCCCACGGGAAGCCTGATGTTTCAAGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACA
TGCAAAGGGCAGAAAGCAAACCCAGTAAATGTTAACTGACAAAAAAAAAAAAAAAAAAAAAGAAA

FIGURE 272

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWCAQIIIGGHEVTPHSRPYMASVRFGGQHHC GGFLLRARWVVSAAHC
FSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRLPGRRARP
PTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKGHLLTLM LCTRSGDSHRRGFCSADSGGPLVCR
NRAHGLVSFSGLWCGDPKTPDVYTQVSAFVAWIWDVVRSSPQPGPLPGTTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 273

GAAGTTCGCGAGCGCTGGCTATGGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTGGCGCTCGGGACAG
GAGACCCAGAAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGACCAGCGTGGCGCGCGCCCTGGCGCCCC
AGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGCGCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCT
ACGACAAGGTACTTTCTTTGTCATGAGGATTCAACAACCCCTGTGGCTAACCCCTGCTTGCATTTACTCTCATCA
AACGCCCTGCAGTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG
GCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGGGCCCTGATGCGGCTGC
AGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTTTAGAGAGTCACTGGCTCTGCCATCAGTG
ACCTGTACAGCCCCAAACGGCTCTTTTCTCTACAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACA
TGGGGGATTATTACCATGCCATTCCATGGCTGGAGGAGGCTGTCACTCTTCCGAGGATCTTACGGAGAGTGGA
AGACAGAGGATGAGGCAAGTCTAGAAGATGCCCTTGGATCACTTGGCCTTTTGCTTATTTCCGGGCAGGAAATGTTT
CGTGTGCCCTCAGCCTCTCTCGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGGATGGCCAGGAATGTCTTGA
AATATGAAAAGGCTCTTGGCAGAGAGCCCCAACACGCTGGTAGCTGAGGCTGTCTCCAGAGGCCAATATACCCC
ACCTGCAGACCAGAGACACCTACGAGGGGCTATGTACAGCCCTGGGTTCAGGCCCACTCTCTACAGATCCCTA
GCCTCTACTGTTCTCTATGAGACCAATTCCAACGCCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCCACC
TGGAGCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAACTTGAGAAC
CATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAGTACCGCATCAGCAAAAGTGCCT
GGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAACCACCGCATTGCTGCCCTCACAGGCCCTGATGTCC
GGCCTCCCTATGCAGAGTATCTGCAGGTGGTGAACCTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATG
CTACGTCACCAAGCAGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCT
CGGTGGAAGCTGGAGGAGCCACAGCCTTCACTATGCCAACCTCAGCGTGCCTGTGGTTAGGAATGCAGCACTGT
TTTGGTGGAACTTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCATGCTGGCTGTCTGTCTGCTGGTGGAG
ATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGGACAGGAATTCCGACAGCCCTGCAGCTCCAGCCCTGAAG
ACTGAACTGTTGGCAGAGAGAAGCTGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTA
GGAGAGGAGAAAGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCACTTTGTCTGTGCCTCGCAAATCAGAGGCAA
GGGAGAGGTTGTTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAAGTCAGAGTAGGATGC
ACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGGAGTTCAGATACTCTCTGTTGGGAACAGG
ACATCTCAACAGTCTCAGGTTGATCAGTGGGTCTTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGG
CAATGAGGACACCTGCAGGAGGGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGC
AGCCCAAGCAGGGAGTGTCCCCCTCCAGAAGCATATCCAGATGAGTGGTACATTATATAAGGATTTTTTTTAA
GTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAAATGTTTATAAATCAAAA

FIGURE 274

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849
><subunit 1 of 1, 544 aa, 1 stop
><MW: 61126, pI: 6.40, NX(S/T): 2
MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEA
RLRDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGY
EKVEQDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLT
GDDCFQVGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRA
GNVSCALSLSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNI PHLQTRDT
YEGLCQTLGSQPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEA
QKIRELAEPWLQRSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVPR
PYAEYLQVVNYGIGGHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIY
ANLSVPVVRNAALFWWNLHRSGEGSDSTLHAGCPVLVGDKWWANKWIHEYGQEFRRPCSS
SPED
```

Important features of the protein:

Signal peptide:

Amino acids 1-19

Leucine zipper pattern:

Amino acids 34-56;41-63

Ribonucleotide reductase small subunit signature:

Amino acids 340-356

N-glycosylation sites:

Amino acids 242-246;482-486

Cell attachment sequence:

Amino acids 27-30

Tyrosine kinase phosphorylation site:

Amino acids 189-198

N-myristoylation sites:

Amino acids 4-10;135-141;153-159;164-170;241-247;303-309;309-315;
457-463;473-479

FIGURE 275

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC
TTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTG
CAGACAGTCTGTCTCCGAGGCACTAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCCTAT
GAGGCCAATGAAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCCCTC
CAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC
AAGTTTGTGTGACGTCAACGGAATCGCTATCTCCTTCCCTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA
GAAAACGTGTCTCTGTTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCTGTGCGCAGCAGCAAGAGATAC
ATATGCGAGTTCACCATCCCTAAATAGGTCTTTCTCCAATGTGTCTCCAAGCAAGATTCAATCATAACTTATAGG
TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAAAAAATTGCAACACAAGATCAATGTCCAT
AGCAATATGATAGCATCAGCCAAATTTTGCTAACACATTTCTTTGGGATTTTGGCCCTTCCCTGGGGTATAGGGGATC
AGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTCTTAGTCTTTTC
TCACTTGTAACAAACCCAGTTTGTTTTCAAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
AGGCTACCTGAAAGATTTTCCCTTGGAGTTTAGCGTATGTTTGACTAACAAAAATTCCCTACATCAGAGACTCT
AGGTGCTATATAATCCAAAAACTTTTCAGCCTGTTGCTCATTTCTGTCCCATGCTGGCAATAATACCTTGTGAGCC
CATTACCCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCTGCCATATCAGAACACAAACCCC
TGAAGAGGTTCTGATTTGATTTTTTTTTTTTTCTTCATGCCTACCCCTTTTTTGGGAAGTTTCCAGCCGCAATTTGA
AATGAAATGACAAGGTGTATATTTGATCAATTTTCATTCCCACCATTCATTACAACCTTAACCTTAAATGGGTA
ACCCTAAGGCATATCAAAGAAGCAGATTGCATGATAAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTT
TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTTTACATTTTCGTATATTTAT
TTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTTTGGAAGCTGAAAACCTGAATTTAAAG
AATGCTATCTTGGAAAATTGCATACGTCTGTGCAATTTTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAG
ATTGTACAAAATAACTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAAG
CAAACAATTTTAAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATATCC
CACTTTGCAAACCTTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTATTGCTCAATAATAAAGCCTGAA
TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 276

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWTEVNALKEIQALQT
VCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDFWLGINDMVTEGKF
VDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGKWSDEACRSSKRYICEFTIPK

FIGURE 277

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCACCCCTAGGAAGCCACCAGAC
TCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCCACGAGCGCTGGCTGAGGGACCGAGCC
GGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAGCGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCT
ACTGCGCGCGCTTCTCCTACCTCTGGCTCAAGTTTTCACTTATCATCTATCCACCGTGTCTGGCTGATTGGGG
CCCTGGTCTGTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCCTGG
CTCCAGCCATCATCCTCATCCTCCTGGGCGTCTCATGTTTATGGTCTCCTTCATTGGTGTGCTGGCGTCCCTCC
GTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGATCTGCCTCATCATGGAGCTCATTGGTGGCG
TGGTGGCCTTGACCTTCCGGAACCAGACCATTGACTTCCTGAACGACAACATTGGAAGAGGAATTGAGAACTACT
ATGATGATCTGGACTTCAAAAAATCATGGACTTTGTTTCAAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACC
GAGATTGGAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACACCTGCT
GCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAATATCGACAAGGAGCGTTTTAGTGTGC
AGGATGTCTACGTGCGGGGCTGCACCAACGCGGTGATCATCTGGTTTATGGACAACCTACACCATCATGGCGT
GCATCCTCCTGGGCATCCTGCTTCCCCAGTTTCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGG
ACATCATCATGGAGCACTCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCA
CGGGATGCTGCTTGTGCTACCCCAATTAGGGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTCTGGGATAGC
ACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACACTCAGTACTGACCAAGCCAGG
GCTGTGTGTGCTGTGTGTAGGTCCCACGGCCTCTGCCTCCCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGC
TTTCCCCGAGGCAGCTCTGGAATCTGTGCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGG
CTACAGGGGAGGGAGAGCCTGAGGCTCTGCTCAGGGCCCATTTTATCTCTGGCAGTGCCCTTGGCGGTGGTATTCA
AGGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGGCATCTGGGGAA
GGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGCCTCTTCTCAGCCTCCAGGTGCCTT
GAGCCCTCTTGCAAGGGCGGCTGCTTCCCTTGAGCCTAGTTTTTTTTTACGTGATTTTTGTAAACATTATTTTTTT
GTACAGATAACAGGAGTTTCTGACTAATCAAAGCTGGTATTTCCCCGCATGTCTTATTCTTGCCCTTCCCCAAC
CAGTTTGTAAATCAAACAATAAAAACATGTTTTGTTTTGTTTTTAAAAA

FIGURE 278

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLESAFLAPAILILLGVVMFM
VSFIGVLASLRDONLYLLQAFMYILGICLIMELIGGVVALTFRNQITIDFLNDNIRRGIEYDDLDLDFKNIMDFVQK
KFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPTCCIRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVII
WFMDNYTIMACILLGILLPQFLGVLLTLLYITRVEDIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 279

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGACACCTGGGAAGAT
GGCCGGCCCGTGGACCTTACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATCCAAGCCACCCTCAGTCCCAC
TGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAG
CATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT
GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCC
CTCGGCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCTGGTCAA
GACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCAC
CCGCTGGTCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCCT
GGTGAACGCCTTAGCTAAGCAGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTG
TCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTCCCTCAG
CATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTCAGCTCTACCTGGGGGCCAA
GTTGTTGGACTCACAGGAAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGA
CAACATCCCGTTCAGCCTCATCGTGAGTCAGGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTATGGTCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGA
AAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTTATAGA
CCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTT
CACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTACACCAAAGGTGACCAACTTATACTCAACTTGAATAA
CATCAGCTCTGATCGGATCCAGCTGATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCAT
CACTGAGATCATCCACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGT
GAAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTG
GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGT
ATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCTGTGAAAAA

FIGURE 280

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQLPLLSAMREKPA GGIPVLGS
LVNTVLKHI IWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTI VEFHMTTEAQATIRMDTSASGP
TRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISL
SIDRLEFDLLYP AIKGD TIQLYLGAKLLDSQGVTKWFNNSAASLTMP TLDNIPFSLIVSQDVVKA AVAAVLSPE
EFMVLLDSVLPESA HRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSS SEALRPL
FTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGW FQPDVLKNIITEI IHSILLPNQNGKL RSGVPVSL
VKALGFEEAAESSLT KDALVLT PASLWK PSSPVSQ
```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 281

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTCCCGCGTTCT
CTTTCCACCTTTTCTCTTCTTCCACCTTAGACCTCCCTTCTGCCCCCTTTCTGCCCCACCGCTGCTTCTGGC
CCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGGGTTGATCTGTGGCCCCCTGTGCTCCGTGTC
CTTTTCGTCTCCCTTCTTCCCGACTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGT
GAGGGTCTCTCTCTCTTGTCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCCACGCTCGAGCCCGCCAGA
CATGTTCTGCTTTTCCATGGGAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCT
GATGTACTGCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCTCCACTGTCCGCTGTCCA
CTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCG
GGCCCCACCAAAGTCTTGTCCAGCACAAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTT
CCCCCTCCCGCTGCCCCAACAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACCTG
CCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGA
GCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC
TGGGAGAAAGAGAGGCGCCGGGCACCCAGCCCCCACTGGCCTCAGCGCCCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGG
CGGAAGACGTACTCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCCTGCATCCTATG
CACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGTACCCCTGCCGTACCCCGAGAA
AGTGGCTGGGAAGTGTGCAAGATTTGCCCAGAGGACAAAGCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAG
GTGTCCCAAGGCACCGGGCCGGGTCTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTTGC
CCTGGAACACGAGGCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCA
GAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGC
AAGACTTCCAGAAAGAGGCACAGCAC'TTCCGACTGCTCGCTGGCCCCCAGGAAGGTCACTGGAACGTCTTCTTAG
CCCAGACCCTGGAGCTGAAGGTACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAAACAGTTGCA
GATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAAGTTGCATTACCCTCAAAAAAAAAAAAAA
AAAAAA

FIGURE 282

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPQPVTPEPQQCCPKCEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFPSRLPNQCVLCSCTEGQIYC
GLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVRHPQDPCSSDAGRKRGPPTPAPTGLSAPLSF
IPRHFRPKGAGSTTVKIVLKEKHKKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEPC
RHPEKVAGKCKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLVKDE
ETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWP PRRSLERLPSPDPGAEGHGQSRQSDQDITKT
```

Signal peptide:
amino acids 1-25

FIGURE 283

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGCGGTTGCGGAGGCTTCCTTGGTGGATTGCAACGAGGAGAAGAT
 GACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGGCG
 GCCTCGCCCTGTTGTGCTGCGCCGCCCGCCGCCCGCCGCTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTG
 GCGGCGGGGCCCGGGGCGAGGTGGACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCCTA
 GGGCGACGCTCCACGCGCCAGGCCCGGAGGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTGCGA
 CTTCCTCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTCCACCACCTTTCAGGCGC
 CGCTCGGCCCTCGCCGACCACCCCTCCGGCGGCGGAACGCACTTCGACCACCTCTCAGGCGCGGACCAGACCCG
 CGCCGACACCCCTTCGACGACCACTGGCCCCGGCGCCGACCACCCCTGTAGCGACCAACCGTACCGGCGCCACGA
 CTCCCCGACCCCGACCCCGATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCACCCACCTGCCACCGAGG
 CCCCCTCTTCGCTCTCCAGAGTATGTATGTAAGTCTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACC
 AGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAAGAGGGCTTTTACC
 TAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGGT
 AAGCAACAGAGGGTGGAACTGAAGTTTATTTTATTTTAGCAAGGGAAAAAAGGCTGCTACTCTCAAGGACCA
 TACTGGTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAATATTTTATATACTTTTATTCTTTACTTTAT
 ATGTTATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAAGCACTAGAGTCGCCAA
 TTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAATAAATCTGCTTTCTGGAAGGGCT
 TTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATAACCATTGGAGTTTGAGGAAAT
 TTGTTGTTGGTTTATTTTCTCTCTAATCAAAATCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGG
 GGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTGGAGACCAAAA
 GTAGATTAAGCAGGAATTATCTTTAAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGGAATAATGTACTGT
 TATCTAAGCATTGCTTGTACTGCACTGAAAGTAATTATCTTTGACCTTATGTGAGGCACTTGGCTTTTGTG
 GACCCCAAGTCAAAAACTGAAGAGACAGTATTAAATAATGAAAAAATAATGACAGGTTATACTCAGTGTAACC
 TGGGTATAACCCAAGATCTGCTGCCACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCTTTCACTGAGCTTGT
 TTCTTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAATT
 CTGGTTTGTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTAAAGAACTTTTAGCTCCTTG
 ACAAGAAGTGCTTTATACTTTAGCACTAAATATTTTAAATGCTTTATAAATGATATTATACTGTTATGGAATAT
 TGTATCATATTGTAGTTTATTTAAAAATGTAGAAGAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTT
 GGGAGGCCAAGGCGGGTGGATCACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCGCTCT
 CTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGTGAG
 AGAGGGGAGACTCTGTCTTAAAAA

FIGURE 284

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGLALLCCAAAAA AVASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATAPTAQAPRTGPPRA
TVHRPLAATSPAQSPET TPLWATAGPSSTTFQAPLGPSP TTPPAAERTSTTSQAPTRPAPTTLSTTTGPAPTTPV
ATTVPAPTTPRTPTPDL PSSSNSSVLPTPPATEAPSSPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHC
ETCKEGFYLN YTSGLCQPCDCSPHGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 285

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCCCTGCTCTGGGGG
AGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCCGTGACGGTGCAGGAAGGCCTGTGT
GTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATTTACCCTGGCCCAGTAGTTCATGGCTACTGG
TTCCGGGAAGGGGCCAATACAGACCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAG
ACTCGGGACCGATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCCCTGAGCATCAGAGATGCCAGAAGA
AGTGATGCGGGGAGATACTTCTTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCT
GTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCCAGGCACCCCTGGAGTCCGGCTGCCCCCAGAAT
CTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTTATGATCTCCTGGATAGGGACCTCCGTGTCC
CCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCCCTCATCCACAGCCCCAGGACCATGGCACCAGCCTC
ACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTACCCGCCCT
CAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCA
CTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGC
CTGAGCTGGAGAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCC
CTGCAGAGCAAAGCCACATCAGGAGTGAATCAGGGGGTGGTTCGGGGGAGCTGGAGCCACAGCCCTGGTCTTCCTG
TCCTTCTGCGTCATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAGGCCAGCAGCGGGCGTGGGAGAT
ACGGGCATAGAGGATGCAAACGCTGTGAGGGGTTGAGCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGAC
AGTCCCCCAGACCAGCCTCCCCAGCTTCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTC
AGCTTCCAGATGGTGAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATC
CACAGATGAGAACTGCAGAGACTCACCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGAGAAGTCAGAGGC
TGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATGTGCAGAGTGAAAAGC
ACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCCTCCCTTTATTTTTTTAACTAAAAG
ACAGACAAATTCCTA

FIGURE 286

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWFREGANTDQDAPVA
TNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVTALTHRPNILI
PGTLESGCPQNLTCVWPWACEQGTTPMISWIGTSVSPDPSTTRSSVLTLPQPQDHGTS LTCQVTFFGASVTTN
KTVHLNVSYPQNLMTVVFQDGTSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPS
NPGVLELPWVHLRDAAEFTCRAQNPLGSQQVYLNVSLSQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRK
KSARPAAGVGDGTGIEDANAVRGASQGPLTEPWAEDSPPDQPPPASARSSVGEGLQYASLSFQMVKPWDSRGQE
ATDTEYSEIKIHR

Signal peptide:
amino acids 1-15

Transmembrane domain:
amino acids 351-370

FIGURE 287

CGCGAGCTGAGAGGAGCAGGTAGAGGGGCGAGGGCGGGACTGTCGTCTGGGGGAGCCGCCCAGGAGGCTCCTCAG
 GCCGACCCAGACCCCTGGCTGGCCAGGATGAAGTATCTCCGGCACCGGCGGCCCAATGCCACCCCTCATTCTGGCC
 ATCGGCGCTTTCACCCCTCCTCCTCTTCAGTCTGCTAGTGTACACACCCACCTGCAAGGTCCAGGAGCAGCCACCG
 GCGATCCCCGAGGCCCCTGGCCTGGCCCACTCCACCCACCCGCCCAGCCCCGGCCCCGTGCCATGCCAACACCTCT
 ATGGTCACCCACCCGGACTTCGCCACGCAGCCGAGCAGCTTCAGAACTTCCTCCTGTACAGACACTGCCGCCAC
 TTTCCCTGTCTGCAGGAGCTGCCCCCTCTAAGTGCAGCGCAGCCGGTCTTCCTGCTGCTGGTGTATCAAGTCTCTC
 CCTAGCAACTATGTGCGCCGCGAGCTGCTGCGGCGCACGTGGGGCCGCGAGCGCAAGGTACGGGGTTTGCAGCTG
 CGCCTCCTCTTCCTGGTGGGCACAGCCTCCAACCCGCACGAGGCCCGCAAGGTCAACCGGCTGCTGGAGCTGGAG
 GCACAGACTCACGGAGACATCCTGCAGTGGGACTTCCACGACTCCTTCTTCAACCTCACGCTCAAGCAGGTCTTG
 TTCTTACAGTGGCAGGAGACAAGGTGCGCCAACGCCAGCTTCGTGCTCAACGGGGATGATGACGTCTTTGCACAC
 ACAGACAACATGGTCTTCTACCTGCAGGACCATGACCTTGGCCGCCACCTCTTCGTGGGGCAACTGATCCAAAC
 GTGGGCCCCATCCGGGCTTTTGGAGCAAGTACTATGTGCCAGAGGTGGTGAAGTCAAGTGAAGCGGTACCCACCC
 TATTGTGGGGGTGGTGGCTTCTTGCTGTCCCGCTTTCACGGCCGCTGCCCTGCGCCGTGCTGCCCATGTCTTGAC
 ATCTTCCCCATTGATGATGTCTTCCTGGGTATGTGTCTGGAGCTTGAGGGACTGAAGCCTGCCTCCACAGCGGC
 ATCCGCACGTCTGGCGTGCGGGCTCCATCGCAACACCTGTCTCCTTTGACCCCTGCTTCTACCGAGACCTGCTG
 CTGGTGCACCGCTTCCCTACCTTATGAGATGCTGCTCATGTGGGATGCGCTGAACCGAGCCCAACCTCACCTGCGGC
 AATCAGACACAGATCTACTGAGTCAGCATCAGGGTCCCCAGCCTCTGGGCTCCTGTTTCCATAGGAAGGGGCGAC
 ACCTTCCTCCAGGAAGCTGAGACCTTTGTGGTCTGAGCATAAGGGAGTGCCAGGGAAGGTTTGAAGTTTGAAGTGA
 GTGAATATTCTGGCTGGCGAACTCCTACACATCCTTCAAACCCACCTGGTACTGTTCCAGCATCTTCCCTGGAT
 GGCTGGAGGAACCTCAGAAAATATCCATCTTCTTTTGTGGCTGCTAATGGCAGAAGTGCCTGTGCTAGAGTTCC
 AACTGTGGATGCATCCGTCCCGTTTGAAGTCAAGTCTTACTTCCCTGCTCTCACCTACTCACAGACGGGATGCTA
 AGCAGTGCACCTGCAGTGGTTTAAATGGCAGATAAGCTCCGTCTGCAGTTCAGGCCAGCCAGAACTCCTGTGTC
 CACATAGAGCTGACGTGAGAAATATCTTTCAGCCCAGGAGAGAGGGGTCCTGATCTTAACCCCTTCTGGGTCTC
 AGACAACTCAGAAGGTGGGGGGATACCAGAGAGGTGGTGAATAGGACCGCCCCCTCCTTACTTGTGGGATCAA
 ATGCTGTAATGGTGGAGGTGTGGGCAGAGGAGGGAGGCAAGTGTCTTTGAAAGTTGTGAGAGCTCAGAGTTTCTG
 GGGTCTCATTAGGAGCCCCCATCCCTGTGTTCCCCAAGAATTGAGAGAACAGCACTGGGGCTGGAATGATCTTT
 AATGGGCCCCAAGGCCAACAGGCATATGCCTCACTACTGCTTGGAGAAGGGAGAGATTAGGTCTCCAGCAGCCT
 CCCTCACCCAGTATGTTTACAGATTACGGGGGGACCGGGTGAGCCAGTGACCCCTGCAGCCCCCAGCTTCAGG
 CCTCAGTGTCTGCCAGTCAAGCTTCACAGGCATTGTGATGGGGCAGCCTTGGGGAATATAAAATTTTGTGAAGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413

<subunit 1 of 1, 372 aa, 1 stop

<MW: 42515, pI: 8.92, NX(S/T): 6

MKYLRRHRPNATLILAIGAFTHLLLFSLLVSPPTCKVQEQPPAIPALAWPTPPTRPAPAPCHANTSMVTHPDFAT
QPQHVQNFLLYRHCRRHFPLLQDVPPSKCAQPVFLLLVKSSPSNYVRRELLRRTWGRERKVRGLQLRLLFLVGTA
SNPHEARKVNRLLLELEAQTHGDILQWDFHDSFFNLTLKQVLFLOWQETRCANASFVLNGDDVFAHTDNMVFYLQ
DHDPPGRHLFVGQLIQNVGPIRAFWSKYYPVEVVTQNERYPYPCGGGGFLLSRFTAAALRRAHVLDIFPIDDVFL
GMCLELEGLKPASHSGIRTSGVRAPSQHLSSFDPFCFYRDLLLVRFLPYEMLLMWDALNQPNTLCGNQTQIY

Important features:

Type II transmembrane domain:

Amino acids 15-34

N-glycosylation sites:

Amino acids 10-14;64-68;184-188;202-206;362-366;367-371

TonB-dependent receptor proteins signature 1:

Amino acids 1-32

N-myristoylation sites:

Amino acids 308-314;316-322

FIGURE 289A

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCAGGAGCGGGGCCCT
GCACACCATGGCCCCCGGGTGGGCAGGGGTGCGCGCCGCGCTGCGCGCCCGCTGGCGCTGGCCTTGGCGCTGGC
GAGCGTCTGAGTGGGCCTCCAGCCGTGCGCTGCCCCACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCA
CGGGCTGGGCTCCGCGCGGTTCTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATAT
CACCAGGATCACCAAGATGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGACATCTGGAAGACAACAGGTCAG
CGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGTGAAGT
CCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTAGATTTGAGTGAAAAACAGATCCAGGGGAT
CCCCAGGAAGGCGTTCCGCGGCATCACCGATGTGAAGAACCTGCAACTGGACAACAACACATCAGCTGCATTGA
AGATGGAGCCTTCCGAGCGCTGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGT
CACCAGCTTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCACCTCTACTGCGACTGCCACCT
GGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCTGCATGGCTCCTGTGCATTT
GAGGGCTTCAACGTGGCGGATGTGCGAAGAGAGTACGTGTGCCAGCCCCCACTCGGAGCCCCCATCCTG
CAATGCCAACTCCATCTCCTGCCCTTCGCCCTGCACGTGCAGCAATAACATCGTGGAAGTGTGAGGAAAGGGCTT
GATGGAGATTCTGCCAACTTGCCGAGGGCATCGTCGAAATACGCTTAGAACAGAACTCCATCAAAGCCATCCC
TGCAGGAGCCTTCAACCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGATATTGCTCC
AGATGCCCTTCCAGGGCTGAAATCACTCACATCGCTGGTCTGTATGGGAACAAGATCACCGAGATTGCCAAGGG
ACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAATGCCAACAGATCAACTGCCTGCGGGTGAACAC
GTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTT
CGCCCCCTGTCAGTCCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCT
GGCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCCGCTGCAGCAGCCCCGCGCCGACTCGCCAACAA
GCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGGATTACCGCAGCAGGTTTCAGCAGCGA
GTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCT
GGTCCGCATCCCAAGCCACCTCCCTGAATATGTACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGA
GGCCACTGGCATCTTCAAGAAGTTGCCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTGCG
AGAGGGAGCTTTTCATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCTGGAGACCGTGCACGG
GCGCGTGTTCGCTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGAGTAACCTTGATCAGCTGTGTGAGTAATGA
CACCTTTGCCGGCCTGAGTTCGGTGAGACTGCTGTCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGC
CTTCACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTG
GCTCGGCAAGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCTTAGGTGCCAGAAGCCATTTTCTCAAGGA
GATTCCCATCCAGGATGTGGCCATCCAGGACTTACCTGTGATGGCAACGAGGAGAGTAGCTGCCAGCTGAGCCC
GCGCTGCCCCGAGCAGTGCACCTGTATGGAGACAGTGGTGGATGCAGCAACAAGGGGCTCCGCGCCCTCCCCAG
AGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAACACCTAACAGCCGTGCCAGAGAGCTGTCCGC
CCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACAT
GTCTACCTCTCCACTCTGATCCTGAGCTACAACCGCTGAGGTGCATCCCGTCCACGCCTTCAACGGGCTGCG
GTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTGGAAGGCTCCTTCAACGACCTCACATC
TCTTTCCATCTGGCGCTGGGAACCAACCCACTCCACTGTGACTGCAGTCTTGGTGGCTGTGCGAGTGGGTGAA
GGCGGGGTACAAGGAGCCTGGCATCGCCCGCTGAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCAC
CCCAACCCACCGCTTCCAGTGCAAAGGGCCAGTGGACATCAACATTTGTGGCCAAATGCAATGCCTGCGCTCTCCAG
CCCGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTGCCCC

FIGURE 289B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCAGCATGGAGGCACC
TGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTCTGGGCTTTGAGGGGCAGCGGTGTGAG
ATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAAAATGCCACCTGCGTGGACGGGATCAACAACCTACGTG
TGTATCTGTCCGCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTC
TGTCAGCATGAGGCCAAGTGATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGGAAG
CTCTGTGAGACAGACAATGATGACTGTGTGGCCCCACAAGTGCCGCCACGGGGCCCAGTGCGTGGACACAATCAAT
GGCTACACATGCACCTGCCCCCAGGGCTTCAGTGGACCTTCTGTGAACACCCCCACCCATGGTCCCTACTGCGAG
ACCAGCCCATGCGACCACTACGAGTGCCAGAACGGGGCCCAGTGTCATCGTGGTGACAGGAGCCCCACCTGCCGC
TGCCCCACCAGGCTTCGCGGGCCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTG
GAACTGGCCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATC
CTTCTCTACAAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGTGCGGCTGGTCTATGACAGC
CTGAGTTCCCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGAATGATGGGCAGTTTCACAGTGTGGAGCTGGTG
ACGCTAAACCAGACCCCTGAACCTAGTAGTGGACAAAGGAACCTCAAAGAGCCTGGGGAAAGCTCCAGAAGCAGCCA
GCAGTGGGCATCAACAGCCCCCTTACCTTGGAGGCATCCCCACCTCCACCGCCTCTCCGCCTTGCGCCAGGGC
ACGGACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAG
GCCCTCCACACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCACCGTGTGCAAGCACGGCCTGTGCCGC
TCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAGGCTGGACCGGCCCACTCTGCGACAGGAGGCCCGG
GACCCCTGCCTCGGCCACAGATGCCACCATGGAAAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCC
GAGGGCTATGGAGGGGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTACCCAT
GGGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAA
CAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACA
GCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGGCTGTGGGCCCCAGTGCTGCCAGCCCACCCGACGCAAGCGG
CGGAAATACGTCTTCCAGTGACGACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGC GGCTGC
CTCGCGTGTTCCTAAGCCCCCTGCCCCCCTGCCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCAT
GTGGGACCCCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAGTA
TATTGTAAAATAAACAAAAATAGAACTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 290

MAPGWAGVGA AVRARLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITR
ITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLNKNKLQVLPPELLFQSTPKLTRLDLSENQIQGIPR
KAFRGITDVKNLQLDNNHISCIEDGAFRALRDLEILTLNNNNISRLVTSFNHMPKIRTLRLHSNHLCDCHLAW
LSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME
IPANLPEGIVEIRLEQNSIKAIPAGAFTQYKKLKRIDISKQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLF
DGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHLAQNPVFCDCHLKWLAD
YLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLVR
IPSHLPEYVTDLRRLNDNEVSVLEATGIFKKLPNLRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRV
FRGLSGLKTLMLRSNLISCVSNDTFAGLSSVRLLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG
KWLRRKRIVSGNPRCQKPFLLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLRALPRGM
PKDVTELYLEGNHLTAVPRELSALRHLLTLIDLSNNSISMLTNYTFSNMSHLSTLILSYNRLRCIPVHAFNGLRSL
RVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHDCDCSLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTTPT
HRFQCKGPVDINIVAKCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGDCTVPINTCIQNPCQHGGTCHLSDS
HKDGFSCSCPLGFEGQRCEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPELNLQHEAK
CIPLDKGFSCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMVLLQTSPCDQ
YEQNGAQCI VVQOEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGD
NDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHSVELVTNLNQTNLNVVDKGTPKSLGKLQKQPAVGINS
PLYLGGIPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDS
VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHIS
DQGEPYCLCQPGFSGEHCQENPCLGQVVREVIRROKGYASCATASKVPIMECRGGCGPQCCQPTRSKRRKYVFO
CTDGSSFVEEVERHLECGCLACS

Signal peptide:
amino acids 1-27

FIGURE 291

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCAGACTCAACTGAGA
AGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCTG
CGGGCATTCTGACCCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGTTGCAAACTGGCAA
AAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCCTTGGAAGCTGGATCTGCATGGCATATTATG
AGAGCGGCTACAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCAACA
GCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGCTCAGCCTTGATCACTG
ATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACAAGGAATGAAC TATTGGCAAGGCT
GGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAGTGGAAAAAAGGCTGTGAGGTTTCC TAAACTGGAAGTGGAC
CCAGGATGCTTTGCAGCAACGCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCCGTTTCCT
CCCAATATTCTTCTCAAACCTGGAGAGGGAAAAATTAAGCTATACTTTTAAGAAAAATAATATTTCCATTAAATGTC

FIGURE 292

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAPTVLDDGSIDYGIF
QINSAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMNYWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:
amino acids 1-19

FIGURE 293

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTACCCAAGGAAAG
TGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTCTCATAGCGACCACCAGAGGA
TGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGC
AAGGAAATCAAAGACGAATGTCCTAGTGCATTTGATGGCCTGTATTTCTCCGCACTGAGAATGGTGTTATCTAC
CAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGT
GGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC
TGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACTACGAC
ATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCAATAAGTCCCCCATGCAGCACTGGAGAAAACAGCTCCCTG
CTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCA
GTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCC
CAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCAGTGCGGGATTTGTTTCAGTTCAGGGTATTT
AATAACGAGAGAGCAGCCAACGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATT
GGTGGAGGAGGATACTTTCCAGAGGCCAGTCCCAGCAGTGTGGAGATTTTCTGGTTTGTATTGGAGTGGATAT
GGAACTCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCATTCGTTGAGAGTTT
TGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCAGTAGCTAGA
ATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 294

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG
GGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIW
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYGEGKCWTDNGPVI PVVYDFGDAQKTASYSP
YGQREFTAGFVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQCGDFSGFDWSGYGTHVGYSSS
REITEAAVLLFYR

FIGURE 295

CAGGCCATTTGCATCCCCTGTCCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGTGTCATGTGTTAAAAA
CGCCAAGCTGAATATATCATGCCCCCTATTAAACTTGTACATGGCTCCCCATTGGTTTTTGGAGAAAAGTTCAAG
CTTTTTACCTTGGTGTCTGCCCTGTATCCCAGTGTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGT
CACTTCCCAGATCTGCTTCTCACCAGAGAGATTCTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATA
GAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAGGAAACA
TTCAAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAGCTTTGACTCAGTTGTT
CCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGCTGCTCTCCATCAACAGATACGAAAGGAAG
AAAAATCTGACTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTT
CATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG
GTCCAACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTCTCAGACAAACAGAAAATCTCCCTCCTC
CACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATG
CAGTGCCCAGTCATTGCTGTTAATTTCGGGTGGACCTTGGAGTCCATTGACCACAGTGTACAGGGTTTCTGTGT
GAGCCTGACCCGGTGCACCTTCTCAGAAGCAATAGAAAAGTTCATCCGTGAACCTTCCTTAAAAGCCACCATGGGC
CTGGCTGGAAGAGCCAGAGTGAAGGAAAAATTTCCCCTGAAGCATTTACAGAACAGCTCTACCGATATGTTACC
AAACTGCTGGTATAAATCAGATTGTTTTTAAGATCTCCATTAATGTCAATTTTATGGATTGTAGACCCAGTTTGA
AACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTTAAAAAATAAACTTGAGTCTTGAATGTGAGCCA
CTTTCCTATATACACACCTCCCTGTCCACTTTTCAGAAAAACCATGTCTTTTATGCTATAATCATTCCAAATTT
TGCCAGTGTTAAGTTACAAAATGTGGTGTCAATCCATGTTTCAGCAGAGTATTTTAATTATATTTTCTCGGATTAT
TGCTCTTCTGTCTATAAATTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAGTGTGTATCATTATCA
AAGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAATCCACCGAAGTGT
TCACTGTCTCTGTTAGGGAATTTTGTGTTGTCTGCTTTGCCTGGATCCATAGCGAGAGTGTCTGTATTTTTT
TTTAAGATAATTTGTATTTTGCACACTGAGATATAATAAAAGGTGTTTATCATAAAAA

FIGURE 296

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLLARRRKKILFYCHFDPDLLLTKRDSFLKRLYRAPIDWIEEYTTG
MADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVPEKLDDLVPKGKKFLLLSINRYERKKNLTLA
LEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCV
LYTPSNEHFGIVPLEAMYMQCPVIAVNSGGPLESIDHSVTGFLCEPDVHFSEAEKFIREFSLKATMGLAGRAR
VKEKFSPEAFTEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 297

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTTCGCCGTTACCTTC
TTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGACAAGCTGCAGGAATTCAGGGATTACT
CCAACTGAAGAAAAAGATGGTAATCTTCCAGATATTGTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTG
CATGAGAGATATGGGCCTGTGGTCTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTA
CTGAAGCAGCATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTATCAA
TCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGTGACTGATTCTCTGAAG
AGTAACCTTTGCCCTCCTCTAAAGCTTTCAGAAGAATTATTAGATAAATGGCTCTCCTACCCAGAGACCCAGCAC
GTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCTATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAA
GATGATCAGGAAGTCATTCGCTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGAT
GGGTCACTTGATAAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTTTTAAGG
AACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTTCATTGACTCCTTAGTACAAGGGAACCTT
AATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGGCCAGTTGCATAATAACTGCAAAATTGTGTACC
TGGGCAATCTGTTTTTTAACCACCTCTGAAGAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGG
AATGGTCCTGTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAACTGTTGAACT
GCCAACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTTATTATTCCTAGAGAG
ACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCCATCTCCACACAAGTTTGATCCA
GATCGGTTTGATGATGAATTAGTAATGAAACTTTTTCTCACTTGGATTCTCAGGCACACAGGAGTGTCCAGAG
TTGAGGTTTGATATATGGTGACCACAGTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAG
GGACAGGTTATTGAAACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGA
TATTAAAATTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACATTTAAAAAAATCTATGTTG
AATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTACTTAA

FIGURE 298

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVSFWFGR
RLVVS LGTV DVLKQHINPNKTS DPFETMLKSLRLRYQSGGGSVSENHMRKKLYENGVTDSLKSNFALLLKLSEELL
DKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHGTWVSEIGKGFLDGS LDKNMTRKKQYE
DALMQLESVLRNIIKERKGRNFSQHIFIDSLVQGNLNDQQILED SMIFSLASCIITAKLCTWAICFLT TSEEVQK
KLYEEINQVFGNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVL YALGVVLQDP
NTWPSPHKFD PDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT TVLLSVLVKRLHLLSVEGQVIETKYELVTSS
REEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 299

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGAGACCGCCGCCCTT
GTCCCGGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACGCTCCTGGCGCATCTGGTGGT
CGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTGCCTGCCTCTCACGTTCACCCCGAGGAGTA
TGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCTCTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTT
CCTCTCAGGAGTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGC
CCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACTACGTATTGGTACATTTTTGTCTTCTGCAGTGGCCCTTCC
AGCTGTCACTGAAATGGCTTTATTCGTCACCGCTCTTGGGCTGAAAAAGAAACCCCTTCTTGATTACCTTCATGACG
GGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTT
TTCCCTCGGAAACTGCTTCTGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATT
GTATTTAGTGCTTTGTAATAAAATATGTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACAATTAAA
AAAAAAAAA

FIGURE 300

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPFTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV
SMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 301

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGACTCGCTGCTGC
TTCGTGTTCTCGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATGGTCCTCCCGGCTCAGAGGAC
CCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAAGTCC
CGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCC
CCCAACCGCCCGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCC
AACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTC
CACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAGAGTTC
CACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTA
GAACGGGGCCGCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCA
GCCACCTGGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATCGGCTG
GTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCCCTACTACCCATCTGGGTGAACCGGGGCAGGC
CACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGG
GTTGGGCCCTCAGGCAGGGAGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTG
GGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCCTGTGGGCAG
GCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTTCTTGCCATCTTGAGGAAAGATA
GCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAG
GAGCCAGTCAGCAGGGTGGGGTGGGGCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTTGTC
GTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCT
CCAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATGGCACA
CCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCCACTAAGGCCACAGCCCATCCGCGTGCTGTGTGTC
CCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCC
TCACCTGTGACACGGGGTTCTCCCGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGC
CGGGCCGCAGAGCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGTGA
AACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGAGCAGGAAATAAAGCTTGCCCCGGGGCA

FIGURE 302

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEA
WGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP
PSKAVEFHQEQQIFIEAKASKIFNCRMWEEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAF
YSTDYRLVQKVC PDYNYHSDTPYYP SG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 303

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCCCTTTATGTCT
TCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTTCTGGTTGGTGTCTCTACTGA
TTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA
TCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCA
GTGAAGGTTTGAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGG
GCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCATCTGACTCCTTGGGGCCAGGCACAGTGGGCA
TTCATGGAGATTCTCCTCAATTCTTCCTTTATTTCAGCTTTCATGACGCTGGTCATTATCTTGCTGCATGTATTCT
GGGGCATTGTATTTTTTGATGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGC
TGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCA
TGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGA
ACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTA
GAGGAAGCACAACTGTGCCTTTTCTGAAAATCCCTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

FIGURE 304

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKGPTQKYLLIFG
AFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGP GTVGIHG
DSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGT
WAFLAAGGSCRSCLKLCLLCQDKNFLLYNQSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 305

[illegible]

FIGURE 306

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGS LPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 307

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAAGAAAAATTTTTTG
GGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAAATTGAGTCAACTAGTGAATTCAAACA
ACTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCTTCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTGAGTC
TGCAGGCATTTAAATCCTTCCTGAGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTT
TAGACAATGAAGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGGCTT
ACCATTCCTTGGAAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCTGACCTGGCGAGCAGGGGTGA
AGATTGGACATTCGTTTGAAGAACCGGCCGATGTATGTACTGAAGTTCAGCACTGGGAAAGGCGTGAGGCGGCCGG
CCGTTTGGCTGAATGCAGGCATCCATTCCCGAGAGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGA
TTGTATCTGATTACCAGAGGGATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTCTTGTTCCTGTGG
CCAATCCTGATGGATATGTGTATACTCAAAC'TCAAAACCGATTATGGAGGAAGACGCGGTCCCGAAATCCTGGAA
GCTCCTGCATTGGTGCTGACCCAAATAGAAACTGGAACGCTAGTTTTGTCAGGAAAGGGAGCCAGCGACAACCCCTT
GCTCCGAAGTGTACCATGGACCCACGCCAATTGCGAAGTGGAGGTGAAATCAGTGGTAGATTTTCATCCAAAAAC
ATGGGAATTTCAAGGGCTTCATCGACCTGCACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCA
AAAAGGCCCCAGATGCCGAGGAAC'TGACAAGGTGGCGAGGCTTGCAGGCCAAGCTCTGGCTTCTGTGTGGGGCA
CTGAGTACCAAGTGGGTCCACCTGCACCCTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGGCGTATGACA
ACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGCTTCTCTGCCAGCTAACCCAGA
TCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGACCATCATGGAGCATGTGCGGGACAACCTCTACTAGG
CGATGGCTCTGCTCTGTCTACATTTATTTGTACCCACACGTGCACGCCTGAGGCCATTTGTAAGGAGCTCTTT
CCTACCTGTGTGAGTCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCTGCCCTCTCCAGCCAGCTCCCTGGAG
TCGTGTGTCTCTGGCGGTGTCCCTGCAAGAACTGGTTCCTGCCAGCCTGCTCAATTTTGGTCTGTCTTTTGATG
AGCCTTTTGTCTGTTTTCTCTTCCACCCTGTGGCTGGGCGGCTGCACTCAGCATCACCCCTTCTGGGTGGCAT
GTCTCTCTCTACCTCATTTT'TAGAACCAAAGAACATCTGAGATGATTCTCTACCCCTCATCCACATCTAGCCAAGC
CAGTGACCTTGCTCTGGTGGCACTGTGGGAGACACCCTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTT
CCTTTAATTTCTCGCAGTCTTCTTGGAAAAATATTTTCTTTGAGCAGCAAATCTTGTAGGGATATCAGTGAAGGT
CTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGTAGACAGAGTTTTGCTCTTGTGTTGCCAGGCTGGAGTGTGA
TGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAGCAATTCTCCTGCCTCAGCCTCTTGAGTAGC
TTGCTTTATAGGCGCATGCCACCATGCCTGGCTAATTTTGTGTTTTTGTAGTAGAGACAGGTTTTCTCCATGTTGGT
CAGGCTGGTCTCAAAC'TCCCAACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTG
AGCCACTGTGCCGGGCGGTCCTCTCTTTT'TAGGCCTGAATACAAAGTAGAAGATCACTTTCTTCACTGTGC
TGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTAGTGTGACCAGGATGGCGGGAGGG
GATCTGTGTCACTGTAGGTACTGTGCCCAGGAAGGCTGGGTGAAGTGACCATCTAAATTCAGGATGGTGAAATT
ATCCCCATCTGTCTAATGGGCTTACCTCCTCTTTGCCTTTTGAAC'TCACTTCAAAGATCTAGGCCTCATCTTAC
AGGTCTAAATCACTCATCTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCT
GTGTTTCTTGTCTGTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
TTTTGTATCTTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCTGCCTCTTGTTTTCACTTACCT
CAGCACGTACCATCTGTCTTTTGTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
TCTTAACCTCCTGCCTAGGATTTGTACAGCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAA
AAAAAAAAA

FIGURE 308

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNRPVDVLVPSVSLQA
FKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNYGAYHSLEAIYHEMDNIAADFEDLARRVKIG
HSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWISQATAIWTARKIVSDYQRDPATTSILEKMDIFLLPVANP
DGYVYTQTQNRLWRKTRSRNPGSSCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGN
FKGFIDLHSYSQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYDNGI
KFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLV

Signal peptide:
amino acids 1-16

FIGURE 309

GGCTGACCGTGCTACATTGCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCCACGCCTGAGTCCAAGAT
TCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTATCTCTTCACCTTCAAGTCCC
CTTTCTCAAGAATCCTCTGTCTTTGCCCTCTAAAGTCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGC
CACAAAGAGACAGATGAAGATGCAGAAAGGAAATGTTCTCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGC
AACAAATTCCAATGAGACTAGCACCTCTGCCAACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCAC
CAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGG
GGTCAGCATAGTACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAGTTCAG
CACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGAGTCCAGCACACCCTCCAGTGGGGCCAGCACAGTCCACCAACTCTGGGTCCAGTGTGACCTCCAGTGG
AGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAG
CACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAG
GGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTCCAG
CACAACCTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCA
CAATTCTGAGTCCAGCACACCCTCCAGTGGGGCCAAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGG
GGCCAAACACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG
CACAACCTCCAGTGGGGTCCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG
GATCAGCACAGTCAACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCAAACACAGCCACCAACTCTGGGTCCAG
TGTGACCTCTGCAGGCTCTGGAACAGCAGCTCTGACTGGAATGCACACAACTTCCCATAGTGCATCTACTGCAGT
GAGTGAGGCAAAGCCTGGTGGGTCCCTGGTGCCCTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGC
CGTGGGGCTCTTTGCTGGGCTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGT
CTACCACCTCATGGCTCAACCATGGCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
GTGGAGTCTTAAGTGTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC
CTGAGCAGCCCCGGAAGCAAGTGCCGATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTT
CATTTCATCCCAGGAGACCCCTCCCAGCTTTGTTTGGATCCTGAAAATCTTGAAGAAGGTATTCTCACCTTTCT
TGCTTTTACCAGACACTGGAAAAGAGAATACTATATTGCTCATTAGCTAAGAAATAAATACATCTCATCTAACAC
ACACGACAAAGAGAAGCTGTGCTTGCCCCGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAAA
CTCCATGCTGGACTCCATCTGGCATTCAAATCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 310

MKMQKGNVLLMFGLLLHLEAATNSNETSTSA NTGSSVISSGASTATNSGSSVTSSGVSTATIS
GSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESS
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS
SGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGA
GTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTA
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNS
ESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESS
TVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS
LVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP
HRPRWSPNWFWRPVS SIAMEMSGRNSGP

Signal peptide:
amino acids 1-20

Transmembrane domain:
amino acids 510-532

FIGURE 311A

CTAAGCCGGAGGATGTGCAGCTGCGGCGCGGCGCGGCTACGAAGAGGACGGGGACAGGCGCGTGC GAACCGA
GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCGCGCCGCGTCTGCGCGTCG
TGCCGCGCCCGCGTCCCCGCGCGAGCGGGAGGAGCCGCGCCACCTCGCGCCCGAGCCGCGCTAGCGCGCGC
CGGGCATGGTCCCTCTTAAAGGCGCAGGCCGCGGCGGCGGGGCGGGTGTGCGGAACAAAGCGCCGCGCGGGG
CCTGCGGCGCGCTCGGGGCGCGATGGGCGCGGCGGGCCCGCGGCGGCGGCGCTGCCCCGGCCGGGCGCTCG
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGCGAGCGGGCTGAGGCGCGCGGAGCCTGCGGCGCGCGGGC
GGCGGCGCGCGGCGGCGGCGGCGGAGCGGCGCGGGCATGGC CGCGCGGCGCGGCGCGCTGGCTCAGCGTGC
TGCTCGGGCTCGTCTGGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCCGGGCTTCGAGCTGAAGCGAGCGG
GCCCACGGCGCGCGCCAGCCCCGAGGGCTGCCGGTCCGGGCAGGCGGCGGCTTCAGGCGCGGCGGGCGCGCG
GCGATGCGCGCGGGGCGCAGCTCTGGCCGCGCGGCTCGGACCCAGATGGCGGCGCGCGGACAGGAACCTTCTCT
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAAGACAA
TTCTTGGAAAGTTTCAAGTTCTTCTCAAGTGAGGGTTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG
GTGTGGACGACTCCTACCGCCCCAGAAAGTCTTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACCTTCTGAGGAGTT
TGAACAGCAGCGAGCCCCCTCTTCTTGGGCAGACAGGCCTGGGCACCACGGAAGAAATGGGAAAACTGGCCCTGG
AGCCTGGTGAGAACTTCTGCATGGGGGGGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAATGGTGCCGC
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT
ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACACCCCAACAAAAACCCACCTACCAGT
ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA
TTGTCTGTATGAGCAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCCTTCA
TGAGGTTTCAGCCCCCGCAGCGAGAGGAGATTTCTGGAATGGGAGTTTCTGACTGGAAAATACCTGTATTTCGGCAG
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCCAGAGGGAAGCCTTGGACGACATTGTATGCAGGTCA
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCC
GGGTGAACCCCATGTATGGGGCTGAGTACATCTGGACCTGCTGCTTCTGTACAAAAAGCACAAAGGGAAGAAAA
TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAGC
TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTTTCTCTCAAACCTCCCTGAAGA
AGCTCGTCCCTTTTCACTCCCTGGGTGCAAGAGTGAGCACAAAGAACCCAAAGATAAAAAGATAAACATACTGA
TTCTTTGTCTGGGCGTTTTCGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGACGTGTCTTATCCCCAATC
AGAACGTCAAGCTCGTGGTTCTGCTTTTCAATCTGACTCCAACCTGACAAGGCCAAACAAGTTGAAGTATGATGA
GAGATTACCGCATTAAGTACCTTAAAGCCGACATGCAGATTTTGCCCTGTGTCTGGAGAGTTTCAAAGAGCCCTGG
CCCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTCTGCGACGTCGACCTCGTGTTTACTA
CAGAATTCCTTCAGCGATGTGAGCAAATACAGTTCTGGGCCAACAAATATATTTTCCAATCATCTTCAGCCAGT
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCCTTACTCAGAAAACTGGCTTCT
GGAGAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
TCCAAGGCTGGGGGCTGGAGGATGTGACCTTTTCAACAAGGTGTGTCAGGCAGGTTTGAAGACGTTTAGGAGCC
AGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTTGTGATCCCAATCTTGACCCCAAACAGCTACAAAATGT
GCTTGGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
TAATTATCTAATTTATTTTTCAAAAATTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
AAGTGGTTTTCTTACATAGGACTCCTTTAAGATTGAGCTTTCTGAACAAGAAGGTGATCAGTGTGTGCTTTGAA
CACATCTTCTGCTGAACATTATGTAGCAGACCTGCTTAACTTTGACTTGAAATGTACCTGATGAACAAAACCTTT
TTTTAAAAAATGTTTTCTTTTGAGACCTTTTGCTCCAGTCTTATGGCAGAAAACGTGAACATTCCTGCAAAGTAT
TATTGTAACAAAACACTGTAACCTCTGGTAAATGTTCTGTTGTGATTTGTTAACATTCCACAGATTCTACCTTTTGT
GTTTTGTTTTTTTTTTTACAATTGTTTTAAAGCCATTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC
CACGTAGGTTTTTTGTTTGTGTTTTGTTTGTCTTTTTTTGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG
CAGTGGCGCAATCTTGGCTCACTTTAACTCCACTTCCCTGGTTCAAGCAATTCCTGCTTTGCTTCCCGAGT
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTTTGTATTTTTAGTAGAGACGGGGTTTACCAT
GCAAGCCAGCTGGCCACGTAGGTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
TGGTAGTTTCAATTCGGCCTAAATAGACCTGGCATTAATTTCAAGAAGGATTTGGCATTTTCTCTTCTTGACCCTT
CTCTTTAAAGGGTAAATATTAATGTTTAGAATGACAAAGATGAATTATTACAATAAATCTGATGTACACAGACT
GAAACATACACACATACCCCTAATCAAAACGTTGGGGAATAATGATTTGGTTTTGTCTTTTCTCTCTGCTG
TGTTATGTGGGTGGAGATGGTTTTTCAATCTTCACTGTTTTGTTTTATCCTTTGTATCTGAAATACCTTTAA

FIGURE 311B

TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
GAGTGTGTTTAGTCTGTTTATTTGCAGTAAACCGATCTCCAAAGATTTCTTTTGGAAACGCTTTTCCCTCC
TTAATTTTATATTCTTACTGTTTACTAAATATTAAGTGTCTTTGACAATTTGGTGCTCATGTGTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCCTGTTTGTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAAA

FIGURE 312

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGARG
DARGAQLWPPGSDPDGGPRDRNFLFVGVMATAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEGS
TSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFWMRADDVYIKGDRLENFLRSLN
SSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYTTHE
VEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPPYQYRL
HSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQREEILEW
LTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQYGYRRVNP
MYGAEYILDLLLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKRINQESG
SFLSNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTCLIPNQNVKL
VLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQFNNESSLFFC
DVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYG
GITCIYKGD LVRVGGFDVSIQGWGLEDDVDFNKKVQAGLKTFRSQEVGVVHVHHPVFCDPNLD
PKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:
amino acids 1-23

FIGURE 313

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCC
TACGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTGACA
GGTGGGAGGCTGGAACATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA
ACAAATGGATGATGTGATATATGCAATTCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT
GGTCAATTAACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT
TTGGAATCATGGTGTCATGGAAAGGGATTACTTTATACTGACTCTGTTTTGGGGAAGCTTTT
TTGGAAGCATTTTCATGCTGAGTCCCTTTTACCTTTGATGTTTGTAAACCCATCTTGGTATC
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCA
TGTTTGGTGTAAGAGTGATTATAACTGGGGATGCATTTGTTCCCTGGAGAAAGAAGTGTCATTA
TCATGAACCATCGGACAAGAATGGACTGGATGTTCCCTGTGGAATTGCCTGATGCGATATAGCT
ACCTCAGATTGGAGAAAATTTGCCTCAAAGCGAGTCTCAAAGGTGTTCCCTGGATTTGGTTGGG
CCATGCAGGCTGCTGCCTATATCTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTCG
AAGACATGATTGATTACTTTTGTGATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAG
GGACTGATCTCACAGAAAACAGCAAGTCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTC
AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA
GAGAAGGTAAGAACCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACAACATTCCTC
AATCAGAGAAGCACCTCCTCCAAGGAGACTTTCCAGGGAAATCCACTTTTCACGTCCACCGGT
ATCCAATAGACACCCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGGG
AAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAGGGGAGAAGAATTTTATTTTACCGGAC
AGAGTGTCATTCCACCTTGCAAGTCTGAACTCAGGGTCCTTGTGGTCAAATTGCTCTCTATAC
TGTATTGGACCCTGTTTACGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTTAAGT
GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA
TCATAGAATTGTCATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG
AGTAAGATTATAAGGTTTGGCATGTGAAAACCTAGAGCATATTTTGGAAATGTTCTAAACCTT
TCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACTGCCATCATTATTTGT
TAAAGATATTTTGCACCTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTTAACTCTCTGAA
TGTAATTTTCGATACTGTGTACATAGCAGGGAGTGATCGGGGTGAAATAACTTGGGCCAGAATA
TTATTAAACAATCATCAGGCTTTTAAA

FIGURE 314

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFIMVSWKGIYFILTLFWGSFFGSIFML
SPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTR
MDWMFLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYF
CDIHEPLQLLIFPEGTDLTENSKSRSNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLD
AVHDITVAYPHNIPQSEKHLLQGDFPREIHFFHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERL
RSFYQGEKNFYFTGQSVIPPCKSELRLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITI
VIFVLQERIFGGLEIIEIACRYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

FIGURE 315

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGA
 CCTCCAAATCATCCATCCACCCCTGCTGTCTGTTTTCATAGTGTGAGATCAACCCACAGG
 AATATCCATGGCTTTTGTGCTCATTGTTGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTG
 GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG
 CTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAGTTCCA
 TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG
 AGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGCTAAAAAA
 CATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCACTTCCCAGATTTACGATGAGGA
 GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCTCTCATTTCATCGTGGGATA
 TGTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGAGCCACAGCCAA
 GTGGAAAGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAAATGCAGATGGGTACAG
 CCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCAT
 CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA
 GCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGGCCTGTGTGGTGT
 TGTCTATGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCAGGCGGAACTGGACTG
 GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCT
 GGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAATGTAACCCATAGAAA
 AGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA
 GGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT
 GGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGG
 GTATTGGGTCTCAGACTGACAACAGAACATTTGTATTTTACATTCAATCCCCATTTTATCAG
 CCTCCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCTGACTATGAGGGTGGGACCAT
 CTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTCAGTTTGAAGG
 CTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTTCAT
 ATGTCCAGTGTCTTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACAGACC
 CAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCTCTCCGGAGCCTGCGC
 ACAGAGAGTACGCCCCCCTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA
 GCAGCGGCAGTACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAGTCAGAAGCC
 ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAATCCATC
 CAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTGCTAGTCACGGACAGT
 GATTCTGCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTTTGA
 GGGCACAGTGTGCTAATGATGTGTTTTATATTATACATTTTCCCACCATAAACTCTGTTT
 GCTTATTCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC
 CTGCTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATCTATAAGCCAG
 CATTACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAACACTACAGGTCCA
 TATCCCTCATTAACACAGACACAAAAATTTCTAAATAAAATTTTAAACAAATTAACATAAACAAT
 ATATTTAAAGATGATATATAACTACTCAGTGTGGTTTGTCCCACAAATGCAGAGTTGGTTTAA
 TATTTAAATATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAAA
 AAAAAAAA

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV
VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLY
DVEISIIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVM
GMIIVFFKSKGKIQAELDWRRKHGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVTHRKAP
QEVPHSEKRFTTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYW
VLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLL
RPYIQHAMYDEEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 317

GCACCTGCGACCACCGTGAGCAGTC**ATGG**CGTACTCCACAGTGCAGAGAGTCGCTCTGGCTTC
TGGGCTTGTCCTGGCTCTGTCGCTGCTGCTGCCCAAGGCCTTCCTGTCCCGCGGGAAGCGGCA
GGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCACCA
GGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTTCCAGAGGTCTCACCTTGCCGAGGCATT
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTGATGGG
GCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTTATATATACTGTACATTCTATTTAAGGT
AAGTAGAATCATCCTAATCATATTACATCAAT**TG**AAAATCTAATATGGCGATAAAAATCATTGT
CTACATTAAAACCTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTAAATCCTGC
CTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATGTTTACTCAA
TGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTTGAACATGGAT
CTTTTGGTTCCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

FIGURE 318

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPPTPEGKLGRFPPMMHHHQAPSDGQTP
GARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPIYGFIFLYILYILFKVSRIILILHQ

FIGURE 319

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAG
GAAAAGAGTTTGGTTGGGAACCCCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCCT
GGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAGAAGACCTACAATTA
CTATAGCACATTGTCAATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAA
CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC
ATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGGAGTGT
GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAACTGTAGATAAAAT
TGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAGATCCTCA
CTCAGTTAAAATTAAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG
AACACGAAGAAGTAAACTCTAGGTGAGAGTCTCAGGATCGTTGGTGAGGACAGAAGTAGAAGA
GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTT
AATTAATGCCACATGGCTTGTGAGTGTGCTCACTGTTTTACAACATATAAGAACCCTGCCAG
ATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAAT
AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGACAGAGCTTTC
TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT
TCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAATGATGGTTACAGTCA
AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTTGCAATGAACCTCAAGC
TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC
ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGC
TGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTTTATACTAGAGT
TACGGCCTTGCGGGACTGGATTACTTCAAAACTGGTATCTAAGAGACAAAAGCCTCATGGAA
CAGATAACATTTTTTTTTTGGTTTGGGTGTGGAGGCCATTTTATAGAGATACAGAATTGGAGA
AGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAACTGTTTGCTTGATGCATGTATTTT
CTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA
GCAATAGTTGAACTTTATGTACATAGAGAAATAGATAATACAATATTACATTACAGCCTGTA
TTCATTTGTTCTCTAGAAGTTTGTGACAGATTTTGTGACTTGTGACATAAATTTGTAATGCATA
TATACAATTTGAAGCACTCCTTTTCTTCAGTTCCTCAGCTCCTCTCATTTTACAGCAAATATCCA
TTTTCAAGGTGCAGAACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTA
TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTTCATTAT
GAAAGGTCAAGCAAAGACAGCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACATA
GTTAAGGAAGTCCAGAAAGAAGCCAAGATATATCCTTATTTTCATTTCCAAACAACACTACTATG
ATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCTATAATAATTATACAACTTCATGCAATG
TACTTGTCTAAGCAAATTAAGCAAATATTTATTTAACATTGTTACTGAGGATGTCAACATA
TAACAATAAAATATAAATCACCCA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTDK
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFH
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIK
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDVMFVTG
FGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLV
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 321

CCGGGCTCCTGGGTGAGGCCGGCAAGTTTGGAGCGTGGTCAGACAATAGGGGCGTGGCTACGG
CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTTGGCTTT
AACAGTACGTGGGCGGCCGGAATCCGGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG
CGGAGCCCAGAAGAAGGGGCGGGGTATGGGAGAAGCCTCCCCACCTGCCCCGCAAGGCGGCA
TCTGCTGGTCCTGCTGCTGCTCCTCTCTACCCTGGTGATCCCCTCCGCTGCAGCTCCTATCCA
TGATGCTGACGCCAAGAGAGCTCCTTGGGTCTCACAGGCCCTCCAGAGCCTACTCCAAGGCTT
CAGCCGACTTTTTCCTGAAAGGTAACCTGCTTCGGGGCATAGACAGCTTATTCTCTGCCCCCAT
GGACTTCCGGGGCCTCCCTGGGAAC TACCACAAAGAGGAGAACCAGGAGCACAGCTGGGGAA
CAACACCCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGGAGAGGTGCT
GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGGAGCTTCGAGGGTGATTTGAA
GGTACCCAGGATGGAGGAGAAGGAGGCTCCTGGTACCCATCCAGAAGGCCACGGACAGCTTCCAC
ACAGAACTCCATCCCCGGGTGGCCTTCTGGATCATTAAGCTGCCACGGCGGAGGTCCCACCAG
GATGCCCTGGAGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCCTGCAGGCCATCCGGGAT
GGACTCCGCAAGGGGACCCACAAGGACGTCCTAGAAGAGGGGACCGAGAGCTCCTCCCCTCC
AGGCTGTCCCCCGAAAGACCCACTTACTGTACATCCTCAGGCCCTCTCGGCAGCTGTAGGGG
TGGGGACCGGGGAGCACCTGCCTGTAGCCCCCATCAGACCCTGCCCCAAGCACCATATGGAAA
TAAAGTTCTTTCTTACATCTAAAAA

FIGURE 322

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27007, pI: 8.68, NX(S/T): 2
MGEASPPAPARRHLLVLLLLLSTLVIPSAAAPIHDADAQESSLGLTGLQSLQGF SRLFL
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLQIDKMTDNKTGEVLIS
ENVVASIQPAEGSFEGDLKVP RMEEKEALVPIQKATDSFHTELHPRVAFWIIKLPRRRSH
QDALEGGHWLSEKRHRLQAIRDGLRKGTHKDVLEEGTESSSHSRLSPRKTHLLYL RPSR
QL
```

Important features of the protein:

Signal peptide:

Amino acids 1-30

N-glycosylation sites:

Amino acids 97-101;112-116

N-myristoylation sites:

Amino acids 80-86;132-138;203-209;216-222

FIGURE 323

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCC
 TGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCGGGCC
 CAGCGCCGACGATCGCTGCCGTTTTGCCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTC
 TCCCTTACGGGGCTCACAATGGCCCAGAGAAGATTCCGTGAAGTGTCTGCGCTGCCTGCTCTAC
 GCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGG
 GACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTG
 ACTTACTTTTCTGTGGTTCATCCGTCATGATTGCTGTTTGCTGTTTCCCTTATCATTGTGGGG
 ATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTGGAAGT
 TTGCTTGTCATTTTCTGTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTATG
 GTTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTATGGATTACCT
 AGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTA
 GTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCTGCTGTGTT
 AGAGAATTTCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
 GGTGTGGGAAGAAAATGTATTCCCTTTTTTGAGAGGAACCAAACAAGTGCAGGTGCTGAGGTTT
 CTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGG
 GCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCTTGAAGAATGACAAC
 TCTCAGCACCTGTCTATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAA
 CACACATCCATGGCAAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAAGAAATG
 TCACAGAAGAAAACCACAAACTTGTTTTATTGGACTTGTGAATTTTTTGAGTACATACTATGTG
 TTTTCAGAAATATGTAGAAATAAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA
 TGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGATGC
 CCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAAC
 ACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTCCGCATCCATGCAAACGAGTCACA
 TATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCAACTAGTATATAAAGTACT
 AATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTC
 TTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACTACCTAAATGTGAT
 TTTTGCTGGTTACTAAATATTCTTACCACTTAAAAGAGCAAGCTAACACATTGTCTTAAGCT
 GATCAGGGATTTTTTGTATATAAGTCTGTGTTAAATCTGTATAATTCAGTCGATTTTCAGTTCT
 GATAATGTTAAGAATAACCATTATGAAAAGGAAAAATTTGTCCTGTATAGCATCATTATTTTTA
 GCCTTTCCTGTTAATAAAGCTTTACTATTCTGTCTGGGCTTATATTACACATATAACTGTTA
 TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGA
 ATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAA
 AGGACTTGTATGCTGTTTTTCTCCCAAATGAAGACTCTTTTGGACACTAAACACTTTTTAAAA
 AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGA
 AAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAATCATTAAAAATGTGACAATTTAG
 AGATTCTTTGTTTTATTTCACTGATTAATACTGTGGCAAAATACACAGATTATTAAATTTT
 TTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCAATTTTACTGTATTTTGTGTAT
 TTTGTTTATTTCTCAGAAATATGGAAAGAAAATTAAAATGTGTCAATAAATATTTTCTAGAGAG
 TAA

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV
HPVMIAVCCFLIIVGMLGYCGTVKRNLALLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGC
SKQAHQEDLSDLYQEGCGKMYSFRLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 325

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTCTGTTTTGAAAAA
GCAGAGATACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTCTTAGAGCAAGACA
ATCACCATCTGAATTCCAGAAGCCCTGTTTCATGGTTGGGGATATTTTCTCGACTGCATGGAAT
CAGAAAGAAGCAAAAGGATGGGAAATGCCTGCATTCCCCTGAAAAGAATTGCTTATTTCCCTAT
GTCTCTTATCTGCGCTTTTGCTGACTGAGGGGAAGAAACCAGCGAAGCCAAAATGCCCTGCCG
TGTGTACTTGTACCAAAGATAATGCTTTATGTGAGAATGCCAGATCCATTCCACGCACCGTTC
CTCCTGATGTTATCTCATTATCCTTTGTGAGATCTGGTTTTACTGAAATCTCAGAAGGGAGTT
TTTTATTACGCCATCGCTGCAGCTCTTGTTATTACATCGAACTCCTTTGATGTGATCAGTG
ATGATGCTTTTATTGGTCTTCCACATCTAGAGTATTTATTATAGAAAACAACAACATCAAGT
CAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAATTCATTGAGCCTTGCAAACAACA
ATCTCCAGACACTCCCAAAGATATTTCAAAGGCCTGGATTCTTTAACAATGTGGACCTGA
GGGGTAATTCATTTAATTGTGACTGTAACTGAAATGGCTAGTGGAAATGGCTTGCCACACCA
ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCCCAGAATACAAGAAGCGCAAAATCAATA
GTCTCTCCTCGAAGGATTTTCGATTGCATCATTACAGAATTTGCAAAGTCTCAAGACCTGCCTT
ATCAATCATTGTCCATAGACACTTTTTCTTATTTGAATGATGAGTATGTAGTCATCGCTCAGC
CTTTTACTGGAAAATGCATTTTCCTTGAATGGGACCATGTGGAAAAGACCTTCCGGAATTATG
ACAACATTACAGGCACATCCACTGTAGTATGCAAGCCTATAGTCATTGAAACTCAGCTCTATG
TTATTGTGGCCAGCTGTTTGGTGGCTCTCACATCTATAAGCGAGACAGTTTTGCAAATAAAT
TCATAAAAATCCAGGATATTGAAATTCTCAAATCCGAAAACCCAATGACATTGAAACATTCA
AGATTGAAAACAACCTGGTACTTTGTTGTTGCTGACAGTTCAAAGCTGGTTTTACTACCATTAC
AAATGGAACGGAAACGGATTCTACTCCCATCAATCCTTACACGCGTGGTACAGGGACACTGAT
GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAACGCCTCATTTAATTCTGTCT
AGTAGTTCCCAGCGTCCTGTAATTTATCAGTGGAAACAAAGCAACACAATTATTCATAACCAA
ACTGACATTCCTAACATGGAGGATGTGTACGCAGTGAAGCACTTCTCAGTGAAAGGGGACGTG
TACATTTGCTTGACAAGATTCATTGGTGATTCCAAAGTCATGAAATGGGGAGGCTCCTCGTTC
CAGGATATTCAGAGGATGCCATCGCGAGGATCCATGGTGTTCAGCCTCTTCAAATAAATAAT
TACCAATATGCAATTCCTGGAAGTGATTACTCCTTTACTCAAGTGTATAACTGGGATGCAGAG
AAAGCCAAATTTGTGAAATTCAGGAATTAAATGTTTCAGGCACCAAGATCATTACACATGTG
TCCATTAATAAGCGTAATTTTCTTTTTCCTTCCAGTTTTAAGGGAAATACACAGATTTACAAA
CATGTACATAGTTGACTTAAGCGCATGAGACACCAAAATCTGTGGCTGCCATCAGAAATTTTCT
ACAGTACATGACCCGGATGAACTCAATGCATGATGACTCTTCTTATCACACTTGCAAATGAAT
GCCTTTCAAACATTGAGACTGCTAGAACCAAGCACTACCAGTATCTCCATCCTTAACGTGCCA
GTCCAGTGATGTGGGAAGTTACCTTTTATAAGACAAAATTTAATTGTGTAAGTGTCTTTGCA
GTGAAGATGTGTAAATAAGCGTTTAAATGGTATCTGTTACTCCAAAAGAAATATTAATATGTA
CTTTTCCATTTATTTATTTCATGTGTACAGAAACAACCTGCCAAATAAAATGTTTACATTTTCTT
TCATA

FIGURE 326

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESERSKRMGNACIPLKRIAYFLCLLSALLLLEGKKPAKPKCPAVCTCTKDNCENARS
IPRTVPPDVISLSFVRSGFTEISEGSFLFTPSLQLLLFTSNSFDVISDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLIHLSLANNNLQTLPKDIFKGLDSLTVNVDLRGNSFNCDCCK
LKWLVEWLGHTNATVEDIYCEGPPEYKKRKINSLSKDFDCIITEFAKSQDLQPYQSLSID
TFSYLNDEYVVIAQPF TGKCIFLEWDHVEKTFRNYDNITGTSTVVCKPIVIETQLYVIVA
QLFGGSHIYKRDSFANKFIKIQDIEILKIRKPNDIETFKIENNWFVVDSSKAGFTTIY
KWNGNGFYSHQSLHAWYRDTDVEYLEIVRTPQTLRTPHLILSSSSQRPVIYQWNKATQLF
TNQTDIPNMEVDVYAVKHFSVKGDVYICLTRFIGDSKVMKWGGSSFQDIQRMPSRGSVMVFQ
PLQINNYQYAILGSDYSFTQVYNWDAEKAKFVKFQELNVQAPRSFTHVSINKRNFLFASS
FKGNTQIYKHVIVDLA
```

Important features of the protein:

Signal peptide:

Amino acids 1-34

Transmembrane domain:

Amino acids 281-306

N-glycosylation sites:

Amino acids 192-196;277-281;422-426

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 310-314

Tyrosine kinase phosphorylation sites:

Amino acids 228-235;378-385

N-myristoylation sites:

Amino acids 172-178;493-499

Amidation site:

Amino acids 33-37

FIGURE 327

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCC
 CTACCACTGCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGA
 AAGAGAAGGGGACAAAGGAACACCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTC
 CAGAAGGATGCCTCCATTCTGCTTCTCACCTGCCTCTTCATCACAGGCACCTCCGTGTCACC
 CGTGGCCCTAGATCCTTGTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA
 CCAGTTGGATGAGTCTCAAGGTCCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA
 CTTACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAAC
 CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTGTGCAACGCCA
 GGCTTGTGCCAGCTTCAATGGGAAGTGTGTCTCTGGAACACCACGGTGGAAAGTCAAGGCTTG
 CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCAGCGTCTGCTTCCACGTCTACTGTGG
 TCATTTTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATAACAGCGAGTGCAC
 ATGCGCTCCAGGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTGATGAAAATGAATGTGA
 GCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCTACCGCTGTGAGTG
 TGGGGTTGGCCGTGTGCTAAGAAGTGTGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA
 TAACAATGGTGGCTGCAGCCACTCTTGCTTGGATCTGAGAAAGGCTACCAGTGTGAATGTCC
 CCGGGGCTGGTGCTGTCTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAA
 TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTTGGTGGCCTGGAGCTCTTCTTGACCAACAC
 CTCTGCGGAGGAGTGTCCAACGGCACCCATGTCAACATCCTCTTCTCTCAAGACATGTGG
 TACAGTGGTTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA
 GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTGAC
 CTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCC
 ACTGGAATCATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAA
 TGAGTTTGAAGAGCCTTACCGGGAAGCTCTGCCCACCTCAAGCTTCGTGACTCCCTCTACTT
 TGGCATTGAGCCCGTGGTGCACGTGAGCGGCTTGGAAAGCTTGGTGGAGAGCTGCTTTGCCAC
 CCCCACCTCCAAGATCGACGAGGTCCTGAAATACTACCTCATCCGGGATGGCTGTGTTTCAGA
 TGAATCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGGTCCCTGTCTT
 CAAGTTTGTGGGCAAAGACCACAAGGAAGTGTTCCTGCACTGCCGGGTTCTTGTCTGTGGAGT
 GTTGGACGAGCGTTCCCGCTGTGCCCAGGGTTGCCACCGGCGAATGCGTCTGTTGGGCGAGGAGG
 AGAGGACTCAGCCGGTCTACAGGGCCAGACGCTAACAGGCGGCCCGATCCGCATCGACTGGGA
 GGACTAGTTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTC
 CCCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTTTCAGACTTCACACTGTGAGTTTCAG
 ACTCCCAGCACCAACTCACTCTGATTCTGGTCCATTTCAGTGGGCACAGGTCACAGCACTGCTG
 AACAAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAACCTAACTGTCCACCCAGAA
 AGACACTCACCCCATTTCCCTCATTTCTTTCTTACACTTAAATACCTCGTGTATGGTGCAATC
 AGACCACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCTAGAAAAATTAACAG
 TTACTGAAATTATGACTTAAATACCCAATGACTCCTTAAATATGTAAATTATAGTTATACCTT
 GAAATTTCAATTCAAATGCAGACTAATTATAGGGAATTTGGAAGTGTATCAATAAACAGTAT
 ATAATTTT

FIGURE 328

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDQHLDSESGPPLCDNHVNGEWYHFT
GMAGDAMPTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPG
GYVYRLTKPSVCFHVYCGHFYDIDCEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQN
NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDVEGCHNNNGGCSHSLGSEKGYQCECPRG
LVLSEDNHTCQVPVLCKSNAIEVNIPRELVGGLELFLTNTSCRGVSNGTHVNILFSLKTCGTV
VDVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE
IMSRNHGIFPFTLEIFKDNEFEFPYREALPTLKLRLDSLYFGIEPVVHVSGLESLVESCFATPT
SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGKDHKEVFLHCRVLVCGVLD
ERSRCAQGCCHRRMRRGAGGEDSAGLQGQTLTGGPIDWED

Important features of the protein:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.

amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537

Aspartic acid and asparagine hydroxylation site.

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

FIGURE 329

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT
GCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC
TGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC
GGGAGGATCACAGAGCCAGCATGTTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG
ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCCTTCAGAAAGGTGGGGATCCCCA
TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTTGTGGTTGTCCTCATCAAGGTGATTC
TGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTG
ACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG
GGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGGACTCGGCCA
CAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTA
GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGATGTTGTTGAA
TCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCC
TGGTCTCCCTGCACTGTCTTGCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGG
AGGAGGCCTCTGTGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGACAAACAGCACGTCT
GTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATA
CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCATCCCTGG
CTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCC
TCATGAAGCTGCAGTTCCCACTCACTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT
TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTTGGATGGGGCTTTACGAAGCAGA
ATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGT
GCAATGCAGACGATGCGTACCAGGGGGAAGTCAACGAGAAGATGATGTGTGCAGGCATCCCGG
AAGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCCCCTGATGTACCAATCTGACCAGT
GGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCAGGAGTAT
ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTGTAATGCT
GCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCAA
AGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCACAGCCTCAGCATTTCTT
GGAGCAGCAAAGGGCCTCAATTCCTGTAAGAGACCCTCGCAGCCCAGAGGCGCCAGAGGAAG
TCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAGCATCCCAGGGAGAGACACAGCCCACT
GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACTTTCCCACTACTGAATGGAAGC
AGGCTGTCTTGTAAGAGCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCA
GCCCTGTCCGTCTTCACCCATCCCCAAGCCTACTAGAGCAAGAAACAGTTGTAATATAAAAT
GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGG
CCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAA

FIGURE 330

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47644, pI: 5.18, NX(S/T): 2

MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYFL
CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA
CFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSLVSLHCL
ACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCSSILDPHWVLTAAHCFRKHTDVFNWK
VRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTP
ATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDT
QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 331

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGGC
TCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGACG
AGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAATCA
ATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATCTACC
TGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGCGCGGC
TCCGGGTCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGTCCTTCT
CCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTGCAAGTCC
TGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGTAGACAACT
TCACTCAGAACCCAGGGATGTTTCAAGATCAAAGGTGAACAAGGCGCCCCAGGTCTTCAAGGTC
ACAAGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCGGGACCACCTGCTGAGAAGGGAG
CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGGCCACCGGGAG
TCAAGGGAGAGGCGGGCTCCAAGGACCCCAAGGGTGTCCAGGGAAGCAAGGAGCCACTGGCA
CCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATTGGCCCCAAAAGGGG
AAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAAAGGGGACAGGGGCA
TGAAAGGAGATGCAGGGGTCTATGGGGCCTCCTGGAGCCCAGGGGAGTAAAGGTGACTTCGGGA
GGCCAGGCCACCAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGATCAAGGACAACCTGGAC
TGCAGGGTGTTCGGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGCCAAGGGTGAGCCTGGCA
GTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGAGTCCAGGAGCCACAGGCC
TGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG
TTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGGGCTGGCAGGTCCCAAGGGAG
CCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAGGATCTTCTGGGGAGCAAGGAG
TAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCCGTGAGGATTGTGCGCAGTAGTA
ACCGAGGCCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGGACAATTTGCGATGACGAGTGGC
AAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTACTCCAAAGGAAGGGCCCTGTACA
AAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAATGTTTCAAGTGTGCGGGCACGGAGAGTA
CCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG
GCGTGGAGTGCAGCGTCTGACCCCGAAACCCTTTCACTTCTCTGCTCCCGAGGTGTCTCGGG
CTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGTTCCCTGGGGACAACCTGAGCAGCCTCTGG
AGAGGGGCCATTATAAAGCTCAACATCATTGA

FIGURE 332

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886
><subunit 1 of 1, 520 aa, 1 stop
><MW: 52658, pI: 9.16, NX(S/T): 3
MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLL
VVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVRVS
HEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT
GPSGPQGPVGKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGDL
GLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPGAKGDQGPGLQGVPGPPGAV
GHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTGLQGQQGRKGESGVPGPAGVKGEQ
GSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGRAEVYYSG
TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLWSCTKNSWG
HHDCSHEEDAGVECSV

Transmembrane domain:
amino acids 47-66 (type II)

N-glycosylation sites.
amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.
amino acids 432-440

N-myristoylation sites.
amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.
amino acids 360-364

Leucine zipper pattern.
amino acids 56-78

Speract receptor repeat
amino acids 422-471, 488-519

Clq domain proteins.
amino acids 151-184, 301-334, 316-349

FIGURE 333

GGGCTGTTGATTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCTG
 CCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTTCT
 CCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCTGGC
 TGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCAACTG
 CTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGTGGGAG
 GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTTTCAGCGAGCCTAGAGAGGGCAGACTA
 TCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGAAGACCGG
 GGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGCTACCAGGT
 CCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCCGGGTGGGCC
 CAGGAGGGGTTCAGAGCCCGTCTGTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGAGCCTGGCCGA
 GCTGCTGCAGGGGGGCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGCGAGTGGCATT
 GCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGCACCAGTGGGGCC
 ATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGCCTCTGGCTCCTTC
 GTAGCCCTGTCCGGGTGTCTACAGCTTCCGGTTCATGTGGTGAAGGTGTACAACCGCCAA
 ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCTGTCTCTCAGCCTTTGCCAATGATCCT
 GACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGACCCTGGGGACCGAGTG
 TCTCTGCGCCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACTCAAGTTTCTCTGGCTTC
 CTCATCTTCCCTCTCTGAGGACCCAAGTCTTTCAAGCACAAGAATCCAGCCCTTGACAACCTT
 CTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAGACTCCCTCTGGCTCCTATC
 CCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAAGAGAAGAGTAGAGCTGTGGC
 ATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTTACCCTCCAGCCACCTGCTGCATC
 TGTTCCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCAAGAAGGAAGATCTGCACTACTT
 TGCGGCCTCTGCTCCTCCGGTTCCCCCAGCCAGCTTCTGCTCAATGCTGATCAGGGACAGG
 TGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAGATGGACAAGCCTCAGCGTACCCTG
 CAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATCTCAGCCAGCACCGTCAGAAGCTGAG
 CCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCACAGGCAGAAGGGTGGGAAGGGCCTGGA
 GTCTGTGGCTGGTGAGGAAGGAAGGAGGTTGATTGTCTAGACTGAACATGGTACACATTCTG
 CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGTCTTCTATGCTGGATCCCAGAT
 GGACTCTGGCCCTTACCTCCCCACCTGAGATTAGGGTGAGTGTGTTTGTCTCTGGCTGAGAGCA
 GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGCATCC
 TCTTGCTTGGCCACCTCCTGAAACTGCTCCACCTTTGAAGTTTGAAGTTTAGTCCCTCCACAC
 TCTGACTGCTGCCTCCTTCTCCAGCTCTCTCACTGAGTTATCTTCACTGTACCTGTTCCAG
 CATATCCCCACTATCTCTTTCTCTGATCTGTGCTGTCTTATTCTCCTCCTTAGGCTTCT
 ATTACCTGGGATTCCATGATTCATTCTTCAGACCTCTCCTGCCAGTATGCTAAACCTCCC
 TCTCTCTTTCTTATCCCGCTGTCCCATTTGGCCCAGCCTGGATGAATCTATCAATAAAACAACT
 AGAGAATGGTGGTCAGTGAGACACTATAGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGGGA
 TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAATAAATATCAAACCTGTATACTAA
 AATTAAAA

FIGURE 334

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECVCEPGRAAAGGPGGAA
LGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSF
RFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRGNLL
GGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

FIGURE 335

[illegible]

FIGURE 336

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRSK
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWL VFDWNTPKKGRRSQW
VRNWAVWRYFRDYFP IQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFPGIR
PYLATLAGNFRMPVLR EYLMSSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSMPGKN
AVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCIFH
GRGLFSSDTWGLVPYSKPITTVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKFG
LPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 337

GGGCGGCGGGATGGGGGCCGGGGCGGCGGGCGCCGCACTCGCTGAGGCCCCGACGCAGGGCCGGGCGGGCCCCA
GGGCCGAGGAGCGCGGCGGCCAGAGCGGGGCCGGAGGCGACGCCGGGACGCCCGCGCAGCAGAGGTTGGCG
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGGA
CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGGCTGTCTGGCCTTCTCTGAAGACCCA
GTTCTGTCTGCACCTGTCTGGTCCGGCTTGTCTTCTGTGGTGAAGTGGTCTGGTTCATCAACTTCTGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCCTACTCACTCTGGAGCCA
ACTGGTCATGCTGTGGAGTGGTGGTCTGACGGAGTGACACTGTTTACGGACCAGGCCACGGTAGAGCGCTT
TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTCGAGATCGACTTCTCTGTGGGTGGACCATGTGTGA
GCGCTTCGGAGTGTCTGGGAGCTCCAAGGTCTCGCTAAGAAAGGAGCTGCTCTACGTGCCCCCTCATCGGCTGGAC
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGGACCGGACACCGTGGTCTGAAGGGCTGAG
GCGCTGTGCGACTACCCGAGTACATGTGGTTTCTCTGTACTGCGAGGGGACGCGCTTACGGAGACCAAGCA
CCGCGTTAGCATGGAGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
CTTACCACCGCAGTCAAGTGCCTCCGGGGACAGTCGAGCTGTCTATGATGTAACCTGAACTTCAGAGGAAA
CAAGAACCCGTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCTCT
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACCGCTCCA
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAGCCTGCCCGAGGCGCTGGACCTCTCTGAA
CTTCTGTCTCTGGGCCACCATTTCTCTGTCTCCCTCTTCAGTTTTGTCTTGGGCGTCTTTGCCAGCGGATCACC
TCTCTGATCCTGACTTTCTTGGGGTTGTGGGAGCAGCTTCTCTTGGAGTTCGAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAAAACCAAAATCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA
ATTCATAGAGGCTGAACAGCAGATTGTGAGCAGGCAGAAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTCAAGCTAATGAAAAAGAATGAAGCAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
CATATGCATGATGAGACTCCCAGAAGGAGAGGAGAGAAAGGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAATCCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCT
AATCAAAGTGTCAAATGACAAAGAATCTTGAAGCAGCAAGAGATGAGCAACTTATCTTGTTCAAAGGATCTTTG
ATCAGATTAAACAGCTCATTTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTTCAACTGTAATTATTGGACTTTTGTAGTCTTAGATGGTCTGACCTCTTGTCTTCAAGGACAGTTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGAAGCTGTAGGAAGGCTGTCTTTAGGCCGGGCACAGTGGC
TTACACCTGTAATCCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCCT
GAGTTCAGGTGATCTGCCCCCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA
ATTTCTTTTAAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCTGTGATCCCAAGTAGCTTGGATTGTA
AACATGCACCACCATGCCTGGCTAATTTTTGTATTTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT
GACCTCAAGTGACCCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCTGAGCCACTGTGCTGGCCTTGA
GCATCTTGTGATGTGCTTATTGGCCATTGTATATCTTCTATCTTCTTTGGGGAAATGTCTGTTCAAGTCTTTG
CCTTTTAAATTTTTATTATTTATTTATTTATTTATTTTGTAGACAGGGTCTTGTCTGTTGCCAGGCTGGAGTA
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT
AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA
TGCCAGGCTGGTCTGAACTCCTGAGCTCAAGTGATCTGCCTGCTTCAAGCTCCCAAAGTGTGGGATTACAGA
CATGAGCCACTGCACCTGGCAAACCTCCCAAATTCACACACACACAAAAAACCTGATTCAAAATGGGCA
GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

FIGURE 338

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213

><subunit 1 of 1, 368 aa, 1 stop

><MW: 42550, pI: 9.11, NX(S/T): 1

MGLLAFLKTQFVLHLLVGFVVFVVSGLVINFVQLCTLALWPVSKQLYRRLNCRSLAYSLWSQLVM
LLEWWSCTECTLFQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKKEL
LYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSM
EVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAYDVDTLNFRGNKNPSLLGILYGKKYEAD
MCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLNFLSWA
TILLSPLFSFVLGVFASGSPLLLITFLGFVGAASFGVRRLIGESLEPGRWRLQ

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 339

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCAG
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTTGC
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT
TACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGGGATA
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCCTGGGATCTGCCTATACCTTCTTTTCTC
TAACCTGGCATAACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG
GTGTTCTCTTGTCTGTTCTCTGTAATGTGGTATGCCATGGGGTCTTTCACAAAGCCTTTCCTCTT
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCTACTTAATATGTAGTCATCCTGCAG
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAT
GCTCTCATAAGACCACTTGTTCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC
GTTTGTGGTTGTATGGGTGTGTCTGTTCCTCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCTTACATGTGGTGGGTGCTCATGTTTATAGAGA
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC
CAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCTGATTC
AGTAGGCCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGATGCTGGTCTTATGAAC
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA
GCACCTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA
ACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTGGGCATGGTGGCACATGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA
AAAAAAAAA

FIGURE 340

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234

><subunit 1 of 1, 143 aa, 1 stop

><MW: 15624, pI: 9.58, NX(S/T): 0

MHHSLQCPGAATRIHLCVCFSEFALALGHFLLISLVGKGLSLSCGVGGROAGLRRLIRPWVRRE
GKINFYTNQDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPSWSGP
CPPGQLHCTCGVLLSFL

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 341

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG
CTGTTGGCGCTGCTCGTGTGCCCCGCGCGGGGTGCGGGCGGCCGGGACCACGGGGACTGGGAC
GAGGCCTCCCGGCTGCCGCCGCTACCACCCCGGAGGACGCGGCGCGCGTGGCCCGCTTCGTG
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG
CCCTTCGCCGACGTCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTTGATCCACAAAGTCCCCTT
TGTGTTACATAATGCTGTCAGGAAGTGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA
AAGCATTCGTTATTTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC
TTTGCTAAGTTGAATATAACCAATATCTGGGTCTGGACTACTTTGGTGGACCAAAAATCGTG
ACACCAGAAGAATATTATAATGTCACAGTTCAGTGAAGCAGACTGTGGTGAATTTAGCAACAC
TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAAGGCTTAATGTTTCTCTGGAAAGCGT
CCCAGAATATTAGCCAGTTTTCTGTC

FIGURE 342

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIAKHS�FIRHPMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ
```

Important features of the protein:

Transmembrane domain:

Amino acids 11-29

N-glycosylation sites:

Amino acids 160-164;193-197;216-220

N-myristoylation sites:

Amino acids 3-9;7-13;69-75;97-103

FIGURE 343

GGCTGGACTGGAACCTCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTCAGCAACTAAAAAAGCCACAG
GAGTTGAACTGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT
AAAATCTGTTTTTTGTTCTCTTGTAACCTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACT
GTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT
CCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAGGTAGCTGAGCCTCTTGGTAGCTGCGG
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGAT**TGA**CAAGCCCGAAGATTTTCATAGGCG
ATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCCGCCATCTAACCTTTT
CATGTCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCT
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA
CTTGCAATTCTCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG
TGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTTATCACAAGGCATCGAGTCTCCTGC
ATTCAGTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG
GGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAGCCAGGGGCAGCCGTCTG
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTCTGAGAGGCCCTCCTATGT
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATGGCTCAGTGTTGGCCCAGGA
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT
AAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT
AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT
TATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG
GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAAGAATTATGGTTATTT
GTAA

FIGURE 344

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:
amino acids 1-15

FIGURE 345

[illegible]

FIGURE 346

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPKNKYPIFFFGTHETAFLGPKDLFPYDK
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDDEDRGVM
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSEEN
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR
SASSSSSSSSSSSDSDSVKPKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSSSDSDSDEVDRISE
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD
EPVKKRGRKGRGRGPPSSSDSEPEAELEEREAKKSAKKPQSSSTEPARKPGQKEKRVRPPEKQQ
AKPVKVERTRK RSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRCLNALEELG
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVNKAGME
KEKAEKLAGEEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHEEGRDSEEGPR
CGSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 347

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
ACACCATTTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTTCTTCCAGTCACTGGCACTTTGAAGCA
AAATATTTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTGGGTTTCATC
AGAAGGACTGGATTTTCAAACCTTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTTGGGAGCCAAAGACCACAT
CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAAATTTGGAGTCTGGCAGACTGAAATGTCCTTTTCGATCCTCAGCAGCC
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTGGCAAAGATACTGCATT
CACTCGATCCCTTGGGCCCTACTCATGACCACCCTACATCAGAACTGACATTTTCAGAGCACTACTGGCTCAATGG
AGCAAATTTATTGGAACCTTCTTCATACCAGACACCTACAATCCAGATGATGATAAATATATTTCTTCTTTTCG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
AGGAGGACAACGCAGCCTGATAAACAAGTGGACGACTTTTCTAAGGCCAGACTGATTGCTCAATTCCTGGAAG
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTTACTCTCCCAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCAACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATGAGTGGATCATGTCAATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTTCTTGGAAACAGACATTGGAACCTGTCTCAAAGTTGTCAGCATTTCAAAGGAAAAGTGAATATGGA
AGAGGTAGTGCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATGGAATTGTCTCTGAAGCA
GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTTCAGCTCTCCTTGCACAGATGCCACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCTGGGATGGAATGCATGCTCTCGATATGCTCCTAC
TTCTAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCAATCACCCAGTGTGGGACATCGAAGACAG
CATTAGTCATGAAACTGCTGATGAAAAGGTGATTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTCAAGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGAGAAGAAGGATTCGGGATGTATTACTG
CAAAGCCCAGGAGCACACTTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCATTGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
CTACATCCAAATCCTTAGCAGCCCAAACCTCAGCCTCGACCACTGCGAACAGATGTGGCACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGCCAAAGTGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAAGTTTTCTACTTAATTTAAAGAAAAGAATTCCTTACC
TATAAAAACATTGCCTTCTGTTTTGTATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTTGCTAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAATTCATTTGAACCAGTTTT
CCAAGAACAATCTTGACACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTACAGTTGTAATGTTTTTA
TGTTTTGAGTTTTTGAATTTATTTGTCATGTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGATAAGGT
GCTTTATTCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCCTATTGAGAACCAGCTACCTTGTGGTAGGGAATAAGAGGTGAGACACAAATTAAGACAACCTCCATTATC
AACAGGAACCTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTC
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTACTGAAGGGCACTAATGTTTTCCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAATAAAAACAAGGAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATTCCTGGCTTTGGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAAATCACAAATAAAGTGAGAGTAATGTAA
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAAATCTAGATTATAACA
AACTGCTAGCAAAATCTGAGGAAACATAAATCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAACC
AATGATATTTTCAGTATATATTTTCTCTTTTTAAAAAATATTTATCATACTCTGTATATTTCTTTTACTGC
CTTTATTTCTCTCTGTATATTGGATTTTGTGATTATATTTGAGTGAATAGGAGAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAATTTTAAAC
AACGGAAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT
GTAGTATGTTTTTGTAAATTTAACAATAAATAAGCCTGCTACATGT

FIGURE 348

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFLG
SSEGLDFQTL LLLDEERGRL LLGAKDHI FLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDI IFKLDTHNLESGRLKCPFPDQQ
PFASVMTDEYLYSGTASDFLGKDTAFT RSLGPTHDH HYIRTDISEHYWLN GAKFIGTFFIPDT
YNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRSLINKWTTFLKARLICSIPGS
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGPYAHKES
ADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPVAGGPTEK
RINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSI SKEKWNMEEVVLEELQIFKHSS
IILNMELSLKQQQLYIGSRDGLVQLSLHRCDTY GKACADCC LARDPYCAWDGNACSRYPATSK
RRARRQDVKYGDPITQCWDIEDSISHETADEKVIFGIEFNSTFLECIPKSQQATIKWYIQRSG
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTLNVIENEQMENTQ
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKG GPKWKHMQEM
KKKRNRRLHRDLDELPRAVAT

Important features of the protein:

Signal peptide:

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 349

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGAGAGGTCATCCTGGAGCATGCCACCGCGGGGAGCAGA
 CAACCTCCCAGGTAAGCTGGGAGCAAGACCTGAAGCTGTTTCTTCAGGAGCCTGGTGTATTTTCCCCACCCAC
 CTCAGCAGTTTCAGCCAGCAGGGACTGATCAGGTGTGTGTCTGGAGTGGGGAGCAGAAGGCGTGGCTGGCAAGA
 GTGGCCTGGAGAAAGAGGTTTACGCGCTTGACCAGCCGAGCTGCCCGTGACTACAAGATCCAGAACCATGGGCATC
 GGGTGAAGGTGGGGGGGCACAGGTGTATGTGCACCTTCTTGTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGGAGGGAAAGGTATTTTAAGGTAACAGTGTGGCACAATAGTTAA
 GAGCACAGTTTTTGGAGCTAGACCGACATAGGTTCAAATTCTCTTCTGTTGCTTCTTAGTTCTGTAGCCCCAGGT
 AAGGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
 AGGGAAGATTAAATGACATAATGTATGTGATGCAACTAGCAAAGTACCAGTCCCATAGTAAGTCATGCCCCACAG
 TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTACTGCAACGACTGGAGCAGAGGCGGCAGCAGGCTT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCGAGAGAGCATCCGCCGGGCACAGGTGAGCC
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGGCCAGGATGAGGTGGAGCAGGAGCGCGGCTCAAGTGAAGCTCGGCTGTCCCAGAGGGACCTCTCTC
 CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCCTGCCC
 CCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTCTGCTATCAGGCAGGGCGTGAGGATG
 AGCTGACAATCACGGAGGGTGAGTGGCTGGAGGTCATAGAGGAGGGAGATGCTGACGAATGGGTCAAGGCTCGGA
 ACCAGCACGGCGAGGTAGGCTTTGTCCCTGAGCGATATCTCAACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC
 AAGACAGTGACAATCCCTGCGGGGCAGAGCCACAGCATTCCTGGCACAGGCCCTGTACAGCTACACCGGACAG
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTGCCCCGGGCCAAGATGGAGTAGATGACG
 GCTTCTGGAGGGGAGAATTTGGGGGGCGTGTGGGGTCTTCCCTCCCTGCTGGTGGAAGAGCTGCTTGGCCCCC
 CAGGGCCACCTGAACCTCTCTGACCTGAACAGATGCTGCCGTCCCTTCTCTCTCCAGCTTCTCCCCACCTGCAC
 CTACCTCTGTGTTGGATGGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG
 ACATGATGGCACCTCGACTCAGGCCGATGCGTCCACCACCTCCCCCGCCGGCTAAAGCCCCGATCCTGGCCACC
 CAGATCCCCCTCACCTGAAGGCCAGGGAAGCCTTGACCCCCAGTGATGCTGCTGTCCCTATCTTCAAGCTGTGAGA
 CCACACCATCAATGATCCAGAGCAACACAGCCAAAAGCTGGAATCGCCCTTATTTCCACCTCACCTCCAAGGGT
 GGAACCTTGCCCCCTTCCATTTCTAGAGCTGGAACCCACTCCTTTTTTCCCATTTGTTCTATCATCTCTAGGACC
 GGAACCTACTACCTTCTCTTCTGTCTGTCATGACCTATCTAGGGTGGTGAAATGCCTGAAATCTCTGGGGCTGGAAC
 ATCCATCAAGGTCTCTAGTAGTTCTGGCCACCTCTTTCCCAACCTGGCTCCATGACCCACCCCACTCTGGATG
 CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCCCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG
 CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCACGAAGGCCAGGCCAGGGCCTGGGCCTCTTGTG
 CTAAGAGGGCAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACCACGGGCAGGGGCCTGCTCCAGCTGCCAC
 GCTCTATCATATGGAGCGAGGTGTTGGGGAAGGCGGGGCAGGCAGCCTGTTGCAGGCAGGGGAAGGAGAAGAGAC
 TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGTGGAAGTAGAGCTGGTCCCTC
 AGCTGGGGGGCAGTCTCTGTCTCAGTGGAGGGGAGGCTTTTACGCCCAACCAACCCCTGGCCCTGCCAGCTGGTAG
 TCCATCAGCACAAATGAAGGAGACTTGAGAGAAGAGGAAGAATAAACAAGTGTGCTTCTGTTCAAGCTGTGTCCAGC
 TTTTCCCTGGGGCTCCAGGACCTTCCCTACCTCCACCACCAACCAAGGGATTTATAGCAAAGGCTAAGCCTGC
 AGTTTACTCTGGGGGTTTCAAGGAGCCGAAAGGCTTAAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA
 TTTAGGGCTCAGGCAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACCTGAGAGAAAGGGGAGGGG
 TCAACAATGAGAGACCAGGAGTAGGTCTATCAGTGCCCCCAGAGTAGAGAGCAATAAGAGCCCAGCCCAGTG
 AGTCCCGCTGTGTTTTCTACCTGGTGATCAGAAGTGTCTGGTTTGGCTTGGCTGCCCATTTGCCTCTTGAGTGG
 GCAGCCCTGGGCTTGGGCCCTCCCTCCGCCCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCCTTCAAGTG
 CACGAGGGGTTAGGCTGCTGTCCCTGAGTCCCTCAATCTGTACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
 TCTCAGGGGGCAGCCTCTCCATGGCAGGCATCCCTGCCCTGGGCTGCCCTCCCCCAGACCCCTGACCACCCCTG
 GGTCTGTCCCCCACCAGAGCCCAGCTCCTGTCTGTGGGGGAGCCATCACGGTGTTCGTGCAGTCCATAGCGCT
 TCTCAATGTGTGTCACCCGAACCTGGGAGGGGAGGGAACACTGGGGTTTAGGACCACAACCTCAGAGGCTGCTTG
 GCCCTCCCTCTGACCAGGGACATCCTGAGTTTGGTGGCTACTTCCCTCTGGCCTAAGGTAGGGGAGGCCTTCTC
 AGATTGTGGGGCACATTGTGTAGCCTGACTTCTGCTGGAGCTCCAGTCCAGGAGGAAAGAGCCAAGGCCCACTT
 TTGGGATCAGGTGCCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCCCACCTGCCCA
 CAGAGAACACAGTGGTCTCCCTGTCCGGGGGCGCTTTTTCTTCTTGGAGCGTCCCTGACGGACAAGTGGAG
 GCCTCTGTGCTGGGCTGCAATGGATGCAAGGGGCTGCAGAGCCAGGTGCACTGTGTGATGATGGGAGGGGGCTC
 CGTCTGCAGGCTGGAGGTGGCATCCACTGGACAGCAGGAGGAGGGGAGTGAGGGTAACATTTCCATTTCCCT
 TCATGTTTTGTTTCTTACGTTCTTTACGATGCTCCTTAAACCCCAAGCCCCAATTTCCCCAAGCCCCATTT
 TTTCTGTCTTTATCTAATAAACTCAATATTAAG

FIGURE 350

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELSDF
EECEETGELFEPPAPQALATRALPCPAHVVFVRYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPDLSPLESSQSDNPGAEPTAFLAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

FIGURE 351A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCACAGACAGAGTCCTACAGAGGGAGAGGCCAGAGAAGCTGACAGA
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG
 GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGTCCTCAGCCCTTCTGAAAACCTTTGCC
 TCTGACCTTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT
 GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCTCCAGACAGGCTCGCATCCCCGGGAGGGG
 CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCCTGCCTCCTGCTCCCCATGTGCCGCTCTCCTGGCTGGTGTG
 AGGCTTCTGCTACTGTGTCCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCCCTCCCCCGGGAGGAGGAGAT
 CGTGTTCAGAGAAGCTCAACGGCAGCGTCCTGCCTGGCTCGGGCGCCCCCTGCCAGGCTGTTGTGCCGCTTGCA
 GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA
 CCTGGGCCAGGCGCCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTCTGCAGTGGGATGGGGAGCCCTGTTAGGCGTGTACAAATATCGGGGGGCTGAACCTCCA
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC
 TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGGAAAGCCCCAGCCCCAGACCCGGAAGAGCCAA
 GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC
 GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCCTTCAAGCACCCAAGCATCCGCAATCC
 TGTGAGCTTGGTGGTGAAGCTCGGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGCCCCAAGTGGGGCCAGTGTCTGC
 CCAGACCCTGCGCAGCTTCTGTGCCCTGGCAGCGGGGCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
 CACAGCCATTCTGTTTACCCGTGAGACCTGTGTGGAGTCTCCACTTGGCAGACGCTGGGTATGGCTGATGTGGG
 CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGTCTCA
 TGAAGTGGGTGATGTCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCCCTTTGAGCAC
 CTCTCGCCATGTGATGGCCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCCGCTT
 CATCACTGACTTCTTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATTGCATCTGCCTGT
 GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCGGGCCCCGATCACGCCATTGTCC
 ACAGCTGCGCCCGCCCTGTGCTGCCCTCTGGTGCTCTGGCCACCTCAATGGCCATGGCATGTGCCAGACCAACA
 CTCGCCCTGGGCGGATGGCACACCCTGCGGGCCCGCACAGGCTGCATGGGTGGTCTGCTGCCCTCCACATGGACCA
 GCTCCAGGACTTCAATATTTCCACAGGCTGGTGGCTGGGGTCTTGGGGACCATGGGGTACTGCTCTCGGACCTG
 TGGGGGTGGTGTCCAGTTCTCCTCCGAGACTGCACAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
 CCGCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
 GTGTGCTGCCCTACAACCACCGCACCGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTCTCTCGCTACAC
 AGCGTGGCCCCCAGGACCAAGTGCAAACTCACCTGCCAGGCCCGGGCACTGGGCTACTATGTGTGCTGGAGCC
 ACGGGTGGTAGATGGGACCCCTGTTCCCCGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG
 CTGTGATCGCATATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTTGCAG
 CAAGCAGTCAGGCTCCTTCAAGAAATTCAGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA
 CATTCTTGTCCGGCAGCAGGGAAACCTGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
 TGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCACAGATGTGGTACTGCTTGGGTCAGTGTGCGCTA
 CAGCGGGCCACTGCAGCTCAGAGACACTGTGAGGCTATGGGCCACTGGCCAGCTTGTGACACTCAAGTCTCT
 AGTGGCTGGCAACCCCAAGGACACAGCCTCCGATACAGCTTCTTCTGTCGCCCGGGCCGACCCCTTCAACGCCACG
 CCCCCTCCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCCGCGGCGCCCTGGGCGGGCAG
 GAAATAACCTCACTATCCCGGCTGCCCTTCTTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT
 CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCTCCTCTCTGCCCTAAT
 GCGCAGGCTGGCCCTGCCCTGGTTTCTGCTGCCCTGGGAGGCAGTGATGGGTAGTGGATGGAAGGGGCTGACAGAC
 AGCCCTCCATCTAAACTGCCCTCTGCCCCTGCGGGTCAAGGAGGGAGGGGAAGGCAGGGAGGGCTGGGCCC
 CAGTTGTATTTATTTAGTATTTATTTCACTTTTATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAA
 CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTGATAGGTATAAGTGGTG
 TGTGTATGCGTGTGTGTGTGTGTGTGAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCTCT
 TTCTGAATTTTATTTTGGGAAAGAAAGTCAAGGGTAGGGTGGGCCTTCAAGGAGTGAGGGATTATCTTTT
 TTTTCTTTCTTTCTTTCTTTCTTTTGTAGACAGAATCTCGCTCTGTGCCCCAGGCTGGAGTGCAATG
 GCACAATCTCGGCTCACTGCATCCTCCGCTCCCGGGTCAAGTGATTCTCATGCCTCAGCCTCCTGAGTAGCTG
 GGATTACAGGCTCCTGCCACCACGCCAGCTAATTTTGTGTTTGTGTTTGGAGACAGAGTCTCGCTATTGTC
 ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCCGACCTGGGTCCAGCAATTCTCCTGCCTCAGCCTCC
 CGAGTAGCTGAGATTATAGCACCTACCACACGCCCCGCTAATTTTGTATTTTGTAGTAGACGGGGTTTTCAC
 CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGGTGATCCACTCGCCTTCATCTCCCAAAGTGTCTGGGATT
 ACAGGCGTGAGCCACCGTGCCTGGCCACGCCCACTAATTTTGTATTTTGTAGTAGACAGGGTTTACCATGT
 TGGCCAGGCTGCTCTTGAATCCTGACCTCAGGTAATCGACCTGCCTCGGCTCCCAAAGTGTCTGGGATTACAGG

FIGURE 351B

[illegible]

FIGURE 352

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLLASLLPSARLASPLPREEEIVF
PEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT
YLTGTINGDPESVASLHWDGGALLGVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSPASG
QGPMC NVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAAAKA
FKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHFDTAIL
FTRQDL CGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTA AHELGHVFNMLHDNSKPCI
SLNGPLSTSRHVMAPVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK
DYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG
RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRPVPRNGGKYCEGRRTFR
SCNTEDCPTGSALTFFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCKLTCQARALGY
YYVLEPRVVDGTPCSPDSSSVQVQGRCIHAGCDRIIGSKKKFDKCMVCGGDGSGCSKQSGSFR
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPPTDVVLPGA
VSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFVPRPTPSTPRPTPQDWLH
RRAQILEILRRRPWAGRK
```

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 353

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCCAGGGAGCTGCCC
GGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGC
TCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCTACCTGAAAGGGCTCTGGATGGAGTGTG
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT
GCGCCGTTCATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACCACCTTTG
CCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGAAGTTTGAGA
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCCCTGC
TTTGCCTGTCCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAG
CCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTGTATCCAAGGAAATAATGTGAATGCGAGGA
AATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACCAA
GACTGAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATATTTATGTGGGTGATTTGA
TAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAA

FIGURE 354

MASTAVQLLGFLLSFLGMVGTLITTTILPHWRRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ
CQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTLFI
LAGLLCMVAVSWTTNDVVQNFYNPLLPSPGMKFEIGQALYLGFISSSLSLIGGTLLCLSCQDEA
PYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 355

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC
 AGGCGGCAGGGCGGGCGGCCAGGATC**ATGT**CCACCACCACATGCCAAGTGGTGGCGTTCTCTCC
 TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGG
 ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA
 GGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCACATCCTGGGACTTCCAGCCATGC
 TGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT
 CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGA
 CACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT
 TTGCCAACATGCTGGTGAATACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG
 GGATGGTGCAGACTGTTCCAGACCAGGTACACATTTGGTGCGGCTCTGTTTCGTGGGCTGGGTG
 CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCTGGCACCAG
 AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTCCTTACAAGCCTG
 GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG
 GTGCCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGTG**TAAT**GTCTTA
 AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCA
 TCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCATCTTTG
 GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG
 TTATTTATGAATTAGAGGCTATAGCTCACATTTCAATCCTCTATTTCTTTTTTTAAATATAA
 CTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAG
 ACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAG
 AAAACTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTC
 CCCACCCCCAACTTGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATT
 TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCA
 AAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC
 AACACCATTTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTTCTGTGCGGGTTCAGAAA
 TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAAAATAA
 ATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG
 AAGGAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA
 GTACAAATTCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG
 ATCACTTGAGCCCAGAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA
 ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCCAGCATTCGGGGAG
 GCTGAGGTGGGAGGATCACTTGAGCCAGGGAGGTGGGGCTGCAGTGAGCCATGATCACACC
 ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAAATAAAAAATAAATAATGGA
 ACACAGCAAGTCCTAGGAAGTAGGTTAAAACCTAATCTTTAA

FIGURE 356

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTEC
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ
SYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 357

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG
 AGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGGCAACCCATGCCTTAGAAATCGCTGGG
 CTGTTTCTTGGTGGTGGTGAATGGTGGGCACAGTGGCTGTCACTGTGCCTCAGTGGAGA
 GTGTGCGCCTTCATTGAAAACAACATCGTGGTTTTTGAAGAACTTCTGGGAAGGACTGTGGATG
 AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGGCTCTT
 TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCTTCTTGGCT
 TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG
 GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGCTCATCCCT
 GTGAGCTGGGTGGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCAA
 AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGCTGATTGTTGGA
 GGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA
 CCTTCCCATCGCACAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC
 AGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTTAACTTTACTATAAAGCCATGCAAATGACA
 AAAATCTATATTACTTTCTCAAAATGGACCCCAAGAACTTTGATTACTGTTCTTAACTGC
 CTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTTCAGCAGAA
 TGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG
 TTCAAGCATCTACTCTTTTTATCATTTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT
 ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAACATTTATATCTCA
 CATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAGTCCATTACACTGAATAAAT
 AGAACTCAACTATTGCTTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTACTATTAATTG
 TTTAAAAACAGCTTAGGGATTAATGTCTCTCCATTTATAATGAAGATTAAATGAAGGCTTTAA
 TCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTTAGCCTAGGAGTTAGAA
 ATCCTAACTTCTTTATCCTCTTCTCCAGAGGCTTTTTTTTTTCTTGTGTATTAAATTAACATT
 TTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAACCTGCTTTTCCAGGGCTATACTC
 AGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATGGTTTTTAGGAAAGTGAAAATATTTTT
 GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT
 TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT
 GTCTTGGTTTTTCATTTGCTTACCACAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTC
 ACCTGCTCCTATGTGGGTACCTGAGTCAAATTTGTCATTTTTGTTCTGTGAAAAATAAATTC
 CTTCTTGTACCATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTATT
 CCAAATTTGATGAACTGACAATCCAATTTGAAAGTTTGTGTGACGCTGTCTAGCTTAAAT
 GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

FIGURE 358

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVM PQWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQ
CKIYDSL LALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 359

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCCC
GCCGCCATGGCTGCCTCCCCCGCGCGGCCTGCTGTCTGGCCCTGACCGGGCTGGCGCTGCTC
CTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAAAAA
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCCGAGGTGCAGCAG
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACTATGAT
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC
GATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTACGCAGATCTTTTCTACC
TACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTTTGATATTTTCAT
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

FIGURE 360

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKLLMLQKREAPVPTKTKVAVDENKAKEFLG
SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRNGHEYYGDDYYQRHYDED
SAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

FIGURE 361

[illegible]

FIGURE 362

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKIN

ENADGSFDYGLFQINSHYWCNDYKSYSENLCHVDCQDLLNPNLLAGIHCAKRIVSGARGMNNW

VEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

FIGURE 363

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCTAGCCCTGCTTGACTGAGAACCCAC
 CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGAAAGAAACACCTGAGCA
 GAATGGAATCATTATTTTTCCTCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT
 TTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGACTTGG
 GGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGACACGCTGTTG
 GCAAATGTCAGGACCAGGTAAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT
 GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC
 ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC
 AGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCGATGTTGCACCCTC
 CCCACCACACCCTGCACCAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT
 ACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT
 ACAGCCCTCTGGAGGGCCTGCCACCTTTATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG
 TGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA
 TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGGGGCTGATGAGGACG
 GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACAGCCTGGACCCACGTGGCCTCCAGGAGG
 CACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGGCACCCACTGTGTCTGC
 AGCAGCACCCCTCAGGACAGCCTGCCCACAGCCAGCGTCATCCTCTGTTTCCATGATGAGGCCT
 GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGCCAGGGCCTTCTGAAGG
 AGATCATCCTCGTGAGCAGCCTCAGCCAGCAAGGACAACCTCAAGTCTGCTCTCAGCGAATATG
 TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC
 GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCATGGATGCCCACTGCGAGT
 GCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT
 CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCAGTATTACCCCTCAAAGGACCTGCAGC
 GTGGGGTGTGGACTGGAAGCTGGATTTCCTGAGGAACTTTGCCAGAGCATGTGAGGAAGG
 CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCGAGAGGTGGTGGCCATGG
 ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTGCTGCGAGGTGGTGAAA
 ACCTCGAACTGTCTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC
 GGGTAGGACACATCTACCAAATCAGGATTCCCATTTCCCCCTCGACCAGGAGGCCACCTGA
 GGAACAGGGTTTCGATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA
 GCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGCAGCTGC
 AAAGGAGACTGGGTGTGCGACATTCCACTGGTTTCTGGCTAATGTCTACCCTGAGCTGTACC
 CATCTGAACCCAGGCCAGTTTCTCTGGAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG
 ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCATGGTGTGGCTCCTTGCAGTGACAGCC
 GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCACAGCACC
 TGTGCTTTGCTGTGAGGAGGAGCAGGTGATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCA
 TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT
 GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG
 CCCGCCAGCAGTGGCGATTTGACCAGATAAATGCTGTGGATGAACGATGAATGTCAATGTCAG
 AAGGAAAAGAGAATTTGGCCATCAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT
 TCATGAAGCTGATCCTTTTGTGTGTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAA
 GAATATAGGAAGTTTCTCCTTTTCACACCTTATTTCAATTGACTGCTGGCTGCTTA

FIGURE 364

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFGE
SQDWVLEAEDEGE EYSPL EGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ
DKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS
LPTASVILCFHDEAWSTLLRRTVHSILDTVPRAFLKEIILVDDL SQQGQLKSALSEYVARLEGV
KLLRSNKRLGAIRARMLGATRATGDVLVFM DAHCECHPGWLEPLLSRIAGDRSRVVS PVIDVI
DWKTFQYYPSKDLQRGVLDWKLD FHW EPLPEHVRKALQSPISPIRSPVVPGEVVAMDRHYFQN
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGH IYQNQDSHSPLDQEATLRNRVRIA
ETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRR LGCRTFHWFLANVYPELYPSEPRPS
FSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ
EQVILQNCTEEGLAIHQHWD FQENGMI VHILSGKCM EAVVQENNKDLYLRPCDGKARQQWRF
DQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 365

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGC
AGCCGGGAGCCATGCGACCCCAGGGCCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCTCCTGC
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG
CAGGAGTGCTTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT
GGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA
TTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTTCAGTGGCT
CACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTTCACATTCAATGGAGCTG
AATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA
ATTCACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG
GATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAATTAAATGCTTTAATTTT
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAG
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCA
CACTGTTTTTTAAATCTAGCATTATTCAATTTTGCTTCAATCAAAGTGGTTTCAATATTTTTTT
TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAATAAAAATTATTTCCAACA

FIGURE 366

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAAGVP
GRDGSPGANVIPGTPGIPGRDGFKEGKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAEC SGPLPIEAI IYLDQGSPEMNSTI
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDA STGWNSVSR IIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 367

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGGATGGC
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTGCT
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC
GGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCCAGC
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGCGGCGG
GTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGGT
GCTGGCGCTCGTGGTCTGCGCTGAGAAAGTTTTCTGCCTCCTGAAGCGAATAAAGGGGCCG
CGCCCGGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 368

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398

><subunit 1 of 1, 121 aa, 1 stop

><MW: 12073, pI: 4.11, NX(S/T): 0

MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVD TGP
PAPT VAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 369

GGCCGTTGGTTGGTGC GCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC
GGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCACG
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAACT
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGT CAGGGGCGCTGCTCACC GACTGGAGCGACG
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT
ATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCCTAAGTAGCCCCCAGAGGCG
CTGGGAGTGTGGCACC GCCCTCCCCTGAAGTTTGCTCCATCTCAGCTGGGGGTCAACCTGG
GGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTCAGC
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAAC TGACAGACTCGCACGTCTG
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTAC
TGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGCTCCCCGCCCTTCCACCTGGCTGTATCGG
GTAGGGCGGGGCCGTGGGTT CAGGGGCGCACC ACTTCCAAGCCTGTGTCCCACAGGTCCTCGG
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAACTGGCACAAGTAAGTCC
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTGAGTATGTGTGGG
CACAGGCTGGCTCCCTCAGCTCCACGTCCTAGAGGGGCTCCCGAGGAGGTGGAACCTCAACC
CAGCTCTGCGCAGGAGGCGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCCCTCAGCTGG
AGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCCACCCCATCCCAGGTCTGTGG
TCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCCCCA
CATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGGA
GGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGCACTGCAGGT
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCACCTCTGCAACCACACCCATGTGGTG
GTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCCGG
CCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC
GTGCCGCGGCCTGCACACCCTTCGGACATCCAGGCACGAGGGTGTCTGTGGATGTGGCCACAC
ATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGGAGGGAGGCAGGGGGT
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGCAGCCTGGTATCGCCAGCCTTAAGGT
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGGAAGATGCTGCTGAGTGTCTCAAGCAGC
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCCCT
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCTCTCCGACCCCGGACAGAGC
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGAGGGAATGGGGGTGGGCTGTGCGCAGCATCAG
CGCCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

FIGURE 370

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE

LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL

APGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

FIGURE 371

GCCGGCTGTGCAGAGACGCC**ATGT**ACCGGCTCCTGTCAGCAGTGA**CTG**CCCGGGCTGCCGCCC
CCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCCCTC
TCGGCCACGGCTGGGTTCGGGGGCCTCGGGCTGGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG
CAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCCGCGGCCCGGACCCCTGAGGCGTCGC
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGGCGCCGC
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGTTATGCGAA
TTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC
TGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAATATGAAGGTG
AAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGAATTCGTCATTATGAAA
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAAAAAGAATGATTTTG
AACAAGGCGAATTATATTTGAGAGAAAAGTTTGAAAATTCAATTGAATCCCTAAGATTATTTA
AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCAACTTTTGGCTATACCC
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT
TCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG
CAAGGT**AA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT
TAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACATGTTTATAAAGTAAAAAA

FIGURE 372

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGLGLGLGLALGVKLAGGLRGA
APAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGAPG
IVVGVSVDGKEVWSEGLGYADVENRVPCPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV
QHYVPEFPEKEYEGEKVSVTTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKNDPLFF
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 373

GACTACGGGGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA
GAGCAAAGATGTTTCAAAC TGGGGGCCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG
CCCAGTTTGGAGGCCTGCCCCGTGCCCCCTGGACCAGACCCCTGCCCTTGAATGTGAATCCAGCCCCTG
CCCTTGAGTCCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT
ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAAAGTGACGTCAGTGATTCTTGGCCTGAAC
AACATCATTGACATAAAGGTCAC TGAACCCAGCTGCTGGAACTTGGCCTTGTGCAGAGCCCT
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCTG
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA
GGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCAGGGCAACGTGTGCCCTCTGGTCAATGAG
GTTCTCAGAGGCTTGGACATCACCCCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA
CAGTTTGTCATCAAGGTCTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT
GCCCCCTCTCCTTTCCACACAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCT
CTTCTTATGCA

FIGURE 374

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLL
SGGLLGILENLPLLDILKPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHVLVLDGDC
THSPGSLQISLLDGLGPLPIQGLLDSLTGILNKVLPPELVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV

Important features of the protein:

Signal peptide:

Amino acids 1-19

Transmembrane domain:

Amino acids 79-97

N-myristoylation sites:

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;
82-88;85-91;86-92;89-95;202-208;233-239

FIGURE 375

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT
AAATATGTCAAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTGTG
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAAA
TTATAATGACCAACACCCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTTGGTGCG
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGAATTGA
TTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGGGACAGA
AGCAGCTGTGAGTCCAACTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT
TCCTGCTCCATGTTTTTGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC
CTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCTAAAACATCAA
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA
GGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTTGGTCATGGAGATGTTTAAATAGTA
AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACACAACCAAATTAAT
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA
GGACTCCACTGCAGTATACAGCACACCATTTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT
TTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT
GGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTGGCATTTATTGCAGCATCATG
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAACATCCATCACAGATGA
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

FIGURE 376

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVAA
LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP
APCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 377

CGCGGATCGGACCCAAGCAGGTCGGCGGCGGCGGCAGGAGAGCGGCCGGCGTCAGCTCCTCG
ACCCCCGTGTGGGCTAGTCCAGCGAGGCGGACGGGCGGCGTGGGCCCATGGCCAGGCCCGGC
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGCCCTCGGGGGGCATCGGCGCGGCC
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCTACAGA
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCGCTGACACCCTGCTCTCAGGCAGC
ACCA GTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAAACATCAATAGCATG
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACG
TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCTTCAAACCTCCACGACAAGGACCCTGAG
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT
ATCTACGTCCTCAGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACGGAG
CAGGTGACCTTAGTGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTG
CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATACCACTTCCTGTCCACACCCCGACC
AGGGGCTAGAAAATTTGTTTGAGATTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG
TGAAAATGGGCTGGGGAAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTCTTG
TGCCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT
GTGGCCAAAATCCCCATCTTCTTGACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG
GAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC
ACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCAGTCTTGGCTTCTTGT
CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC
CCAGTGATTTTCATGGTGATCATTAAGAAAGAAATCGCAACCAAAAAAAAAAAAA

FIGURE 378

MARPGMERWRDRLALVTGASGGIGA A VARALVQQGLKVVG CARTVGNIEELAAECKSAGYPGT
LIPYRCDLSNEEDILSMFSAIRS QHSGVDICINNAGLARPD TLLSGSTSGWKDMFN VNV LALS
ICTREAYQSMKERNVDDGHI ININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ
MRPTEQVT

Important features of the protein:

Signal peptide:

amino acids 1-17

N-myristoylation sites.

amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205

Short-chain alcohol dehydrogenase.

amino acids 30-42, 104-114

FIGURE 379

GAGCGGAGTAAAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTAGC
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCGACCGTGACGAGAAGCCACG
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACTCCCT
CTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA
GAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTTCAAGTCTTGATTTGTGGCTTACCT
CAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTGCTTCTTCAGAAATGTTTTTTTACAATCTC
AAGAAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGTATTTGGACTCATTTGGGGATT
GATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA
AATACTAGACTTAAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGGA
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCCTTCT
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATATTGTTGTGAATGG
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAATAAAAG
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGTGCTGCTCCATCCACTG
TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTGATGAACTCTAATTCTGTACATA
AAAATTTTAAAGTTATTTGTTTGTCTTTCAGGCAAGTCTGTTCAATGCTGTACTATGTCCTTAA
AGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGTTTGTATAAATCTTTTGT
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAAACATGGATTGATTTCTATAACACATTTAT
TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAATCATTCTGTGCTTTGTTCTC
AATAGATGTAACGTGTTAGACTACGGCTATTTGAAAAAATGTGCTTATTGTACTATATTTTGT
ATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC
AAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGAAGGTTAATTATTGTATATTTTAA
AAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT
AAACATTGGGGCAATTTAATAACAGCATTAAAATAGTTGTAACTCTAATCTTATACTTATTG
AAGAATAAAAGATATTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTTCACATACAT
GAATGTTCAATTTAAAAGTTTAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTATTTCC
ATATTTGGGTAAATTTTGCTTTTATTATATTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTGTGCTGCATTAAATTGCTTG
GAAAGTGTTAACATTATATTATATAAGAGTATCCTTTATGAAATTTTGAATTTGTATAACAGA
TGCATTAGATATTCATTTTATATAATGGCCACTTAAAATAAGAACATTTAAAATATAAACTAT
GAAGATTGACTATCTTTTCAGGAAAAAGCTGTATATAGCACAGGGAACCTAATCTTGGGTGTA
ATTCTAGTATAAAACAAATTATACTTTTATTAAATTTCCCTTGTAAGTGCAGCTAGCTTCT
ATGGTGCCCTATATTTCATAGTATTTATTCTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCT
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTTCGTCATTATAATATGCTACCACATGT
AGCAATAATTACAATATTTTATTAAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT
TCCAAATCTCTCTTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA
TTGCCAGGT

FIGURE 380

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAEENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVPVTTNKRTNVSGSIR

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 381

AAC TTCTAC **AT**GGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC
ATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTT CAGGTGCAGAGTCTCAGTTGCCCCG
GAGCACCTCCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCCAGTTCTGGTT
TCATGCCAGCCTGTAAAAGGCCATGGAAC TTTGGGTGAATCACCGATGCCATTTAAGAGGGTT
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTTCATTT CAGTAGCCACCAG
CCACCTGTGGCCGTTGAGTGCTTGAAAT**GAG**GAACTGAGAAAATTAATTTCTCATGTATTTTT
CTCATTTATTTATTAATTTTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTTGG
ATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACAT
TTATTTTTTTATTCTTTTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGTGCC
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA
GTAGCTGGGACTACAGGCATGCACCACAATGCCCACTAATTTTTGTATTTTTTAGTAGAGACG
GGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAACCTCCTGGCCTCAAACAATCCACTTGCCTCG
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCTGGCCTAAACATTTATCTTTT
CTTTGTGTTGGGAAC TTTGAAATTATACAATGAATTATTGT TAACTGTCATCTCCCTGCTGTG
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGT
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC
CATGAGATCCACTTTTTTTAGCTCCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAATGACAGGA
TTTCGTTCTTAATTTCAATTAAAATAACCACACATGGCAAAAA

FIGURE 382

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRI PVLVSCQ
PVKGHGTLGESMPFVKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

FIGURE 383

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACCATGATCAGCGCAG
 CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAG
 TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC
 GCTTTCCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACA
 ACCAAATAAATAATGCTGGGATTCCCTTCAGATTTGAAAACTTGCTGAAAGTAGAAAGAATAT
 ACCTATACCACAACAGTTTAGATGAATTTCTTACCAACCTCCCAAAGTATGTAAAAGAGTTAC
 ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTCCTTATCTGG
 AAGAATTACATTTAGATGACAACCTCTGTCTCTGCGAGTAGCATAGAAGAGGAGCATTCCGAG
 ACAGCAACTATCTCCGACTGCTTTTCCTGTCCCGTAATCACCTTAGCACAAATTCCTGGGGTT
 TGCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTTTCATCACCAT
 CTCTTCAAGGTCTCACTAGTCTAAAACGCTTGGTTCTAGATGGAAACCTGTTGAACAATCATG
 GTTTAGGTGACAAAGTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGCGGAATT
 CCCTGACTGCTGCACCACTAAACCTTCCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA
 ACCCATCAATCGGGTGCCCCCAAATGCTTTTCTTATCTAAGGCAGCTCTATCGACTGGATA
 TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC
 AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT
 TACAATCACTACCTGTGAAGGTCAACGTGCGTGCGGCTCATGTGCCAAGCCCCAGAAAAGGTTT
 GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA
 GCACCATTCAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCAAGGACAGTGGCCAG
 CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG
 GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTACCTCTGATACCATTCTATA
 TCTCTTGGAACCTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAACTGGGCCATA
 GCCCGGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA
 CAGCCCTGGAGCCTGATTCACCCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT
 ACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAACTGCACCCCTTCGAATGTACAACC
 CTACAACCACCCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACCTTTGG
 CTGCCATCATTGGTGCGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTGGT
 ATGTTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAA
 AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACTCTATCCTGGAAATCAGGGAACTT
 CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAAATACACACCA
 TATTTCTCCTAATGGAATGAATCTGTACAAAAACAATCACAGTGAAAGCAGTAGTAACCGAA
 GCTACAGAGACAGTGGTATTCAGACTCAGATCACTCACACTCATGATGCTGAAGGACTCACA
 GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

FIGURE 384

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRC DAGFIYCND RFLTSIPTGIPEDATTL
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNL PKYVKELHLQENNIRTITYDSL SK
IPYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAA PVNLPGTNLRKL
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGI FDDLDNITQLILRNNPWYCGCKMKW
VRDWLQSLPVKVNVVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ
GQWPAPVTKQPD IKNPKLTKDQQTGSPSRKTITITVKS VTSDTIHISWKLALPMTALRLSWL
KLGHS PAFGSITETIVTGERSEYLVTALEPDSPYKVC MVPMETSNLYLFDETPVCIETETAPL
RMYNP TTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSK
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNL YKNNHSES
SSNRSYRDSGIPDS DSHSHS

Important features of the protein:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.

amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645

Amidation site.

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

FIGURE 385

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCCAGGCTTCTTGG
 CAGCCCTGCCGGGCCACTTGTCTTC**ATG**TCTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG
 GGCGTGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA
 GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC
 GCTGTGGTCCCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT
 GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCTAGAACAGAGGCTGCCTGAAATCAACCT
 GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGC
 CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC
 TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA
 GCTGACCCTCCAGCCCGGGTTTTGGAAGCTCCCACATGCCTGGATCCACACTGATGCCTCCTT
 GGTGTACCCACGTTTCGGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT
 GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG
 CCTCATGACCAAGCCCGCTGCTCAGGCTACTGCCTGTCCCACCAACTGCTCTTCTTCTCTG
 GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT
 CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCTACCCG
 GGACATCTTCATGGAAAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT
 CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTTCGGGGAGCCTGA
 TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTTCGAGGAGAGTGAA
 GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA
 TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCCTCATCCTCCCGAG
 TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTTATATTTTTTTTAGTAGAGAC
 AGGGTTTCATCATGTTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCACCTC
 AGGCTCCCAAAGTGTTGGGATTAT**AGG**TGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAA
 GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC
 TAGATGGCTGCTCCTCCCAACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCTTATACA
 TCCTGGCAGAATAACCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA
 GCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCA
 TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA
 GCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCGGG
 AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

FIGURE 386

MSARGRWEGGGRRACRGSGLLARAQGAERVTSSEQRPAMASLGLLLLLLLLTALPPLWSSSLPG
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL
SLRVGMLGEKLEAAIQRSYLHYLKLSDPKYLRELFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ
DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ
GPLQQSQDYINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS
WQKQQEGCFGEFDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP
PGFKQFSCILIPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRPPTSGSQSVGL

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

FIGURE 387

GGTCTGAGTGCAGAGCTGCTGTCATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAGTTGTTCCAGGGG
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCCGGTT
TCCTTAAGACAGATGGGAGTTTTGTGGTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG
TTGTATCTCCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGA
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA
TGAAATCTTCAGGTCCACCTTCTTACTTTATTTAAAGGGAATCGTGGGGCTGGACAGACTTTC
TAATGAACCCAATGGTTATGATGATGGTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTG
GCAAATCTAGCAGCGGCAGCAGTAAACAGGCAAAAGTGGGGCTGGCAAAAGGAGGTAGTCAG
GCCGTCCAGAGCTGGCATTTCACAAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAA
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT
ATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTTATAGAAAATGCCATTAATAAA
TTATATGAACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAA
AAAAAAAAAAAAAAAAAAAA

FIGURE 388

MAAALWGFFPVLLLLLLSGDVQSSEVPGAAAEGSGSGVGIGDRFKIEGRAVVPGVKPQDWIS
AARVLVDGEEHVGFLKTDGSFVVHDIPSGSYVVEVVSPAYRFDVVRVDITSKGKMRARYVNYI
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMVLPLLIFVLLPKVVNTSDPD
MRREMEQSMNMLNSNHELDPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:

Signal sequence:

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

FIGURE 389

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCCATGGCGTGGAGCCTTGGGAG
 CTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTGGGAATGGTACCACCTCCCGAAAATGTCAG
 AATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA
 CCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC
 CTTGACGGAATGTGATTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC
 TGAATTTGCAGATGAGCATTGAGCTGGGTAAACATCACCTTCTGTCTGTGGATGACACCAT
 TATTGGACCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC
 CCTAAAATTGAGAATGAATACGAACTTGGAATATGAAGAATGTGTATAACTCATGGACTTA
 TAATGTGCAATACTGGAACCGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT
 TGAGGTCCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAGGGTTTCTTCC
 TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC
 GGTCCCCTCCTGGATGGTGGCCGTATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT
 CCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTTACAAGAAGACAAAGTACGCCCTTCTCCCTAG
 GAATTTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT
 TTTCTCCTTTCCATTGTGCGATGAGAATGATGTTTTTGACAAGCTAAGTGTGATTGCAGAAGA
 CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCCGCCTGGGCAGGG
 GCCCCAAAGCTAGGCTCTGAGAAGGAAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC
 ACATCTGCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA
 CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGCA
 AAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCATGATGTTTTTCAAGTTGGC
 CACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTAATTGTGAGA
 AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTGAGGCAGGCGG
 ATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA
 AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA
 GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC
 ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG
 AGAAACAGAAATACTTAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT
 TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT
 GCTACACAGAGCACGGACTTTTGGATTCTTTGCAGTACTTTGAATTTATTTTTCTACCTATAT
 ATGTTTTATATGCTGCTGGTGCTCCATTAAAGTTTTACTCTGTGTTGC

FIGURE 390

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551

><subunit 1 of 1, 325 aa, 1 stop

><MW: 37011, pI: 5.09, NX(S/T): 4

MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLADS
LHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPQYDFEVLRLNLEPWTTYCV
QVRGFLPDRNKAGEWSEPVCETTHDETVPSSWMVAVILMASVFMVCLALLGCFSLWCYVYKKT
KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNPGDSCSL
GTPPGQGPQS

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

FIGURE 391

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCGATGAGGA
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCCAGCACTGCCC
AGATCACTGAGGCCCAGGTGGCTGAGAACCGCCCCGGGAGCCTTCATCAAGCAAGGCCGCAAGC
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG
AGAGGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA
TCTGGCTCATGGTGAAATAAGCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA
TCCTGGCAAGTGACCCAGCTCTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCCAGGAGC
GGCGATGCACTCGCACTGCAAAATGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT
GATAGATGGGGGACTGTGGCTTCTCCGTCACCTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCCTGCGCCACCTGCTTCAC
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCTGTTTTACAGATAAGGAACTGAGGC
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT
TAGAAATAAATGAAAACACCTGA

FIGURE 392

MRKHLSSWWLATVCMLLFSHLSAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQG
RKLDIDFGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK
LHQQVLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWLMMVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

FIGURE 393

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGCCAA
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG
ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCTTCTGCCCTCCTTTG
CTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCTGCTTCTC
TGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGG
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT
AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC
TGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAAACGTGTTTTCAAAAACCACCACAAT
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAACCTTTGTTCTCATC
GTGTCACAACCTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG
CGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC
CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTCTACAAGCTCT**TGAATGTCTAGA**
CCAGGACCTCCCTCCCCCTGGCACTGGTTTTGTTCCCTGTGTCAATTTCAAACAGTCTCCCTTCC
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT
GAAGAGTCTACAGAGAAGATTCTTGTATTTATTACAACCTCTATTTAATTAATGTCAGTATTTT
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC
ATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT
ACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATTGTTAAAAAACAGAGAGGGATG
CTTGGATGTAAAACTGAACTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC
AGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAAAGTAAACGATAAAATGTGGATTAAA
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTTCAATTTCCACCCACACTCGCCAGCTCAC
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

FIGURE 394

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARPFPCPPLLATASQMOMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVKG
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNHHN
RTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAALTKA
LGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 395

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT
TTCCTGATGATTTATAGACTCAAAGAAAACTATGTTCAGAAGCTCTCTTCTCTTCTGGCCTC
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA
AGCTGGAAATCTTTCATTTTGCTTGTCAGTGGGGTAGGTCAGTCTTAGTTTTTATTTTT
TGAAATTTCAACTTTCAGATTCAGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT
GATGCTGAGGTTTGGGGT

FIGURE 396

MFRSSLLFWPPLCLLSLFLLLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT
CEGLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

FIGURE 397

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTTG
TGTCTCTGGTGGTTCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAAATGCAGAAATATCAATAGAACCTACTG
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCCTATCCTTTTTTTAGAAACACAAAT
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCTGACAGCTCC
AGAGAAGTGGGAAGAGAAATCCAGAAGACCTTCCTGTTTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTTCCTT
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
AAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGATTCTAAAATTTCTCATCAGGA
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGGAGGAGGTGTCCACACAAGGAACATT
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT
TTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGAAACGTTACAGTACTCATACACCCC
TCAGCTCCAAGACTTAGACCCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA
AGAGCCATCGACGACCCTGGTCTGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTCGCT
GTCCAGCTTCGACCAGGATTGAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGCAATTCATGGAGGAATGGGGGTTATATGTGCAGATGGAAAACTGATGCCAACA
CTTCCTTTTGCCTTTTGTTCCTGTGCAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTGAGTGTCTGTGAGAA

FIGURE 398

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGKVKVTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPPFLETQI
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHPANLILYIGNEFDKRFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS
RTIPDKTVIEYEDVRTTDCAGPEEQELSLQEEVSTQGTLLSQAALAVLGPQTLQYSYTP
QLQDLPLAQEHTDSEEGPEEEPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEE
GLLSRLYEAPDRPPGENETYLMQFMEEWGLYVQMEN

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 240-260

N-glycosylation sites.

amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526

Tyrosine kinase phosphorylation site.

amino acids 385-392, 518-526

N-myristoylation sites.

amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor

amino acids 1-278

FIGURE 399

CCGGCGATGTCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA
ATCCCCGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTTGCAACAGGGGAC
TATTCAATTTTGTATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAAT
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATC
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTTCATTGGGGCCCATAATATTCCTAATGCAAAT
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT
AAGAAGAATGAGGAGACAGTAGAAGTGAAC TTCACAACCACTCCCCTGGGAAACAGATACATG
GCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTG
ACTCCATATTTTCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC
CCACAAACAGGCGTCCCTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAGGTT
CTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT
CAAAACCATTGCAGAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG
GGTCCAGTGCAGTGGCTTGCCACTCAAAAGAAGGCAGCAGACAAAGTCGTCTTCTTCTTTCC
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC
TCTCAAGACCTCTTCCCCCTTGCCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATTCAT
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTG
TAG

FIGURE 400

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLIPGDLRDLRVEPVTTTSVATGDYS
ILMNVSUWLRADASIRLLKATKICVTGKSNFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGCLDHIMKYKKKCVKAGSLWDPNITACKK
NEETVEVNFTTTPLGNRYMALIQHSTIIGFSQVFEPHQKKQTRASVVI PVTGDSEGATVQLTP
YFPTCGSDCIRHKGTVVLCPTGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH
ERIKTSFSTTTLLPPIKVLVVPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGP
VQWLATQKKAADKVVFLLSNDVNSVCDGTGKSEGPSSENSQDLFPLAFNLFCSDLRSQIHLH
KYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHVKKQVSAGKRSQACHDGCCSL

Important features of the protein:

Signal peptide:

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.

amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201
and 283 - 287

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

FIGURE 401

GGGAACAGGGAACTATCAGCCCGTCGGCCTCCGGGCCCTGCATTCTCTAGCCATGGACCG
GGACCTTTTTCGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTCGGAG
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCCTGGGGTCGGCCGCCGAGCCAGCCCG
GGGCCCCGCCGCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA
GATACAGAAATTCATCTCCAAAAAGCGGATCTGCTTTTTCGCACTTTCCTGGAAATCAGA
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC
TTTAGAGCAATTCATGGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTTCCGAGATAT
TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTTCGGGAATTCGGTTTTTTCAT
GGTGTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC
TCTTTGTCCCTTAAGAGATGTGCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA
CCAACTGGTGACATCATTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT
AGCAGTATCTCTGTATAGCTCTTCTCTCCACCACACCTATCTGGTATTAAATTAGGTGT
AATTAGCTCTGAAGAGCTTCCTTTATACTACAGGAGAAGTGTGAGCTAAATAGCAATTC
TTTGGAGTCCATGAAAATGTCATGCAGAGTTCTTTGGGATTTGTTAATCCAGGAGTAGT
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAACAATC
CGCATCTTGGGCTTTAAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA
TGTGGATGCTATGAATGAATACAATAAAGCTTTGGAAATAGACAAACAAAACGTGGAAGC
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA
TTTTGAGCTTGCATTAGAAAACTGTCCAACCTCACAGAAATGCAAGAAAATACCTCTGCCA
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTTAAATGCTGAAAG
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA
GAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA
AGAAAAGCAGAAAACAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAAA
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTTCAAGTGTTCCTC
TGCTGATGAATCAGTGTCTTCATCATCATCCTCTTCCTCTTCTGGTCAAAAAGGCATAA
GAAACATAAGAGGAACCGTTTCAAGTCTTCTCGCAGTTCCAGAAGGCATTATCTAGGGC
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCCAGCTAATAC
TTCAGCATCTTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTTCATCTTC
ACTTGAAATACCGGATGATTTTGGAGTGTACTCCTATTTATTTAAAAAGTTAACTATAAA
ACAGCCTCAGGCAGGTCTTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA
CAGCTCCATTATGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA
AGACAGTGGTATTGATGATCCTGACCACGGGTAGGCTTAGGTTTATGTGTGTGTATGTGT
CTTAGTTTTTAACAAAAAATTA AAAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG
AATAAGGATATAAAGAATATTTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA
TCACAAAAGAGTAAAAAAATTTTACAAAATTA AAAATGTTTAAAGTTAAAAAGCTCTAGG
AAGCTAAGGTCAATTTATTATTGGAGAAATAAAATTATTTTATGAATTTACTGT

FIGURE 402

MDRDLRLRQSLNCHGSSLLSLLRSEQQDNPHFRSLLGSAAEPARGPPPQHPLQGRKEKRV
NIEIQKFISKKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELFF
RDIERGDIVIGRISSIREFGFFMVLIICLGSGIMRDIAHLEITALCPLRDVPSHSNHGDPL
SYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPHLSGIKLGVISSEELPLYRRSVELN
SNSLESYENVMQSSLG FVNPGVVEFLLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNVREALVARGALYATKGS LNKA
IEDFELALENCPTHNRNARKYLCQTLVERGGQLEEEEEKFLNAESYKKALALDETFKDAED
ALQKLHKYMQKSLELREKQAEKEEKQKTKKIETSAEKLRLKLLKEEKRLKKKRRKSTSSSS
VSSADESVSSSSSSSSSGHKRHKHKRNRSESSRRHSSSRASSNQIDQNRKDECYPVP
ANTSASFLNHKQVEKLLGKQDR LQYEKTQIKEKDRCP LSSSSLEIPDDFGVYSYLFKKL
TIKQPQAGPSGDIPEGIVIIDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

Important features of the protein:

Signal peptide:

Amino acids 1-23

Transmembrane domain:

Amino acids 138-155

N-glycosylation sites:

Amino acids 288-292;508-512;542-546

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 300-304;472-476;473-477;517-521;598-602

N-myristoylation sites:

Amino acids 218-224;222-228;271-277;348-354

Amidation site:

Amino acids 52-56

Cell attachment sequence:

Amino acids 125-128

FIGURE 403

CCGAGGCGGGAGGAGCCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTC
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATA
GGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTT
ATGACAAACTTTT CAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA
CTGCCTACTTTTGTGATTCAACCTTTT CAGCCCATTAGCACCTGAGCCAGTGCTTTTCTGGAGCTC
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAAGAAGTACA
TGTCAGAAAATAAGGGAGTTCCTCTGCATGGGGGTGATGAAGACAGACCTTTTCCAGACTTTG
ACCCCTGGTGGACAAACGACTGTGAGCAGAAATGAGTCAGAGCCCATTTCTTGCCAAC TGCACTG
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCCTGTTGGAGGAAGAGATTCAGCATTTTTTGT
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTTCGCCAAGTGGTGGCGCTGCT
TTCCTGAGCGGTGGTTCCCATTTCTTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT
TACGTGAGCTTTTTCTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT
GCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCAGTGCCGAAGACATTGTC
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTGACACCACCCACTGGAAGG
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCACTGCGATGGAACCGCTTTCTCAGAAC
TGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGAAAACCAGGTTGAAAGGGGAA
AAATAAAAACAAAAACGATGAAACTGCAAAAA

FIGURE 404

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIIVVYK
VLATLGLILLTAYFVIQPFSPLAPEPVLGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPLHG
GDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMILLEDAPRKFERLHPLVIKTGKP
LLEEEIQHFQYPEATEGFSEGGFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFPVFTHL
PFPKASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRHCQSVAMPIEPGD
IGYVDTTHWKVYVIARGVQPLVICDGTAFFSEL

FIGURE 405

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCTGGACTCCC
 GTCTCCTCCTGTCTCCGGCTTCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCTCTCCGGCGCAGCTTCT
 CAGCGGACGACCCTCTCGCTCCGGGGCTGAGCCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG
 TTTGGCTGCTGCTTCCCCGCGGGTGCCACTGCCACCGCCGCCCTCTGCTGCCGCCGTCCGCGGGATGCTCAG
 TAGCCCCGCTGCCCCGCCCCCGGATCCTGTGTTCCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAAGTAGTC
ATGGTGCTGTGGGAGTCCCCGCGGCAGTGACAGCAGCTGGACACTTTGCGAGGGCTTTTGCTGGCTGCTGCTGCTG
 CCCGTCATGCTACTCATCGTAGCCCCCGGTGAAGCTCGCTGCTTTCCCTACCTCCTTAAGTGACTGCCAAACG
 CCCACCGGCTGGAATTGCTCTGGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACACCTGTAAA
 TTTGATGGGGAATGTTAAGAATTGGAGACACTGTGACTTGCCTCTGTGAGTTCAAGTGCAACAATGACTATGTG
 CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTTACCTGCGACAGGCTGCATGCAAAACAGCAGAGT
 GAGATACTTGTGGTGTGAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC
 TCTGGAGAAACTAGTCAAAAGGAGACATCCACCTGTGATATTGCCAGTTTGGTGAGAAATGTGACGAAGATGCC
 GAGGATGTCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCTCTGCGCTTCTGATGGGAAA
 TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT
 CGATGTCAAGATAACACAACACTACAACACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT
 GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT
 GGGAAAGTGTGAGCATTCTATCAATATGCAGGAGCCATCTTGAGGTGTGATGCTGGTTATACTGGACAACACTGT
 GAAAAAAGGACTACAGTGTTCTATACGTTGTTCCCGGCTCCTGTACGATTTAGTATGTCTTAATCGCAGCTGTG
 ATTGGAACAATTGAGATTGCTGTCATCTGTGTGGTGGTCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA
 ATTCACAGACAGAAGCAAAATACAGGGCACTACAGTTGAGACAATACAACAAGAGCGTCCACGAGGTTAATCTAA
 AGGGAGCATGTTTTCACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA
 GACAAGAGATCTACACATGTTGCCTTGCATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATT
 GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTCTGTAATGTAATAAATACTATTTATA
 TCACACAATATAGTTTTTTCTTTCCCATGTATTTGTTATATATAATAAATACTCAGTGATGAG

FIGURE 406

MVLWESPRQCSSWTLCGFCWLLLLPVMLLIIVARPVKLAAPFPTSLSDCQTPPTGWNC SGY
DDRENDLFLCDTNTCKFDGECLRIGDTVTCVCQFKCNNDYVPVCGSNGESYQNECYLRQ
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTT TK
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY
TGQHCEKKDYSVLYVVPGPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQ
KQNTGHYSSDNTTTRASTRLI

FIGURE 407

CTCGCAGCCGAGCGCGGCCGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCCTGGCAG
 ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT
 GTCCAGACTGAGGCCCCATTTGCATTGTTTAACTACTTAGAAAATGAAGTGTTTCAATTTTAA
 CATTCCCTCCTCCAATTGGTTTAAATGCTGAATTACTGAAGAGGGCTAAGCAAAACCAGGTGCTT
 GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGGCGCTCTCCCCGTGTCTCTCCACGACT
 CGCTCGGCCCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGACGTGCC
 CGAGCTCCTCCGGGGGTCCCGCCCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCG
 TCTTGGACATGCCAGGAATAAAAAAGGATACTCACTGTTACCATTCTGGCTCTCTGTCTTCCAA
 GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT
 GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA
 ACCAAAATGGCGGGTATTTATGCATTCCCCGGACAAACCCTGTGTATCGAGGGGCCCTACTCGA
 ACCCTTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA
 ACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGCAACC
 AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCCACCCAGATCTGCA
 TCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCAGT
 GCTTAGACATTGATGAATGTCGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTTCTGGAT
 CCTATTCTTGTACATGCAACCCTGGTTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATG
 TGAACGAGTGTGCCACCGAGAACCCTGCGTGCAACCTGCGTCAACACCTACGGCTCTCTCA
 TCTGCCGCTGTGACCCAGGATATGAACCTTGAGGAAGATGGCGTTTATTGCAGTGATATGGACG
 AGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCCGGCACATACTTCT
 GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT
 GTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA
 AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT
 GTCTTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACG
 TGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCCAAATGCAAGCCACGACCCGCTACCCCTG
 GGGCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA
 CGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC
 TGGACTTGGAATGATCACTGTCAACACTGTCTCATCAACTTCAGAGGCAGCTCCGTGATCCGAC
 TGCGGATATATGTGTGCGAGTACCCATTCTGAGGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT
 CATTGGCACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT
 TAGGCATTTTCTGTGAACGTTTTCCCCGAAGAGTCAGCCCCGACTTCTGACTCTCACCTGTA
 CTATTGCAGACCTGTCAACCCTGCAGGACTTGCCACCCCCAGTTCCTATGACACAGTTATCAA
 AAGTATTATCATTGCTCCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT
 TCCACTATTTTCAAAGAAAATAGATTAGGTTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGT
 GAACAGCTTGCTGTCACTTCTTCACCTCTTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCA
 AAGACCCGGGAGCTGGCGGGGAACCTGGGAGTAGCTAGTTTGGCTTTTTCGTACACAGAGAA
 GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTTAGAGAATGTGTTTCAAACCATGC
 CTGGTATTTTCAACCATAAAAGAAGTTTCAGTTGTCCTTAAATTTGTATAACGGTTTAAATCT
 GTCTTGTTTCAATTTGAGTATTTTAAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGA
 CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTTCTTT
 GAGGACCCCTTAATCTTGCTTTCTTTAGAATTTTACCCTAATTGGATTGGAATGCAGAGGTCT
 CCAAACCTGATTAAATATTTGAAGAGA

FIGURE 408

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGGYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAPPLSAPNYPTISRPLICRFGYQMDESNQCVDVDECATDSHQCNPTQICINTEGGYTCSCTDGYWLLEGQCLDIDECRYGYCQQLCANVPGSYSCTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSILICRCDPGYELEEDGVHCSDMDECSFSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTCYNLQGGFKCIDPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAYYIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPRIQLDLEMITVNTVINFRGSSVIRLRIYVSQYPF

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.

amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248, 267-273, 310-316

Aspartic acid and asparagine hydroxylation sites.

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

FIGURE 409

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGGCTCA
 GGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT
 TCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT
 TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGCTGGG
 AAGATCCAAAAAGGAAGAGAATTGAGTTTGGTTCGGCCCTTTCCAGGACTGAACATGAAGAGT
 TATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA
 GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGGAGGTTCA
 TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGACCTTGCGT
 GACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCAGTGGGCACA
 GGCTTCAGTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT
 TTATACAGTGCACCTAATTCAGTTTTTCCAGATATTTCCCTGAATATAAAAAATAATGACTTTTAT
 GTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC
 AACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT
 CCCGAATCAATTATAGGGGGCTATGCAGAAATTCCTGTACCAAATTGGCTTGTGGATGAGAAG
 CAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG
 TTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC
 TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGTGCACGGAACCTGAGGAT
 CAGCTTTACTATGTGAAATTTTGTCACTCCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT
 CAGACTTTTAATGATGGAATATAGTTGAAAAGTACTTGCGAGAAGATACAGTACAGTCAGTT
 AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACCTGGAC
 ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCCAG
 GAATACAAGAAGGCAGAAAAAAGTTTGGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT
 TACATCCGGCAAGCGGTGACTTCCATCAGGTAATTATTCGAGGTGGAGGACATATTTTACCC
 TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTATGGAAAAGGATGGGAT
 CCTTATGTTGGATAACTACCTTCCCAAAGAGAACATCAGAGGTTTTCATTGCTGAAAAGAA
 AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT
 TTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTTTTTTGGGGGGAGATGTTTACT
 ACAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG
 GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTGAAATAGGAAGTTTTA
 ATTTCTTCTAAGAGTAAGTGAAAAGTGACAGTTGTAACAAACAAAGCTGTAACATCTTTTTCTG
 CCAATAACAGAAGTTTGGCATGCCGTGAAGTGTTTGGAAATATTATGGATAAGAAATAGCTC
 AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTTTGGGGAAAAGATTCTCAAATGTATAA
 AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATAAAAAGTAAAAA

FIGURE 410

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGD SGQPLFLTPYIEAGKIQKGRELSLV
GFPFGLNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP
YVVT SNMTLRDRDFPWT T T L S M L Y I D N P V G T G F S F T D D T H G Y A V N E D D V A R D L Y S A L I Q F F Q I
FPEYKNND FYVTGESYAGKYVPAIAHLIHS LNPNVREVKINLNGIAIGDGYSDPESIIGGYAEF
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TGCSNYY
NFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLTEIMNNY
KVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRQAGDFHQV
IIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 411

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCCCCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCGCTCTTCTGTGCGAGGTGAGTGAGAACAAGTTCGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGC
CAGCATTGCCCGAGCTCACGGGCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGAGCTCAAACGCTCAAGGTGCTGCGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTACGCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCCCTCCCTGCGGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACCTGCTGCAGTCACTGCCCTCCAGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTGCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCGGAG
GCCGGCCAGCAGCAAGCAGCAGGACCGCTGCCCCAGTCTCAGGCCCCGAGGGGCGAGGCTAGCTTCTCCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGCGCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTTCTCCCTCTGAGACTCACGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGCTCTCTCCCTGGAGGCCAGCTCTGCCCGAGGGCTGAG
CTGCCACCAGAGGTCTGGGACCTCACTTTAGTCTTGGTATTTATTTTCTCCATCTCCACCTCCTTCATCC
AGATAACTTATACATTCCAAGAAAGTTCAGCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCCTTTCCCC
TTGTCTTATTTAGCGATGCCGCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCAG
CCATGGGACGGTCAACCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA
AAGGCCAGGCTGGAGCTTGCTCTTCACTTTTGTGGCAGTTTGTAGTTTTTGTTTTTTTTTTTTAAATCAAA
AAACAATTTTTTTTAAAAAAAGCTTTGAAAATGGATGGTTTGGGTATTAAAAAGAAAAAAACTTAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGT
TGAAGTGTGTTTCTTTCCCTGGGCGCAGGGTGACGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCCTGGGAGGGAGGTTTTTTTGTGTTTGTGTTTGGGTTTTTTTGGTGTCTTGTGTTTCTTCTCCTCC
ATGTGCTTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGTTGGCTAATCCCCGATGAACGGTGCTCCATTGCGACCTCCCCCTCCTGCTGCTGCCCCGCTCTCCA
CGCAGTGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGAGGTGCCCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGTTCCCGTCCCTGGCGC
CTGGAGTGACACAGCCAGTCGCGACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGTCCCCACCTT
AGAAGGGTCCCCGCCTTAGATCAATCAGTGGACACTAAGGCACGTTTTAGAGTCTCTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAA

FIGURE 412

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF
AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHFLMLSGIPDTVFDLVELEVKL
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWIYSLK
TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEG
KLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQHLHRLT
CLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLTFLPADIG
LLQNLQNLAITANRIETLPPELFCRKLRLHGLGNNVLQSLPSRVGELTNLTQIELRGNRLEC
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 413

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGAAGCCGTGGGGGTTTTGAGCTCATC
TTCATCATTCATATGAGGAAATAAGTGGTAAAAATCCTTGGAAATACAATGAGACTCATCAGAA
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAG
AAAGGGAAGTGAAGCACTGCTCCAAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGACCC
CAGCCACAACGACACTGGATTATCCTATAACCTCCTTTTTCAACTCCAGAGTTCAGATTTTC
ATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCACAGCTGGATCTCA
AAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG
TAACCTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTAATGACTTTGACACCA
TGCCTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTGAGTGGGGCAA
AAATACAAAAATCAGATTTCCAGAAAATGCTCATCTGCATCTAAATACTGTCTTCTTAGGAT
TCAGAACTCTTCTCATTATGAAGAAGGTAGCCTGCCCATCTTAAACACAACAAAACCTGCACA
TTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGCGTGATGGAATCAAGACTTCAAAAA
TATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAAATGCAACGAAATC
TTAGTTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG
ACCTTTTTCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAAACACTTTTCAGATCCGAAATG
TGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTTGACTACTCAAATACTGTAATGA
GAACTATAAAATTTGGAGCATGTACATTTTCAGAGTGTTTTACATTCAACAGGATAAAATCTATT
TGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATGCACAAATGCCACACATGC
TTTTCCCGAATTATCCTACGAAATTCCAATATTTAAATTTTGCCAATAATATCTTAAACAGACG
AGTTGTTTTAAAGAAGTATCCAACCTGCCTCACTTGAAAACCTCTCATTTTGAATGGCAATAAAC
TGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAACACACCCTTGGAACACTTGGATCTGA
GTCAAAATCTATTACAACATAAAATGATGAAAATGCTCATGGCCAGAAACTGTGGTCAATA
TGAATCTGTATACAATAAATTTGCTGATTCTGTCTTCAGGTGCTTGCCCAAAAGTATTCAAA
TACTTGACCTAAATAAATAACCAAAATCCAACTGTACCTAAAGAGACTATTTCATCTGATGCGCT
TACGAGAACTAAATATTCGATTTAATTTTCTAATGATCTCCCTGGATGCAGTCACTTTCAGTA
GACTTTTCAGTCTGAACATTGAAATGAACTTCATTCTCAGCCCATCTCTGGATTTTGTTCAGA
GCTGCCAGGAAGTTAAACTCTAAATGCGGGAAGAAATCCATTCGGGTGTACCTGTGAATTAA
AAAATTTTCATTTCAGCTTGAAACATATTTCAGAGGTCATGATGGTTGGATGGTCAGATTCATACA
CCTGTGAATACCCCTTTAAACCTAAGGGGAAGTAGGTTAAAGACGTTTCATCTCCACGAATTAT
CTTGCAACACAGCTCTGTTGATTGTCAACATTTGTTGGTTATTATGCTAGTTCTGGGGTTGGCTG
TGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC
AAACATGGCACAGGGTTAGGAAAACAACCCAAGAACAACTCAAGAGAAATGTCCGATTCCACG
CATTTATTTTCATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCCAATCTAG
AGAAGGAAGATGGTTCTATCTTGATTTGCCTTTATGAAAGCTACTTTGACCCTGGCAAAAGCA
TTAGTGAAAATATTGTAAGCTTCATTGAGAAAAGCTATAAGTCCATCTTTGTTTTGTCTCCCA
ACTTTGTCCAGAATGAGTGGTGCCATTATGAATTTACTTTGCCCACCACAATCTCTTCCATG
AAAATTTCTGATCATATAATTCTTATCTTACTGGAACCCATTCCATTCTATTGCATTCCCACCA
GGTATCATAACTGAAAGCTCTCCTGGAAAAAAGGCATACTTGGAAATGGCCCAAGGATAGGC
GTAAATGTGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCA
GAGAAATGTATGAACTGCAGACATTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT
CTCTGATGAGAACAGATTGTCTATAAAATCCACAGTCCCTTGGGAAGTTGGGGACCACATACA
CTGTTGGGATGTACATTGATACAACCTTTATGATGGCAATTTGACAATATTTATTAATAATAA
AAATGGTTATTTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACA
CCTTCACAAGTTTATAAGGGCTTATGGAAAAAGGTGTTTCATCCAGGATTTGTTTATAATCATG
AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGTAATCCCAGCACTATGGGAGGCCAAGGTGG
GTGACCCACGAGGTCAAGAGATGGAGACCATCCTGGCCAACATGGTGAAACCCCTGTCTCTACT
AAAAATACAAAAATTAGCTGGGCGTGATGGTGCACGCCTGTAGTCCCAGCTACTTGGGAGGCT
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG
CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA
ATGGAAAACATCCTCATGGCCACAAAATAAGGTCTAATTCAATAAATTATAGTACATTAATGT
AATATAATATTACATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGGAAAAA
CATATTAATATGTTATAAACTATTAGGTTGGTGCAAAACTAATTGTGGTTTTTGCCATTGAAA
TGGCATTGAAATAAAAGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGTCTGG
GAGGTTGGATTACAGGGAGCATTTGATTTCTATGTTGTGATTTCTATAATGTTTGAATTGTT
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 414

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQL
QSSDFHSVSKLRVLIILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN
TTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNKV
DLLWDDFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFYIQ
QDKIYLLLTkMDIENLTISNAQMPHMLFPNYPTKFQYLNfANNILtDELfKRTIQLPHLKTLI
LNGNKLETLSLVSCFANNTPLEHLDLSQNLLQHKNdENCsWPETVVNMNLSYNKLSDSVFRCL
PKSIQILDlNNNQIQTVPKETIHLMALRELNIaFNFLtDLPgcSHfSRlSVLNIEMNFILSPS
LDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLEtYSEVMMVGWSDSYtCEYPLNLRGTRLKDV
HLHELSCNTALLIVTIVVIMLVGLAVAFcCLHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI
FVLSPNFVQNEWCHYEFYFAHHNLFHENSdHIILILLEPIPFYCIPTRYHKLKALLEKKAYLE
WPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

FIGURE 415

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCGGGCCGAGCCACCTCTTCCCTCCCCGC
TTCCCTGTGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCCCAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACAGGCCAGACCAGGGGCGCTCG
CTGCCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGAGTGGCGGGCGGACGGAGAAAAACAACCTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG
CCGCTCCCCGCCCCCAGCCCTGGCATCCAGAGTACGGGTGAGGCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTCCG
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
ACCGGATTATTTTCAAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTTAGAAGTGCAGGGCACCTTACAGA
GGCCCCCTGGTCCGGGACAGCCGACCTCCCCCTGCCAACTGCACCTGGCTCATCTGGGCGAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCGCTTAACCTACGCTCCCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCAGCCCTCTGCAGCTGCCCCGGGGCAACGTACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCTGCAGGAAG
AGTTTCAGTGCCTGAACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCCTGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCTGACCCCAAGACCCGCTCCCTCCCTGCCTTGCAATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGTGGACCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCGACTACTGCGTAGTCTCACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTTACCACACAGTTGCTTGGAGCA
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGCTATTGCTTGCTTGGGACAGACCCCTGTGGCTTAGGCT
CTGGCTGGGAGCTGGCGAAGCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT
CTGGTGCCACAGCCTGCTACCTGCCTGTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTGCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCATTACAG
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTTCATCGCCCTGGGCTGCACCTGCAAGCTCATGGCA
TTCGCAACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC
CTTCTACGGGCAGCTCATTGCCAGGGTGCCATCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATA
ACTCAGTGTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGGCCAGGTG
CCCGCCGTGCTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGTGGGGCTTGCTCCCTCGAA
CCAAACACCCCGGCTCGGGCTCTGAGGCCAGATCCAGGTACACCTTCTGCTGCTCCCTTGAGGGCTTAGATG
GTGGCACAGGTCCAGCCCGTGAGGGCGGGGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA
AGGCTCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACTTTTAGAGGTGGGTGAGCCTCCCCTCC
ACCACTTCCCTCCCTGTCCCTGGATTTTCAAGGACTTGGTGGGCCCTCCGTTGACCCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
TCACCACCACCTGCTCCCCACGCCACCACATTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAC TAGAGA
CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

FIGURE 416

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQEETFQCLNHRCVSAVQRCGDGDGSDGAGCSSDPFPGLTPRPVPS
LPCNVTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRLAVRFTALDLGFGDAVHVYDG
PGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLPWDRPC
GLGSGLGAGEGLGERCYSEAQRCDGSDCADGTDEEDCPGCPPGHFPCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPDGSDGDEWDCSYVLPRKV
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYGQLIAQGA
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRRLMRRLVRRLRRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPEGPTRSPPGPHTAVLALEDEDDVLL
VPLAEPGVWVAEAEDEPLLT
```

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 417

GTCGTTCTCTTCTCTCGCGCCAGTCTCTCTCCCTGGTTCTCTCAGCCGCTGTCGGAGGAGAGCACCCGGA
 GACGCGGGCTGCAGTCGCGCGGCTTCTCCCCGCTGGCGGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCTAG
 AGCCTCCCTTGCGGCTCTCTCTGCCCCGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
 GCCCCGGAGGCGGCGGTGGATGCGGCGCTGGGCAGAAGCAGCCGCGGATTCCAGCTGCCCCGCGGCCCCGGGCG
 CCGCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCTCTGTCAGCCGCATC
 GCCCCGCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCTGCTTGGATTCTTAGCACCACACAGCTCAG
 CCAGAACAGAAGGCCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATGTGACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
 GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCCATGGCCAATG
 ATTGAGAAATTACCTTGTGCTGCCCTGACTGACCGAGAATGCACCTGCCCCACCTGGCATGTTCCAGTCTAACGCT
 ACCTGTGCCCCCATACGGTGTGCTGTGGGTTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG
 TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
 CTGAGTCAGAACCTGGTGGTGTGATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCCCTC
 TCCAGCTCCACCTCACCTTCCCTTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAACCCCATGAAGTCCCT
 TCTCCACTTATGTTCCCAAGGCATGAACCTCAACAGAATCCAACCTCTTCTGCCCTCTGTTAGACCAAAGGTACTG
 AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
 CCAAACCTTCAGGTAGTCAACCACCCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG
 GCCACTGGGGGCGAGAAGTCCAGCAGGCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
 CATTTTGACATCAATGAGCATTTGCCCTGGATGATTTGCTGCTTTTCTGCTGCTGCTGGTGCTTGTGGTGATTGTGGTG
 TGCAATATCCGAAAAGCTCGAGGACTCTGAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGAAAAGGCCA
 GGGCTGAAGAAATCCATGACTCCAACCCAGAACCAGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
 ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTCTTTGCAATGCCAGTGAG
 AGGGAGGTGCTGCTTTCTCCAATGGGTACACAGCCGACCACGAGCGGGCTACGCAGCTCTGCAGCACTGGACC
 ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCCGAGAGAAACGATGTTGTGGAG
 AAGATTCGTGGGCTGATGGGAAGACACCACCCAGCTGGAAACTGACAAACTAGCTCTCCCGATGAGCCCCAGCCCCG
 CTAGCCCCGAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA
 CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
 TCCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCCTGGAC
 CCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG
 ATCCCCAGGCTGAGGACAAACTAGACCCGCTATTTCGAAATTAATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
 CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA
 ATTTAGTGGCAGGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTGTGTTTGGGGTGTGTGTGTGTGTGTGT
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 TCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCCTTGCCAGGTGTAAGTGTGTGAA
 ATACCCACCCTAAAGTTTTTTAAGTTCCATATTTTCTCCATTTTGCCCTCTTATGTATTTTCAAGATTATCTG
 TGCATTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
 TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTCACACCTACTTTTT
 AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAGAAAATTTAAGA
 CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCATATTATGAG
 CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTCACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC
 TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
 GACAACTGGGCCACCAAGAACTTGAACCTTCACTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT
 GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
 TTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGCTGGGATTCTTTACCAAT
 ACTTTAATTAATAATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTGCAACTATGCTCCATTTACAAATG
 TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAGGTGGCGTGGACTCCCTTGTGTGGGTGGGGTTTGTGG
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTGA
 AAAAAAAA

FIGURE 418

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATGQ
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAAL
TDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAY
TDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSPGTAFPRPEHMETHEVPSSTYVPKGMN
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPS
MEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVVCSIRKSSRTLK
KGPRQDPSAIVEKAGLKKSMPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNAS
EREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDVVEKIRGLMEDTTQL
ETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRCSTSSGS
SALSRNGSFITKEKKDQTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE
IIGVKSQEASQTLTLLDSVYSHLPDLL
```

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

FIGURE 419

ATGGCTGGTGACGGCGGGGCGGGCAGGGGACCGGGGCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
 ATCACCGCCTGGCCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
 AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
 GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA
 GAGGCCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTAC
 CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC
 CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG
 CAGAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCCAGCCACTGAGA
 GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG
 GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
 AATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAAGTGCCAATGAG
 AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
 GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGCGCGAC
 GAGGAGAAGATCTACCACAAGATGAGCATTTCCGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
 CTGCTCTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
 CAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
 ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG
 TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
 GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG
 GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
 GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
 GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
 CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC
 GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATC
 GGTGTGGTCATGGGCCATGAGTTGACGCATGCCCTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG
 CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA
 TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG
 GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
 AACCACCAGCTCTTCTTCTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCAGAGGGG
 CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCTCTGCGG
 CACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA
 GAAATGGCCAGCTGTCAACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTTGGGAGGAAGCAA
 ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG
 TGCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTACCCCT
 GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

FIGURE 420

MNVALQELGAGSNVGFQKGTQRLGSRQTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHS
TCLTEACIRVAGKILESIDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL
KHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDNFME
VLKAVAGTYRATPFFTUYISADSKSSNSNVIQVDQSGLFLPSRDYYLNRTANEKVLTAFLDYM
EELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL
EFLSFLLSPLELSDSEPVVVYGM DYLLQQVSELINRTEPSILNNYLIWNLVQKTTSSLDRRFES
AQEKLETLTGTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTA
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLY
NFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNHPKALNFGGI
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQT
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFQAQVWCSVRTPESSHEGL
VTDPHSPARFRVLGTLNSRDFLRHFGCPVGSPMNPGLCEVW

Type II Transmembrane domain:
amino acids 32-57

FIGURE 421

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGCC
GCCTCTCCGCACGATGTTCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG
GTCCGGGTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG
CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCG
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCCTGGCAGTGCTGGTGCCCTT
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGAGCAGGAA
GAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACGGGCAGC
GCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGCCCTTCACGT
GGCCTCCCCGGAGCTCCACCCCTCTTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCGCGA
GGACGACGAGTTCTACCGGCGCATTAAGGGAGCTGGGCTCCAGCTTTTCCGCCCTCGGGAAT
CACAACCTGGGTACAAGACATTTCCGCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACAGAA
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCCTGAACACTGT
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCCCCTGCACTGTCTCAA
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGACATTTCAGCTTGAGCTGGATGGAC
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTCGTGG
GCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA
CCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCTGGGACGCTGCTTGC
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTCTCTGTCGGGACCCCCCTGCCTTCCTGC
TCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA
CAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGG
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

FIGURE 422

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531

><subunit 1 of 1, 327 aa, 1 stop

><MW: 37406, pI: 9.30, NX(S/T): 1

MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACL~~SL~~GFFSLLWLQLSCSGDVARAVRG
QGQETSGPPRACPPEPPPEHWEEDASWGPHRLAVLVPFRERFEELLVFVPHMRRFLSRKKIRH
HIYVLNQVDHFRFNRAALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVASPE
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTGY
KTFRHLHDPAWRKR~~DQ~~KRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD
CDKTATPWCTFS

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 423

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATACCAGATC
TCACCAGAGAGTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCCTGGATGCT
GCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCCCTC
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT
GTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAAGTGGT
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAGTAACAG
CTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT
CTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGGAAGATTA
TAACTGTGATGCAAAGTTACCTATGTCTGCAAGTTCAAGGACTAGGGCAGGTGGGAAGTCAG
CAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCCTGGAA
GAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCCTTCTTTTTCCTT
TTTCTTCACCTTCATTTAGGCTTTTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATA
ATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

FIGURE 424

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965  
<subunit 1 of 1, 175 aa, 1 stop  
<MW: 19330, pI: 7.25, NX(S/T): 1  
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD  
ADLACQKRPSGKLVSVLGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD  
VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD
```

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

FIGURE 425

CGGACGCGTGGGCGCCACCTCCGGAACAAGCCATGGTGGCGGCGACGGTGGCAGCGGCGTGG
CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC
AACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT
GTGGCCAGCGAGTGGGCTTACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC
CTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGGAGCCT
GACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCGCACCTACAGTGTCTCATTCCCCATGTTT
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG
GCTTGGGACCCAACTGTGTCAGTGGAGGAGGTCAGACCCCAGATCACAGCGCTCGTGAGGAAG
CTCATCCTACTGAAGCGAGAAGACTTATAACCACCGCGTCTCCTCCTCCACCACCTCATCCCG
CCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAGAGACCCACTGA
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCCTTGTGGGGGAAAAATTCTAGTAT
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAGAGCTCTTGACCAG
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA
GCAATAATCTCCACCCAAGGCTTCTGTAACTGGGACCAATGATTACCTCATAGGGCTGTTG
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATTC
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAATAAAAACTTGCATCCAAC
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCTCTGTATTA
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAAACAATCCAAACAATACCTCACGATATA
AAATAAAAATGAAAGTATCCTCCTCAAAA

FIGURE 426

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLVKYRGSVSLVVNVASECGFTDQH
YRALQQLQORDLGPHHFNVLAFFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH
PAFKYLAQTSKGKEPTWNFWKYLVPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

FIGURE 427

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**AT**GGGGGTGGAGATTGCC
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTCTT
CTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT
GCCGGCCACTCA**IGAG**AGTGTTTTTTGTGTAAAGTATTTTTTTAGAATACTGTTGACTTCTTCAT
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTTAGG TTC
AAGGTCATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATCTTCACTA
TTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG
GGTGCCCCTGACACATTTATGTAGTGATCCCACAAATGTGATTGTTAATTTAAATGTTATTCT
AATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAGTTTTG
AGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

FIGURE 428

MGVEIAFASVILTCLSLAAGVSQVVLLQPVPTQETGPKAMGDLSCGFAGHS

FIGURE 429

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG
CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCAGGCAAATGGTGCTGACCATCTTT
GGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGCAAT
GTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGCAGGA
TCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTGGGTCAAG
TACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCAACCATTGAG
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT
CATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC
TCAAAAGTCAAATTAAATTCTTCCCAATGCCCCAACTAATTTGAGATTCAGTCAGAAAATA
TAAATGCTGTATTTATA

FIGURE 430

><ss.DNA57834

><subunit 1 of 1, 176 aa, 1 stop

><MW: 19616, pI: 7.11, NX(S/T): 0

MVLTIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH
GYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

Important features:

Signal peptide:

Amino acids 1-26

N-myristoylation sites:

Amino acids 48-54;153-159;156-162;167-173

FIGURE 431

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCCA
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA
GAGACATTGAGAGGCCAAATTCGGAAAAAGAAAACATTTCGTCTTTTGGGAGAACAGATTATTT
TGA CTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAATCAT
GACTTGAAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGA
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCAAATAAA
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG
CAGACACTTTTTTGGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG
AAGGACTGGAGGAAGGTGAAGTGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 432

MSRSSKVVVLGLSVLLTAATVAGVHVKQQWDQQLRDGVIRDIERQIRKKENIRLLGEQIILTE
QLEAEREKMLLAKGSQKS

FIGURE 433

GAATTCGTGTCTCGGCACTCACTCCCGGCCCGCCGACAGGGAGCTTTCGCTGGCGCGCTTGGCCGGCGACAGGA
CAGGTTCCGGGACGTCCATCTGTCCATCCGTCCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCC
CGCTGCCGTGCTGCTGGGCCCTTCTCTCCCGCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGAAGAAGCCA
AGCCTTACCCGCTATTCCCGGGACCTTTCCAGGGAGCCTGCAAACTGACCACACACCGCTGTTATCCCTTCTCTC
ACGCCAGTGGGTACCAGCCTGCCTTGATGTTTTCACCAACCCAGCCTGGAAGACCACATACAGGAAACGTAGCCATT
CCCCAGGTGACCTCTGTGCAATCAAAGCCCCCTACCGCCTCTTGCCCTTCAAACACACAGTTGGACACATAACTTT
TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATATACCAGGACACCACAATTTCTTGG
TGGAAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTTATCCAGATGATGAAGTTACAGCA
ATAATCGCTTCTTTCAGCATAACCACTGTGCAGCGTTACAGACAATGGGTCGTATATCTGTAAGATGAAAATAAAC
AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCTCTCACTTACTAAGCAGCCTGAGAGC
ATGAATGTCAACAGAAACACAGCCTTCAACCTCACCTGTCAAGCTGTGGGCCCGCCTGAGCCCGTCAACATTTTC
TGGGTTCAAACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCGGCGTGCTAACTGTTCCAGGCCTGACG
GAGATGCGGTCTTCACTTGTGAGGCCACAAATGACAAAGGGCTGACCGTGTCCAGGAGTGAGATCAACATC
AAAGCAATTTCCCTCCCCACCACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCTGGGTT
CCTGGTTTTGATGGATACTCCCCGTTAGGAATTGCAGCATTCAGGTCAAGGAAGCTGATCCGCTGGGTAATGGC
TCAGTCATGATTTTTAAACACCTCTGCCTTACCACATCTGTACCAATCAAGCAGCTGCAAGCCCTGGCTAATTAC
AGCATTGGTGTCTTCTGCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTTGGATTCTAGCAAGCAGCACTGAA
GGAGCCCCCATCAGTAGCACCTTTAAATGTCACTGTGTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG
ATGAAGCCTCCGACTAAGCAGCAGGATGGAGAAGTGGTGGGCTACCGGATATCCACGTGTGGCAGAGTGACAGGG
ATTTCCAAAGAGCTCTTGGAGGAAGTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT
ACGTGCACAGTGAGGATTGCAGCCGTCAACAGAGGGGAGTTGGGCCCTTCACTGATCCAGTGAAAAATTTATC
CCTGCACACGGTTGGGTAGATTATGCCCCCTCTTCAACTCCGGCGCCTGGCAACGCAGATCCTGTGCTCATCATC
TTTGGCTGCTTTTGTGGATTATTTTGAATGGGTGATTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG
GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATTCTGAATTAGTGGTGAATTATATAGCAAAGAAATCCTTC
TGTCGGCGAGCCATTGAACTTACCTTACATAGCTTGGGAGTCAGTGAGGAACTACAAAATAAACTAGAAGATGTT
GTGATTGACAGGAATCTTCTAATCTTGGAAAAATCTGGGTGAAGGAGAGTTTGGGTCTGTAATGGAAGGAAAT
CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTTGGACAACCTCTTACATCGGGAG
ATCGAGGAGTTTCTCAGTGAGGCAGCGTGCATGAAGAGCTTCAGCCACCCAAATGTCAATTCGACTTCTAGGTGTG
TGTATAGAAATGAGCTCTCAAGGCATCCCAAAGCCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCAT
ACTTACTTACTTTATTCCCGATTGGAGACAGGACCAAAGCATATTCTCTGCAGACACTATTGAAGTTCATGGTG
GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTTCATCGAGATTTAGCTGCTCGAACTGCATG
TTGCGAGATGACATGACTGTCTGTGTGCGGACTTCCGGCCTCTCTAAGAAGATTTACAGTGGCGATTATTACCGC
CAAGGCCGATTGCTAAGATGCCTGTAAATGGATGCCATAGAAAGTCTTGACAGCCGAGTCTACACAAGTAAA
AGTGATGTGTGGGCATTTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCCTGGGGTCCAG
AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCCGAAGACTGCCTGGATGAAGTGTAT
GAAATAATGTAATCTTGTGAGAACCGATCCCTTAGACCGCCCCACCTTTTCAGTATTGAGGCTGCAGCTAGAA
AACTCTTAGAAAGTTTGCCTGACGTTCCGGAACCAAGCAGACGTTATTTACGTCAATACACAGTTGCTGGAGAGC
TCTGAGGGCCTGGCCAGGGCCCCACCTTGCTCCACTGGACTTGAACATCGACCCTGACTCTATAATTGCCTCC
TGCATCCCCGCGCTGCCATCAGTGTGGTCAAGCAGAAAGTTTATGACAGCAAACCTCATGAAGGACGGTACATC
CTGAATGGGGGCGAGTGAGGAATGGGAAGATCTGACTTCTGCCCCCTCTGCTGCAGTCAAGCTGAAAAGAACAGT
GTTTTACCGGGGAGAGACTTGTAGGAATGGGGTCTCTGGTCCCATTCGAGCATGCTGCCCTTGGGAAGCTCA
TTGCCCGATGAACTTTTGTGTTGCTGACGACTCCTCAGAAAGCTCAGAAAGTCTGATGTTAGGAGAGGTGCGGGGA
GACATTCCAAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTTGTCTT
CCTTACCAAGTGAATCCATGGCCCCAAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCAATTAATAATACATAA
TATATATTTATTTAAAGAGAAAAAATATGTGTATATCATGAAAAGACAAGGATATTTAATAAAACATTACTTA
TTTCATTTCACTTATCTTGCATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACCTTTGTACAGAGTTG
AAGTTGTTTTTCAACTTCTTTTCTTTTTCATTACTATTAAATGTAAAAATATTTGTAAATGAAATGCCATATT
TGACTTGGCTTCTGGTCTTGATGTATTTGATAAGAATGATTAATTTTCTGATATGGCTTCATAATAAAATTGAA
ATAGGA

FIGURE 434

MGPAPLPDLLLGLFLPALWRRATTEAREEAKPYPLFPFPFPGSLQTDHTPLLSLPHASGYQPALMFSPPTQGRPHHT
GNVAIPQVTSVESKPLPPLAFKHTVGHIIILSEHKGVKFNCSINVPNIYQDTTISWWKDGKELLGGHHRITQFYPD
DEVTAIASFSITSVQRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPESMNVTRNTAFNLTCQAVGPPE
PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSCEAHNDKGLTVSQGVQINIKAIKPSPTTEVSIRNSTAHSI
LISWVPGFDGYSPPFRNCISQVKEADPLGNGSVMI FNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL
ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQQDGELVGYRISHVWQSAGISKELEEVEVGQNGSRARISV
QVHNATCTVRIA AAVTRGGVGPFPDPVKIFIPAHGWVDYAPSSTPAPGNADPVLIIIFGCFCGFILIGLILYISLAI
RKRVTQETKFGNAFTEEDSELVVNYIAKKSFCRRRAIELTLHSLGVSEELQNKLEDVVIDRNLILGKILGEGEFGS
VMEGNLQEDGTSLKVAVKTMKLDNSSHREIEEFLSEAACMKDFSHPNVIRLLGVCIEMSSQGIPKPMVILPFMK
YGD LHTYLLYSRLETGPKHIPLOQTLLKFMVDIALGMEYLSNRNLFHRDLAARNCMRLDDMTVCVADFGLSKKIYS
GDYYRQGRIAKMPVKWIAIESLADRVYTSKSDVWAFGVTMWEIRTRGMTYPYPGVQNHMYDYLLHGHRLKQPEDC
LDELYEIMYSCWRTPDLPDRPTFSVLRRLQLEKLLES LPDVRNQADVIYVNTQLLESSEGLAQGPTLAPLDLNLIDPD
SIIASCTPRAAISVVTAEVHDSKPHEGRYILNGGSEEWEDLTAPSAAVTAEKNSVLPGERLVRNGVSWSHSSML
PLGSSLPDELLFADDSSEGSEVLM

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

FIGURE 435

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGATG
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGGAT
CCAAGC**ATG**GAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTCCTG
CTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC
CCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCTGCCTG
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCA
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC
CAGTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA
GCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT
ACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG
GTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT
CCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTTATATCTGGAAACC
AAAACCCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACTTTCCTTGTGGAC
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC
ACAGCAGATTTTCATTGTCAAGATTCTGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCTTGCTCAGCAACCTGT
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAGCTTCAGGAGTGCAAC
TTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGCCTTATGACCTCTACCATCCC
CTTCCTCGGTGGGAGGCCACCCCATGGACCGGTGCTCCTCCTCGTGTGGGGGGGGCATCCAG
AGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCATGTCACTTCAGTGGAAGAGTGG
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTTGACTGCCCTAAA
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCCAAAAACAAAGCCCCAC
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAAACCAAAGAGAACTTCCAGTCGAG
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTGAGAGGAG
CCCTCG**TAA**GTTGTAAAAGCACAGACTGTTCTATATTTGAAACTGTTTTGTTTAAAGAAAGCA
GTGTCTCACTGGTTGTAGCTTTTCATGGGTTCTGAACTAAGTGTAATCATCTCACCAAAGCTTT
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

FIGURE 436

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTCAGGASYSRLRRCLSS
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPSCLKCQAK
GTTLVVELAPKVLDDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR
GQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHLYLETKTLQGTKGENSLSSSTGTFLVDNS
SVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFPSCATCGG
GYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYDLYHPLP
RWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL
AQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKKLPVEAK
LPWFKQAQELEEGAAVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

FIGURE 437

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT
CTTTATGTCTTTCTCCTCTTCCTATTCTGTGCATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC
AGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTTGAAATCTGGCATGAGATG
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCCTGCCCTATTCCTCCTCCCAAGTCTGT
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTGTAGCCACCT
CCCTGTCAGCCAGTATTAACATGTCCCCCTTCCCCCTGCCCGCCGTAGATTACAGGACATTCGC
CCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC
CATGATGTTACAATCCCACCTTGCCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCCTGAGGAAAAACCAAAGGGAAGCAACAGG
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT
GGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACA
ATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA
AAACAAAATTCTCTAACACTGAAA

FIGURE 438

MWLPLGLLSLCLSPILSSPSLKSQLQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGMEH
RNHLCFCDLYDRATSPPLKCSLL

FIGURE 439

GTTTCCTCATAGTTGGCGTCTTCTTAAAGGAAAAACACTAAAATGAGGAACTCAGCGEACCGGGAGCGACGCAGCTT
 GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCGAGGTGTCTGAGGGGCTGG
 GGCAAAAGGTGAAAGAGTTTTCAGAACCAAGCTTCTTGGAAACCCATGAGCCATGAAGTCTTGCTGCACATTATACCGT
 CTGAGGGTAGCAGCTCGAAACTAGAAAGAGTGGAGTGTTCAGGGACGGCAGATATCTCTTTGTGTGACCTTGGC
 GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATTGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
 AGGCCCTGAGTGCACACTGGCTTGCCTCCTCCTAGCCACAGCAGCAGCTGCTTTTGTGCTGACTTGAAACGAGGTCCCTCAG
 GTCACCGTCCAGCGCTGCGCTCCACCGTCCGAGGAGCCCGGAGGCACTGTGATCTTGGGCTGCTGGTGGAACTCCCA
 AGGATGAATGTAACCTGGCGCCTGAATGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGTGTGCTCATCACC
 CACGGGACCCCTCGTTCATCACTGCCCTTAAACAACCACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCTGCG
 GGGGCTGTGGCCAGCGTGGCAGCCACTGTGACACTAGCCAATCTCCAGCACTCAAGTTAGATGTGCAGCAGCT
 ATTGAAGTGGATGAGGGAACACAGCAGTCATTGCTGCCACCTGCGCTGAGAGCCACCCCAAGCCAGGTCGCG
 TACAGCGTCAAAACAAGATGGCTGGAGGCTCCAGAGGTAACCTACCTGATCATGCGCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAAACC
 TCCGGCTCCAGCGACAGGCTACGTTGTGCGCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC
 CAAACCATCATCGTCACCAAGGCCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAATCCCAACCCCAAGGTCG
 ACCTGGGCCAAGGATGGGTCCAGTGTACCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCTCATCGAC
 ACCACAGCGAGGAGGACTCAGGCACCTACCGCTGCATGCCGACAATGGGGTTGGGCAGCCCGGGGAGCGGTC
 ATCCTCTACAAGTTCAGGTGTTTGAACCCCCCTGAGGTCACCATGGAGTATCCCGAGCTGGTTCATCCCCCTGGGG
 CAGAGTCCCAAGCTTACCTGTGAGTGGTGGGAACCCCCCGCCTCGTGCTGTGGCTGAGGAATGCTGTGCC
 CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGGCCCTGCGCGTGTCTCAGCATGGGGCTGAGGACGAAGG
 GTCTACCAAGTGCATGGCCGAGAACGAGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
 ATAACCCCAAGGCTATGGCAGGATGCTGAGTGGCTAGCTGGCACAACCTCTGTATCACCTTCCAAACTCCGGAAC
 CCTGACAGATGCTGAGGGGGCAACCGGCGCTCCCGAGACCCCAAGCTCAGTGGGGCTGTCTCCCGAAGTGT
 CCAGGAGAGAAGGGGAGGGGGCTCCCGCCGAGGCTCCCATCATCTCAGCTCGCCCCGCACTTCCAAGACAGAC
 TCATATGAACTGGTGTGGCGGCTCCGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAACAC
 CGCAAGCAGGTACAACATCTCTGACGATGGACCATCTCTGGCATTCCAGCCAACAGCAGCCGCGCTGACCTC
 ACCAGCTTGACCCCGGAGCTTGTATGTAAGTGGAGATGGCAGCTTACAACCTGTGCGGAGAGGGCCAGACAGCC
 ATGTTACCTTCCGAACCTGGACGGCGGCCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC
 GACCTTGAGGCCAGTCCCGAGCAGCAGCCAGCCAGACCAAGCGGCGCTCTCCCCCCAGAGCTCCCGACAGG
 CCACCATCTCCAGCGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGTTGGGTTCCCAATC
 CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACAGCGCCATCCCCCA
 TCCGGCTGTCCGTGGAGATCACGGGCTTAGAGAAAGGCACCTCTACAAGTTTCGAGTCCGGGCTCTGAACATG
 CTGGGGGAGGCGAGCCAGCCAGCGCCCTCTCGGCCCTCAGTGGTGTGGGCTACAGCGGCTCGCGTGTACGAGAGG
 CCGTGGCAGGTCCTTATATCACTTACGGTACGGTCACTGAATGAGACACCATCATGCTCAAGTGGATGTATCAT
 CCAGCAAGTAAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGACAATGATAGT
 GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCATCCATCAGCCACCTGCGAGCTGAGAGACCTCCTAC
 GACATTAAGATGCAGTGTCTCAATGAAGGAGGGGAGCGAGTTCAGCAACCTGATGATCTGTGAGACCAAGCT
 CGGAAGCTTTCTGGCCAGCTTGGTGCAGTGCACACCCCAACTCTGGCCCCACACAGCCGCGCTTCTGAAACC
 ATAGAGCGGCGGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGGGGTCTGCT
 CTGGGCTCCATCTGTTCTCATCATCGTCACTTTCATCCCCCTCTGCTTGTGGAGGGCTGGTCTAAGCAAAAAACAT
 ACAACAGACCTGGGTTTTCTCGAAGTGCCTTCCACCTCTGCGGCTATATACTATGTTGCCATTGGGAGGACTC
 CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGAGCGGCTGTGCTAATGGGATCCCATG
 AATAGGGGCTGCCCTCCGGTGCAGTGGGCTACCGGGCATGAAGCCCCAGCAGCACTGCCAGGCCAGCTTCAG
 CAGCAGAGTGACCCAGCAGCTGCTGAGGCAAGCCATCTTGGCAATGGATATGACCCCCAAGTACCAGATC
 ACGAGGGTCCCAAGTCTAGCCCGGACGAGGGCTTTCTTATACACACTGCCGACACTCCACTCACCAGCTG
 CTGCAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAAGGGTGGAGAGGCC
 CCGGACAGTCTGTCTTGGAAAGCAGTGTGGACCTCCATTTCACTCAGGGCCCCATGCTGCTTGGGCTTGTG
 CCAGTTGAAGAGGTGGACAGTCTGACTCTGCAACCTGCAAGTGAGTGGAGGAGACTGGTGTCCCCAGCACCCTGAGG
 GCTACGTAGGACAGGAACCTGGAATGCAGTCTCCCCGGGGCCACTGGTGGTGTGCTTTTGAACACCACTCT
 CTCACAATTTAGGCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAAAGAAAAA
 AGAGACAGAGAAAAATTTGTTATTTTCTATTATAGCCATTTTATATATTATGCACTTGTAATAAATGTA
 TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTTGGAGAGGAAAAAAGAAAGCTGCCA
 CTTAACAGGAGTACCCAGGAAAGACACCGCAGCAGGCTGGCGGGGACAGACTCTTAACCTGGGGCTCTGCAGTG
 GCAGGGCAGGCTGCAGGAGGCCCAAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTTCATCAGCAGCA
 TGAGGGGAACAGCAAGGGGCAAGTATACAGCCTGGAGACACCCACAGATGGCTGGATCCGGTGTACGGGAA
 ACATTTTCTAAGATGCCATGAGATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAAGAAACCTCCAGAA
 CAATAATCCGTGGCAACATATCTCTGTAAAAACAAACACTGTAACCTCTAATAAATGTTTGTCTTCTCCCTGTAAAA

FIGURE 440

MLRGTMTAWRGMREVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPPR
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN
LQDFKLDVQHVIEWDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQIVN
ASQDEDEGMYKCAAYNPVTQEVKTS GSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSLILEC
VASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA AVILY
NVQVFEPPEVTMELS QLVI PWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV
LSMGPEDEGVYQCMANEVGS AHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM
LRGQPALPRPPTS VGPASP KCPGEGKGAPAEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGEGQTAMVTFR
TGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASETSVYVTWIPR
GNGGFP IQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRVRALNMLGESEP
SAPSRPYVVS GYSGRVYERP VAGPYITFTDAVNETTIMLKWMIYPASNNTPIHGFYIYYRPT
DSDNDSYKKDMVEGDKYWSHISHLQPETSYDIKMQCFNEGGESEFSNVMICETKARKSSGQP
GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSI VLIIVTFIPFCLWRAW
SKQKHTTDLGFP RSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRCPSAA
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPKSSPDEGSFLYTL PDDS
THQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSGPPCCLGLVPVEEVDSPD
SCQVSGGDWCPQHVPV GAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 441

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC
TCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG
GCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTTTCTGCTGGATGGTTTTCGCT
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGCAGGG
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACCTACATGTGGGACCCACCA
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAATGGAT
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG
GCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCCG
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC
AGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCACGGAATGACCGACA
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAACACTCTGAGATATATA
ACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA
CTGAGAATCGAGAGATGCTTCCGTTTTTGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC
CTGATTTCAAATCCAACCTCAGAGCTGCTCCTATCAGGTCGGTGGACGTCTACAATGTCATGT
GCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC
TGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA
AGACCATGCACATTGTAAATACATTATTCTTGATAATTCTATACATAAAAGTTCCTACTTGT
TAAA

FIGURE 442

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDYL
TPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSL MPLWWNGSEPLWVT
LTKAKRKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAAIYH
ERIDVEGHYGPASPQRKDALKAVDTVLKYM TKWIQERGLQDRLNVIIFSDHGMTDIFWMDKV
IELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNF
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

Important features of the protein:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

FIGURE 443

AGTGACTGCAGCCTTCCTAGATCCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC
ACCAGTGTGTGAGGGGAGCAGGCAGCGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA
GCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCATCCT
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAAG
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCCTTCATCC
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTATAAGA
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCCGAG
AGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTCCCTGTCC
CAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTAACATTCTTGTG
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC
CAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTCTACATTAAAAAT
ATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 444

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA
LSQASTDPKESTSPEKRDMDHFFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS
LGTEEQRPL

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 445

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCAGTCCACCATGATCCATCTGGGTCACAT
CCTCTTCCTGCTTTTGCTCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCCCTGTGCGCACGCCACGCCGCAGCCCCGCCCAAGATGG
CAAAGTCTACATCAACATGCCAGGCAGGGGCTTGACCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATC
CTGGATGGTGTGTGGTGGCACAGGAACCCCCGCCCAACTTTTGGATTGTAATAAAACAATTGAAACACCA

FIGURE 446

MIHLGHILFLLLLPVAAQTPGERSSLPAFYPGTSGSCSGCSLSLPLLAGLVAADAVASLLIVGAVFLCARPR
RSPAQDGKVIINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

FIGURE 447

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACC**ATG**ACGCTCCTCCC
CGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAAGTGCCCTCGGCCAGGC
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC
GGTGCTGCGGCCGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTG
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT
CCAGAGCCTGCTGGTGCTGCGCCGCCGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCC
CCGTT**CAGTGTGA**CCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT
TGGGGGTAGAAGGAGCTCAGCACCTCTTCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG
CTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAG
TGTACGTGTATTATTAAACTGATGAACACATCCCCAAAA

FIGURE 448

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHELLARGAKWGQALP
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDED RYPQKLAF
AECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGC
TCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

FIGURE 449

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA
AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT
TGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCCGCTGGCTACCAT
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTATCCATCCTTTAAATCTGCACAT
GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACTGGGGAT
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAATT
AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA
GTTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGAAAAATTACT
TCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTGAAACCTTGCA
AAAGGCCGGCTTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCAGTGTCTGTTCTGATTCTGG
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA
TCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAGTGAAGTTCAGACTTCATATGA
CATCGTCTTGTTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTACTTTTCTCAACTTTGA
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACCTTTAGTTAAGGGGGA
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGGCCTTAATACAGTTTTAAC
CACTGATAAATCAGATTTGTTCAATTAACAGTATTGGGATTGTGCCCTCTGTGAGAGAAAAGGA
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATCTTTTCCCAAGAACTCTTAC
TAAAGCACAAATTTTAAAGCTCTTTCTGTCTATGATTATGCTGTGAAGAAGCCATGGCTTGC
ATATCCTCACTATAAGCCCCCGGAGAAATGCCCCCTCTATCATTCTCCATGATCGACTTTATTA
CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAGCCCACAACGC
TGCACTCCTTGCTTATCACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA
TGAGAACTTAAACTGAACTATGAAGTGAACACTCCTTTTTCCCCTCCTAGTTCCAAATGA
CTATCAGTGGCAAAAAAGAACAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT
TATCATTGTTTAATAAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA

FIGURE 450

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCEGAELRAPDKIAIIGAGIGGTSAAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGOEYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEEASNWFIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGMLNRTLLETQLQAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVCSGLLQASKSNLISGSVMYIEEKTCTKYTGNTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLTDDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTQAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSSIILHDLRYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL
```

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.

amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121, 119-125, 260-266, 384-390, 459-465

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23, 232-243

FIGURE 451

[illegible]

FIGURE 452

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGKVVD
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAFGVDT
ELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRFSISAS
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS
KDGPSYFTVVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:
amino acids 1-20

FIGURE 453

[illegible]

FIGURE 454

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLTVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLLEDGKGRCFPDP
NFKSTALVVDGELYTGTVSSFQGNTPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGDDDKIYFFFSETGQFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRDD
GFPFNVLQDVFTLSPSPQDWRDTLFGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSPLYQPQLATRPWIQ
DIEGASAKDLCSASSVSPSFVPTGEKPCEQVQFQPNVTNLTACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLLLVTGQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQTDEGGSPVPII
STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAV
HPKTCPVVLPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPPLSIQDSFVEVSP
VCPRPVRVLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 455

TAAGATGAGGGCATCCCTCACGTTACACCCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC
AAGCGGGCTTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT
ATTTGGGTTTAGGGACTGATCCCTTGCAGTTTACTTCTGGATCACCATGAATGGCCAAGATGG
TGGCAGAACACGCTGTGGACCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG
GGAACCGTGTTAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAAATTCGAGGCCC
GAGTGACTAACGTCTCTGTACACGGAAATGGGTACTTGGTGGCATAGAGAAAACACAATTAGC
CACTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCTACACTTCTCACTCAGGTGCACCCCT
TCTGCTGTCTTTCCCCAACGTACTGGGTCCCGAGCGTGGTGGGTATTTGCCCACTGGGTGC
CAGCTCAGCAGCCCCCACCCTCTCTTTATTCTCTCCAAAGCTGGTCTTTCTGACTATCATTGT
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC
TGTGGCAAAGGACAGCTGGAAGAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC
GAGGCCATGGCACTCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT
ACCCGGGGTGCTGGTGTCTGGCTTGCACTCTGGCCCAGTTCAGAGAAAGTTGCAGAGATCAGGG
GCCAAGGATGTCATAGCCCCAGGTTGTCCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCCTAGTTCCTCACTCCA
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG
GTTCAAGGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA
TCTCACCGTTACTTCAGTTACCCTTGCAAGGGGGCCAGGGAGTCAAGAAATATACCGTGTTCTC
CAGGGTTTAAGCCGGCCATGCCTTCCCGAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC
CCCACAACTGAAGGAAGGAGATCCTTCCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA
AAGCTTGAGAAGATGGACCCTTTGCCCACCAGGGTTAATTCTTGGTGGGGCAGCTCGGCTGTG
ATCAGGGCAACCAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT
GTCCCTAACAGCAGCCTGGAGCTACCCCAATCCCTCACAGCCTGACCTCCTCATTCATCA
GATCTCGTGCCG

FIGURE 456

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPQRTGSRAWVVFATLGASSAAPH
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

Important features of the protein:

Signal peptide:

Amino acids 1-28

Transmembrane domain:

Amino acids 64-78

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 103-107

N-myristoylation sites:

Amino acids 53-59;94-100

FIGURE 457

CCCGCGCGCCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTC
 GCGCCGGCCGTGCGCCCGGCTCTGGGGGCGCCAGGAACTCGGTGCTGGGCCCTCGCGCAGCCC
 GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCCGCGCG
 GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTC
 ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCC
 CTTGTGACCCCCACTCCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCT
 CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC
 TTTGGTCTTGGAACACACCGAGGACGGCTCAACATTCATTTCAGGCCTGGAGGACGGCGATCTA
 TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG
 CACCCACCCGCTTCTCGGGTGTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG
 GTCACATCATAAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC
 AGCAGTGGGATGGACGCAGTATTTCTGCCAATTTCAGACCCAGAACTCCAGTGCTGAACCTC
 CTGCCGGAGCCCCAGGTGGCCCGCTTCATTGCGCTGCTGCCCCAGACCTGGCTCCAGGGAGGC
 GCGCCTTGCCCTCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAATGACCTATTCTTT
 GAGGCCCCCTGCGTCGGGATCCTCTGACCTCTAGACTTTTCAGCATCACAATTACAAGGCCATG
 AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCAACATCACCCGCATCTACAGCATTGGG
 AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCGGACAAGCCTGGGGAGCATGAG
 CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG
 TTGCTTCTGCTCCTGATGCAGTTCTGTGCCATGAGTTCTTCTGCGAGGGAACCCACGGGTGACC
 CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
 GCCTACCACCGGGGTTTCAGAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACAGAGCATC
 GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG
 GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCC
 ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCCTTTGTGCTAAGT
 GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTACCCATTTCGACATGACTCGCACCCCGTGG
 GCTGCCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT
 GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC
 GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC
 AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCTGTGACAAGTTCCCTCAC
 GAGAATGAATTGCCCCAGGAGTGGGAGAACAAAGACGCCCTCCTCACCTACCTGGAGCAG
 GTGCGCATGGGCATTGCAGGAGTGGTGGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT
 GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT
 CTGCTGACCCAGGGGACTACATGGTGAAGTGGCAGTGGCCAGGGGCTACCATTTCAGTGACACGG
 AACTGTGCGGTACCTTTGAAGAGGGGCCCTTCCCCTGCAATTTTCGTGCTCACCAAGACTCCC
 AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGC
 CTGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG
 ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT
 TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 458

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60, NX(S/T): 6
MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTLWLQGGAPCLRAEILACPVS DPNDLFLEAPASGSSDPLDFQHH
NYKAMRKLMKQVQECPNITRIYSIGKSYQGLKLYVMEMSDKPGHEHELGEPEVRYVAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNP DGYEIAYHRGSELVG
WAEGRWNNQSIDLNNHFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVV RDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLT PGDYMVTASAEGYHSVTRNCRVT FEEGPFPCNFVLT KTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```


FIGURE 459

TAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA
AGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT
GGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAGAAGTATCAGTGACAGCGA
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCACCAAT
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCTGCCCC
TACAACTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAAAACAAAT
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

FIGURE 460

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFVPSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFPW
FRNFPPIPIPESAPTTPLPSEK
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

Important features of the protein:

Signal peptide:

Amino acids 1-20

N-glycosylation sites:

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 80-84

N-myristoylation sites:

Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;
538-544;560-566;637-643

Zinc carboxypeptidases, zinc-binding region 2 signature:

Amino acids 498-509

Zinc carboxypeptidases:

Amino acids 391-411

FIGURE 461

AGCAGGAGCAGGAGAGGGACAATGGAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCTC
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTCTGGT
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCCACT
GAGGTGGCTGTCATAGGCTTCTTCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC
ATGGTGCAAAAATTCCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC
TACAACATCACTGGGAACACCATCTGCCTCTTTGCGCTGGTAGACAATGAACAACCTGAATTTA
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATGAGCCGTTTCATTGAGATCAACAGC
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA
GAAAATGGGAAGGTGATATCATTTTTTCAAACCTAAAGGAGTCTCAACTGCCAGCTTTGGCAATT
TACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCCGTAGAGCATGTG
CAAACTTTTGTGATGGATTCTTAAGTGGAATAATTGTTGAAAGAAAATCGTGAATCAGAAGGA
AAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACCTACATATGGCCAAGTATCTACTTTA
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGACACACACACGCACACAC
ACACACACACAGAGCTTCATTTCTGTCTTAAAATCTCGTTTTCTCTTCTTCTTCTTTTAAA
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTCATACTCTGTAAGCCCAT
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA
TTCCTAGAGAAAGATTGTTCCAATTTGTCAATTAATATCAAGTTTGTATACTGCACATGACTT
ACACACAACATAGTTCTCTGCTCTTTTAAGGTTACCTAAGGGTTGAACTCTACCTTCTTTTCA
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA
AATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC
ATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA
TAAATAAAAGGCAATCATGTTATA

FIGURE 462

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDPAAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRLVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAAKLF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNFCDF
LSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 463

CTCGCTTCTTCCTTCTGGATGGGGGCCAGGGGGGCCAGGAGAGTATAAAGGCGATGTGGAGG
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGGATGCACCGGCCAGAGGCC
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC
CCTGGAGGAGGCAAGTATTTAGCACCACCTGAAGACTACGACCATGAAATCACAGGGCTGCGG
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAACTTGGAGACTCCTGGGACGTG
AACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA
AAAGTCTTTGTGCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCAG
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAACCTCA
CCCGTGGGTGCTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAAATAAGCTTCT
GCAGAAAA

FIGURE 464

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVVKL
GDSWDVKLGALGGNTQEVTLQPGYITKVFAFQAFLRGMVMTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:
amino acids 1-22

FIGURE 465

CGGACGCGTGGGTCCGGCGGCCCTGAGGCTGCACCGGGCACGGGTGCGCCGCAATCCAGCCTGGGCGGAGCCGGAG
 TTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCCGAGAGCTCGGGGACCCCGT
 TGCTGCTGCTGCTACTACTGCTGCTCTTGCCAGTGCCAGGCGCCGGGGTGTTCAGGACATATCCCTGGGC
 AGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCTTGGCGCACCGTCAAGCTGGAGGAGCCGGTCTCGAAGC
 CAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGC
 TGGCCCCAGGATACATAGAAACCCACTACGGCCCCAGATGGGCAGCCAGTGGTGTGGCCCCCAACCACACGGATC
 ATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCTCTGCACCTGCTTGGGATGAGTG
 GCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA
 CCCACGAGATCTTTCGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG
 CGGGCATGACCAGCCTTCTGGTGGTCCCCAGAGCAGGGGCGAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGG
 AACTGTACATTGTGGCAGACCACACCTGTTCTTGACTCGGCACCGAACTTGAACCACACCAACAGCGTCTCC
 TGAAGTCGCCAATACGTGGACCAGCTTCTCAGGACTCTGGACATTGAGGTGGCGTGAACCGGCTGGAGGTGT
 GGACCGAGCGGGACCGCAGCCGCGTCAAGCAGGACGCCAACGCCACGCTCTGGGCTTCTGCACTGGCGCCGGG
 GGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGTGTCTACGGGCGCGCCTTCCAGGGCGCCACAGTGGGCC
 TGGCGCCCGTTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCTCGGAGCTCCCCATCG
 GCGCGCAGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCTGCGTGG
 AGGCTGCGGCCGAGTCCGAGGCTGCGTCATGGCTGCGGCCACCGGCCACCCGTTTCCGCGCGTGTTCAGCGCTT
 GCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGCGCGGCTTGCCTCTCCAAATGCCCCGAGCCCGGAC
 TCCCGGTGCCCGCGCGCTCTGCGGGAACGGCTTCTGTGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGG
 AGTGCCTGCGACTCTGCTGCTTTGCTCACAACCTGCTGCTGCGCCCGGGGGCCAGTGCGCCACGGGGACTGCT
 GCGTGCCTGCGTGTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTT
 GCACGGGCACCTCTCCACTGTCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGAGTGGCT
 ACTGCTGGGATGGGCGCATGTCCACGCTGGAGCAGCAGTGGCCAGCAGCTCTGGGGCTGGCTCCCACCCAGCTC
 CCGAGGCTGTTCAGGTGGTGAACCTCTGCGGGAGATGCTCATGGAACCTGCGGCCAGGACAGCGAGGGCCACT
 TCCTGCCCTGTGAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCAC
 CGCATATGGTGCCAGTGGACTCTACCGTTCACCTAGATGGCCAGGAAGTGAATTGTGCGGGAGCCTTGGCACTCC
 CCAGTGCCAGCTGGACCTGCTTGGCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCC
 AGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTT
 GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCAGCCTTCTGTGACAAGCCAGGCTTTGGTGGA
 GCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGC
 CTCTGCTCCAGGGGCGCGCTGGCTGGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGATGCAGCTGGG
 GCTGCAGAAGGGACCTGCGTGCAGTGGCCCCAAAGATGGCCACACAGGGACACCCCTGGGCGCGCTTCAAC
 CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCTGAGAACTCTCATGAGCCAGCAGCC
 ACCCTGAGAAGCCTCTGCCAGCAGTCTCGCCTGACCCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCT
 GGTGAGAGGTAGCTCCTAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAACCTGAACTG
 CAGGGGCGAGCCAGTGAATCACCGACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCCGAGTGGAGCT
 TCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCTGAGGGCTGGAGAACACTGCTTGGGCACACT
 CTCCAGCTCAATAAACCATCAGTCCCAGAAAGGTCACACAGCCCTGACCTCCCTCACCAGTGGAGGCTGG
 GTAGTGTGGCCATCCCCAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCCA
 GCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTTCGACTGAGTCCCACTCC
 CCTGCAGCCTGGCTGGCTCTGCAAAACAAACATAATTTTGGGACCTTCTTCTGTTTCTTCCCACCTGTCTT
 CTCCCTTAGGTGGTTCTGAGCCCCACCCCAATCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGAC
 AGCCTCTCCCCATTCTGTGTGTGTCCGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAA
 AAGAAAGACATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCAGCACTTTGGGAAGCCGGGTAGGAGG
 ATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTAAAA
 TTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTG
 AGTTCAACACTGCAGTGAGCTATGGTGGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCTGTCTCTAA
 AATAAATTTTAAAGGACTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 466

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788
><subunit 1 of 1, 813 aa, 1 stop
><MW: 87739, pI: 6.94, NX(S/T): 5
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MGWRPRRARGTPLLLLLLLLLLWVPVGAGVLQGHIPGQPVTPHWLVDGQPWRTVSLPEEVS KPDMLVALEAEGQ
ELLELEKXNHRLAPGYIETHYGPDGQPVVLAPNHTDCHYQGRVGRFPD SWVVLCTCSGMSGLTILSRNASYYL
RPWPPRGSKDFSTHEIFRMEQLLTWKGT CGHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT
RHRNLNHTKQRLLEVANYVDQLRLTDIQVALTGLEVWTERDRSRVTQDANATLWAFLOWRRGLWAQRPHDSAQL
LTGRAFOGATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECD CGPGQCECDLCCFAHNCS
LRPGAQCAHGDCCVRCCLKPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGY CWDGACPTLEQQ
CQQLWCPGSGHAPAECFQVNVNSAGDAHGNCGCGDESGHFLPCAGRDALCGKLQCQGGKPSLLAPHMVPVDSTVHLD
GQEVTRCGALALPSAQDLGLGLVEPGTCQCGPRMVQCSRRCKNAFQELQRLCTACHSHGVCNSNHNCHCAPGW
APPFCDKPGFGGSMDSGPVQAEHNHDTFLLAML LSVLLPLLPAGLAWCCYRLPGAHLQRCSWGCCRDPACSGPKD
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLPAVSPDPOADOVOMERSCLW

Important features of the protein:

Signal peptide:

Amino acids 1-27

Transmembrane domain:

Amino acids 702-720

N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

Tyrosine kinase phosphorylation site:

Amino acids 236-244

N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;
400-406;402-408;454-460;504-510;510-516;517-523;580-586;
601-607;661-667;687-693;717-723;719-725

Amidation site:

Amino acids 200-204

Neutral zinc metallopeptidases, zinc-binding region signature:

Amino acids 342-352

FIGURE 467

[illegible]

FIGURE 468

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL
VTKMCHIGCPDIPSLGLGPYVSIACCQTSLCNHD
```

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

FIGURE 469

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCAGAGCAAAGGTATTTGCAGT
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAACTGTTTCTCTGGA
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG
AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTGTTGGC
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCAAGCAAGGAAGTAGAATCTTTTGC
AAGAAAAAACTACGGAGTAACTTTCCCATCTTCCACAAGATTAAAGATTCTAGGATCTGAAGG
AGAACCTGCATTTAGATTTCTTGTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTGGAA
GTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTGAAGT
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTATG
AGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATTTTA
AACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTAGTGCGTT
CTCAGCTCATTTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTTT
TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAGGATGTTACCCAAAG
CAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACTTCCTCTGACCATACT
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTGGATTCAAGAGCACTGT
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACACAAATGTT
GAAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC
AGGATTTTGTTTTTTCTTTTAAAGTACAGGTTCTAGTGTTTTACTATAACTGTCACTATGTA
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT
CATCAAAAAAAAAAAAAA

FIGURE 470

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFFPCNQFGESEPRPSKEVESFA
RKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVVIKKKEDL

Important features of the protein:

Signal peptide:

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

FIGURE 471

GCCCTAACCTTCCAGGGCTCAGCTCTTTGGAGCTGCCATTCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG
 TCGGGCGAAGAAAAGAAGCAAACTTGTTCGGGAGGGTTTCGTCAATCAACCTCCTTCCCGCAAACCTAAACCTCCT
 GCCGGGGCCATCCCTAGACAGAGGAAAGTTCTGCAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC
 GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGC
 ACCGGGTGGCGCTGCCCGAGTGGAAACGACAGTTTGCAGAGCCTCGGCTGCAAGTGGCCTCTCCTCCCGCGGTT
 GTTGTTCAGTGTGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG
 CTCCTACTCGCGTTTCGCTTCTTCTCTCGGTTCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG
 GGTCTACCGAGACCGATCCGCGAGCGTTTGGCCCGGTTCGTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGAA
 GGACTGGCGGGTGGGGTAGGGAGGTGGCGGCGGGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG
 AGTTATGTTACTTTGCCACTTCTTACCGGACAGTTTCAGTTCGCCGATGGGAAAACCCGAGACCAAATCCTTGA
 TTGGCAGTATGGAGTTACTCAGGCCCTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTACACGCGTACAGCCA
 CAGGTGGAAAAGAACTTGGACTTTCTCAAGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGA
 GCCCAGAAGCTTACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA
 CAATTACTATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAAT
 GGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCTCT
 CGATTTTCCATTTTATGGCCACTTCTTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT
 CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCCAGTGTATCCAGAAA
 TTCAACTGTTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA
 TAACCTGGGAAGCTTCACATTCAGGCAACCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTC
 TGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAAGTCGGACTGTCCGATGCATTTGTCTGTGCCA
 CAGGATCCAACAAATTTCCCAATGTTTCGAAGAAGAAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAA
 AATTACCAACATTTTCGGCTGTGGAGATGACCCCATTAACCCACATGCCCTCCAGTTTAAACAGATGTGGCCCCCTGTGT
 ATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG
 GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC
 TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTTCAGGGTCTTAACCTACCACCAGAAGAGCAGT
 GACTTCTCAGTTTCCACAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC
 TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGAACCTCCACGCTGGCCTCATCATTGGAATCCTCATCCT
 GGTCTCATTTGTAGCCACAGCCATTTCTGTGACAGTCTATATGTATCACCACCCAACATCAGCAGCCAGCATCTT
 CTTTATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAGAAGAGGCTCTGGACATCCTGCCTATGCTGA
 AGTTGAACAGTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGCTAAAATTTCTAGGACAGAACACACC
 AGTACTGGTTTACAGGTGTTAAGACTAAATTTTGCCTATACCTTTAAGACAAACAAACAAACACACACAAAC
 AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGGTAAACAA
 AAAACTAAAACCTTATACAAGATACCATTTTACACTGAACATAGAATTCCTAGTGGAAATGTCATCTATAGTTCACT
 CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAG
 GGATCAGAAAAAAAATCATAATAAGCTTTAGTTCATGAGGG

FIGURE 472

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTOAFPHTEEEEVEVD SHAYSH
RWKRNLDFLKAVDTNRASVGQDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYIISRIYGPSDS
ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV
HRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTTFQATLLMD
GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRTIYEYHRVELQMSKIT
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCWSCSKLQRCSSGFDRHRQDWVDSGCPEESKEK
MCENTEPVETSSRTTTTVGATTTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLKDNGASTD
DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAMKFRR
GSGHPAYAEVEFPVGEKEGFIVSEQC

Important features of the protein:

Transmembrane domain:

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.

amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

FIGURE 473

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCG
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCTGAGCCTCGGGCTCCGGCCCGGACCT
GCAGCCTCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGCGC
TTTAAAAGTGCTACTAGAACAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG
AAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTGTTCA
GCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTC
GGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCCTCCTCCTCTTACGAACCGCACTGT
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTG
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGCTGGCCCTGCTCATCCTCTGTGTATC
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTGCGAGGACATTAG
TACAACGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCC
TGCTGCCAGTGCCCGCTGACTCAGTGCAGACCTGCGGGCCGGTGGCTTGTCTCCCATCCATG
TGCTGTGAGGAGGCTGCAGCCCCAACCCGCGCACTCTTGGTTGTGGGGTGCATTCTGCAGCC
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTC
ACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGT
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCACTCTCAAT
CCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT
GTTCCAGTCCAGTCTCATTCTGAAAACCTTTACAGCAGCTACTGATTTATCTAGATATAACAAC
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG
AGTGGCGCTGTCTATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA
GCAGTCTGGACCTTGATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTG
AAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCA
GAGTATACTTTTTCTTCCAGAAATAATTTATACCGCCTATGAAATATCAGATAAATTACCT
TAGCTTTTATGTAGAATGGGTTCAAAGTGAGTGTCTTATTTGAGAAGGACACTTTTTTCATC
ATCTAAACTGATTTCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGT
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTCCAGAATCC
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA
GGGAATGTGGTCGAGAAAGGGCAGCCCATTGCCAGAAATTAACACATATTGTAGAGACTTGTA
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC
TCTGCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGT
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT
GGATGAAGCAGCTGTAACCTAGTGTAGTTTGACCAGGACATTGTCGTGCTCCTTCCAAT
TGTGTAAGATTAGTTAGCACATCATCTCTACTTTAGCCATCCGGTGTGGATTTAAGAGGAC
GGTGCTTCTTCTATTAAAGTGCTCCATCCCTACCATCTACACATTAGCATTGTCTCTAGAG
CTAAGACAGAAATTAACCCCGTTCAGTCAAAAGCAGGGAATGGTTCATTTACTCTTAATCTT
TATGCCCTGGAGAAGACCTACTGAACAGGGCATATTTTTTAGACTTCTGAACATCAGTATGT
TCGAGGGTACTATGATATTTTTGGTTTGGAAATTGCCCTGCCCAAGTCACTGTCTTTAACTTTT
AAACTGAATATTAAATGTATCTGTCTTCTCT

FIGURE 474

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVTCLHRFKEDWGFQKCKPCLDCAVVNRFQKANCSATSDAICGDCLPG
FYRKTCLVGFQDMECVPCGDP PPPYPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMEKKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLPSCMCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFATAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

Important features of the protein:

Signal peptide:

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

FIGURE 475

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAATG
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATGAAG
CTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT
CGCGCGCCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA
TCGAACCCCGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGACAAATGC
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG
CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG
TCCCACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG
GGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA
CAGGTCCTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGCATAGACCGCCCCCT
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGC
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

FIGURE 476

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTLVVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIIRTCHRPSC
TTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

FIGURE 477

CCCACGCGTCCGGGACAGATGAACCTTAAAGAGAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAC
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTGAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTT
TCTTTTCTTTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAA
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACAGGGT
GGTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCACAAATGAGAACTGGA
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAATGGATGATCCCTTTAGAT
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCACGCGCCAGTATTTACAGGACAAAGAAACAGTCTTAA
AATATCAGAAAATACAGCTGAAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG
TATCCAAAACACAGATCAGCCCCAATCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCATGATATA
TCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCTCACAGCGCTGGA
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCATGACAATGCCCCACA
GTTTGGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGC
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCAATTTTTGATGCCTCAGAAAAATATTGCAACGAC
CTTTCAAATCAATCCTTTTTCTGGGAAATCTTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAATCTTACAA
AATAAATATACAGGCAATGGACGGTGGAGGCCCTTTCTGCAAGATGTAGGGTTTTAGTGGAAGTATTGGACACCAA
TGACAATCCCCCTGAACTGATCGTATCATCTTTTCCAACTCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGC
TGTTTTTAAGATTAATGACAGAGACTCTGGAGAAAATGGAAGATGGTTTGCTACATTCAAGAGAATCTGCCATT
CCTACTAAACCTTCTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA
GTACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAATAACGGTCCTGGT
CTCCGACGTCAATGACAACGCCCCCGCCTTCAACCAAACCTCTACACCTGTTCTGTCGCGGAGAACCAACAGCCC
CGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGAGACTCGGGCACCAACGCCAGGTCACCTACTCGCTGT
GCCGCCCCAAGACCCGACCTGCCCTCGCCTCCTTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCT
CAGGTGCTGGACTACGAGGCCCTGCAGGCTTTGAGTTCGCGGTGGGCGCCACAGACCGCGGCTCCCCGCGCT
GAGCAGAGAGGCGCTGGTGCCTGCTGGTGTGCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACCCGCTGCA
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGGCCCGGGCGGCGGAGCCGGGTACCTGGTGACCAAGGTGGTGGC
GGTGGACGGCGACTCGGGCCAGAACGCCCTGGCTGTCTGCTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCTGG
TGTGTGGGCGCACAATGGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGGACGACGCAAGCACAGGCTCGT
GGTGCTTGTCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGACGGCTT
CTCCAGCCCTACCTGCCCTCTCCCGGAGGCGGCCCGGCCAGGCCAGGCCGAGGCCGACTTGCTCACCGTCTA
CCTGGTGGTGGCGTTGGCCCTCGGTGTCTTCGCTCTTCTCTCTCGGTGCTCCTGTTCTGTCGGCGGTGCGGCTGTG
CAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTCGGTGCCCGAGGGTCCTTTCCAGGGCATCTGGTGGACGT
GAGGGGCGCTGAGACCCTGTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACAGTGAGTT
CAAGTCTTGAACACAGTTATTTCCGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATTCACCTT
CCGAAATAGCTTTGGATTTAATATTCAGTAAAGTCTGTTTTTGTAGTTTCATATACTTTTGGTGTGTACATAGCCA
TGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA
CCCCGTGGTTTTTACAATGTTTTCATCTTTTTTGCATTATAAACAACCTGGGTTTAAATTTAATGAGTATTTTTT
CTAAATGATAGTGTAAAGTTTTAATCTTTTCCAACTGCCCAAGGAATTAATTACTATTATATCTCATTACAGAA
ATCTGAGGTTTTGATTCATTTACAGAGCTTGATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGCTCTA
TTAAGAAGGCATATCTACATTTCCAACTCATTCTAACATTCTATATATTCGTGTTTGAAGAACATGTCAATTA
TTTCTACATCATGTATTTAAAAAGAAATATTTCTCTACTACTATGCTCATGACAAAATGAAACAAAGCATATTGT
GAGCAATACTGAACATCAATAATACCCCTAGTTTATATACTTATTATTTATCTTTAAGCATGCTACTTTTACTT
GGCCAATATTTTCTTATGTTAACTTTTGTGATGTATAAACAGACTATGCCTTATAATTTGAAATAAAATTATAA
TCTGCCTGAAAATGAATAAAAAATAAACATTTTGAATGTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 478

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLLDSHTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDI
NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGLNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGELSLLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYETQAP
ENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYELVNSY
KINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN
GKMVCYIQENLPFLLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPLRKTEHNITVLV
SDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPQDPHLPLASLV
SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVLDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVVAVDGDSQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVLDGFSQPYLPLPEAAPAQAEADLLTVYLV
VALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFGHLVDVRGAETLSQSYQYEV
LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ
```

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

Amidation site.

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

FIGURE 479

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCTGGGAATTTAAGGGACCCACACTACCTTCCC
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCA**AT**GGGACCTGTGCGGTTGG
GAATATTGCTTTTTCCTTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG
ACGATGACACAGAACGCTTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAGCTAC
AGGCGGAAC**T**GAGTCGCACCGGT**C**GATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAG
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTTACGCTGAGCGCAAGGGCTCACTGAGAT
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGTGAAGG
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACATACCTCAAGA
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC
AGGAGCAGCCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCAGCTGCTGAAACTGCAT
GTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG
GAAGCCACCCCAA**A**CTTGACCGAGAAGATCTTT**GA**CCCTTGCCTTTGAGCCCCCAGGAGGGGA
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTTCAGGGTGTGTT
TATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCCTGCTCCTAGAGATG
AACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT
AACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG
GACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA
GCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAACTTCTATATCGCTATT
AACTTTTTTCTTTTTTTCTA

FIGURE 480

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVLE
LGQVLDTGKRKRHPYVSSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMTATLKGL
VQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQLQNFLCEGHVL
PAAETACLQETWTGKEITDGEEKTEGEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:

Signal peptide:

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

FIGURE 481

GGCGTGTGCAAGGCGGGGTCCGGCCCGCGCAGGTTCGGGTAAGCGCGTCTAGGGCGCTGCGCGG
CGCAGCGAAAAATGGCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCCTGCTTTGTGCCTCTGA
CCTGCTGCTGCTGCTGCTACTGCTACCACCGCTGGGTCTGCGCGGCCGAAGGCTCGCCCGG
GACGCCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGGATATTCGCGATTACAATGA
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT
TCCAGAGCACAAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA
CTATGACGTCCAGAGGTTTCAATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG
CTACGCTTGGGAGATCAAGGACTTTTGGTCCGTCAAGACAGGTGTGCTGATGTAACCTCTGGA
GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG
GAATAAAAGAGAAGACCTGTGATGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG
GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT
TCTAGTGTCTTCTAGAAAGGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTCCCATTTACACTTGGTGAG
TCATCAACTCTACTGAGATTCCTACTCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT
GATCAGATAGCAAATTCGATCAGAGAAGACTTAAAACTCTTGACTTAATTGAGTAAACTCT
TCATGCCATATACATCATTTTTATTATGTTAAAGGTAAATATGCTTTGTGAATCAGATGTC
TGTAGCCAGGAAGCCAGGGTGTGTAAATCCAAAATCTATGCAGGAAATGCGGAGAATAGAAAA
TATGTCACTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG
AGAACTCTTGGTGTCTGTCAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTTTCC
TTATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTTATATGTTCCATTTAATGTGACAGTTTTT
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT
TTGTTTTCTAAACATTTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTTCGTATAGAGTAACATG
ATGTGCTACTGTTGATGTCTGATTTTGGCGTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG
AACATTTATATACAGATGTCATTTCTAAGAACTAAATTTCTTTGGGAAAAACCCTCAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 482

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

Important features of the protein:

Signal peptide:

Amino acids 1-32

N-glycosylation site:

Amino acids 201-205

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 85-89

Tyrosine kinase phosphorylation site:

Amino acids 50-59

N-myristoylation sites:

Amino acids 30-36;138-144;153-159;176-182

Amidation site:

Amino acids 207-211

FIGURE 483

[illegible]

FIGURE 484

MALPPGPAALRHTLLLLLPALLSSGWGELEPQIDGQTTWAERALRENERHAFTCRVAGGPPTPRL
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDQAQNPW
LTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV
SSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

FIGURE 485

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT
GGTCATTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGGCGCTTCTGTGGTGG
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCCTGTACCCCTCATTCTCGCTGC
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTC
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAAACATTTCTGTTATC
TAAATAAAACAGTGAAGTTTGTGTTGACTAAAAAA

FIGURE 486

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLFTSTILGTYVEAGAAKSNEEEIVNKSEFGRFPRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

Signal peptide:

Amino acids 1-21

N-glycosylation site:

Amino acids 38-42

N-myristoylation site:

Amino acids 27-33

FIGURE 487

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCGATGTGGAGCGCG
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT
ACGCACCACC GCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG
CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCCTGCTCTGGA
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCCCTGTCA
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCCAGT
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC
TCTGCAGGTCACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCTCAAGTGCCTTTGTG
ATTAAAGAATGTTGGTCTATGAAA

FIGURE 488

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAPVLLGLLLALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN
NQEVSFAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:

Signal peptide:

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196

Endoplasmic reticulum targeting sequence.

amino acids 218-223

FIGURE 489

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGCAGCTTCTCAGGGCCGGAGCCAGTTCTTGGAGGAGACTCTGC
 ACAGGGCATGGATCACTGTGGTGCCCTTTTCTGTGCCTGTGCCTTCTGACTTTGCAGAATGCAACAACAGAGAC
 ATGGGAAGAACTCCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGGAGCTCAGTTTTTCTCTCGTCA
 ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCAGGGCTACAACCTGACCTTGCAGACACCCACCAT
 CCAGTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC
 CCAGGCAGGAGGTGAGCATGCCCCGGGGTCAGCACGCCATGCAGTTCCTCCGCCGAGCTGACCCGGGACGCCCTGCAA
 GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAAACAACTC
 ATCTCTGCTGAATAACTACGTCTTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA
 CATCAGCTTCTGGCACAACCAAAGCCTGGAAGGCTACACCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA
 ACAGCCCTGGGGGGCTGGAGCCCTGAGGGCTGTGCTACAGAGCAGCCCTCCCACTCTCAGGTGCTCTGCCGCTG
 CAACCACCTCACCTACTTTGCTGTTCTCATGCAACTCTCCCCAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT
 TACGTACATCTCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCTGCTGCACCTTCCATTT
 CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCTCCGTGCTGCTCCTGAACATCGCCTT
 CCTGCTGAGCCCCGCACTTCGCAATGTCTCCTGTGCCCGGGTCAGCATGCACGGCTCTGGCCGCTTGGCCGCTGCACTA
 CGCGCTGCTCAGCTGCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCCTCGGGCGTGTCTACAA
 CATCTACATCCGCAGATATGTGTTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGTGCTTTC
 CCTCTCTGTCAAGAGCTCGGTATACGGACCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT
 CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGCACAGTGTCTGGTTCATGGGCTACGGCGGCTCAC
 GTCCCTCTTCAACCTGGTGGTGTGCTGGCCTGGGCGCTGTGGACCCCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC
 AAGTGTGAGGGCCTGCCATGACACTGTCACTGTGCTGGGCTCACCGTGTCTGGGAACCACTGGGCTTGGC
 CTTCTTTTCTTTGGCGTCTTCTGTGCTGCCCCAGCTGTTCTCTTCAACCATCTTAAACTCGCTGTACGGTTTCTT
 CTTTTTCTGTGGTTCTGCTCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCCTTCAGCTC
 CTCCCAAACAACACAGTAGTCCGGGCTCCTGGCCTGGAATCCTCAGCCTCTCTGGCCGCCAGTAGCCTGAGGCT
 ACGGCTCCTGCTAGAGAGGGTGGCAGGCCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAGGGGCTTTTC
 CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGTCTCCGGGCGAGA
 TCCAACCTTACCTGGGGCGAGCAAACTTTGTCTGGTACCTGGGCCCAGCTCGCCAGGGATGTGGGCAGAGCACCA
 GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCTGCCACTTCTC
 ACAGACCTTAGGTATCCACAGCTGTGACATGGGGCAAGCAGCTTTGTTTCAGCCTAACCCAGGAGCTTAGTAAA
 AATTGCATAAGACCAGGGGGAAGAGTGTGAGCGTGGGGTGGGAATTCCCGCGGCCCTCCACCTGCTTGTAGGGC
 AGGATCTCATTACAGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT
 CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTTA
 ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCCCACCTTCCCAAAGATTGGGAGGTTCCGCCGTTCCAGAGG
 CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAGTAGCCCATCCCGCAGTTTTCTTGGGGGCA
 GAGGAAAACGCTTCTTCTCCTCCAGCTGAATCAGCTGGATCCCAGTGTCTGGCTGTTTGGTGATTGGGCAAGA
 TTGAATTTGCCAGGTAGGCGTGAGAGTGTGGGTTTTAAATTGGAAGCTCAGGCCATAGTTTTAGAGAATCACCC
 TTACCCAGACCTTCATGAGACAGTGCTCATGAAGCCAGTGCGTTTTCCAGAACGAACACTAGGCGGCACCGTTG
 GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAGACCCCATGCAC
 CAGCTGGAGGGGCGGTAACCTGCAGGACTGCGCCTACTGAGTGACCCATTTCTCCAGGAGGAAAGGCAAGACAG
 CTTACACGGCCATTTGTCTCTTTTCCCAATGCGGCGGTGCACTTTCGCTCTTGGGGGCTGCACCCAGACATAGC
 TGGCACAGAGCAGGGTGCTCAGGTGGTGGGTGCTCAGGGCCCTGCCCCAGGCCACTGGGCGGTTTTGATGACCT
 CAAAGGTCACAGGCAGAAAATAGGAGCAGGATTTCCCCTGGGGAAAAGTTATCCTGGGACATCTTCTGCTCTTCT
 GTACATTTCTAGATGCAAATAACTCCTTACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT
 CCAATGCCAGCTCTGCCACTTGCTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCCCTCAGTTTTCC
 TATTTGTAAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAGAATTCAAATAAGAGACTTGGCA
 CAGAGTAAGTGCTCAGTAAAAA

FIGURE 490

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQNATTETWEELLSYMENMQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTLOTPTIQSLAFKLSCDFSGLSLTSATLKRVPQAGGQHARGQHMQFPAELTRD
ACKTRPRELRLICIYFSNTHFFKDENNSSLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNIAFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWMIAIEGFNLYLLGRVYNIYIRRYVFKLGV
LGWGAPALLVLLSLSVKSSVYGPCTIPVFDSENGTGFQNMSCWVRSPVVHSLVMGYG
GLTSLFNLVVLAWALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCRSEAEAKAQIEAFSSSQTTQ
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domains:

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

N-glycosylation sites:

Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;
179-183;394-398;400-404

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 274-278

N-myristoylation sites:

86 GLSLTS
101 GGQHAR
157 GAQLSH
255 GCSISI
311 GSACTA
420 GGLTSL
467 GTTWAL

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 246-257;318-329

Eukaryotic thiol (cysteine) proteases histidine active site:

Amino acids 410-421

G-protein coupled receptors family 2 proteins:

Amino acids 273-302;314-343

FIGURE 491

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT
GAGGGGCACCAGACAGAGGATGAGGAGAGAGAGTCCGACACGGGCTGCCCTGAGAGACATTTC
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA
ATACTCCCTCAATCAAGCTATCCGGAAAGAATTACAAGAAATGCCAGAACTGCTTGGGTGG
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC
GGGAGGCACCCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA
CCTAATAGGCAGTTCGTAATTAGGCAGCTAAAAGTTTTTCTAGGCATTTATGCAAGCCTCC
CAGGCCATTTTCAGCACTCATCGAAGACTCTATTCCTACATGTAGTCCCGAAGTTGGAGGCC
TGAGAACCCCTACCTGATAGACCCAGAGAACCAAAACGTGACCCTGAATGGTCCTGGGGGCTG
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCCACACAGCCCT
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC
TCTCTATAACCCCTCCAACCCAACCTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC
GGGGAGTCTCGTCCCTCATCCCTGGTGGAGTCATTAGCATCTTCCGCAGCGACTCAGCCCT
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCTGGCACTCAGCCTGATCCACCTCTGTGT
TCAACTCTACCGTATGATGGACAAGGGCGTCTCAGCTACTGGCGAAAGCCAAGGAACTGGCT
GGAGGTAGCCTCTCTTGTGTCATTTTCTTTTGAAAATAACAATAAACTGTTTATATCTTGAA
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATGTCAGTTTTCTC
CCTCTGTAGTGTTAATCTCAAAACAGCATTTGAGATCAGGTATCATTTAGTGTTGTTACAGTT
ACCGTCATGTACCACACGAATTTAGCCAAGGTGGTGGTCCCATAAGATCATATGGTGCTAAG
AAATTTCTGTCACCTAATGACATCTTGATTCTGACCTTGATGTAGGCCTAGGCTAAATATGT
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTTAAAAATAAAAAA

FIGURE 492

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTTLDDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRHLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHLVCVQLYRMMDKGVLSYWRKPRNWLEVASLVSFSEK
```

Important features of the protein:

Signal peptide:

Amino acids 1-30

Transmembrane domain:

Amino acids 250-267

N-glycosylation site:

Amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 2-6

N-myristoylation sites:

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

FIGURE 493

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCAGAGAAAAGCTTCTGTTTCGT
 CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC
 CCCACTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG
 CGCACAGTTCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA
 ACAGAAATGCTCTGCCCTTGGAGAAGTGTAAACCTAGGGCTACTGTTGATTTTGACTATCTTC
 TTAGTGGCCGAAGCGGAGGGTGCTGCTCAACCAAACAACCTCATTAATGCTGCAAACTAGCAAG
 GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC
 TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT
 TGTTGCCCTCCTATCGCATTAAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC
 CAGCCTTCCTGCACAAAAGCCTACAGGAAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT
 GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTCGGACCTTCAGATTCGTCCAGTG
 GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT
 GGATATCACCTCCAAGTGTTAGTTACACCTGAAGTACCTGCTTTCAAAACAGGAATAGAAGT
 GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT
 TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGACTGTTAAGAGTACATGCCACTGG
 GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG
 TACATAGAGCTACTTCCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTCCATATATC
 ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC
 AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC
 TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT
 CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC
 CAAGAAACAACAACAAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT
 GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAATGGATTCTCATT
 CATACCCTTGTATAATTGGAATTTTGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT
 GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTGTGCAGGACAGTAAAT
 AATGAAAACCAAATTTCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTG
 TATCCTTTCAGAATATTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA
 TTTATGTGTCCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA
 CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC
 ATGACAAGTAGAGCTACCTCATTCTTTTAAATGGTTATATAAAATTCCATTGTATAGTTATAT
 CATTATTTAATTAAAAACAACCCTAATGATGGATATTTAGATTCTTTTAAGTTTTGTTTATTT
 CTTTTAAGTTTTGTTTGTGGTATAACAATACCACATAGAATGTTTCTGTTTCATATATCTCT
 TTGTTTTTGTAGTATATCTGTAGGATAACTTTCTTGAGTGGAATTGTCAGGTCAAAGGGTTTGT
 GCATTTTACTATTGATATATATGTAAATTGTGTCAAATATATATGTCAAATTCCTCCAACA
 TTGTTTTAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTCCTGCTTCTACAG
 TTGCCACTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA
 CTATTTAATAAAAATGGATTTATA

FIGURE 494

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13, NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAEAGAAQPNNSLMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRYCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTCH
VSHLTGNKSLYIELLPVPGAKKSALYIPYIILTIIILTIIVGFIWLLKVNGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVDTDLHTL
```

Important features of the protein:

Signal peptide:

Amino acids 1-24

Transmembrane domains:

Amino acids 78-98;267-286

N-glycosylation sites:

Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;
218-222;233-237;247-251;298-302

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 112-116

N-myristoylation sites:

Amino acids 103-109;259-265

FIGURE 495

CCAGGTGCACAGCGCATCGCCCCGAGGCTGTACCGCCCTGCCCCGCCCACCCCAGCTGTCCTG
 GACCCAGGGGCAGGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT
 TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCAGGAACCAGTACCACCTGCACCA**ATGGG**
 GCTGTCCCGGAAGGAGCAGGTCTTCTTGGCCCTGCTGGGGGCCTCGGGGGTCTCAGGCCCTCAC
 GGCACCTATTCTCCTCCTGGTGGAGGCCACCAGCGTGCTCCTGCCACAGACATCAAGTTTGG
 GATCGTGTGTTGATGCGGGCTCCTCCACACGTCCCTCTTCTGTATCAGTGGCCGGCGAACAA
 GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCCTGGAATCTC
 CTCCTACACTTCTAATGCTGCACAGGCTGGTGGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT
 GGTGCTGATCCCAGAGGCCCAGCATCGGAAAAACCCACGTTCTTGGGGGCCACGGCTGGCAT
 GAGGTTGCTCAGCCGGAAGAAGAGCTCTCAGGCCAGGGACATCTTTGCAGCAGTCACCCAGGT
 CCTGGGCCGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGCAGGCCGAAGGTGC
 CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA
 ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGCCTCCACCCA
 GATCACGTTTCGTGCCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTTCGCTCTA
 CGGCTCCGACTACAGCGTCTACACTACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG
 CAGGCTCCTCGTGGGGCTGGTGCAGAGCCGCCCGGCTGCCCTGCTCCGTACCCGTGCTACCT
 CAGCGGCTACCAGACCACACTGGCCCTGGGCCCGCTGTATGAGTCACCCTGTGTCCACGCCAC
 GCCCCCGCTGAGCCTCCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCCTGGAGCCTGCGT
 CTCAGCCATCCGGGAACCTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCCTTTGA
 CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA
 CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCCCTCCTGCACGAGGGCTAC
 GGGTTACAGCAGGAGACCTGGCCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT
 GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG
 TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGCTGGCCCTGGTG
 GCGGTGGTGGGGCTGCCTTGGTCCAGCTCTTCTGGTTGCAGGACT**TAGT**GGGAAGGCGGAGGT
 GGGCCCCCACAGAGCCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTCTGAGCCCTGAGC
 GCCGTGGGGCCTTGCTCTGTGGCTCTGCCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT
 CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCCTCCCGGCGTCCCTCCCCCAACCTCC
 TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG
 TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG
 CACAGGGGTCCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT
 GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCTGG
 GGGCTTCTGCTGGGCCAGCCCGGCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT
 TGTTTTTATTAAAGCATCATGGACACAGCAAAAAAAAAAAAAAAAAA

FIGURE 496

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENGTGVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPEEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS
LPQNLTVEGTGNPGACVSAIRELFNFSSCQGQEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYIILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMI PADAP
AQWRAESYGVVWAKVVFVVLALVAVVGAALVQLFWLQD
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domain:

Amino acids 428-449

N-glycosylation sites:

Amino acids 67-71;135-139;304-308;325-329;410-414

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 133-137

N-myristoylation sites:

Amino acids 50-56;123-127;165-171;207-213;234-240;
259-265;311-317;314-320;331-337;398-404;
413-419;429-435

GDA1/CD39 family of nucleoside phosphatases proteins:

Amino acids 43-59;202-215

FIGURE 497

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG
 AGTTCACCTGTCTCAGGAACCACCTGAGCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA
TGGCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCGTGGTGGTGCCTCCA
 CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG
 CCCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC
 TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCCTCCACCTGAAATTCATTG
 CTGGTTTCGGAGTGCGCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTCGCGCCCCAG
 AGCCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCGTGACCCAGAGCTCCA
 TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG
 ATGGCAGTAACAGCACCTCCCACGCGCTGCTGGTCCTGGTGCAGAAGCACATTAAAGCTGTCT
 TGAGTAACAAGCTGTGCCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA
 CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCAGATCCGCTATTCCATGGTCAGTGTGC
 CCACTGTCAACAGTGACTACATTTCCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAACC
 CCATCATCTGCCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT
 CCATGGCCACCGTGGGCCTCTCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG
 CCGGTGCCCTCAACCTGGACATCACAGGGCAGCTGAGGTGGATGACAACCTGCTGAACACCT
 CTGCTCTGGGCCGGCTCATCCCGGAGGTGGCCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC
 TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACAACAAACGCCACCCCTGCGGC
 TGCAGCCCTTCGTGGAGGTCTGGCCACAGCCTCCAACCTCGGCTTTCCAGTCCCTCTTCTCCC
 TGGATGTGGTAGTGAACCTTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA
 CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT
 CAGGTGCGCACACTGATGGGCACCGTTTTTTGAGAAGCCCTGCTGGACCATCTCAATGCTCTC
 TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTGAGATCTTT
 GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCTGAGGCAAGACCACT
 GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA
 AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTA
 TCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCCTTCCCTCCTCCTTCT
 CCTCCCTCTTCCCTCATCTCCCCCTCCTTCTCTGCCCCACCCAGGGGGGAGCAGACTGCT
 CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAAACAACCTTCTCTTGAGCTGC

FIGURE 498

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAAANFTFKVFRAPPELELTLPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIAVLSNKLCLISISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSYISLEVNAVLFLLGNPIILPTDAT
PFVLPRLHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPEPMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV
VNLRLQLSVSKVKLQGTTSVLGQVQLTVASSNVGFIDTDQVRTLMGTVFEEKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVVISSGLFYQS
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

Transmembrane domain:

Amino acids 217-236

N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

FIGURE 499

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAGC
CCTTATGCTGCTCACCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTGCTGTCACTC
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG
CACACCAGAAGAGCCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTGACATA
TAACACCACCTGCTGCAACAAGGACAAGTCAACAGCGCAGGACCCCGGCCCACTCCAGCCCT
GGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAGACTCATT
CCATTGGCTGCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG
GTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCCAC
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCTTATACTCTGCTG
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC
ATATGTACCCCATCCCCCATACTCACCTCTTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA
AAAAAAAAAAAAAAAAAAAA

FIGURE 500

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878

><subunit 1 of 1, 125 aa, 1 stop

><MW: 13821, pI: 8.60, NX(S/T): 2

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGITYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:

Signal peptide:

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

FIGURE 501

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG
GGCTGGGGGCTGCTGACATGTGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCCCTTCAGGAGT
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT
CCACACTACCAGGGCCAAGTGAGCTTCTGGACCCCAGCTATTCCCTGCATATCAGCAATCTG
AGCTGGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAACTCATGAGAAACAGA
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTGACTGCTCCTTGGGAACCCC
AGTCCTGAGCTTGGTTTCTTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTCTTTCCAGG
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA
ATAAAGTCAAATTAAGTGACCACA

FIGURE 502

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLLLQEGSQRRRLWRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPGKEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLIFLLLVLAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

Transmembrane domain:

Amino acids 144-165

N-glycosylation site:

Amino acids 99-103

N-myristoylation site:

Amino acids 106-112

FIGURE 503

ACGGGCCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCAG
TCGGGCCGTTCTTCGCGCCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC
CGCACCCAGGTTTCGGCCCGTAGGCGTCTGGCAGCCCGGCGCCATCTTCATCGAGCGCCATGGC
CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTCTGCT
GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTAAAAGC
TCTTACCCTCCACTATGACCGCTATAACCACTCCCGCAGGCTGGATCCCATCCCACAGTTGAA
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAAGTCATACAGTGTGAGAACA
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT
TGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCCTCTGAAGACCAGTATGTACTAAGAGG
TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC
TGGAAAGCAGCACGGCTTTGCCCTCTTCTCTGATTATTATTATAAGTGGTCTCGGCGGATTC
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA
GCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA
CCGTTACCAGAGATTACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTCAC
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGCTTTTACAGGACAACA
AGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACCTGGTGGAATACTAGGATA
TTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCTTATCC
TCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA
TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG
ACGATAAAAGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT
CTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGGATATTCAAAGTTCTGTG
GTGTTATGTCCAGTGTAGCTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA
AATACTTATGTGTTGTATGTGAGTGAACATGCAGATGTATATTGCAGTTTTTGAAGTGATC
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTA
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTAGTTTTAGGTGGTTGTAGC
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTTGGTATTATATTATTTGATGTTTG
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC
TTTTGAGCTCTGAAGCTTTGAATCATTCAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA
CCTTCTGTAGGAAAAGGTGGAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG
CAAAAATGCTTGAAACCTCTATATTTCTTTCTGTTTCTAAGAGGTAAAGGTCAAATTTTCAAC
AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT
CTGTTTCAATCTTAAAAAGAATCA

FIGURE 504

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPO
LKCVGGTAGCDSYTPKVIQCQNKGWDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSSEDQYVL
RGSCGLEYNLDYTELGLOKLKESGKQHGFFASFSDDYYKWSADSCNMSGITIVVLLGIAFVV
YKFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPLHGGS
SYSVCSNSDTKTRTASGYGGTRRR
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318

FIGURE 505

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGCACGGGCATACCTGC
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTACCTTTTGAAGGACAAGATGCATT
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA
GCAGGGCTGTGCTCTTCCCTGCCGCCACCGGCCAAAGAGGTCCTCATCACTGCCATTGAACC
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCTGCTGGCCGAACCTG
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT
CAGACTTCCGCACCGTCTGCAACAACGTCATCCCCAAGAGCATCCCAGACATCCGCCGGCTCA
GCGCCAGCCTCTCCAGCCACCCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCACGGCCATCAGAAGGACATCTGGGCGC
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG
TACCTCCCTGAGAGACTGGCCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA
AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTCTCCTTGATGTTTCTGGAAGACACATC
TGATTATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCTGGCCCAGGATCTAAAACTT
TCTAAGTTTCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTACCTCACCTTGAATCTAACAAATCAA
GTATTTCTGCAGGTCCAATGGTCTAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTATTGTGGTAAAAAACACATCACGTAAAATG
TACCATCTTAACCATTTTAAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC
AGACCCCCGGAACCTTCTCATCTTGTAATTCTGAAGTTCTATACCCACCGAACAACCTCCTCTT
TTCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGAGAGT
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTGTATTCT
GGAAAAGTGTTTCTTCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT
GTACACTTGCTGTACCTATTTTTTATTTAAACAATATTCATCTATGGTATAATAAAGATGTCAT
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 506

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLYNAAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVVELLYEF
LLAELEISPDQLQISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 36-40;84-88;105-109

FIGURE 507

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAAACTGAGAAGTGATTGCTCGAGGCCTTC
CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAGGCCAGCTTGTATTATAAAGACAT
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA
GAAATATGCTCAGCAAGTCTTGCGAGAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCGGAAGTTCTCCAGTAAAGTCCA
GACCTCTTGGAAGTCTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTGC
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAAGTGGGCCACACCCTGAA
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACCAGTTGAGGGATATTCAGAACATGTTGG
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCACTGTCTGACCTTGAATATTAT
TCCAATGACTTATTTGTTGCTGTTTTATTTAAGAGTGTGATTCAACTGGCTTCAAGCAATG
GTAAAAAAGGAAACCCTGCCATTCTGGGTACGACTCTTCTTTTGAAGCAGGTGGCAGAAAAA
ATCCCACTGCAGCCAAAACATTTAGGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCCCCACA
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT
GGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
ATGAACTTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAAA
GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACTCA
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCAT
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAAGTCTTTAATTTAAAAACACAAAAAAAT
TTTAGCTCTTCCCACTTTTTTTTTCTATTATTTGAGGTCAGTGTGTTTTGTTTGCACACCAT
TTTGTAATGAACTTAAGAATTGAATTGGAAAGACTTCTCAAAGAGAATTGTATGTAACGAT
GTTGTATTGATTTTTAAGAAAGTAATTTAATTTGTAAACTTCTGCTCGTTTACACTGCACAT
TGAATACAGGTAACATAATTGGAAGGAGAGGGGAGGTCACTCTTTTGATGGTGGCCCTGAACCT
CATTCTGGTTCCCTGCTGCGCTGCTTGGTGTGACCCACGAGGATCCACTCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG
GAGAAGGTCACAACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG
GAAGCTGTCCTGGAGGTCCCTGGTCCGAGAGGGACATAGAATCTGTGACCTCTGACAACTGTG
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCAGCAATTATTACAATTCTTGAATTCCTT
GGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTTAGATCTAACGTGTTCCAGTGTCTGT
CTGAGGTGACTTAAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACACCC
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCAGTATTATAAATTGTGTA
TTTAA

FIGURE 508

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLKDIKCTLVFGVWILYILKLNYTTEECMDKMKMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMA LLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGH TLNQFDVVIRLNSAPVEGYSEHVGN
KTTIRMTYPEGAPLSDLEYYSNDL FVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVIIKETAFDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTP LHYFDSQCMAAMNFQTMHNVTTETKFL LKLVKEGVVKDLSSGGIDR
EF
```

Important features of the protein:

Transmembrane domains:

Amino acids 11-27;281-297

N-glycosylation sites:

Amino acids 30-34;180-184;334-338

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 2-6;109-113;223-227

N-myristoylation sites:

Amino acids 146-152;150-156;179-185;191-197

FIGURE 509

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCTTCCGCTCCAACATGG
CTAGTTCCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCCCGCCAGGCTAGACAGTGGAGTGCCGCACA
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT
TGGTCGATCTTCGAGCCAAAGATGCGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG
TGCTGCCGCCGGGTACTGTCCTGGGTGCCAGTGCTCGTTATTGTCCTCGTCGTGCTCTGGTCC
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCACAGCAGCCAAACCAGAAG
TTCCACTTGTCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG
CAGATGCTTGTTGATATGGCCAAAAAGCTACCGGTTTACACAAGAACTGGAAGTGGAGGTCAG
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG
TTCTCAAACTAGCCCTTTTTTTTCTCCCATCTTCTGAAAACCACTATGGAGATTTTCTCCA
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTCTGTGTTGCTATATCACATATCTATC
CACATATGCATACCTCTATTTATCTTTCGTCAAGCCATCTTATGTTTCTGATGCATTTCAAAG
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTTAAATTTACA
TACAAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAAAGTGTACACATCTGT
GTAACATAACCCCCAATAAAATTGCCATCACCTCAG

FIGURE 510

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLYLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLRKAKSYMFSN
```

Important features of the protein:

Transmembrane domain:

Amino acids 24-45

N-myristoylation sites:

Amino acids 11-17;12-18

FIGURE 511

CAGCCGGGGCG**ATG**CGGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGGCGA
GCTACGCGCGGAAATGGCAGCAGATGCGGCCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA
ACGGGGTCCGCAGCCCCGTTCCCAACCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG
CCGCAGGAGAGAGGAGCCTGTCACCCTGTGGAGAATGCACTCCAGTTCTAGTCGTTGCCCCCT
TGGCACCCGCCGACACTGCTAGTGCCCCCATCCCAAAGTGAGCATTCTTTGTGTGTAGCACA
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA
AAGCCCTGCCGTTTCTCCTGCCTTGGCTTGGGAAGCCT**TAGGA**ACAGAAGCTCCCTGGGAGC
ACAGAGCGGTTTTAAACTGGCCAACACCTTAACGCCCAGAGCCGCCCTCCTCTCGCTGCCACT
TTGGAATAAAGAGACTAGAGATTCACTGGACGCTTCTCCCGGCATCACAAGACTTGACTGC
TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTTGTTTATTAAAG
AGTGAATTTTTTAAATTAATAATCATGTTTTTAAACAGAGATGGACATTTTATTGATGGAAAAA
ATCACGTTAAGTTAGAAAGCTCTCAAAAGTACCTGGTATTTACAACCTCCCTGTGAGGGAGGGC
GAACTCGATCTCAGAGTTTTATTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA
TTTGCCCAAAATGGCATATTTTAAATTTGGCCCGAGACCAGAACCCAGTTTCTCTGGGATTAT
TTGTTAGTAATCGTTTTTACAGGCTGAGCATTAACCTAACCTCCAAAGCTTGAAGGACTTTTTCTC
ATTTTCACTTGTTTTCTCTAATAAAAAATAATGCTGTAATTTCAACTTCACAAGATGAGGCCTC
ATGGAAGAGTGTTTACCAAAATATTAATAATACCTTTGACAGAAAAAATCAAGCGAACTCTTT
GCCAACCAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAAATCACTGG
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTTAAGGCTTTAT
GGTATTAAAAAATAAACTGTACAAAAATATAGATTTTCCCCTATCCCCTACCCCTGGAAAGTA
ATATACTGAAGTCTCATCATACTGTTTTGGGGATTCCAGTAATTAAAATCTCTAGTGAACAAA
GACCTGTTTCAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCTCCTTGTAGTCAC
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTATTCCACCAACAA
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTTCTCCTTTACTTGTTAAAGTGA
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC
CAGTGTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA
GAATCTTGCTTTACATACAAGAGGTGTTGCGTTTTCATTTTGCGGCTAATGTCCAAACGCTG
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAACTCTAATCTA
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCAGCTACTCCAGCTGTTGGACCTGC
TGCCTTAGAACCACAGATTGGTACCTCGTGCC

FIGURE 512

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGLVWQKLLWGAASALSLAGASLVLSLLQRVASYARKWQQMRPIPTVARAYPLV
GHALLMKPDGRGKGRRSSWSATGSAAPFPSPDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFVVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP
```

Important features of the protein:

Signal peptide:

Amino acids 1-25

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 75-79

N-myristoylation sites:

Amino acids 3-9;17-23;145-151

Amidation site:

Amino acids 73-77

Leucine zipper pattern:

Amino acids 8-30

FIGURE 513

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC
 CCACTGCTCCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCTGTTCGGGGCCCA
 GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTCAGCCCATCCCCAGTT
 CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCCGTGGACTGAGTGGCAGGCCATCCT
 ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG
 ATCCTGCAAGCCCTGCCTTCTTCTCCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC
 ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCCTCCAGCTCAGCCACTGCAC
 TGAGAACATGGACTCTCTGTGGGGCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA
 CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTGAGGGCCCTCAAGGAGAG
 CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCCTAGAGTCCAAGAGAATCCTGGTGATCA
 GAGAAGGGTCCCCGAGGTCACCGGGGATGCACGGTCTGCATTTCCGCCCCCTGCCGGGACAA
 TGGAGGCCCTCTCTCCCTTTGTGCCCCGGGCCCGGGCCTCTGCAGACAGACCTCCATGCCCA
 GAGGTGAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA
 CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG
 GAGGGGGCCAGCCTCATCCCACTGCCAGCTGACCCTCAGTTCTCAAAGACAGTGAGTGA
 GGACAGGCCTCAGGCTGTCTCTTCAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC
 ACCAGGGCAGACACTCACCCCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCCCAG
 TACACACAAGTTTCCCCCTGCTGCCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC
 CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGGAGAAGGAGGCGGCCCTT
 CCAGCGCATCAACAGTGCACTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCCTC
 ACGGCCTTCCCACACTTTGTCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC
 TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCCTGGGCCT
 ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGAAGAA
 GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCTTCTGCCACCTCTTCTGA
 TTCCAGGACTCAGCCAGGTACCTCGCTGATTCCTGCCCCCTTCCCAGCTGCAAGCAT
 GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC
 CCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT
 TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCCAGAGGTGAGAACCAGAGATC
 CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGAAATGCCATCTCGAGCCCCTACAGCTC
 TACGGGAGGCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCACTGCCAGCTG
 ACCCTCAGTTCTCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTCAC
 ACCCAGTGTGAAAAGACGGCAGATACAGCACAGGGCAGACACTCGCCTCCAGGGGTGGC
 TCCCCCAGATCCCAGGCCTCTAGGCCCCGTATATGCAAGTTTCCCCTGCTGCCACGCAGG
 CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA
 GACCTGGACCGGGAGAAGGAGGAGGCATTCAGCGCATCAACAGTGCACTGCAGGTTGAG
 GACCAGGCCATCTAGGACTGCAGACCCTCACGGCCTTCCCACACTTTGTCTCACTTGCA
 ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG
 ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT
 GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC
 TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT
 CTC

FIGURE 514

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
MDSLWGPAGSHPFVHNTSLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSSYSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFPLLPRRRGEPLMLPPPPELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTSIIPAPFPAASMDA
GMRRTRHGTSAPAAAAAAPPSTLNTLGLSLEWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK
```

Important features of the protein:

N-glycosylation sites:

Amino acids 105-109;187-191

Glycosaminoglycan attachment site:

Amino acids 38-42

N-myristoylation sites:

Amino acids 15-21;130-136;180-186;307-313;361-367

Amidation site:

Amino acids 315-319

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 106-117

FIGURE 515

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGCGCTCCGCTCT
 CAGCCACCTCACGGCTGCCAGGAGTGC CGCGGGAGTTTGCCCCGAGCGCGGGGAAGTTTCCTC
 CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGGCAGCGGCCCCGCGAGGTTACTT
 TATGGAATTGGGCTCTTAGAGAACAAAGAAAAGACTGAAGTTTTACGGGAAAACAAATCATGTG
 GTCTTCAGATTCTGAAATAAGGAGAAATGCAGCCATCTGAAATGGTCATGAACCCCCAAACAAG
 TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG
 ATTGGAAGAACACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAAGTAACTTCAGGATGG
 GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT
 ATCACCAACCAGAACCCCAAGTTTCACATGCCTGAGGATGTACGAGAAAAAAGGAAAATCTT
 CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTACAAAGAGGGGAT
 CAAGCTTTAAGTAAGTCCACAGGGTCACCAACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT
 AAGACTGTTTTTAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTCACCCTTTAAACAAA
 AGTTTAGTCAAAGATAATAAATGGAAGAAAACCTGAGGAGACCCAAGAGAAACGAAGGTCTTTC
 CTTCAGGAGTTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTTCATACA
 GTATCCAGAATCTATGTAGAAGATAAACACAAAATCTTATATTGTGAGGTACCTAAGGCTGGC
 TGTTCCAATTGGAAGAAGATTCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC
 TCCCACAATGCTGTCCACTACGGGAAGCATTTGAAGAAGCTAGATAGCTTTGACCTAAAAGGG
 ATATATACCCGCTTAAATACTTACACCAAAGCTGTGTTTTGTTGTTGATCCCATGGAAAGATTA
 GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG
 GCAATTATCAAGAAATATCGACCAAATGCCTGTGAAGAAGCATTAATTAATGGATCTGGAGTC
 AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTAC
 TGGGAAAAGGTCAGCAAACCTCTGCTATCCGTGTTTTGATCAACTATGATTTTGTAGGGAAATTT
 GAGACTTTGGAAGAAGATGCCAATTACTTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA
 TTTCCCAACTTTAAGGATAGGCACTCTTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG
 TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTATTACTTGACTAT
 TTAATGTTTTAATTATACAACCTCCACTTTTGTAGTTTGCATTTCATTTTCTAAAACCTGTATAT
 ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT
 TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC
 ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTTGAGTTGCTCTAAAATGTTTG
 GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA
 TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC
 TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTTAGCAGTCTGTGGCATATTAA
 TCAAACCTGTTGAATTGTTTTCTTACACCCCTGGAATCTTTCTATCAACTATAATGATAAATCC
 ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA
 ATATGAGAATATAGCAGAAAAACCA

FIGURE 516

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKFHMPEDVREKKENLLLNSESTRLLTKTSHSQGGDQA
LSKSTGSPTEKLIIEKRQGAQTVFNKFSNMNWPVDIHPLNKSLVKDNKWKKTEETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRIVYEDKHKILYCEVPKAGCSNWKRIIMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGITYTRLNTYTKAVFVRDPMERLVSAFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVSCLKCYPC
LINYDFVGKFETLEEDANYFLQMIGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYLDYLMFNYYTTPLL
```

Important features of the protein:

Signal peptide:

Amino acids 1-24

N-glycosylation sites:

Amino acids 159-163;243-247;324-328;437-441

Glycosaminoglycan attachment site:

Amino acids 53-57

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 177-181

Tyrosine kinase phosphorylation site:

Amino acids 329-337

N-myristoylation sites:

Amino acids 116-122;236-242

FIGURE 517

GGAAC TTCC CAGGCACCC TGTGTGGCCGCACTGCTCCCTCTGGCCCAACCATG C C TCTGTCCAGCCACCTGCTGC
 CCGCCTTGGTCTGTTCCTGGCAGGGTCCTCAGGCTGGGCCTGGGTCCCCAACCACTGCAGGAGCCCTGGCCAGG
 CCGTGTGCAACTTCGTGTGTGACTGCAGGGACTGCTCAGATGAGGCCAGTGTGGTTACCACGGGGCCTCGCCCA
 CCC TGGGCGCCCCCTTCGCCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA
 GCTGGCTCCGAGACAGGGCAGGGGCCGCACTGGAGGGTCTGGGCCTCACTCAGACCACACACTGGGCACCGACT
 TGGGCTGGTACATGGCCGTTGGAACCCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAACCCCTGC
 GAGAGGCAGCCTCCTCTTGCAAGCTGAGGCTCTGGTACCACGCGGCCTCTGGAGATGTGGCTGAACTGCGGGTGG
 AGCTGACCCATGGCGCAGAGACCCTGACCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG
 CAGTGACCACAGGCCGATCCGGGGTGACTTCCGAGTGACCTTCTCTGCCACCCGAAATGCCACCCACAGGGGCG
 CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCACCCCCAGGCCAACTGTCCCCGGGACACC
 ACCACTGCCAGAACAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAACCTGCGGGGACCTGTCTG
 ATGAGAACCCACTCACCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCTGGGCCCATGGAACCGCTCGG
 AAGGTGGTCCCGGAACACCGTGTGGTGGTCTGAGCGCCCTCCTGGCCACGCCGTGACCACAGCCGGAACA
 GTGCACAGGGCTCCTTCTGGTCTCCGTGGCCGAGCCTGGCACCCCTGCTATACTCTCCAGCCCCGAATTCGAAG
 CCTCAGGCACCTCAACTGCTCGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCTCCAGCTGT
 TCCTGCAGACTCTGGGGCCCCGGCGCCCCCGGGCCCCCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG
 CCTGGGTCCGAGACCGTGTGTGACATCCAGAGCGCCTACCCCTTCCAGATCCTCCTGGCCGGGCAGACAGGCCCGG
 GGGGCGTCTGGGTCTGGACGACCTCATCCTGTCTGACCACTGCAGACCACTCTCGGAGGTGCCACCCCTGCAGC
 CGCTGCCTCCTGGGGCCCCGGGCCCCAGCCCCCAGCCCCCTGCCGCCAGCTCGCGGCTCCAGGATTCCTGCAAGC
 AGGGGCATCTTGCCTGCGGGGACCTGTGTGTGCCCCCGGAACAACCTGTGTGACTTCGAGGAGCAGTGCGCAGGGG
 GCGAGGACGAGCAGGCCTGTGGCACCACAGACTTTGAGTCCCCCGAGGCTGGGGGCTGGGAGGACGCCAGCGTGG
 GCGGCTGCAGCTGGCGGCGTGTCTCAGCCCAGGAGCCAGGGGTCCAGTGCAGCTGCTGTGGGCACTTCTGT
 CTCTGCAGCGGGCCTGGGGGAGCTAGGCGCTGAGGCCCGGGTCTCTCACACCCCTCCTTGGCCCTTCTGGGCCCCA
 GCTGTGAACTCCACCTGGCTTATTATTTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACCTTTGAGCGGGACACAT
 GCAGCTGGTACCCAGGCCACCTCTCAGACACACACTGGCGCTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA
 CCACAGGCCAAGGCCACTTTGTGCTCCTGACCCCCACAGACCCCTGGCCTGGGGCCACAGTGCCACCTGCTCT
 CCAGGCCCCAGGTGCCAGCAGCACCCACGGAGTGCTCAGCTTCTGGTACCACCTCCATGGGCCCCAGATTGGGA
 CTCTGCGCAGCAGCCTCTGAGACGGGAAGGGGAGGAGACACCTGTGGTTCGCGGTGAGGACCCAGGGCAACCGCT
 GGCAGGAGGCCTGGGCCACCCCTTTCCACAGCCTGGCTCCCATGCCAGTACCAGCTGCTGTTCGAGGGCCTCC
 GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCGGTGCGGCCGGGGCCCCCTGCTGGGCCCCCTAATTACT
 GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCCTGGAGGCCAAGGTCTCTGGAGGCGGCAGGCCAATGCCTCGG
 GCCATGCTGCCTGGGGCCCCCAACAGACCATACCACTGAGACAGCCCAAGGCACTACATGGTGGTGGACACAA
 GCCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCCCTGGCCCAGCCTGCTT
 GTCTGACCTTCTGGTACCACGGGAGCCTCCGACGCCAGGCACCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC
 ACCAGGTGCTCAGCCTCAGTGCCACCGCGGGCTTGCTGGCGCCTGGGCAGCATGGACGTGCAGGCCGAGCGAG
 CCTGGAGGGTGGTGTGTTGAGGCAGTGGCCGAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC
 AGGACGGGCCCCCTGCCCTCAGCCAGGTTCTGTGATTTTGGTCTGGCCTGTGTGGCTGGAGCCACCTGGCCGGGC
 CCGCCTGGGCGGATACAGCTGGGACTGGGGCGGGGAGCCACCCCTCTCGTTACCCCCAGCCCCCTGTGGACC
 ACACCCCTGGGCACAGAGGCAGGCCACTTTGCCTTCTTTGAACTGGCGTGCTGGGCCCCGGGGGCGGGGCCCT
 GGCTGCGCAGCAGCCTCTGCGGCCACCCAGCCTCCTGCCTCCGCTTCTGGTACCACATGGGTTTCTCTGAGC
 ACTTCTACAAGGGGAGCTGAAGTACTGCTGCACAGTGTCTCAGGGCCAGCTGGCTGTGTGGGGCGCAGGCGGGC
 ATCGGCGGCACCACTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCCAGATCGTGTGTTGAAGCCA
 CTCTGGGCGGCCAGCCAGCCCTGGGGCCCATTGCCCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTGCCAGC
 AGCCTGCCCCCAGCCCGGGGAACACAGCCGCACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGCCCTCCTATTGC
 TCATGCTCCTGGTGTGCTGGGACTTGGGGGACGGCGCTGGCTGCAGAAGAAGGGGAGCTGCCCCCTCCAGAGCA
 ACACAGAGGCCACAGCCCTGGCTTTGACAACATCCTTTTCAATGCGGATGGTGTCAACCTCCCCGCATCTGTCA
 CCAGTGATCCGTAGACCACCCAGACAAGGCCCGCTTCTCACGTGACATCCAGCACTTGGTCAGACCCCTAGCC
 AGGGACCGGACACCTGCCCGGCCAGGCTGGGACAGGCTGCAGGTCTCAGGATATGCTGAGGCCTGGGCGTTCCC
 TGCCCTGTGCTGACTCTGTTGCTCTGTGAATAAACACCTGGCCCATGAGGGCCGCCCAAAAAAAAAAAAAA
 AAAAAAAAAAAAAA

FIGURE 518

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
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GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALLEGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETLTLWQSTGPGWPGW
QELAVTTGRIRGDFRVTFSTRNATHRGAVALDDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGWSRNRHAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPGTPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPRAPAPQPLPPSSRLQDSCKQGHLAGCDLCPPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRQWRRVSAQESQGSSAAAAGHFLSLQRAWG
QLGAEARVLTPLLGPSPGSCSELHLAYYLSQSPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALLSRPQVPAAPTECLSFYHLHGPQIGTL
RLAMRREGGEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTMALDD
VAVRPGPCWAPNYCSFEDSDCGFSPGGQGLWRRQANASGHAAWGPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLTSKEHRPLAQPACLTFWYHGSRLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMVDVQAERAWRVFEAVAAGVAHSYVALDDLLLQDGPCPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPQPPVDHTLGTGTEAGHFAFFETGVLGPGGRAAWL
RSEPLPATFASCLRFWYHMGFPEHFYKGELKVLHSAQQQLAVWGAGGHRHQWLEAQVE
VASAKEFQIVFEATLGGQPALGPIALDDVEYLAGQHCQQPAPSPGNTAAPGSVPAVVGSA
LLLMLLLVLLGLGRRWLQKKGSCPFQSNTEATAPGFDNILEFNADGVTLPASVTSDF
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

Transmembrane domain:

Amino acids 1075-1092

N-glycosylation sites:

Amino acids 203-207;281-285;339-343;756-760

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 514-518;1100-1104

N-myristoylation sites:

Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;
523-529;540-546;678-684;707-713;791-797;870-876;921-927;
937-943;954-960;1036-1042;1071-1077

Amidation site:

Amino acids 1093-1097

Cell attachment sequence:

Amino acids 191-194

FIGURE 519

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAACATCAGCTCCTGGCATCTGTAAGGATGCT
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT
CTCCTTTTCTTCCCTGCCTAGAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTGTCTACCAGACCTTCTGTGACATGACTTC
TGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCAT
GCAGCATTTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTTCGTTTCAGTTCCGGGTGTTTAA
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAAGTTACTGGCTGTAACTGAGCA
TCACTGCATCGGTGGAGGAGGGTTCTTCCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC
CGCCTTTGACTGGGATGGATATGGAATCACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA
GGCGGCTGTACTCTTGTTCATAGATTGAGACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA
ATCACATCAATTTGCA

FIGURE 520

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
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HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGLIYQKYPVKYRSGKWCNDNGPAIPVVYDFGDAKKTASYYSYGQ
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSADFWD
DYGTHVKSSCSREITEAAVLLFYR
```

Important features of the protein:

Signal peptide:

Amino acids 1-26

Glycosaminoglycan attachment site:

Amino acids 86-90

N-myristoylation sites:

Amino acids 23-29;88-94;127-133;136-142;265-271

FIGURE 521

GATCAGTGTGTGAGGGAAGTCCATCATGAGGTCTGACAAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCCTTCGTTAATTGACTACA
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG
ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAATGATTTTTTTGTTGAAA
TAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA
ACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAAAC'TCCAGCTCCACTTTCCCTATG
TACCTGTGCCATGACAGGACTAACAGACAGAATGACCTTTCTGGAAGAGTAAAAAATTCATGCTTTTCAGTTT
TGTTCCACTTCTGGATTGAGGATTACGACTATCATTTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCA
CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCCTCAAC
CATACCAACCTAAGTTTGTGAGTTTGTGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA
ATTTTGTCCAGAGTTGAGGGGAAGATGGTATTGTGGTGTTTTCTCTGGGGTCACTGTTTCAAATGTTACAGAAG
AAAAGGCTAATATCATTGCTTCAGCCCTTGCCCGAGATCCACAGAAAGGTGTTATGGAGGTACAAAGGAAAAAAC
CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAATGATCTTCTTGGTCATCCCAAAACCA
AAGCTTTTATCACTCATGGTGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAAGCTTCAAAA
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCCCTCTATAAAGAGAATGCTATGA
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCAGATCGAGCAGTCTTCTGGATCGAGTTTGTCTATGC
GCCACAAAGGAGCCAAGCACCTGCCATCAGCTGCCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA
TTGGGTTTCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTTCTGTCAAAAAT
TTAATAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAAATTCAGAAAGACCTGATGGGGTAATCCTG
TTAATTCAGCCACATAGAATTTGGTGAAAACCTTGCTATTTTCATATTATCTATTTCTGTTATTTTATCTTAGCT
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTCTTTCTGTTGATTTTCTTAGGTGCTTT
ACTCTCTTCTCTCATTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA
TGATGTCATTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCTGGTGTGCGCCCAACAC
ATGGATATAAAGAGGTAAAAAATTAATTCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTCTATGA
GATTAGCTGGCTATGAGAAACATAATGATGTTTTCTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGCTGTATTTCCATAGAC
CTCATCTAGATGTGATGGCCTACATTTCTGCCATCACTCAACCAATACCTTTTCTGTTTTCTTGATGATAAAAA
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTCTCACATAGAGAACATGTCAGTAAGAT
ATTCAGGTGAACAGATATTTTTGGGATTAGTAACTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT
TTATTTGATAGTACACTTAAAGAAGATTTATATGTTTATTCTTTAAAAATGATGAATACTCATAATCTTATCTC
TATAATCAAAAGTATAATTTACTGTAGAAAATAAAGAGATGCTTGTCTGAAAGTAAGATCAGTGAAGTCTTT
TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC
CTGCATAACAAATAGTATTATATATTAATATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGAATA
ATGTTTACACTAGTAAGCAAAATATGTTAATCTTCTCATTTTTTTACTGTGATATAATCTTAGTGATATGCCTATT
AATAGTTTTTAAATAAAATAAATTGGCTTATCTGGCTTTTTGAAAATTTTGAATTTCTTACAGATGTTGATTAGGTA
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAATAAATAAGTATTTTTCTTGTGTATGTATACA
ATAAATATAAATAAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTTA

FIGURE 522

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
><subunit 1 of 1, 527 aa, 1 stop
><MW: 60284, pI: 8.31, NX(S/T): 3
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PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDDFFVEIRGT
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLT LRISVGGNMER
SCGKL PAPLSYVPVPM TGLTDRMTFLERVKN SMLSVLFHFWIQDYDYHFWEEFY SKALGR
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED
GIVVFSLSLSLFQNVTEEKANIIASALAIQPKVLWRYKGKKPSTLGANTRLYDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVP MVGVPIFGDQLDNIAHMKAKGA AVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSA AHD
LTWFQHYSIDVIGFLLTCVATAIFLFTKCF LFSCQKFNKTRKIEKRE

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domain:

Amino acids 489-510

N-glycosylation sites:

Amino acids 131-135;313-317;518-522

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 67-71;340-344

Tyrosine kinase phosphorylation sites:

Amino acids 122-131;136-144

N-myristoylation sites:

Amino acids 19-25;276-282;373-379;377-383

Amidation site:

Amino acids 338-342

FIGURE 523

GGCTGCGGGGTCGGCACGGAAGATGCACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG
GGGGTGGCTGGCCCTTGCTGTCTCCTGCCCGGGTCTTGGTCCAGGCCCTGAGCTACCTGTG
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG
TGTTTGGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAACTGGAGGCTCCCCA
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTGGGCCCTTCGACTCTTGGAGGCCCTGCT
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTTCTAGCCTCAGACTTCACAGATATT
GTGCCAGGGGTGAGCACCCTGTTTTCTTGGTCTCACTCTCCTGGGCACTGGTGTCTTACACT
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCCGCCCTCTTCTGCCAG
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTGCTGAGTCTGGTTCGTCTTACAAAGCC
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCCACTGGCTGGTGATGACATTCTGGCTTGT
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GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG
TTCTACATGGTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTTCTCCAG
GGGCGATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTTCTGATTGGCAGT
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAAATCCACAGACATCTGGCAGGGCTGC
CTAAGGAAGTCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGCC
ACAGATCTAGCTGGGAAGAGAACCGAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA
ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG
GTTGCTGTGGAGGACTCTTCTCCTCAGTCATCACCCTGGCTGTGGGTGAACTTGCCCTAAAA
ACAGGAAATGTGTCTAAGATCAATGCCGCCTTTGGAGATAACAGTCTTGCCTATTGTCCACCT
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCCAGCAAGAGCTC
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA
GCAGAGGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA
GCACCTACCCAGAACCCAGCAGCCACGCAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT
GTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCCAGCCTGCA
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC
TCAGAGCTAGAGGAGCCGCTGGAGCCCAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG
TGGGTGTCAATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT
GAGTCTATCCAAACGGAAGTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC
TGAACACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT
GAGAAAGGAAATCCCACTTCTGACACCTGTGTCTTGGGCACATCACTGTACCTCTGAATCT
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAACA
TCACAGACCCCAACCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATTC
CAGTCAAAATTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTGTCTGTG
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCTATTTTATTTGAGGTTCTTGTTACAATT
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAATATATTCTAACTGTATTATGTTA
TGAAATCTCTTGGTAAGATAATTTGCATGCTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA
ATAACTAACATAACTGAAAGTGCAAATGTCA

FIGURE 524

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLLWGWLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMHLHLLQLGVWKRHWDAALTSLQKELEAPHRGWLQLQEADLSALRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFVWFVAGAHWLVMTFWLVAQQSDIIDSTCHWRLF
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMMLLENIILLLLATDFLQGASWTSLQTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGLRKSCGIAGGDKTERRDSPRATDLAGKRTE
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTQVAVEDSFLSHHHWLWVKLALKTG NVSKI
NAAFGDNSPAYCPPAWGLSQQDYLQRKALSAQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAATQGEPTKEGADAVSGTQKGKTGGQQRGEGQQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRRLGKSSPAQPASHPVGLAPFPDTMADISP
ILGTGPCRGFCPSAGFPGRTLSISELEEPLEPKRELSHHAAGVWVSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

Transmembrane domains:

Amino acids 35-50;269-287;293-313

N-glycosylation sites:

Amino acids 416-420;467-471

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

N-myristoylation sites:

Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;
390-396;473-479;529-535;536-542;558-564;603-609;
643-649

Amidation sites:

Amino acids 354-358;568-572

Leucine zipper pattern:

Amino acids 112-134

FIGURE 525A

AGTGCCCTCTGTCATTTAATCTCCACGGAGTCCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC
AATCGTTCTGTTAAGACTGTCCTTGGGTCCATTATGTGAGCAATGAAATCGGTGCTGCCATTACTAAACCCCTTACT
GTGTGCTGGCATTGTGTATGCATGCATGTGTGTGCGTGACACGTGTGTGTTTGCCTGTACATGTGCATGTGTGTG
TTGTGTGCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCCAACCCAGGAGGAGACTG
TGCCTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAATGCACGTTGCCTTCCAGTTCTCTG
TGTGACCTTGGGCAAGTCACTTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG
ACCATTACATATGAAGAGAAATGTGTGTGCAACATTTCAGTTAATAATCACAAGGTGGAGGAGTGCCTGCTCAGA
CCCAGAGCTGACACAGGGAACCTCTCCAGAAGGCTGCAGGGCTTCCCTCCCAACCCCTCCAACGGGCCACTTGCTG
AGCCCGTGTATCTGTTTCAGTGGAATGCCAATTATGAATTCAGTGCTTTCCTTGCTGAAAGAGAGGCGTGGAA
ACTCTGTGCCCCAGCTTGGTGCAAAGCCCCCTTGTGTGCTATCTTATTGACCTCCCAAATAGCATGGTAAGGTCA
GTACTGTCACTTCCCCCACTTTGAAGATGAGGAGAGCACAAATCTAGATGGAAATGGAGGTCACGCAGTGGAAA
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTCTTCCATTCCACGCTACGCTTGAAGCTCAATCTCTC
TTCCTGGTTGATTCTCCCCACTTCCCCACCCCCAGATATATCCCATCGCTGCTTGGTGGACAGTAGCCATGACTG
GGTTTTGGTAAAGGTTGCTGAATAATCAGGCTGCTGGTTAGTTTTACATTTTACCTTTTCCAGTGAAATGGGGC
CCCATGAAAAAGGCAGCTCAAGTTGTAAATTACTCAAAGGAAGGACAGAAAGGTCTTCTGTTTGCACCTACCCTA
AGGATTTGGGGTAGACACTGGGAATTTACTAATTATGAATTCAGTGCTTTCCTTGCTGAAAGAGAGGCGTGGAA
TCAACGCTGAGTGAAGGCATCAAGTTTAAGCTGCTAATTACTTCTGATCATGCAGAATAAAAGCTACGTCCCTT
GAAATACACCAGGCAGCTAAACATAATCTTTCGCTTTCGCTAGTGTGGTTAAGGAATCCAGATGTTACTGCAAT
AACCCTCCATAAAACAAAAGGAACACCCAGCTGTGAGAACTGGCTTCTCAGCATTCGTCCCAGCAGAGGCTCTTC
CGGGGCCAGCCCTGGAAGAACCATCAGGGTCTGATGGTTGCCCTGTTTTCAGCACAGCCCTTATTGGCAGGCAG
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACAACTTCTGACAGTGAACAGGAGTAAACATG
GGACCCACCCGAAACCTTTGTCTGTTGACTTCTTAGCAAAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCGGGTAT
AGGAGACCATGACTTGAGCAGACTGATATAAGTGAATGCAACATATTTAGATGGCACAACCTTAATTTAGATTT
ATCAGTGCTAATATAGAAAAAGCTAGTATTTATTGGGGCTTATTAGATTTTTAGTCTGAATCCTCACAACCTTACG
AGGGGGTTCGTTTTACAGACTATGATCTTGCATGATTTCCCCAAAGATGCTCATTAAGTATATGGTGAAAGTAGA
ATTTGAATACAGAAGACCTGGTTCTGCTACTTTCTGTGTTTCTATTTGGTTCAAACAGCCCTTCTTCTTTCAA
ACAACCTTCAGTGCAATTCATGGTTTTGGAAAATAAATCTGATTTTGAATTCAGACAATAAGTGCATTTTTAATG
TTTTATTCTTTATCTTGAAAACTGATATATTTATGAAATGATATGTGCTCACTCAGTGTCAACACTTCAAACAA
CACAGACAGTACAATGACAAATTGGAGATCAGCTCTAATCTCGGCCCCCAATTTAATGCAATGCTGAATATCTT
CTGAACATAGTCCATCCCACACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGGACTTCTGCAG
TCAAGAGAGCTGGGAAACTCTTGGACAGTCACAATGTGCATTTGGGTATTAAAGGCTCTGCAAAGTCTGCACCA
AATAAACCCCTTGGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA
ACACAGGTTGGCATTCTTCTAGAGAGTGTGCTGTGAAAACACTGGTCTCACAGCACCGTGCATTCATCCAGCA
GGTATTTACCAAGCAGGACTTTGGGCCAGGTCGGTCTAGGCTCTGCAGGTGGACCAGCCCTGACCTCCA
TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCATTGAGAAAACGAAGAAACACACAGGTACTTTTCAGATG
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGTCTGTTTTGAGACAATCTTCTCGACAATGAGATA
GAATGAACCATGCAAACCTTTGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGAAAAATCCTTTGACATATAT
ACATACAAATAAAGATACATGTGTATAATTTTATGTAATTGACATCACATTATATGCTGGCACCTGCCTTTTTTG
CTTAATGAAAATGTCAAAGGTAATATTACCAATCAATCAATATATTTCAACCATCGTGTTAATTTCTGCAGAGCA
CTTATTCAGCACATACTGCATTTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT
TCCCCTTCTGAAATGATCTCCTTAGAATAAATTTCCCCAAATGTATTGCTGGGTTCAAAGGCATGAACATTTTA
CATTTTTATACAATAATGTCAAACCTACCTTCCGGAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA
ATGCCCATTTTCTAAATGCTTACTATGACTGGTTTCCAACACATTTTAATTCTTGTTCATCTGATAGGCAAA
AAATGATATTTAATTTTTATTTGATTGATAATGACCTGAACGTGCCATTAGCCTTTTGCATGTATTCTTTTAT
GAAACATCTGTTCTATCCTTCGTCAATGTTCTCTTCATATGTTAACTTTTCTTATTGATTTGTTAGAGCACTT
TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGCTTTAGTTTTGCTTATCAAGTTT
AAAGCCATTACAGAGATGTTGTAATGTGTATGTTGTTAAATTTATGCTTATTTTGTGTTTTCTGATGCTCATAT
GTTTAGAATGGTCAAGCAATCCCAACTTATGATTACATAAATATTCTCCCATATTTGCTCTTAGCATTTTTTTTC
TTTTTCATGTAACCCCTTGTCTTTTCAGGAATTTACTTTGCGGTAAGAAATGGGCTGGCTTCCAGTTTTATGTTTC
CCAAATGGTGATTACAGCTGTTCCATTTCCATATTTCTCCCTTATTAGAAATGACCACTATATTATGTTCTAAAATA
TCTGCGTACTTGTGTCCCTTCCATATAATCTCAGTTCATCTCTTTGAGCTATCTTTTGATTCTTTTTCAAACCAC
ACTGCTTTACTGAACGTGCATCATCTTATACATTTTAAATACTCAGCAAGACAAGTTTCTCAATGCCACTCTTTT
TCAGAGTTTTCTGGTGGTTGTAAGATGTTTATTCTTCTGGATAAACTTTAGAAATCACTCTTTTTGTCCAAGGTA
AAATATATCCCACTTGAATCATACTGAATATACAGACTAATTCAAGGAAAAATGTATGCTTTTATGCAATTGA
GTCTTCTTATCCAATAAAAAAGATGAATTTCCATGTATTGAAATCTTCACTGAGACTTATTTTTGGCTTTTCA

FIGURE 525B

CATGTCCTGCAAATGTATTGTTAAATTTATTTTTAGGTATTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA
TTGTTTTAATAGTTTTTCTATTATTTTGGGTTTTCTGGAATACAACCTTATTATCTACAAATTATGATTGTTTT
GCCTTTTCCAATGTTCACTAACTGTTTTTATATTCTTGTCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT
GCAATACTAATGA

FIGURE 526

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLPLLNPYCVLAFVYACMCVRAHVCVCVYMCMCVLCACVCTCRKKVMCGNGEFQ
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP
```

Important features of the protein:

Signal peptide:

Amino acids 1-28

N-myristoylation sites:

Amino acids 80-86;94-100

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 13-24;34-45

FIGURE 527

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCCTCTGAACTTCCTAAAGATATC
AAGATGATATCACCAGACTTGCCCTTTTGGACAATTGTCCTTGATCATAGTTAGTTGGACAACCT
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA
GCCAGCTTAACAACCTTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACTTACTAACATGGATTGTATTACTCAGC
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAACTTAATCCTGATCCA
TGTAACCTTTGGCATTTATCCTTATTCCGACTATGGCAATTCTTGGAATACTTACACTGTT
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCTCTTTTA
CTCCATGCATTATGCAACTTTATGTAAGATTGGACTTAAGGAATGATGAAGATAATTTATGTG
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA
GAAGACAAGTCTATTTTACAATATTGAAAATAGGAAATTAGTTTTGTAATGTTTGAGGGAAG
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT
ATCAACTGTAAA

FIGURE 528

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLNLRYYFK
LNPDPCCKPLAFILIPTMAILGNTYTVSIKSSKLLKTTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM
```

Important features of the protein:

Signal peptide:

Amino acids 1-25

Transmembrane domains:

Amino acids 91-108;128-143;167-186

N-myristoylation site:

Amino acids 141-147

FIGURE 529

GCGAGCCGGGTCCCACCATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA
AAGTTAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT
TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT
TTGTCTGATCCAAACTATGGGGTCCATCTTCCGGCTGTGAAACTGCGGAGGCACGTGGAGATG
TACCAATGGGTAGAAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG
ACGAGGTATTCTACAACACTGAATGGAGGTGAGAAATCATCAACAGCAAAAACCTTCGACCGA
GAGATTGGCCACAAAACCCCAGTGCCATGGCAGTGGAGTCATTCATGGCAACAGCCCCCTTT
GTCCAAATTGGCAGGTTTTTCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC
CTGAGCCTATCCAAGCTGGAGGACCCTCATGTGGACATCATTGCGCGTGGAGACTTTTTCTAC
CACAGCGAAAAATCCCAAGTATCCAGAGGTGGGAGACTTGCCTGTCTCCTTTTCTATGCTGGA
CTGAGCGGCGATGACCCTGACCTGGGCCCAGCTCACGTGGTCACTGTGATTGCCCGGCAGCGG
GGTGACCAGCTAGTCCCATCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAACTAAGGAGCAACTCCATGAAGACCTGGGGC
CTGCGGGCAGCTGGCTGGATGGCCATGTTTCATGGGCCCTCAACCTTATGACACGGATCCTCTAC
ACCTTGGTGGACTGGTTTCTGTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCCTGGCGGCTGGCTGGCTCTTCTACCGACCC
CTGTGGGCCCTCCTCATTGCCGGCCTGGCCCTTGTGCCCATCCTTGTTGCTCGGACACGGGTG
CCAGCCAAAAAGTTGGAGTGAAGAACCCCTGGCACCCGCGGACACCTGCGTGAGCCCTGAGG
CTGGTTGTACAATGCCCACGCCTGCCTGGCTGCTTTCACCTGGGAGTGCTTTCGATGTGGGCA
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTCACGTGTTGTGTCCATAGCTTTAGTCT
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCCCAACTACTCTCACA
CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC
TGTCATATTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG
TAGCTGAATAAGGGGTCAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG
GTGCCTGTGCTATAAATGAGTTTCTTCACATGAAAAACACAGCCAGCCCCAAGATGACTTATCT
GGGTTTAGGATTCAATAGTATTCACCTAAGTCTTATTACATGAGCAATTTTCATCAAATCTCCA
AACTCTTAAAGGATGCTTTCGGAAAAACACGCTGTATACCTAGATGATGACTAAATGCAAAATC
CTTGGGCTTTGGTTTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAAGTGTTCTTA
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG
TATTTTTTATTAAAAGTTTTGTAATAAATTTCTAAATTATCA

FIGURE 530

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of 1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTSTRREHVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIIFTNEGRALKT
ATSLAEGLSLVVSPDSIHVSAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVKLRRHVE
MYQWVETTESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLLHHGDFSAAEEVFHRE
LRNSNMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFAFCVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKE
```

Important features of the protein:

Transmembrane domains:

Amino acids 34-53;365-388

N-glycosylation site:

Amino acids 4-8

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 140-144

Tyrosine kinase phosphorylation sites:

Amino acids 99-107;220-227

N-myristoylation sites:

Amino acids 35-41;93-99;310-316

Cell attachment sequences:

Amino acids 221-224;268-271

FIGURE 531

AAAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGAGAGAAATGGGCAATAA
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTTCCCCCCTCTTT
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAAGTGCCTGGCTATTTTCAGA
TAAGACTTCACTGAGTGACTGTTTCAGCCCATGATTTACCCTGCAGTTTAAACAGGCTCAGGAAT
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG
GACCATTTCTGCCTTTTTTCACTATTACATCCCCCGCCTGTAGCCCAGCCTGCCATACAGTAGA
TACTCAATAAATATTTGCTGAATGATAACCAATAA

FIGURE 532

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758  
<subunit 1 of 1, 100 aa, 1 stop  
<MW: 10316, pI: 8.52, NX(S/T): 0  
MGNNCYFKSLGAVILPSASATFVVLCVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA  
NCLAISDKTSLSDCSAHDLPCLTGTSGIRSHQLSAGHLGL
```

Important features of the protein:

Signal peptide:

Amino acids 1-47

N-myristoylation site:

Amino acids 58-64

FIGURE 533

CGGGGTGTACGAAAGAGAAACCCGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAG
CTGAGCCCATGAGCTCCCAGAGCTAACCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG
TAGTCCCCATCCTGGAGGGGCAGGCTCTGCGCATCTGCTCCTGGCATGGCGCTGCGGCACCTC
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG
CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCCAGGCGCAAGTCTGTGTGGT
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA
ACCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCC
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCTCC
CTCTTCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTAC
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCTCAGACGTGGGGTCTGCAGGAAAG
GAGGACCCACCACGACAGGGCAGACCCCCAATACCTGCTCCTCCTTGAAGTCCAGCTCCACCC
GAGGACAGACGCAGCCGGCCTCCGCCAGGCCCTCCTGAGCAGCCATCGCTTCAGTGGTGCTGG
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTGAGGCGGGAGCGGCCCT
GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGAGGCCCGTATCAGCAATGTCTGACCTGG
AGGCCGAGACCACGCCACGCACTTGCGGGCAGGGACCCGGAGGCCGACCCCTTGCGGGGAACC
AGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCCTGGGCACAGCCTCGGCTCTGGGT
CCCTCCGCCTCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCAC
AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC
CTTGGGGGGTCCGGGCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC
CAGAGCCCACAGCGGGCAGGACTCCTCCAGCACCACCACACCCAGTGGCCCCGAGACCCCTCTG
AGAACAGTGAGGCTGGTCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC
CTAGGAACCAGCTGCCTGAGACCAGGGTGCTCTGGGCTGTCTCCCGCGTGGCGGAGACCCC
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG
CAGAAATTCATTGTGCAGAAAAGTCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC
CCCATGCCTGGCTGATCCCTGCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCTCCCGGAGTTCTTG
GAGAAAGGCGCCGCTCGTGGCCGCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 534

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMентаQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPGEAAAMIPPPQSSDVGSAGKEDPPRQ
GRPPIPAPP
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

**N-myristoylation sites: **

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

FIGURE 535

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA
GGACTGCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCCATGG
CCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC
TGGTTGTGCGTCTTGTAATGAAGTGAATTTCCCATTTGCTACTAAACTGCTTTGGACAACCTG
GTACAAAGTGGATAACCATTTCTCTACACATACAGGCGGCCCCCTTCGAACTCACTATGGATACA
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACCT
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA
TGAACAATGCCCCACCAAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTTCGAGTTG
TGTCCCATACCAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAGTGAC
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCTGCCCCACCACAAAAGGA
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGAAA
TTGTGGTATGTGGTATGTAAATATTTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGT
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

FIGURE 536

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783
><subunit 1 of 1, 210 aa, 1 stop
><MW: 24022, pI: 9.51, NX(S/T): 1
MACILKRKSVIAVSFIAAFLFLLVVRLVNEVNFLLLLNCFGQPGTKWIPFSYTYRRPLRT
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPT KGYEEDVG
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKT VGIY
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE
```

Important features of the protein:

Signal peptide:

Amino acids 1-27

N-glycosylation sites:

Amino acids 148-152

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 6-10;191-195;201-205

N-myristoylation sites:

Amino acids 41-47;87-93;91-97;167-173;178-184

FIGURE 537

GTTTTATTGACAATACATGCATCATATCTTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCTTGGGAGCCTGGGGTTGGCCT
TCTACCTGCCTTTGGTGGTGACTACACCTAAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTCACCTGTGGCCTTGGCTATAAGG
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCATTCTCATTTGGCAAGGAATTTGAG
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTTGGACAGGAAGCTTCCGGTTCACCTGGAGA
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCTTTCAAGCCAACCTCCCAC
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG
GTAAAAAAGCTTGAGACTTGTCAAGAGGCTCTATTTTGGGTTGAGGGTCTTCCCTCCTAACTTG
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGAAGGAAGGTGGCGTCAGCC
TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTGGTGAGGATTGTCCTCTGTGCG
CTAAGGGGGGGCCTGCAGCAGTGAAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT
TAGAGGGAACACTCCCACAGCCAAAAGATGAGTGGGAGAAATGGAGGGGACAACTCCTGGG
AGCTATGCGCAGTAACCTAACTTCCTTATGTCCCATGGATCTCTTCTGATCTTCCCTGCCCA
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCTGGGAAGAGTTCTAAGAAGCTTGCA
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCCTCTTCTGAGCTGT
GTATTCATGTAGAGGGATGTATTCAGCCTTTTGTAGTGAACATTTTTTTTCAATAAAAGTAATT
CACAGTAA

FIGURE 538

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPLVVTTTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDGVRRKCQTQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFRFT
WRLARGVISTDDEVFKPFQANSHFVKFKYAQEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYSKPHHPKWKKKVASALGIGIAIGVGGV
LVRIVLCALRGGLQQ
```

Important features of the protein:

Signal peptide:

Amino acids 1-30

Transmembrane domain:

Amino acids 225-244

N-glycosylation site:

Amino acids 45-49

N-myristoylation sites:

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

FIGURE 539

GCGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGCATGAATTCAGCCCAGCGCAC
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCAGACAGGACTATGAAGAGCTAGAA
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTCTTCGTCAGCTGACAAAGACATCA
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA
ACTGATGTTTCAGAAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAAGATAGTCTCCATGAGGACCATGTCAATATAC
TTATTGATGTATCTCTAGTACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT
GTGGAATTAATTAATAA

FIGURE 540

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPAVLSTRQDYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAQKHQATINFLKTEVE
RKSKMIRDLQNEDSRKRPRDLQWKIVSMRTMSIYLLMYL
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-myristoylation site:

Amino acids 54-60

FIGURE 541

[illegible]

FIGURE 542

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936 .
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQQLGTDGPLVTDPEETHKSTKAAHPTDDTTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTSKGKCRQLSRLCRNRCR
```

Important features of the protein:

Signal peptide:

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

FIGURE 543

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTGAGAGCAAAACC
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCCAGTCCC
GCTCCGCCTTTGAAGGGTAAAACCCAAGGCGGGGCCTTGGTTCTGGCAGAAGGGACGCTATGA
CCGCAGAATTCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA
ATGTGACCCTGAAGTGTGAGGCTCATTCCAGAAATGTGACATTTGTGCTGCGCAAGGTGAACG
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCTTCACGGACC
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTTGAAGCTCCCT
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCATCTTCAGCTGCATCTCCATCCTTCTCC
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA
TGGAAGGGTATCTCTCTCGACGGCAGACCCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG
CACTGAAAGTGTAGCAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT
TAAGTTTCTCGTCTTA

FIGURE 544

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTCLKCQAHSQNVTFVL
RKVNDSGYKQEQAENEAEPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSEESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV
```

Important features of the protein:

Signal peptide:

Amino acids 1-16

Transmembrane domain:

Amino acids 135-153

N-glycosylation sites:

Amino acids 44-48;55-59;64-68

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 171-175

Tyrosine kinase phosphorylation sites:

Amino acids 61-69;87-95

N-myristoylation sites:

Amino acids 12-18;203-209

FIGURE 545

GGCGGCCCCGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG
CTCTCTCTCAGCCGCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGC
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG
GGCGCAGCATGCCGCCACCAAGTGCAACGAGCCGTCACGGAGCTCAGCATCACCTCCAGGGG
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCAAAGCTCTTCAT
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTATGTCCATCCCCAAGGGGAACTCAGC
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA
GAGCCTGGAGGAGCAGAACGAGGTATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC
TCTGGTTTCGCGCATCGGCTCCGTCAACATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT
GGGCTACGTGGACCCCGTGGAAGCCGGCAGGTTTTCGGACAACACAGGTCTGGTTCGGACACCA
CATCCCTCCCCATCCGCAGGATGTGGAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTTCAGCCTTAGCCCATTATAAACTCGTTTAC
ATCCACCCTTTTCATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCTCATG
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTTCATTGCTTCATCGCCAAGTGTACTGAGACC
ACCCTGGACACCCTGCTTTTTTGCCACAACCTGAGTACTCGGTGGCACTGCCAGAAGCCCAACCC
AACCCTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCCTAAACCCTAGAAATCCTCAGTGACA
AAGGCTGTCCTGAGGTAGGAAA

FIGURE 546

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517

><subunit 1 of 1, 458 aa, 1 stop

><MW: 51778, pI: 7.81, NX(S/T): 2

MMLIPMASVMAVTEPKWVSVWSRFLWVTLLSMVLGSLALLLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSKVKKVMSIPKGNSALRRVMEETYYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRLGY
VDPVEAGRFRFTTQVLVGHHPHPQDVEKQMQUEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLLMNLILMQAGYPPITIRKEQRSDYYHVLEAANECDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQPNHSGFKETLPVKP

Important features of the protein:

Signal peptide:

Amino acids 1-46

N-glycosylation sites:

Amino acids 275-279;446-450

Tyrosine kinase phosphorylation sites:

Amino acids 216-225;217-225;244-232

N-myristoylation sites:

Amino acids 35-41;235-241;266-272;368-374

Amidation site:

Amino acids 119-123

FIGURE 547

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG
CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG
GCATTTCCACAAGACGCCAAGATGGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC
CTCCTGCTCTCAGCCTCAATCCTGGTCCTCTGGATGCTCCAAGGCTCCAGGCAGCTCTCTAC
ATCCAGAAGATTCCAGAGCAGCCTCAAAGAACCAGGACCTTCTCCTGTCTAGTCCAGGGTGTCTC
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA
GCTGAAAAGAATAAGGAGCTGCCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC
ACCATCATTTGGATCTCTTGCTGCGGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG
ACAAGGAAGTGGAGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGGCCAGGGATCTCTGTCC
ATCTTGCTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACA
GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCC
TCTCCAGTCCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCCGGCCCCCTG
CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC
CCCGACCTGCCCCCTACTGCCAGCTGGTGCCAACCTTCTGATGGGTCTGGGCCAGGCCAGC
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG
GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA
GGTGTCTTGGCAGGGGGACAGGAGACTGTAACAGGCCCAGGTCTTGTGCAGCCCCCTGAATGC
ACGCCCCCTTCGGTCTGTTCTTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG
GCTCTGGCCCCCTTCCATGCCAAAGTCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCTTAGGACAAGGCAGACACCCACCATGCGG
GCCTCAGGTGGCAGAGAGGCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG
GTGACCACGGCTGCTGGACCCCTTCCCTGTTTACGGCAGGCCCAGCCCCCTCTCAGAACCTGCTG
CCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT
CTCCACCCACCCAGCACCCGTCCCAATGTGGCCTCAGCTTGTCTCTCCCTTCCCCAACT
ATGCATTCAATTCAGCAATAAATGAGCCTTTGCTGCA

FIGURE 548

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIPMGTOGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLSVQGVPDF
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRAQPTDSGTY
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPTNAGILAATIIGSLAAGALLISCIAYL
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGHDAGDNNI
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEPENHQYQQDLLNPDAPYQCQLVPTS
```

Important features of the protein:

Signal peptide:

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

FIGURE 549

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA
 AGAGCTTCCTTGTTTCTGGAATGTTCTTTCCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC
 TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCCTCACCCTTGCTCTT
 CACCAGCCCCCTGCTCCCCCTCTTCTCTTGGGGCTGTTGTGCTTGTGATACTTTTTTTTTTGT
 GTGTTTGACACACATCTTCTTCTCACCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC
 TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCACTGGGGTGGGGGTGCTGCTGGCA
 CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCTATGGGACACTGCACAGTACACC
 TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGCTCCCTGCGGTGTGTGTTG
 GTTGGGATCCTCCACAGTGACAGACGGTGCCTCTGCCCACGTTTCCACACAGCTCTTTTGCT
 TGTGGAGCTCACCCTTTTGCAGAGAGCTCATTTCCTGCGGTCTTTGGCCTGCAGAAGTAAAA
TGAGGGGTGGTGAATTACACCCTGCTGGTTACACATGGAAACTCAGGAGTGAGAATTTGT
 GGAGACAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA
 GAAGCGGGGTGGGGCCTGCACACCGAGTCTTCCAGTGAGTCCAGTGATGCTCTCTCTCTTC
 TCCCAGTCACTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTAGTATTT
 GCGGACTTGAAGTCGGACGAGATGGAGCTGCTACTCAGCCTACGGAGATGAGACAGGCGTG
 CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGCTG
 GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGACGCTCTTCCAGCTGAAGCAG
 AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAGC
 AGCAGCTCTGTTCTGGAGTTCATGTGATGAAGTCTATCCCGACGTTTCTGTGGATATCTCC
 ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACAGCCATTTGAACCTG
 GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGGCTCTCGG
 CCGTCTGTTCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACACCCTGGGAAGC
 CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGACGTCACCCACGACCCCTATGAGTTTCTTCAG
 TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA
 TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTGTCATCAGACAAGGACTTTGATCCTGTC
 CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTGAGCA
 GAGTCTCCAAGCCCCACGAACCCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT
 GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG
 GCGTGTGGCCATCGTGTGAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG
 AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA
 CGTGTGGCTCCAGCCCTTGTTTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCCTGGGG
 TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTCTGTATCAGTCCAGTGTGTTT
 CTGTCATAGTTTGTGTCTCCCAGGCAGGCCATGGTAGGGGCCTCGCAGGGGCCATTGGGGAGC
 ACAGGGCCAGGCTGGGGTGAGGAGAGCTCCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA
 GGAGTGTGTTCTGCCTGCCCGTTACAGTGGAGCGTTCCGTGTCCATAAAACGTTTTCTAACTG
 GGAA

FIGURE 550

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVLMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSPTARAGPGQAWSLRC
VLVGILHSDRRRCALPTFPHSSFACGAHPFAESSFPCGLWPAEVK
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

N-myristoylation sites:

Amino acids 53-59;64-70;97-103

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 74-85

FIGURE 551

CGCCCTTAGCATGGGTTTCTGCCGAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCAT
 GACCCTGGCCCTGGGTACCTTGCCCTGCCCTTCCCTACCTGTGAGCTCCAGCCCCACGGCCTGGTGAAGTGAAGTGA
 GCTGTTCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCAGCCCGTGGCAATGTACACAGCCTTCTCTGTCTCTC
 CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA
 CTGCCCCGCCGTTGGCCTCAGCCCCATGCACTTCCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT
 GCCCACCTTGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATC
 ATGTCTCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCTCT
 ATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG
 CCTGGGCAGCCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCCCGCAACCTGCCCTTCCAGCCT
 GGAGTATCTGCTGTTGTCTTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG
 TGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACACGCTCCCAACCCCTGCATGGAGTGCCCTCGTCACTT
 CCCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCCTGGTGTGAAGGACAGTTCTCTCTC
 CTGGCTGAATGCCAGTTGGTTCCTGCGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAACTTCTCTACAA
 ATGCATCACTAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACCAAAA
 GAGGGTGTCTTTGCCACCTGTCTCTGGCCCCCTTCTTCGGGAGCCTGGTGCCTTGAAGGAGCTGGACATGCA
 CGGCATCTTCTTCCGCTCACTCGATGAGACACGCTCCGGCCACTGGCCCCGCTGCCCATGCTCCAGACTCTGCG
 TCTGCAGATGAACCTTCAACAGGCCAGCTCGGCATCTTACGGGCCCTTCCCTGGCCTGCGCTACGTGGACCT
 GTCGGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG
 GCTGCAGCCTGGGGACCTTGTCTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCCACTGCAGCAC
 CCTCAACTTCACCTTGGATCTGTACGGGAACAACCTGGTGACCGTGACCGCGGAGATGTTTGGCCAGCTCTCGCA
 CCTGCAGTGCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCTTCCGCTGACCGG
 TCTGCAGGTGCTAGACCTGTCCCAATAAGCTGGACCTCTACCACGAGCACTCATTACGGAGCTACCACGACT
 GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACCTTCAGCTTCTGTCG
 TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCCCACAACAACATCCACAGCCAAGTGTCCAGCAGCTCTGCAG
 TACGTGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA
 CTTCTTCCAAGGCCGTGAGCGGTTTGATCTGGCTGGACTTGTCCAGAACCCTGCGACACCTCCTGCCCAAAC
 CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG
 CCTCCACTTCTTCCCAAACCTGGAAGTCCCTGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCT
 GCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCTGTCGCCCGCGCTTCTTTTC
 CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC
 CCTGGCGAGTGCCCTGCAAATACTAGATGTAAGCGCCAACCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGA
 CTTCTTCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCA
 GGGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCTGGATGAGGCCCTCTCCTGGGACTGTTTTCGCCCTCTC
 GCTGCTGGCTGTGGCTCTGGGCTGGGTGTGCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTT
 CCACCTGTGCCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC
 CTTCTGTGCTTTCGACAAAACGACAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCGAGCTGGAGGA
 GTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCTCTTTGAGAA
 CCTGTGGGCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACGGACCGGGTCACTGGTCTCTT
 GCGCGCAGCTTCTGTGCTGGCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGTGGTGTATCTGAG
 CCCTGACGGCCGCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGGCCCCA
 CCAGCCCAGTGGTCAAGCGAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCACTTCTATAA
 CCGGAACCTTCTGCCAGGACCCACGGCCGAATAGCCGTGAGCCGGAATCCTGCACGGTGCCACCTC

FIGURE 552

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWFLKSVPHFSMAA
PRGNVTSLSLSSNRIHHLHDSDFAHLPRLRLNLKWNCPVGLSPMHFPCMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSHTNIMLDSASLAGLHALRFLFMDGNCY
KNPCRQALEVAPGALLGLGSLTHLSLKYNLTVPRLNPSSLEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSLSWL
ASWFRGLGNLRVLDLSENFYKCIKTALQGLTQLRKLNLSFNYQKRVSAHLSLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRY
DLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPNCTLNFTLDL
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHE
FTELPRLEALDLSYNSQPFQGMQGVGHNFSAHLRTRLRHLSLAHNNIHSQVSQQLCST
RALDFSGNALGHMWAEGLYLHFFQGLSGLIWLDSLQNRLLHTLLPQTLRNLPKSLQV
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAP
FSKAKELRELNLNLSANALKTVDHSWFGPLASALQILDVSNPLHCACGAAMDFLLEVQ
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMHLH
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVFDKTQSAVADWVYNELRGQLEEC
RWALRLCLEERDWWLPKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQR
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDN
YNRNFCQGPTAE
```

Important features of the protein:

Signal peptide:

Amino acids 1-30

Transmembrane domain:

Amino acids 818-835

N-glycosylation sites:

Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;
469-473;474-477;513-517;567-571;694-698;731-735

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 347-351

Tyrosine kinase phosphorylation site:

Amino acids 863-871

N-myristoylation sites:

Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;
563-569;607-613;695-701;794-800;929-935;945-951;
1010-1016

Amidation site:

Amino Acids 974-978

Leucine zipper patterns:

Amino acids 204-226;644-666;814-836

FIGURE 553

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGCGGGGTGTGTGTCCTCT
GTTAAGAGTGCTACTCGCCCGGGGTTGATCTGTGCATGCCACTCCTGGGTCAGACGGTGAGGT
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCTT
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATCATGGCATTGCTGGTGGACCGAGTGCGGGGC
CACTGGCGAATCGCCGCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCCCTC
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCATTTCGTG
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCAAAAGTCTGCCG
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT
CTGCAGAACAAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCCT
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCTTTGGAATGGTG
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT
GAATTACAAGTGAACCTCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAATATTTGGTCCCTGGTCA
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT
TATTGGATCATTTGGGAACACTTCACCTGTCACCTATAACATGTTCCGACACTTCAAGTTCTGC
ATTACTTTATTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA
AGTAGGAGTAAACTGGCACAACGTCCTTAAATGGGTTTTTTGTGGAGAAAAGAATGTTGTCCCA
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

FIGURE 554

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFPNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVFTNLSLQNNITIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVILNSYYDVKFNFLGMVFAALGVLTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFEPVFGEGGIFGPWSVSALLMVLLSGVIAFMVNL
IYWIIGNTSPVTYNMFGHFKFCITLFGGYVLFKDPLSINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP
```

Important features of the protein:

Signal peptide:

Amino acids 1-27

Transmembrane domains:

Amino acids 46-60;75-90;153-167;192-208;221-237

N-glycosylation sites:

Amino acids 43-47;92-96;97-101;238-242

N-myristoylation sites:

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

FIGURE 555

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG
 CAGGAATGTAAGCACTGTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG
 TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCCATGCCTGTTTTCTGGAACCAGTCCCTGGA
 GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC
 CAGGCAGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC
 AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGACTCTAACCAGGTTCTTCAGACCCA
 AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT
 TTTCTACGGGGGTCTCTGGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC
 CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC
 GCTCATGCCCCCTCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCAGATGCACC
 TACTGCCCTCACCACCTTGAACCCCCGGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT
 TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCGCTGCAGCGGAGTTACCCGTGTGGGTTCTCTG
 AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCCTAGTGCAAGTCAACCG
 GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTCGCCAAGACGAGTCCGACGCCCC
 GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT
 AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA
 GGGCGCACCCCCGTGCCCCCTCCCGCCGCTGTGCTGCGGTGGCCACGCTCTCTGGACTGGCCG
 CCTACCCTTGCCCTTGCGGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG
 ACAGTTGTGCGGCCGTGGGCAACTGTTGGTTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG
 TGATGTACCAGAGCGCGTCTTCCACCTGTGAGCCTTTGCCACCCGCGCCGCTGCTGCTGGC
 ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG
 CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCTCTGCACTTCAG
 GGTGGAGAATGGTCCAAATCCCACGGTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT
 CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGCAAGGACAGTCCTTCCAGCCAACCCAG
 CCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCCGGGCACCAGTGACCTGCCAGCCCCAGC
 CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCGCTAAGCTGCA
 GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA
 AAGGAGGGTCCATGTGTGCAGCCCACCCCTGTCTTGAGCCCGTCTACCAAAATAAAGTTGTAG
 TGATTCCA

FIGURE 556

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLGHLIDSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHRGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALT
```

Important features of the protein:

Signal peptide:

Amino acids 1-45

N-glycosylation site:

Amino acids 6-10

N-myristoylation sites:

Amino acids 97-103;144-150

FIGURE 557

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTCAGCATTTC
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTCACCAAGCCACC
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGTCTGCTCT
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTCATGGGGACA
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTGACCT
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG
TGAGGGGGGATGAAGGATAAGCCCATTTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTGACCATTCGTGAGTCTGTGTT
CCATACTCCACTGAGTGTGGGCACTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG
CTCATGTTGCCTTTGACCACCATTTCCTTAAGGAGAGCCAGCTGATTGCTGTGAGGATAAGAGC
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG
TATTCCCTTTGGAACCTCCCATTCTTGTTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAAATA
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA
AAGTATAAGACTAAGTGATAAACTGTCTTCCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG
TACTCTGAAAAACAAGGGGG

FIGURE 558

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVVSLLLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTTFAGLCYFNYHDVGICRAVAMLWKL
```

Important features of the protein:

Signal peptide:

Amino acids 1-15

Transmembrane domains:

Amino acids 71-88;126-140

Glycosaminoglycan attachment site:

Amino acids 12-16

N-myristoylation sites

Amino acids 8-14;58-64;78-84;108-114;148-154

FIGURE 559

CCCAGCCCCGCGTTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC
 AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC
 CTGGGTTTTCACTTCCTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC
 CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG
 CCCAGCAGCCTCCCGCCCCACGCCCCGGATGCTCACCTGGATGCCAACCTCTCAAGACCCTG
 TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG
 GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTACCTGCGCAGCCTGGTCCTGGGGGAC
 AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCTGCGG
 AGGCTGGACTTGTGAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC
 TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC
 GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC
 GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTG
 ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCTCAACGTCAGCTACAACGTCCTGGAGTGG
 TTCCTCGCGACCGGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAACAG
 CTGCTGTTCTTCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCTCCTGCTGCGCGACAAC
 AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCAGTTC
 CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC
 AGCGACCTCGCAGATCTCCGCTTCCCTGGACATGAGCCAGAACCAGTTCAGTACCTGCCAGAC
 GGCTTCCCTGAGGAAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG
 CTTACATTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACAG
 CTGTGCGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTCAAC
 CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC
 ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCCTGCCAGCTGCCTCGGACCGGGTGGG
 CCCCCCTAGCTGTGTGGATTTAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG
 TGGCCTGGGGGCATTGCCAGACTGCCCATTCCAAGGGACCTCCCTGACCTACTTAGACCTCTC
 AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA
 GGTCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT
 TGGGAATCTCAGGGACTTAGATCTGTGCGGGAATTGCTTGACCACCTTCCAAGGTTTGGGGG
 CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAAACTCGCTCACAGCCCTTCCCCAGAAGGC
 TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG
 CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT
 CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCCGGAGGTGTGCCTCGGGA
 CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT
 CACCCTGCTGGTGGCCTGCACTGTCTATCGTCCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT
 CAAGAGCCGCTGCCACTGGTCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCG
 GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG
 ACGAATTGAAGTTTCAATTAAAAATTTAATATGTTTCCATTCCCTCATCGCCACCCACCCCG
 CCCCACCACCGCCCAAGTTCTTTTTCCATCATTATAATTATCCTTATTATCTTGGTAAAT
 ATTTATTAAGTGACTTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA
 AAAAAAAAAAAAAA

FIGURE 560

><subunit 1 of 1, 692 aa, 1 stop
><MW: 76366, pI: 6.07, NX(S/T): 11
MELLPLWLCLGFHFLTVGWRNRSQTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR
MLTLDANPLKTLWNHSLQPYPLLESLSLHSLCHLERISRGAFQEQGHLRSLVLGDNCLSEN
YEETAALHALPGLRRDLDSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEGLE
ERLRELDLQRNYIFEIEGGAFDGLAELRHLNLAFNNLPCIVDFGLTRLRLVNLVSYNVLEW
FLATGGEAAFELETLDLSHNQLLFFPLLPQYSKLRITLLLRDNNMGFYRDLYNTSSPREMV
AQFLLVDGNVTNITTIVSLWEEFSSSDLDLRLDMSQNFQYLPDGFRLKMPSLSHLNLH
QNCLMTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLRLFNLSNQLLGVPPG
LFANARNITTLDMSHNQISLCPLPAASDRVGPSCVDFRNMASLRSLSEGCGLGALPDC
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD
LDLSGNCLTTFFPRFGGSLALETDLRRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG
VDGWGALQHGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVLIPLSC
LTLVACTVIVLTFKKPLLQVIKSRCHWSSVY

Important features of the protein:

Signal peptide:

Amino acids 1-18

Transmembrane domain:

Amino acids 651-672

N-glycosylation sites:

Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;
312-316;408-414;427-431;500-504;622-626

Glycosaminoglycan attachment site:

Amino acids 533-537

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 566-570

N-myristoylation sites:

Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;
308-314;396-402;416-422;420-426;471-477;
484-490;497-503;522-528;545-551;555-561;610-616

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 657-668

Leucine zipper patterns:

Amino acids 48-70;492-514

FIGURE 561

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAGT
TTGGGCTGGAAGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGTACTTCA
TAAATACACGGAAGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG
AGGAAGAGATGATTTTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA
GGAGTCTCGGGGGCGTGAAGTTGACCCCTGTGCCTGAGCCCGAGGCATTTCAGAGCTGATTCAGA
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA
GAGCCACCCTCACACCAGCGGTCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC
TTTTGAAGAAATTCAGCAGATAAATTGAAAGTGCCGGAAGCGAAAGCAGAACTGGCAATAG
TTCTCCTGCCTCGGTGGAGCGGGAAGACAGATGCTTACAAAGTCTGAAAACAGAAATGAG
TCAGAGAGGAAGTGGACAGTGCCTTATTCATTACAGCAAAGGATTTTCGTTGGCATCAAATCT
AAGTTTGTTTTACAAAGATTGTTTTTAGTACTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCC
AAACAAAATATATTATTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

FIGURE 562

```
></usr/seqdb2/ssť/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLVGLALWWVPGQSDLHGRRFSDLKVCGDEECSSMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKEYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELDVPV
EPEAFRADSEEDGEAFSESTEGLQGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDK
LKVPGSESRTGNSSPASVEREKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYK
DCF
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-glycosylation site:

Amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 67-76

N-myristoylation sites:

Amino acids 205-211;225-231;277-283

Amidation site:

Amino acids 28-32

FIGURE 563

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG
TGTGACCCATCTTTTCAAATTCCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT
GCTCCTACCCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGCTGGGTGAGCCCCAGGCCTGGTTGCTG
GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT
GACCGGCAGTTCCTCAGCTCCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACCTTCTG
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTCGG
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA
CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTCATGTTAT
GAAAA

FIGURE 564

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSITLGRYLRQLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

N-myristoylation sites:

Amino acids 4-10;12-18;93-99

Leucine zipper pattern:

Amino acids 102-124

FIGURE 565

CGGCACGAGTAAAATGGAGATAATATCACCATGCACTCAGCCCTAGCCACTGCATTGCTGTTA
CTGATAACCATTA CTGCTGCTACGTCGTTTTTTTTGATGGCTCAGCCCTTAGGGAAGGGGGATCA
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA
CCCACCCTGAGGTCGGGACCTGGGTTCCTTCCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCCTGCCTGTGACGGAGGCCCCAGCCA
TCTCC

FIGURE 566

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLLIPLLLLRRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGPSPSQWALPCL
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

Glycosaminoglycan attachment site:

Amino acids 58-62

FIGURE 567

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA
ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG
GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT
GATGACTTGCATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGA**CCGTGGCTC
CAGCCACCCCGGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

FIGURE 568

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLLGLAASSWLGGQNASDHSLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRRMLAMPIDLDTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

Important features of the protein:

Signal peptide:

Amino acids 1-18

N-glycosylation site:

Amino acids 20-24

N-myristoylation sites:

Amino acids 5-11;9-15;17-23;18-24

FIGURE 569

GGTGCCAAGGGTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTCAT
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTTGGCTGGCAATCTTCTGTA
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT
GGAGCCCTCCACACCTTGCTCTGTGTGCCTCTCATTCTGATTTGAATTCTTATTTTGCTATA
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG
CTGTCTTATGGAAGTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA
CAACTACAATTTGTTGTGCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATCTTTGGGTT
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG
GTTTGAAAGTGTAAGCAAATCGTACATTTCCCAAACACTTTGTAAAGAAGGAATGGGTAGTG
TCAACTAAAGGAAATGGTGTGCATCCCAGCAAAGAAAGAGACCGAAAGCAAAGTCATAAACC
ATGCCACGAGCTCAGCTGTCTGCTCCGTGTCCTCTCCATACCCTTGTTGACTGTGCTCATA
TTAGCCAGAGACCTAAGTGCTCTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTCAC
TGTCTACTTCTGATCCTCTCTTCTGTGTCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT
GGCCCGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGCGCTTCTCTGATATCATCTTCCAT
CCATGGAAAAGGAGGAGAATGGAAACAGAGCCGAGTGATTCTTTACACCATCACCCCTTACC
AACCTCTGGCTCCCAAACCTGCCACTGTTCAGGGAGACACAGACCATGTACAAGGCGAGCCAG
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCCTCACCCACGACGTGCCCTACCACGACTAC
TTCTACACAATCAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC
ACTTATTTGGCTGAGATGCACAGACAATCTCCCAAAGAGAAGGCCAGCAAGACTACAACGGTG
CGGAGGAGGAAGCGTCCCATGCCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCG
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCCACACAG
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAACTC
TGGATGTTGGAATACACCACGCAGACCCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAGG
TTACCCAGTCTCAGACAGAATGGGCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT
GAGCTCCAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGCGACTACACGTCGGAAAGTGAAGAAAAG
AGGAATCGCTATCATTGACAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT
ACATAGACCATATAAATATATATATATAAATATATATATATACAGAATATAAATATATATATT
ATATACAGATTTTAAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC
GCCCTGTGCTGGCCGGAGCAGCGTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCCACCTCTGTTCCCCACCCCTTCCCTTGC
TGGCCATTCTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCTAAG
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCCTTTTGA
TTTGTTCCTCAAAATAAAGAGAATCTTTTCTTCCCTAAAAA

FIGURE 570

><subunit 1 of 1, 425 aa, 1 stop
><MW: 49786, pI: 8.84, NX(S/T): 3
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE
DLSGRQYVNEVFNFVSVDKLYDLLFTNSPFQRDFMEQRRFSDIIFHPWKKEENGNSQSRVIL
YTITLTNPLAPKTATVRETQTMKASQSESECYVIDAEVLTHDVPYHDYFYTINRYTLTRV
ARNKSRLRVSTELRYRKQPWGLVKTFIEKNFWSGLEDYFRHLESELAETSTYLAEMHRQ
SPKEKASKTTTIVRRRKRPVPHLEEVMSPTTPTDEDVGHRIKHVAGSTQTRHIPE
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWQGLRLQERLPQ
SQTEWAQLLESQQKYHDTLQKWREIIKSSVMLLDQMKDSLINLQNGIRSRDYTSESEK
RNRYH

Important features of the protein:

Signal peptide:

Amino acids 1-28

Transmembrane domain:

Amino acids 312-334

N-glycosylation sites:

Amino acids 73-77;114-118;183-187

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 97-101

Tyrosine kinase phosphorylation sites:

Amino acids 144-153;188-196

N-myristoylation sites:

Amino acids 201-207;291-297

Leucine zipper pattern:

325-347

FIGURE 571

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAAT
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAAATCCCTGTGGATAAGGGTGGACGGCTGCTCTGTCAACTT
TGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTGGAAAGGTATGCATCGTGACAGAGCGAGACAC
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGGTTCCGAATGTTTTCCG
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGA
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTCACAGA
GGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG
AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTACATTACAGACTTCAACATAGCGACGGT
AGTGAAAGGAGCAGAAAGGGCTTCTCCATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCAGGTGTA
CATGGACAGAGGCCCCGGATACTCGTACCCTGTGCACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG
GGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCATCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT
CCACTACTCTCCACGTGGTGCAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG
CGTGTCCAGCCTTCATGACATACAGAGCGTGCCTTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGC
ACTGATGCCCCGCTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGATTCT
AGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGATGGCACAAGGACAGCTG
CCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGGAGGAATTTCATCATATTCAACAGAGAGAAGCT
CAGGAGGCAGCAGGGACAGGGCAGCCAGCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCAAAGCAAGCT
CCAGGACGGGTGCAACAACAACCTCCTCACCCACACCTGCACCCGTTGGCTGCAGCAGCTGAGCCCCACTTGTG
CTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCTCTTTGTGCCCTGATGGTCCCTGTCTC
ACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTTCTGGTCCCATCTCCAT
GACTGATTCACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGGAGAACCCTAATTAGGTAGGAAACATGAAAAACCTTTGA
TATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCCATTCCCCAAAGCAATCAA
ACCGTCATGACTTTTGCAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCCGAAAAACACAGCCCTGACAGCAA
AATAAAGGTCTGATATGTTGGCCCTTCTATGGAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT
CATGTGCATTCTCTGGCAGGCCACAGTCTTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTCAGCAGTCTCT
CACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCATTGAGATGAGAGTTGGGTGCTGAGCATTG
GTTACTCCTGCAGAGTGTAATCAGCACCCCATCCAAGTGGCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAC
TCTCTATCAGCTTTTCAAGGTTTTCTCTCCTGGGAAGGGTGTAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTCAGG
AGGAAAATGGGTTTACACAAAAAGCAAATACATTCTGATCTGCTCAGGGAGAAGCTTGCCTTTGAACCTGGAAGA
TGTTGGGATGAGCAGGGAAAGCTTAGACTTTGGAGTCAGGTTTGTGTTTCAGAATCCAGCCCTGCTGGCTACTAAC
TAACTGGGAGACCTTAGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT
GGCCTTTTTTGTGTCAGCATAATCGTCATCATTATTTAGATACTTTCTTCTTCACTCACCCAGCAGGTGAGTTTTT
TGTGCAAAACAAACCTGTTTAGGATTCTTCCAAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTATCTCTGCG
TGAAGTTTCGACTGTGTTTTTATTTTTTTCATCCAATTTTCACTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCTCTTTAGATTTCTTAAAGACATTTTAAATGATGTTAGGTTTTATATTTTTTATTTTTTAA
AAAAGAAATAGTCAGTGTTTTTCTCTTTCAACCGAGACTATTTCTGGATTGTGTGCTCCTCGTCAGTTGACTTGT
TTTGCACACTTTTCTTTACTTCATGTCCCCATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGC
CTGCTCCTCTCCCTACTGTGACCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGAA
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGTTCTGTTCAAGTTGGCATTCTTGTGTTG
GAATAAACTATTTCTTGG

FIGURE 572

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110

<subunit 1 of 1, 364 aa, 1 stop

<MW: 42195, pI: 7.40, NX(S/T): 1

MKYMNKQKCIERDEVNRFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVFQVYMDRGPYSGYSPVDWWSLGITAYELLRGWRPYEIHVS
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWD
VFKKALMPGFVPNKGRLNCDPTFELEEMILES KPLHKKKKRLAKNRSRDGTDSCPLNGH
LQHCLETVREEFIIFNREKLRRQQGQGSQQLDTSRGGGQAQSKLQDGCNNLLTHTCTR
GCSS

Important features of the protein:

N-glycosylation site:

Amino acids 285-289

N-myristoylation sites:

Amino acids 123-129;290-296;337-343;339-345;348-354

Serine/Threonine protein kinases active-site signature:

Amino acids 92-105

FIGURE 574

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRGCVSRSCSRQRRPQHLEPSAGPASACAAA VAVSVPATVPPKQLPLHG
QVNICGCPLLFFLLFQLLLLLPLPSRSRKPPTQLTLAQLQTVSSAQLYLAPRAPLRHWTH
RRVIFYCKVASLYIFLSPPPPSVSGVPYSPANSWSCALVPLLGSVPPHPPAPSPCCSG
QTMLKMLSFKLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRMMSQ
LELLSGGEMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNTECGKLLLEEIKCALCSPH
SQSLFHSPEREVLERDLVLP LLCKDYCKEFFYTCRGHIPGFLQTTADEFCFYARKDGGL
CFPDFPRKQVRGPASNYLDQMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVSQSGIKGGDERGLLSLAFHPNYKKNKG
LYVSYTTNQERWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSLRLDVD TDMCNVPYSIPRSNPHFNST
NQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYSEEP
SLLEFKPFSNGPLVGGFVYRGCQSERLYGSYVFGDRNGNFLT LQQSPVTKQWQEKPLCLG
TSGSCRGYFSGHILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCCS PGWEGDFCRTAKCEPACRHGGVCVRPNKCLCK
KGYLG PQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV
```

Important features of the protein:

Transmembrane domains:

Amino acids 63-80;186-201

N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

Glycosaminoglycan attachment site:

Amino acids 417-421

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

FIGURE 575

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT
 CTGGCTTCCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG
 GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT
 CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCCT
 CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAGTGAACCTGTCAGTTCTGCCCCACACA
 GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG
 GAAGAGGAGCCGACAGCAGAGGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA
 TGAGCAACCCAGCTTTCCAGACAGTCACTTTTCCCAGTGGTCATACCTGGTCTGGAAGATTC
 CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC
 CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA
 AAACGAGGCAGCGAACCCACACGTGGAAGTCTGATACCGCTTGCAAGAGGGAATTGAATAGAT
 GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCCGCAAGCAACAAC
 TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTTCAGACACAGGGGAAACC
 ACTGCCTCTTTCAGTCTTTCTCCCAGATTCCAACAGTCAGTGTTACAGCATTTTACCTTGTTT
 ACCTCCCTGAGAAGACGTTGCAGCTCACTACCCCGAGTGGGCACTGGGAGCCTCTGCTCAGGT
 GGGAGACAGATGCCCCCACATGCACATCTGGTGTATTATGAAGCAGATACTGGGGCTTCATAA
 ACACAGAAGGGGCGAGGAAGTAGCCCCAGGGCATAGTGTGGGGCCTCCTGACTAAAAGTAGCTT
 GCAAACCCCTGCCTATAACAGCCACTTCCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA
 CCGCTCTTCCTTTAGTTCTTCACTCTGTATAGACCCTGCCAGAGCAGCTCAGGGTGGAGCAG
 CTGCAGCCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT
 CCAGAGGAGTCAATTCCTTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG
 AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCATTTAGGTCTTGCTGCTCAT
 CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTGAGGGAAGAAGGCTTTATCCAGGTGCTAC
 AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCACTGACTAAAATTAGGGGTT
 TATATAGCAGGGAAGAAATGTAACATCATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG
 AGGAGTTGGCCAACAGGCAGCAGGTGGTCACCTGGGGAATCATGATGGGTGAGGGGTCTGGCT
 TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTAGTTTCTTGATAACCGTCTGGGAGGATTG
 CTGGCTGGTTTTCTGAGAAAGGAATTGAGATGACATAAATGTAAATTTCTCCTTGGGTTTCAA
 GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAAACCATAAACATCAGTTCTATGGGACA
 ATTGGGCCCATTTCAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCCTGGAGAAG
 TTCCTGGGGCCTACAAGAACTAGAGAGGCTTCTGGCAAAGCTCTATGCTGTCTATCCTCT
 CTTCTCTCCTTGACAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCAATA
 AGTAGAAAACTGAAGGGGGGTGGGAGGCACATGGATTTGAACCAGAGACCGCTTGGCCTGCAG
 GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTC
 CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAAACAA
 CCCATTCTGCTCTCTCTTTCTCTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC
 TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAAGCCAACGTTATC
 CTAGAAAAGCTTTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG
 CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTTGTCT
 GAGATAAGGAGGAACCTGTCCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC
 TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG
 TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC
 AGGTTCTGAGCCTTGGGGGACCAGTTACCCCTACATCCCAGGCTTCTGTTGTCCCTTGCCCTG
 CCTGTAAGGAATAAAGTTGCTTTGCTTA

FIGURE 576

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALEFVLVALESLLLSPCPGTSSSTLTRTFFPSLVSCVQVPFSWIPCLECFLEYFL
ILAEDVLQLFSGNANMQVNQ
```

Important features of the protein:

Signal peptide:

Amino acids 1-29

Transmembrane domain:

Amino acids 47-62

N-myristoylation sites:

Amino acids 25-31

FIGURE 577

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA
CATCGGATAGTTCCCAAGTTGATACAAAACCTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA
TGTTCAAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTTCTATTTTTCTGATGATACCAGAAAT
TGGACAGCCAGTAAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA
GAAGACATGGAATTTTTGAAGAGGTACGCAGGAACTGATATGCACTGGATTGGACTAAGCAGG
AAACAAGGAGATTCTTGGAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATAGGCC
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA
TTTATCAATTCAGAGCAATTCATCCTCCTCTTTCCATCTTTGATTACAGTTAATAGGCTATA
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

FIGURE 578

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR
```

Important features of the protein:

Signal peptide:

Amino acids 1-42

N-glycosylation sites:

Amino acids 78-82;130-134;146-150

N-myristoylation site:

Amino acids 131-137

FIGURE 579

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC
TGCTGTCTCCTTAGCTGCTCACATATGGATACTTTACAGTTTCAGGATTCCACTGCAATGAGC
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC
AAGCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG
GAAGCCCCAAGTCAGCCGCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAAT
ACTGAAAAAGCATCATTTTGAACAGCCATTTCTTCTTTTGGCAAACTGAAGAGGGTTCAC
ACAACTTATTTTAAAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG
TCAGCCTTGTGCTGTTGAGGAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC
TGTGGGAACTACTCATTTCTTGGCATTCTTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC
TGAGTGATATTAAATCTCAGCATTGTTGTGCAAAAAAAAAA

FIGURE 580

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNESPVLPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

Important features of the protein:

Signal peptide:

Amino acids 1-35

Tyrosine kinase phosphorylation site:

Amino acids 61-70

Amidation site:

Amino acids 48-52

FIGURE 581

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA
CCCTCCCTTTCCCTTGTGTGTAGGGCCGCGCTCCACCCCCACCTCGCCGGAGTCCGGGGCG
GCCCCGGTGTCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCAG
GGAAATCTCCGACCAGGCCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTTGAATTATCTGTG
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG
ATGGACTTTCTGGTCCTCTTCTTGTTCACCTGGCTTCGGTGCTGATGGGTCTTGTTCTTATC
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCCTGGCCAGGGGAGGAGCACAGATATTTTCC
TGTATAATTCCAGAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG
AGAAACCACACCTTCATTGTCCTGCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC
TGGGAAGTATTTGGCTACTGTGAGGAGCTGGAGTTGTCTTGCAATTACCTTCTTCTGCCCTAT
CTGCTGCTAGGTGTAAACCTGTTTTTTTCCACCTGACTTGTGGAACCAATCCTGGCATTATA
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACTGCATCGGGGCCTGG
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT
GTGAGCACCACTTTTCTGGTCCACTTGGTGGTGTGTCAGATTTATAACCAGGAGACTTACATC
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTCAGTACCTGTTCTGACT
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTGCTGGTTCTGAGCTTCCTCCTGGGTGGCTAC
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC
TGGGCCTGGTGCCAGCGTTGTCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC
CGGAACATTCACTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA
TGTCATGAGAGGAAGAAACAAGAATGACAAGTGTATGACTGCCTTTG

FIGURE 582

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFYFLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIIPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYQCQELELSLHYLLLPYLLLGVNLFFFTLTCG
TNPGIITKANELLFLHVYEFDEVMFPPKQNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLTFFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

Important features of the protein:

Signal peptide:

Amino acids 1-29

Transmembrane domains:

Amino acids 100-116;201-217;256-275

N-glycosylation sites:

Amino acids 65-69;284-290

N-myristoylation sites:

Amino acids 32-38;77-83;120-126;322-328

Cell attachment sequence:

Amino acids 292-298

DHHC zinc finger domain:

Amino acids 140-204

FIGURE 583

CCGCGGAAGTGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT
 AGGCTGGGCGAAGAGTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT
 GACGGGAAGGCCAGTGCAGCGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC
 CTCGTCTCTCTTCTGCTTCAGAGGGAGAGCAGGCCCGTCGCCCCATTTCTGCAACAGCCAGAGGACCTGGTG
 GTGCTGCTGGGGGAGGAAGCCCCGGCTGCCGTGTGCTCTGGGCGCCTACTGGGGGCTAGTTCAGTGGACTAAGAGTGGG
 CTGGCCCTAGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG
 CATGACCTCCACATTAGGCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTCAGGCTACACAAGCAGGCCTC
 CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCTCTGTGTCT
 CTGGTTGCTGGAGTTCTTGCGAACCTGACATGTGCGAGCCGTGGGGATGCCCGCCCTACCCCTGAATTGCTGTGG
 TTCCGAGATGGGGTCTGTGGATGGAGCCACCTTTCATCAGACCCTGCTGAAGGAAGGGACCCCTGGGTCACTG
 GAGAGCACCTTAACCTTGACCCCTTTAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCCGAGCCAGGCC
 CTGCCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA
 CACACTGTGCAGGAGGGAGAGAAGGTCATTTCTGTGTCAGGCCACAGCCACAGCCAGCCTCCTGTACAGGCTACAGG
 TGGGCAAAAGGGGGCTCTCCGGTGTCTCGGGGCCCGCGGGCCAAAGGTTAGAGGTCTGGGCGAGACGCCCTCGTTCTG
 ACTGAGCCCGTGTCTGCGAGGTGAGCAACGCCGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT
 GGGCCGATTCTGCAGGCAAGCCGGAGCCCGTGTCTGTCAGCTGGGGGAAGACGCTTCTTCAGTGCCTGCGCTGG
 CGCGGGAACCCGCTTCCACGGGTAACTGGACCCGCCCGGTGGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG
 CGTCTTCCGTGGTGGGGCCCGAGGACGCGAGGCGACTATGTGTGAGAGCTGAGGCTGGGCTATCGGGCCTGCGG
 GCGGCGCCCGGAGGCTCGGCTGACTGTGAACGCTCCCCAGTACTGACCGCCCTGACTCTGCGCCTGCCTTC
 CTGAGGGGCCCTGCTCGCCTCCAGTGTCTGTTTTCGCTCTCCCCCCCCAGATGCCGTGGTCTGGTCTTGGGAT
 GAGGGCTTCTGGAGGCGGGTTCGAGGGCCGGTCTCTGGTGGAGACATTCCTGCCCCAGAGAGCCGCGGGGGA
 CTGGGTCCGGGCTGATCTCTGTGCTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC
 AGTGCCCGGAACCGGCTGGGCGAGGGAGGTGCCCAGGCCAGCCTGGGCGGTAGAGACTTGCTGCCCACTGTGCGG
 ATAGTGGCCGGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTTCATCACTGGGGTGGCCCTCTGCTGCTGGCGC
 CACAGCAAGGCTCAGCCTCTTTCTCCGAGCAAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACCGCTCCAGT
 TCACGAGGTCTGAAGAAGAGGAGACAGGCAGCCGCGAGGACCGGGGCCCATTTGTGCACACTGACCAAGTGTAT
 CTGGTTCTGGAGGAGGAAGGACTCTGGAGACCAAGGACCAACCAACGGTTACTACAAGGTCCGAGGAGTCACT
 GTGAGCCTGAGCCTTGGCGAAGCCCCCTGGAGGAGGTCTCTTCTGCCACCACCCTCCCCCTTGGGGCCCCAGGG
 ACCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC
 TATCTCACACACCCCACTCTGAGCTTTACACAGCTACATCAAACCCACATCCTTTGGGGCCCCAGATCTGGCC
 CCCGGGACTCCCCCTTCCCATATGCTGCCTTCCCCACACCTAGCCACCCGCTCTCCAGACTCAGTGTGACAT
 CTTTCCAATGGAAGAGTCTGGGATCTCCAACCTGCCATAATGGATTGTTCTGATTTCTGAGGAGCCAGGACAAG
 TTGGCGACCTTACTCTCCAAAAGTGAACACAAGGGGAGGGAAAGATCATTACATTTGTGTCAGGAGCATTGTGATA
 CAGTCAGCTCAGCCAAAGGAGATGCCCCAAGTGGGAGCAACATGGCCACCAATATGCCACCTATTCCCCGGTG
 TAAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG
 GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG
 CATAGGATAGATGAAGATGAAGAGCATACCAGGCCCCACCTGGCTCTCCTGAGGGGAACCTTTGCTCGGCCAAT
 GGAAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCCAAAATGGCCACCATCTTGATTTTACTTTCTTAAA
 GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAAATATTGGGATAA
 AAATATTTATGTTTAAATAATAAAAAAAGTCAAAGAGAAAAAAA

FIGURE 584

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
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IALGGQORDLPGWSRYWISGNAANGQHDLHIRPVELEDEASYECQATQAGLRSRPAQLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTLTFFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLASAPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVDASFLTEPVSCSVSNAVGS
NRSTALDVLFGPILQAKPEPVSDVGEDASFSCAWRGNPLPRVTWTRRGGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAEEARLTVNAPPVVTALHSAPAFLRGPARLQCL
VFASAPDAVVWSWDEGFLEAGSQGRFLVETFPAPESRGGLGPGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRRDLLPTVRIVAGVAAATTTLLMVITGVALCCWRHKSAS
ASFSEQNLMRIPGSSDGSSSRGPEEEEETGSREDRGPIVHTDHSDLVLEEEGTLETKDPT
NGYYKVRGVSVSLSLGEAPGGGLFLPPSPPLGPPGTPTFYDFNPHLGMVPPCRLYRARAG
YLTTTPHPRAFTSYIKPSTSFGPPDLAPGTPPFPYAAFPPTPSHPRLQTHV
```

Important features of the protein:

Signal peptide:

Amino acids 1-20

Transmembrane domain:

Amino acids 511-531

N-glycosylation sites:

Amino acids 143-147;301-305;484-488

N-myristoylation sites:

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;
387-393;460-466;473-479;494-500;495-501;514-520;528-534;
554-560;592-598;608-614

Amidation site:

Amino acids 500-504

Cell attachment sequence:

Amino acids 149-152

Multicopper oxidases signature 1:

Amino acids 445-466

Immunoglobulin domain:

Amino acids 326-377

FIGURE 585

GCCCGCCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG
 GGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGCTAAGAACAGGCAGTTTGTGTCTGGCTGG
 CTGCAGATACCCAGAGGCAAAAGAGACCGAAGCCACCCGAGGGACCCACGGACGGACAGAT
 GGTAGGCGCGAACCCGAGAGGACCGGCGGAGGCTGAGCACCGAGAGCCGCCAAGGAAGAGAAA
 CTAACCACAGCCAAGTTACCCCGCCGGCTTTCCTTCGCTGCGCTAAGGAATGAAACCTTCCA
 GCTCGATCTGCTCTTCGTCTGCTTCTTCTCCTCCTCAGTCAAGAGCTGGGCCTCCAGAAGAGAGG
 ATGCTGTCTGGTGTCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT
 CTATTCCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTCTGGGACAGCCAGTGACGCTACT
 TTGCGCCATCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGT
 GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACTGTCTAGGGGAGCA
 CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA
 GGCCGCCATCCGCTCCCGCCCCGCACGCCTCACAGTCTTGGTGCCGCCTGATGACCCCGTCAT
 CCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGACCTCTCAACCTCACCTGCCACGCAGA
 CAATGCCAAGCCTGCAGCCTCCATCATCTGGTTGCGAAAGGGAGAGGTATCAATGGGGCCAC
 CTACTCCAAGACCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCTCTTCATCTC
 CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTCTGCCACCAACAAAGCCATCCCCGG
 AGGAAAGGAGACGTGCGTCACCATTGACATCCAGCACCTCCACTGGTCAACCTCTCGGTGGA
 GCCACAGCCAGTGCTGGAGGACAACGTCTGCTACTTTCCACTGCTCTGCAAAGGCCAACCCAGC
 TGTCAACCCAGTACAGGTGGGCCAAGCGGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA
 CAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCGTCTCCTGTGAGGTGACCAACGCCCTG
 GGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCC
 CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA
 TCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCTGAGCAATGAGAAGACCTG
 ACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGCCCCGT
 GTGGGAGCCGGGGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCAC
 CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCG
 CCGCCGGACCGCATCGCCTGGTCTGGAAGGAGAACGTTCTGGAGTCGGGCACATCGGGGCGC
 TATACGGTGAGACCATCAGCACCGAGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATC
 GTGCGGGCCGACTTCCAGACCATCTAACAAGTGCACGGCCTGGAACAGCTTCGGCTCCGACACT
 GAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG
 TCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCTCGTCTCTT
 ATGGCAACCATCGTGGCGTTCTGCTGTGCCCCGTTCCAGAGAAGTACGGGAGGGAGATCCGGG
 ATCTCAGGGAGGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGAGAGCAAGTAAGCAG
 GAGTGCAATGAACAGGGGTCCTAACAGTGTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG
 CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTTGA
 CCTGGACTAGACTGAACTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT
 TCAGTCAGGAACTGTACAGAAAGATAGGGGGAAAAGCGGTTTGTGGTTTGATCCTTGCTCTAC
 AAGAGCTGTTAGTCTAGAGAGACCCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC
 TCACCAGAAAAGCAGGTCACTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT
 TGCTTTGAGAAAACCTTAA

FIGURE 586

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFFLFSQELGLQKRGCCCLVLGYMAKDKFRRMNEGQVYSFSQQPQDQVVV
SGQPVTLTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLRKGEVINGATYSKTLRLDGKRESIVSTLFI SPGDVENGQSIVCRATNKAI PGGKET
SVTIDIQHPPVLNLSVEPQPVLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVTNALGSTNLSRTVDVYFGPRMTTEPQSLLDLGSDAIFSCAWTG
NPSTIVWMKRGSGVVL SNEKTLTLKSVRQEDAGKYVCRAVVPRVGAGEREVTLT VNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSWKENVLES GTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKGAGLEAESVPMAVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

Transmembrane domain:

Amino acids 534-555

N-glycosylation sites:

Amino acids 167-171;253-257;324-328;498-502

Glycosaminoglycan attachment sites:

Amino acids 523-527;574-578

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 204-208;370-374;588-592

Tyrosine kinase phosphorylation sites:

Amino acids 40-49;300-308;389-397

N-myristoylation sites:

Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;
374-380;436-442;478-484;539-545;543-549;
568-574

Amidation site:

Amino acids 202-206

Leucine zipper pattern:

Amino acids 8-30

FIGURE 587

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCTCGAAAAATCAATGGTATTTGCATTTCTC
CCAAGAAGGTTGCTTGCCAAAACCTTTTCGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA
AAATGACAGTCTGTCAGCTCATTGAAGGCACTAGATACCCTGCCTGCAGGTACCACTATTCCC
CCACAGAGGGGTTTGTTCCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA
GAAGAGATTACACTACATCTGAGATGGAGACCTTTCTCTGCTGCTGCTCAGCCTGGGCCTGG
TTCTTGCAAGCATCAGAAAGCACAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA
CATTCAGAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAATGACAAAGAGTGTT
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCACT
ACAGGCAAACAATTCCCCAGGTGCCAATACCATAGTGTTACCTCATTAGAGAAGATATTGACA
GTGCTGACAGGTCATTCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAAATCCACAG
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTTATTCTTGTTTAAACCTTT
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTCTGATTATTTATTCTAACTGGAGGAGTG
AAAAATCCAAAATTGTGGATAATTCAATTAAAGTTATGACTGATACCG

FIGURE 588

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEASESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMSKDDMSSTLLTFRSLHYNDPKGNSGNDKECCNDMTVWRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLMSWLVCCKSL
```

Important features of the protein:

Signal peptide:

Amino acids 1-16

N-glycosylation sites:

Amino acids 61-65;89-93;111-115

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 105-109

N-myristoylation sites:

Amino acids 12-18;88-94;144-150

Microbodies C-terminal targeting signal:

Amino acids 197-201

FIGURE 589

CAGTCCTGCCGGGACGGTGAGCGCATTTCAGCACCCCTGGACAGCACCGCGGTTGCGCTGCCTCC
AGGGCGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC
TGCACTTGCCGCCGCTTTCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCAGGCTCGCGCCCGAAGCA
GAGCCATGAGAACCCAGGGTGCCCTGGCGAGCCGCTAGCGCCATGGGGCCCCGGCGAGGCGCTG
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT
TGTTGCGCCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCTCCTGGTGAATCTGTCT
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG
CGGACACCGTCTGGCGCCCGGCGCATGCCAAGTCATTGGCTTCTGGACACCTTCTGGCGTCC
AACGCGGCGCTGAGCGTGGCGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCACTG
CGCTACGCCGGACGCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG
TCCTGTTGCTGCGCCTGCCGCCCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG
CTCCATGCCGTGGGCTTCTGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC
CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC
GCCACCTGCACCCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTACCGTGAACGCCCAGTGGGGCATCCTCAGCAAG
TGCTGACCTACAGCAAGGCGGTGGCCGACCCGTTACGTACTCTCTGCTCCGCCGGCCGTTT
CGCCAAGTCTTGGCCGGCATGGTGACCGGCTGCTGAAGAGAACCCCGCGCCAGCATCCACC
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGACACAGAGTGAAGAGAACCCCGCGCCCA
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCTGCTGACGACACACTGA
GGGCTTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG
CCACAGAGATGCCACTGGGGACCCCCAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

FIGURE 590

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLSLGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRLRP
RYAGLLLGCawGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCQRMDTVTMKALALLADLHPSVRQRCLIQQRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRP
FRQVLAGMVHRLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

Important features of the protein:

Signal peptide:

Amino acids 1-24

Transmembrane domains:

Amino acids 46-60;85-103;130-150;175-192;246-264

N-glycosylation sites:

Amino acids 47-51;348-352;355-359

Tyrosine kinase phosphorylation site:

Amino acids 286-295

N-myristoylation sites:

Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;
349-355

G-protein coupled receptor proteins:

Amino acids 72-112

7 transmembrane receptor (rhodopsin family):

Amino acids 22-294

FIGURE 591

AACATGGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTGCTCCGGCTGCCCTGGCGGGTG
 CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAAACTCTGCGCGGACGAC
 GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTTACAGGCCCGGATTTGTCGTTTT
 GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA
 GTTTGGGCTGGAAGTGTTGGACGCACTTTTGGATATTTTCCAAAAGATTTAATCCAGGTAGTT
 CATGAATATACCAAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTGTTGTTTGAT
 GGAGGAAGAGATGATTTTTCATAATTATAATGTAGAAGAACTTTTAGGGTTTTTGGAACTGTAC
 AATTCCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAACTTTACAGGATATGGAAAAAAC
 CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACCTCAGAGGAAAGT
 GATAGTGTATTCTCAGAAAACACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC
 TCCCATGCAAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA
 GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAAACAACAAACCAGCAATAGTTCT
 CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAAGAAATGACTCTA
 GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCACTTGTATCTGATGATGAGACAACCAGA
 CTCGTTACTTCATTAGAAGATGATTTTGTATGAGGAATTGGATACTGAGTATTATGCAGTTGGA
 AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG
 GAAGATATGAAAACCTCCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT
 TCAAATGAAGAGGACAAGGTTTCAGCTAACTGTGCCCCCTGGCATCAAAAATGATGATAAAAAT
 ATACTAACAACCTGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT
 ACGATGGATTTAGAGAGCTCTAGTTTCAGAGGAAGAAAAAGAAGATGATGATGATGCATTAGTC
 CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT
 GATGGTCTTTTTTATTGTAGACATTCCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT
 CACATTAAAGGAAAAGGGAGGGGAGTTCAGGAATCCAAGAGGGGCCTGGTACAAGATGAGACA
 GAATTAGAGGATGAAAATCAAGAAGGCTTTAAAACAGAGCCCATAAACTATTGACCCTCTGAGG
 TTTCAATTGGAAAGAAAGTGTAAGTGTGCAATTATCCATTACAGTAAAGGATTTTATTGGCTTCAA
 AATCCAAAAGTTTATTTTAAAAGGTTTGTGTTAGAACTAAGCTGCCTTGGCAGTGTGCAATTT
 TTGAGCCAAACAATTCAAAAATGTCATTTCTTCCCTAAATAAAAATCACCTTTTAAAGCTAGAG
 CGTCCTTACAACTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT
 AATTGCAAAATGATTTAGAATGTCATGAAAAATATGAACATTTTCTGTGGAAATGCTTTAAGA
 ACATGTATTTCCATTATCCTATTTTTAGTGTACACCAGCTGAATACGGAGCAATGGTGTTTAT
 AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC
 ACTAACTATCTCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT
 AATATTTAAAAA

FIGURE 592

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLLVWLLVLRPLPWRVPGQLDPSTGRRFSEHKLCADDECMMYRGEALEDFTGPDC
RFVNFKKGDPVYVYYKLARGWPEVWAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTDET
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP
VEANSEESDSVFSSENTEDLQEQFTTQKHHSHANSQANHAQGEQASFESFEEMLQDKLKVP
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTKFGSTADALVSDDETTRLVTSLED
DFDEELDRTEYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE
DKVQLTVPPGIKNDDKNILTTWGDTIFSIVTGGEETRDTMDLESSSSEEEKEDDDDALVP
DSKQKGKQSATDYSDDPDNDGLFIVDIPKTNNDKEVNAEHHIKGKGRGVQESKRGLVQD
ETELEDENQEGFKTEPIKL
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249;249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

FIGURE 593

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC
ACATGCTGTTCCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC
TTCTACAATGTCTGAAGAAGTGACCTACGCGACACTCACATTTCAGGATTCTGCTGGAGCAAG
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCCATTGCGG
TCATGCTGCTCTGGGCTCTGGTAACTCTTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG
GATGATGTTTTTGCAGATATCTAATGACATTAACCTCAGATTCAGAGAAATTGAGTCAACTTCA
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACCTTGTC
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC
CATCAAACCTGTGCCAAGAGCTAATCATTCACTTTCAGACCACAGATGTAATCCATGTCCTAA
GATGTGGCAATGGTACCAAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC
TAACAGTAGAAAGGACTGCATAGACAAGAACTCCACCCTAGTGAAGATAGACAGTTTGGAAGA
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG
GGACTCCTCTGGCAGAAGTTGGTTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGTAAGT
CTCTAACTATTGAGGGTAAACACAAGCTTTCATGGAATCCTGGGAAAATTAATAATGATTGT
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAAGGATGTGC
TTATTTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTGCGA
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATCTCCAA
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAACTACGGTACCAGAGCAAGG
GCGAATTCTGCA

FIGURE 594

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80, NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLNRKRGHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINSDEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFKLSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNPCPKMWQWYQNSCYFFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

Important features of the protein:

Transmembrane domain:

Amino acids 42-62

N-glycosylation sites:

Amino acids 91-95;101-105;176-180

N-myristoylation sites:

Amino acids 17-23;97-103

FIGURE 595

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC
ATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCCTATGCTGACA
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG
GATGAACATAATAGGCCCATTCACACATAACCAGGTATGTAATGTAATGGAACCAAACCAAAC
AACTGGCTTCGTACAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT
CTGTTTTTATATGGAATCAGATGAGTCCACGGAATTAAATTCAAGCCAAACCAGTATACAAAG
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTGTTGGGTGATCGCATCCTCAA
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTTCAA
GACATTGGGGCGTGCAATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCTTCACT
GTTTCGTAACCTGGCCATGTTTCCTGATACCATTCGAAGGTTGATTCCTCCTCTTTGGTTGAA
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAACTGTATTGTGGAGCT
GATGGAGATTGGCTGGTTCCTCTTGGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG
GGTTCCTGCCATGGAGCCTCAAAGGCCGCTGCTTCTTAGTTGGCCATCTTGGCCCCACCCGA
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 596

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVVLLDTTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISERDAAQKIYVEMKFRTLDCNSIPWVLGT
CKETFNLFYMESESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLAHQDIGACIALVSVRVFYKKCPFTVRNLA MF PDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVP LGRCICSTGYEEIEG SCHGASKGRCF
```

Important features of the protein:

Signal peptide:

Amino acids 1-22

N-myristoylation sites:

Amino acids 192-198;274-280;278-284

Receptor tyrosine kinase class V signature 1:

Amino acids 192-209

Ephrin receptor ligand binding domain:

Amino acids 34-207

FIGURE 597

A C A C T G G C C A A A C A A A A C G A A A G C A C T C C G T G C T G G A A G T A G G A G G A G A G T C A G G A C T C C C A
 G G A C A G A G A G T G C A C A A A C T A C C C A G C A C A G C C C C C T C C G C C C C C T C T G G A G G C T G A A G A G G G
 A T T C C A G C C C C T G C C A C C C A C A G A C A C G G G C T G A C T G G G G T G T C T G C C C C C C T T G G G G G G G G
 C A G C A C A G G G C C T C A G G C C T G G G T G C C A C C T G G C A C C T A G A A G A T G C C C T G T G C C C T G G T T C T T
 G C T G T C C T T G G C A C T G G G C C G A A G C C C A G T G G T C C T T T C T C T G G A G A G G C T T G T G G G G C C T C A
 G G A C G C T A C C C A C T G C T C T C C G G G C C T C T C C T G C C G C C T C T G G G A C A G T G A C A T A C T C T G C C T
 G C C T G G G G A C A T C G T G C C T G C T C C G G G C C C C T G C T G G C G C C T A C G C A C C T G C A G A C A G A G C T
 G G T G C T G A G G T G C C A G A A G G A G A C C G A C T G T G A C C T C T G T C T G C G T G T G G C T G T C C A C T T G G C
 C G T G C A T G G G C A C T G G G A A G A G C C T G A A G A T G A G G A A A G T T T G G A G G A G C A G C T G A C T C A G G
 G G T G G A G A G C C T A G G A A T G C C T C T C T C C A G G C C C A A G T C G T G C T C T C C T T C C A G G C C T A C C C
 T A C T G C C C G C T G C G T C C T G C T G G A G G T G C A A G T G C C T G C T G C C C T T G T G C A G T T T G G T C A G T C
 T G T G G G C T C T G T G G T A T A T G A C T G C T T C G A G G C T G C C C T A G G G A G T G A G G T A C G A A T C T G G T C
 C T A T A C T C A G C C C A G G T A C G A G A A G G A A C T C A A C C A C A C A G C A G C T G C C T G C C C T G C C C T G
 G C T C A A C G T G T C A G C A G A T G G T G A C A A C G T G C A T C T G G T T C T G A A T G T C T C T G A G G A G C A G C A
 C T T C G G C C T C T C C C T G T A C T G G A A T C A G G T C C A G G G C C C C C A A A A C C C C G G T G G C A C A A A A
 C C T G A C T G G A C C G C A G A T C A T T A C C T T G A A C C A C A C A G A C C T G G T T C C C T G C C T C T G T A T T C A
 G G T G T G G C C T C T G G A A C C T G A C T C C G T T A G G A C G A A C A T C T G C C C C T T C A G G G A G G A C C C C C G
 C G C A C A C C A G A A C C T C T G G C A A G C C G C C C G A C T G C G A C T G C T G A C C C T G C A G A G C T G G C T G C T
 G G A C G C A C C G T G C T C G C T G C C C G C A G A A G C G G C A C T G T G C T G G C G G G C T C C G G G T G G G G A C C C
 C T G C C A G C C A C T G G T C C C A C C G C T T T C C T G G G A G A A C G T C A C T G T G G A C A A G G T T C T C G A G T T
 C C C A T T G C T G A A A G G C C A C C C T A A C C T C T G T G T T C A G G T G A A C A G C T C G G A G A A G C T G C A G C T
 G C A G G A G T G C T T G T G G G C T G A C T C C C T G G G G C C T C T C A A A G A C G A T G T G C T A C T G T T G G A G A C
 A C G A G G C C C C C A G G A C A A C A G A T C C C T C T G T G C C T T G G A A C C C A G T G G C T G T A C T T C A C T A C C
 C A G C A A A G C C T C C A C G A G G G C A G C T C G C C T T G G A G A G T A C T T A C T A C A A G A C C T G C A G T C A G G
 C C A G T G T C T G C A G C T A T G G G A C G A T G A C T T G G G A G C G C T A T G G G C C T G C C C C A T G G A C A A A T A
 C A T C C A C A A G C G C T G G G C C C T C G T G T G G C T G G C C T G C C T A C T C T T T G C C G C T G C G C T T T C C C T
 C A T C C T C C T T C T C A A A A A G G A T C A C G C G A A A G G G T G G C T G A G G C T C T T G A A A C A G G A C G T C C G
 C T C G G G G G C G G C C G C C A G G G G C C G C G C G G C T C T G C T C C T C T A C T C A G C C G A T G A C T C G G G T T T
 C G A G C G C C T G G T G G G C G C C C T G G C G T C G G C C C T G T G C C A G C T G C C G C T G C G C G T G G C C G T A G A
 C C T G T G G A G C C G T C G T G A A C T G A G C G C G C A G G G C C C G T G G C T T G G T T T C A C G C G C A G C G G C G
 C C A G A C C C T G C A G A G G G C G G C G T G G T G G T C T T G C T C T T C T C T C C C G G T G C G G T G G C G C T G T G
 C A G C G A G T G G C T A C A G A T G G G G T G T C C G G G C C C G G G G C G C A C G G C C C G C A C G A C G C C T T C C G
 C G C C T C G C T C A G C T G C G T G C T G C C C G A C T T C T T G C A G G G C C G G G C G C C C G G C A G C T A C G T G G G
 G G C C T G C T T C G A C A G G C T G C T C C A C C C G A C G C C G T A C C C G C C C T T T T C C G C A C C G T G C C C G T
 C T T C A C A C T G C C C T C C C A A C T G C C A G A C T T C C T G G G G G C C C T G C A G C A G C C T C G C G C C C C G C G
 T T C C G G G C G G C T C C A A G A G A G A G C G G A G C A A G T G T C C C G G G C C C T T C A G C C A G C C C T G G A T A G
 C T A C T T C C A T C C C C C G G G A C T C C C G C G C C G G A C G C G G G T G G G A C C A G G G C G G G A C C T G G
 G G C G G G G A C G G G A C T T A A A T A A A G G C A G A C G C T G T T T T T C T A A A A A A

FIGURE 598

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLSSLERLVGPQDATHCSPGLSCRLWDSIILCLPGDIVPAPGP
VLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLVSFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALPWLNV SADGDNVHLVLNVSEEQHFGLSLYWNQVQGP KPRWH
KNLTGPQIITL NHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFP LLKGHPNLCV
QVNSSEKLQLQECLWADSLGPLKDDVLLLETRGPQDNRS LCALEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQLWDDDLGALWACPM DKYIHKRWALVWLACLLFAAALSLILL
LKKDHAKGWLRL LKQDVRSGAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLLFSPGAVALCSEWLQDGVSGPGAHGP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRL LH PDAVPALFRTVPVFTLPSQLPDFLG
ALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
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Important features of the protein:

Signal peptide:

Amino acids 1-20

Transmembrane domain:

Amino acids 453-473

N-glycosylation sites:

Amino acids 118-122;186-190;198-202;211-215;238-242;
248-252;334-338;357-360;391-395;

Glycosaminoglycan attachment site:

Amino acids 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-556

N-myristoylation sites:

Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;
692-698;696-702;700-706

FIGURE 599

GGTCCTTAATGGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCTGGAGCCAA
GTGCAGGAGCACCCTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCTGCTTCATCCTCCCTGGCATCTGAGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTGTTTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATGTTCTGTACTGATATTTAA
ATAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 600

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFLH
YDCGNKTVTPVSPPLGKKLNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 601

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT
GCTTCCTGAACTAGCTCACAGTAGCCCGGCGGCCAGGGCAATCCGACCACATTTCACTCTCA
CCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGCTCT
CCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC
TCTGTCTGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT
ATTTCTGCCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGACCTGGAATTTG
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGGCCCTGACA
GTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAA
TAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTTCGCCCTCTGCAACTACAAAT
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTTCCTGTTTCAGGATCAC
CAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA
ATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG
TAGTCCATCAGAAATTGGCAGTCACTTCCAGATTGTACCAGCAAATACACAAGGAATCTTTT
TTGTTTGTTCAGTTTCATACTAGTCCCTTCCAATCCATCAGTAAAGACCCCATCTGCCTTGT
CCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCTTCTGTGTCCATTAAAGACTCTGATAATTGTCTCCCTCCATAGGAATTTCTCCCA
GGAAAGAAATATATCCCATCTCCGTTTCATATCAGAACTACCGTCCCGATATTCCTTCAG
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA
TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA
AATACTGTGAAAAA

FIGURE 602

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGED

FIGURE 603

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAATATGCATCTTGACAGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCCACCATGCTGCTGGCCAGGCCGGAAGGAGCTGCAGAAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

FIGURE 604

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675

><subunit 1 of 1, 247 aa, 1 stop

><MW: 25335, pI: 7.00, NX(S/T): 0

MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHG VNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 605

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAGATGG
TCCCCGGCGCCGCGGGCTGGTGTTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCACG
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATTCACC
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCAGGACC
AGATTGCTCTGGTGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCCAGGAGC
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGGCCGAGACG
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG
TCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGGTAGAAGA
GTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGAAAAGGGTTTGGG
CGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCT
GGTGTTTGGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAAGCTTCTCATCAGGGTTG
CAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 606

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI
HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVII SDNAVDNDSFYV
EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

FIGURE 607

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCCATGTGGCTGC
 CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA
 GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA
 TTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT
 CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAAGACCGCACGTTCA
 CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA
 GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA
 CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCACAAGAGGAACCACT
 ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT
 TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACTTCTCCG
 AACCTCTGACTAAAGACATGGCCACTTAGAGAGATGGATCTGCAGAGCCTTCCCTGCCCTGGCC
 ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCTCGGGATGCAGTGACT
 GAGATAGGGGCCCTGGGCTCCGCCCTGGGCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC
 AGCTCAGGGACTTAGCCAGGTCTCTCCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG
 TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG
 GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTTGGGGGAGACCCCCCAG
 CCCTAGACTTCCATCATTCCGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCC
 GTGTTTTTAAATTTTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC
 CTCTCTGATCCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTAGGGCATGAGG
 GGCTGGATGGACCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT
 GGGAACCTCCCTGGCCCCGGCCGGTGCTTGTCTCCCCCTCCCACCTCTTCTCCTCCTAGCT
 CCCCAGCTCCCTGCCTATTCCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT
 GACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTCAGGCCTCAAGAACCACCTCCAGGTGGGGA
 GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCTCCCTTTTTCGGTGATGTTGAAATCATG
 TTAATAATGAAAACGTGCTAGGGAAGTGTTCTGTCTCCTCACAGGCTTCACCCACGGCGAT
 GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCTCACACCAAAGGGACCT
 TCCCATGTGAGATGTGCTCCCGCCCCACCTGCCACAAGCAAAACACACACATGTTCCGGC
 ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGTTCTAATAGGGAGTAC
 TGACTGTCAGCAGTGATAAAGGAGAGGGGACCTCTGGTCCCTAGCATGGCAGCCAGAGCCT
 CCCCTCTTCTTGTCTTCAGCCAAAGAGAACTTCTCTGACTTTGAACTGAATTTAGGTCTC
 TGGCCAATGATGGGCCTGAAAATTCATAATGGCCAGAGAGGAGAGTTCGAGCCCGGCTAAGA
 TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGGCCCTACCTCC
 TGGAATGCTTTCTTGATCCAGCTTCCCAGAGATCCGACCAGACCCAGGGAGGACGGCACCGC
 TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTACCAGCTGGACTCAGGGGCGAGGGGACATG
 GCGCTTGTCAACGTGATGTCTTTTCCCACCGTTTCTTCTGTTGATATTCAATGAATC
 CGTCAATCTCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 608

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGSLTVQCHYKQGWETYIKWWCRGVRWDTCKI
LIETRGSEQGEKSDRVSIKDNQKDRTFTVTMEGLRRDDADVWCGIERRGPDLTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHYMLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMNFSLEPLTKDMAT
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

Transmembrane domain:

Amino acids 151-170

N-glycosylation site:

Amino acids 190-194

Tyrosine kinase phosphorylation site:

Amino acids 95-103

N-myristoylation sites:

Amino acids 66-72;125-131

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 5-16

FIGURE 609

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTGTAAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAAAAAAACCTTGTAATCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

FIGURE 610

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

Amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 192-196;225-229

N-myristoylation sites:

Amino acids 42-48;46-52;136-142

SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FIELD OF THE INVENTION

[0001] The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

BACKGROUND OF THE INVENTION

[0002] Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment.

[0003] Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Pat. No. 5,536,637].

[0004] Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and nerve growth factor receptor.

[0005] Membrane-bound proteins and receptor molecules have various industrial applications, including as pharma-

ceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

[0006] Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF THE INVENTION

[0007] In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

[0008] In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0009] In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0010] In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

[0011] Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

[0012] Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide

probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

[0013] In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

[0014] In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93%

amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

[0015] In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

[0016] In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

[0017] Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

[0018] In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as

defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

[0019] In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

[0020] In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

[0021] Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

[0022] In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

[0023] In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

[0024] In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

[0025] In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

[0026] In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF THE DRAWINGS

[0027] FIG. 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO276 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16435-1208".

[0028] FIG. 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in FIG. 1.

[0029] FIG. 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO284 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA23318-1211".

[0030] FIG. 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in FIG. 3.

[0031] FIG. 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO193 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA23322-1393".

[0032] FIG. 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in FIG. 5.

[0033] FIG. 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO190 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA23334-1392".

[0034] FIG. 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in FIG. 7.

[0035] FIG. 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO180 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA26843-1389".

[0036] FIG. 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in FIG. 9.

[0037] FIG. 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO194 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA26844-1394".

[0038] FIG. 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in FIG. 11.

[0039] FIG. 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO218 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA30867-1335".

[0040] FIG. 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in FIG. 13.

[0041] FIG. 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO260 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA33470-1175".

[0042] FIG. 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in FIG. 15.

[0043] FIG. 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO233 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA34436-1238".

[0044] FIG. 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in FIG. 17.

[0045] FIG. 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO234 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA35557-1137".

[0046] FIG. 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in FIG. 19.

[0047] FIG. 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO236 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA35599-1168".

[0048] FIG. 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in FIG. 21.

[0049] FIG. 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO244 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA35668-1171".

[0050] FIG. 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in FIG. 23.

[0051] FIG. 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO262 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA36992-1168".

[0052] FIG. 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in FIG. 25.

[0053] FIG. 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO271 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA39423-1182".

[0054] FIG. 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in FIG. 27.

[0055] FIG. 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO268 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA39427-1179".

[0056] FIG. 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in FIG. 29.

[0057] FIG. 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO270 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA39510-1181".

[0058] FIG. 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in FIG. 31.

[0059] FIG. 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO355 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA39518-1247".

[0060] FIG. 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in FIG. 33.

[0061] FIG. 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO298 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA39975-1210".

[0062] FIG. 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in FIG. 35.

[0063] FIG. 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO299 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA39976-1215".

[0064] FIG. 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in FIG. 37.

[0065] FIG. 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO296 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA39979-1213".

[0066] FIG. 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in FIG. 39.

[0067] FIG. 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO329 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA40594-1233".

[0068] FIG. 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in FIG. 41.

[0069] FIG. 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO330 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA40603-1232".

[0070] FIG. 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in FIG. 43.

[0071] FIG. 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO294 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA40604-1187".

[0072] FIG. 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in FIG. 45.

[0073] FIG. 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO300 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA40625-1189".

[0074] FIG. 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in FIG. 47.

[0075] FIG. 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO307 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA41225-1217".

[0076] FIG. 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in FIG. 49.

[0077] FIG. 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO334 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA41379-1236".

[0078] FIG. 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in FIG. 51.

[0079] FIG. 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO352 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA41386-1316".

[0080] FIG. 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in FIG. 53.

[0081] FIG. 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO710 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA44161-1434".

[0082] FIG. 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in FIG. 55.

[0083] FIG. 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO873 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA44179-1362".

[0084] FIG. 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in FIG. 57.

[0085] FIG. 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO354 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA44192-1246".

[0086] FIG. 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in FIG. 59.

[0087] FIG. 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO1151 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA44694-1500".

[0088] FIG. 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in FIG. 61.

[0089] FIG. 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO382 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA45234-1277".

[0090] FIG. 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in FIG. 63.

[0091] FIG. 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1864 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA45409-2511".

[0092] FIG. 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in FIG. 65.

[0093] FIG. 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO386 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA45415-1318".

[0094] FIG. 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in FIG. 67.

[0095] FIG. 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO541 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA45417-1432".

[0096] FIG. 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in FIG. 69.

[0097] FIG. 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO852 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA45493-1349".

[0098] FIG. 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in FIG. 71.

[0099] FIG. 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO700 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA46776-1284".

[0100] FIG. 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in FIG. 73.

[0101] FIGS. 75A-75B show a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO708 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA48296-1292".

[0102] FIG. 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in FIGS. 75A-75B.

[0103] FIG. 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO707 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA48306-1291".

[0104] FIG. 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in FIG. 77.

[0105] FIG. 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO864 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA48328-1355".

[0106] FIG. 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in FIG. 79.

[0107] FIG. 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO706 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA48329-1290".

[0108] FIG. 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in FIG. 81.

[0109] FIG. 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO732 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA48334-1435".

[0110] FIG. 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in FIG. 83.

[0111] FIG. 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO537 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA49141-1431".

[0112] FIG. 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in FIG. 85.

[0113] FIG. 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO545 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA49624-1279".

[0114] FIG. 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in FIG. 87.

[0115] FIG. 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO718 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA49647-1398".

[0116] FIG. 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in FIG. 89.

[0117] FIG. 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO872 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA49819-1439".

[0118] FIG. 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in FIG. 91.

[0119] FIG. 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO704 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA50911-1288".

[0120] FIG. 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in FIG. 93.

[0121] FIG. 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO705 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA50914-1289".

[0122] FIG. 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in FIG. 95.

[0123] FIG. 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO871 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA50919-1361".

[0124] FIG. 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in FIG. 97.

[0125] FIG. 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO702 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA50980-1286".

[0126] **FIG. 100** shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in **FIG. 99**.

[0127] **FIG. 101** shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO944 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA52185-1370".

[0128] **FIG. 102** shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in **FIG. 101**.

[0129] **FIG. 103** shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO739 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA52756".

[0130] **FIG. 104** shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in **FIG. 103**.

[0131] **FIG. 105** shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO941 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA53906-1368".

[0132] **FIG. 106** shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in **FIG. 105**.

[0133] **FIG. 107** shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1082 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA53912-1457".

[0134] **FIG. 108** shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in **FIG. 107**.

[0135] **FIG. 109** shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1133 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA53913-1490".

[0136] **FIG. 110** shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in **FIG. 109**.

[0137] **FIG. 111** shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO983 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA53977-1371".

[0138] **FIG. 112** shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in **FIG. 111**.

[0139] **FIG. 113** shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO784 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA53978-1443".

[0140] **FIG. 114** shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in **FIG. 113**.

[0141] **FIG. 115** shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO783 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA53996-1442".

[0142] **FIG. 116** shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in **FIG. 115**.

[0143] **FIG. 117** shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO940 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA54002-1367".

[0144] **FIG. 118** shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in **FIG. 117**.

[0145] **FIG. 119** shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO768 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA55737-1345".

[0146] **FIG. 120** shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in **FIG. 119**.

[0147] **FIG. 121** shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO1079 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA56050-1455".

[0148] **FIG. 122** shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in **FIG. 121**.

[0149] **FIG. 123** shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO1078 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA56052-1454".

[0150] **FIG. 124** shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in **FIG. 123**.

[0151] **FIG. 125** shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO1018 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA56107-1415".

[0152] **FIG. 126** shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in **FIG. 125**.

[0153] **FIG. 127** shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO793 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA56110-1437".

[0154] **FIG. 128** shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in **FIG. 127**.

[0155] **FIG. 129** shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO1773 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA56406-1704".

[0156] **FIG. 130** shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in **FIG. 129**.

[0157] **FIG. 131** shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1014 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA56409-1377".

[0158] **FIG. 132** shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in **FIG. 131**.

[0159] **FIG. 133** shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1013 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA56410-1414".

[0160] **FIG. 134** shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in **FIG. 133**.

[0161] **FIG. 135** shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO937 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA56436-1448".

[0162] **FIG. 136** shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in **FIG. 135**.

[0163] **FIG. 137** shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1477 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA56529-1647".

[0164] **FIG. 138** shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in **FIG. 137**.

[0165] **FIG. 139** shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO842 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA56855-1447".

[0166] **FIG. 140** shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in **FIG. 139**.

[0167] **FIG. 141** shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO839 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA56859-1445".

[0168] **FIG. 142** shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in **FIG. 141**.

[0169] **FIG. 143** shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO1180 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA56860-1510".

[0170] **FIG. 144** shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in **FIG. 143**.

[0171] **FIG. 145** shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO1134 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA56865-1491".

[0172] **FIG. 146** shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in **FIG. 145**.

[0173] **FIG. 147** shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO1115 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA56868-1478".

[0174] **FIG. 148** shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in **FIG. 147**.

[0175] **FIG. 149** shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO1277 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA56869-1545".

[0176] **FIG. 150** shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in **FIG. 149**.

[0177] **FIG. 151** shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO1135 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA56870-1492".

[0178] **FIG. 152** shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in **FIG. 151**.

[0179] **FIG. 153** shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO827 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA57039-1402".

[0180] **FIG. 154** shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in **FIG. 153**.

[0181] **FIG. 155** shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO1057 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA57253-1382".

[0182] **FIG. 156** shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in **FIG. 155**.

[0183] **FIG. 157** shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO113 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA57254-1477".

[0184] **FIG. 158** shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in **FIG. 157**.

[0185] **FIG. 159** shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO1006 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA57699-1412".

[0186] **FIG. 160** shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in **FIG. 159**.

[0187] **FIG. 161** shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO1074 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA57704-1452".

[0188] **FIG. 162** shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in **FIG. 161**.

[0189] **FIG. 163** shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO1073 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA57710-1451".

[0190] **FIG. 164** shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in **FIG. 163**.

[0191] **FIG. 165** shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO1136 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA57827-1493".

[0192] **FIG. 166** shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in **FIG. 165**.

[0193] **FIG. 167** shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1004 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA57844-1410".

[0194] **FIG. 168** shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in **FIG. 167**.

[0195] **FIG. 169** shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO1344 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA58723-1588".

[0196] **FIG. 170** shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in **FIG. 169**.

[0197] **FIG. 171** shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO1110 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA58727-1474".

[0198] **FIG. 172** shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in **FIG. 171**.

[0199] **FIG. 173** shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO1378 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA58730-1607".

[0200] **FIG. 174** shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in **FIG. 173**.

[0201] **FIG. 175** shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO1481 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA58732-1650".

[0202] **FIG. 176** shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in **FIG. 175**.

[0203] **FIG. 177** shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO1109 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA58737-1473".

[0204] **FIG. 178** shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in **FIG. 177**.

[0205] **FIG. 179** shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO1383 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA58743-1609".

[0206] **FIG. 180** shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in **FIG. 179**.

[0207] **FIG. 181** shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO1072 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA58747-1384".

[0208] **FIG. 182** shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in **FIG. 181**.

[0209] **FIG. 183** shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO1189 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA58828-1519".

[0210] **FIG. 184** shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in **FIG. 183**.

[0211] **FIG. 185** shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO1003 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA58846-1409".

[0212] **FIG. 186** shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in **FIG. 185**.

[0213] **FIG. 187** shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO1108 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA58848-1472".

[0214] **FIG. 188** shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in **FIG. 187**.

[0215] **FIG. 189** shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO1137 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA58849-1494".

[0216] **FIG. 190** shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in **FIG. 189**.

[0217] **FIG. 191** shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO1138 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA58850-1495".

[0218] **FIG. 192** shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in **FIG. 191**.

[0219] **FIG. 193** shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO1415 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA58852-1637".

[0220] **FIG. 194** shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in **FIG. 193**.

[0221] **FIG. 195** shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO1054 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA58853-1423".

[0222] **FIG. 196** shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in **FIG. 195**.

[0223] **FIG. 197** shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO994 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA58855-1422".

[0224] **FIG. 198** shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in **FIG. 197**.

[0225] **FIG. 199** shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO1069 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA59211-1450".

[0226] **FIG. 200** shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in **FIG. 199**.

[0227] **FIG. 201** shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA59212-1627".

[0228] **FIG. 202** shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in **FIG. 201**.

[0229] **FIG. 203** shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO1129 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA59213-1487".

[0230] **FIG. 204** shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in **FIG. 203**.

[0231] **FIG. 205** shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO1359 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA59219-1613".

[0232] **FIG. 206** shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in **FIG. 205**.

[0233] **FIG. 207** shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO1139 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA59497-1496".

[0234] **FIG. 208** shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in **FIG. 207**.

[0235] **FIG. 209** shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO1065 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA59602-1436".

[0236] **FIG. 210** shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in **FIG. 209**.

[0237] **FIG. 211** shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO1028 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA59603-1419".

[0238] **FIG. 212** shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in **FIG. 211**.

[0239] **FIG. 213** shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO1027 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA59605-1418".

[0240] **FIG. 214** shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in **FIG. 213**.

[0241] **FIG. 215** shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO1140 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA59607-1497".

[0242] **FIG. 216** shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in **FIG. 215**.

[0243] **FIG. 217** shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO1291 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA59610-1556".

[0244] **FIG. 218** shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in **FIG. 217**.

[0245] **FIG. 219** shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO1105 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA59612-1466".

[0246] **FIG. 220** shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in **FIG. 219**.

[0247] **FIG. 221** shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO1026 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA59613-1417".

[0248] **FIG. 222** shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in **FIG. 221**.

[0249] **FIG. 223** shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO1104 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA59616-1465".

[0250] **FIG. 224** shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in **FIG. 223**.

[0251] **FIG. 225** shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO1100 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA59619-1464".

[0252] **FIG. 226** shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in **FIG. 225**.

[0253] **FIG. 227** shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO1141 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA59625-1498".

[0254] FIG. 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in FIG. 227.

[0255] FIG. 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO1772 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA59817-1703".

[0256] FIG. 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in FIG. 229.

[0257] FIG. 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO1064 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA59827-1426".

[0258] FIG. 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in FIG. 231.

[0259] FIG. 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO1379 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA59828-1608".

[0260] FIG. 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in FIG. 233.

[0261] FIG. 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO3573 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA59837-2545".

[0262] FIG. 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in FIG. 235.

[0263] FIG. 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO3566 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA59844-2542".

[0264] FIG. 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in FIG. 237.

[0265] FIG. 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO1156 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA59853-1505".

[0266] FIG. 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in FIG. 239.

[0267] FIG. 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO1098 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA59854-1459".

[0268] FIG. 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in FIG. 241.

[0269] FIG. 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO1128 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA59855-1485".

[0270] FIG. 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in FIG. 243.

[0271] FIG. 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO1248 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA60278-1530".

[0272] FIG. 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in FIG. 245.

[0273] FIG. 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO1127 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA60283-1484".

[0274] FIG. 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in FIG. 247.

[0275] FIG. 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO1316 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA60608-1577".

[0276] FIG. 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in FIG. 249.

[0277] FIG. 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO197 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA60611-1524".

[0278] FIG. 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in FIG. 251.

[0279] FIG. 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO1125 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA60619-1482".

[0280] FIG. 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in FIG. 253.

[0281] FIG. 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO1158 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA60625-1507".

[0282] FIG. 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in FIG. 255.

[0283] FIG. 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO1124 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA60629-1481".

[0284] FIG. 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in FIG. 257.

[0285] FIG. 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO1380 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA60740-1615".

[0286] FIG. 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in FIG. 259.

[0287] FIG. 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO1377 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA61608-1606".

[0288] FIG. 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in FIG. 261.

[0289] FIG. 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO1287 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA61755-1554".

[0290] FIG. 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in FIG. 263.

[0291] FIG. 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO1249 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA62809-1531".

[0292] FIG. 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in FIG. 265.

[0293] FIG. 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO1335 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA62812-1594".

[0294] FIG. 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in FIG. 267.

[0295] FIG. 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO3572 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA62813-2544".

[0296] FIG. 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in FIG. 269.

[0297] FIG. 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO1599 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA62845-1684".

[0298] FIG. 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in FIG. 271.

[0299] FIG. 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO1374 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA64849-1604".

[0300] FIG. 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in FIG. 273.

[0301] FIG. 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO1345 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA64852-1589".

[0302] FIG. 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in FIG. 275.

[0303] FIG. 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO1311 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA64863-1573".

[0304] FIG. 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in FIG. 277.

[0305] FIG. 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO1357 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA64881-1602".

[0306] FIG. 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in FIG. 279.

[0307] FIG. 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO1557 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA64902-1667".

[0308] FIG. 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in FIG. 281.

[0309] FIG. 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO1305 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA64952-1568".

[0310] FIG. 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in FIG. 283.

[0311] FIG. 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO1302 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA65403-1565".

[0312] FIG. 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in FIG. 285.

[0313] FIG. 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO1266 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA65413-1534".

[0314] FIG. 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in FIG. 287.

[0315] FIGS. 289A-289B show a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO1336 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA65423-1595".

[0316] FIG. 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in FIGS. 289A-289B.

[0317] FIG. 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO1278 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA66304-1546".

[0318] **FIG. 292** shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in **FIG. 291**.

[0319] **FIG. 293** shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO1270 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA66308-1537".

[0320] **FIG. 294** shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in **FIG. 293**.

[0321] **FIG. 295** shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO1298 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA66511-1563".

[0322] **FIG. 296** shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in **FIG. 295**.

[0323] **FIG. 297** shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO1301 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA66512-1564".

[0324] **FIG. 298** shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in **FIG. 297**.

[0325] **FIG. 299** shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO1268 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA66519-1535".

[0326] **FIG. 300** shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in **FIG. 299**.

[0327] **FIG. 301** shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO1327 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA66521-1583".

[0328] **FIG. 302** shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in **FIG. 301**.

[0329] **FIG. 303** shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO1328 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA66658-1584".

[0330] **FIG. 304** shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in **FIG. 303**.

[0331] **FIG. 305** shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA66660-1585".

[0332] **FIG. 306** shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in **FIG. 305**.

[0333] **FIG. 307** shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO1339 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA66669-1597".

[0334] **FIG. 308** shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in **FIG. 307**.

[0335] **FIG. 309** shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO1342 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA66674-1599".

[0336] **FIG. 310** shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in **FIG. 309**.

[0337] **FIGS. 311A-311B** show a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO1487 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA68836-1656".

[0338] **FIG. 312** shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in **FIGS. 311A-311B**.

[0339] **FIG. 313** shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO3579 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA68862-2546".

[0340] **FIG. 314** shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in **FIG. 313**.

[0341] **FIG. 315** shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO1472 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA68866-1644".

[0342] **FIG. 316** shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in **FIG. 315**.

[0343] **FIG. 317** shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO1385 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA68869-1610".

[0344] **FIG. 318** shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in **FIG. 317**.

[0345] **FIG. 319** shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO1461 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA68871-1638".

[0346] **FIG. 320** shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in **FIG. 319**.

[0347] **FIG. 321** shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO1429 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA68879-1631".

[0348] **FIG. 322** shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in **FIG. 321**.

[0349] **FIG. 323** shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO1568 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA68880-1676".

[0350] **FIG. 324** shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in **FIG. 323**.

[0351] **FIG. 325** shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO1569 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA68882-1677".

[0352] **FIG. 326** shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in **FIG. 325**.

[0353] **FIG. 327** shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO1753 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA68883-1691".

[0354] **FIG. 328** shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in **FIG. 327**.

[0355] **FIG. 329** shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO1570 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA68885-1678".

[0356] **FIG. 330** shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in **FIG. 329**.

[0357] **FIG. 331** shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO1559 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA68886".

[0358] **FIG. 332** shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in **FIG. 331**.

[0359] **FIG. 333** shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO1486 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA71180-1655".

[0360] **FIG. 334** shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in **FIG. 333**.

[0361] **FIG. 335** shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO1433 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA71184-1634".

[0362] **FIG. 336** shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in **FIG. 335**.

[0363] **FIG. 337** shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO1490 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA71213-1659".

[0364] **FIG. 338** shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in **FIG. 337**.

[0365] **FIG. 339** shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO1482 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA71234-1651".

[0366] **FIG. 340** shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in **FIG. 339**.

[0367] **FIG. 341** shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO1409 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA71269-1621".

[0368] **FIG. 342** shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in **FIG. 341**.

[0369] **FIG. 343** shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO1446 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA71277-1636".

[0370] **FIG. 344** shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in **FIG. 343**.

[0371] **FIG. 345** shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO1604 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA71286-1687".

[0372] **FIG. 346** shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in **FIG. 345**.

[0373] **FIG. 347** shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO1491 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA71883-1660".

[0374] **FIG. 348** shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in **FIG. 347**.

[0375] **FIG. 349** shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO1431 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA73401-1633".

[0376] **FIG. 350** shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in **FIG. 349**.

[0377] **FIGS. 351A-351B** show a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO1563 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA73492-1671".

[0378] **FIG. 352** shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in **FIGS. 351A-351B**.

[0379] **FIG. 353** shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO1571 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA73730-1679".

[0380] **FIG. 354** shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in **FIG. 353**.

[0381] **FIG. 355** shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO1572 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA73734-1680".

[0382] **FIG. 356** shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in **FIG. 355**.

[0383] **FIG. 357** shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO1573 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA73735-1681".

[0384] **FIG. 358** shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in **FIG. 357**.

[0385] **FIG. 359** shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO1508 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA73742-1662".

[0386] **FIG. 360** shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in **FIG. 359**.

[0387] **FIG. 361** shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO1485 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA73746-1654".

[0388] **FIG. 362** shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in **FIG. 361**.

[0389] **FIG. 363** shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO1564 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA73760-1672".

[0390] **FIG. 364** shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in **FIG. 363**.

[0391] **FIG. 365** shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO1550 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA76393-1664".

[0392] **FIG. 366** shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in **FIG. 365**.

[0393] **FIG. 367** shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO1757 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA76398-1699".

[0394] **FIG. 368** shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in **FIG. 367**.

[0395] **FIG. 369** shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO1758 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA76399-1700".

[0396] **FIG. 370** shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in **FIG. 369**.

[0397] **FIG. 371** shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO1781 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA76522-2500".

[0398] **FIG. 372** shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in **FIG. 371**.

[0399] **FIG. 373** shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO1606 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA76533-1689".

[0400] **FIG. 374** shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in **FIG. 373**.

[0401] **FIG. 375** shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO1784 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA77303-2502".

[0402] **FIG. 376** shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in **FIG. 375**.

[0403] **FIG. 377** shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO1774 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA77626-1705".

[0404] **FIG. 378** shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in **FIG. 377**.

[0405] **FIG. 379** shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO1605 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA77648-1688".

[0406] **FIG. 380** shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in **FIG. 379**.

[0407] **FIG. 381** shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA81754-2532".

[0408] **FIG. 382** shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in **FIG. 381**.

[0409] **FIG. 383** shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO1865 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA81757-2512".

[0410] **FIG. 384** shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in **FIG. 383**.

[0411] **FIG. 385** shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO1925 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA82302-2529".

[0412] **FIG. 386** shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in **FIG. 385**.

[0413] **FIG. 387** shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO1926 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA82340-2530".

[0414] **FIG. 388** shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in **FIG. 387**.

[0415] **FIG. 389** shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO2630 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA83551".

[0416] **FIG. 390** shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in **FIG. 389**.

[0417] **FIG. 391** shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO3443 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA87991-2540".

[0418] **FIG. 392** shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in **FIG. 391**.

[0419] **FIG. 393** shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO3301 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA88002".

[0420] **FIG. 394** shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in **FIG. 393**.

[0421] **FIG. 395** shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO3442 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA92238-2539".

[0422] **FIG. 396** shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in **FIG. 395**.

[0423] **FIG. 397** shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO4978 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA95930".

[0424] **FIG. 398** shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in **FIG. 397**.

[0425] **FIG. 399** shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO5801 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA115291-2681".

[0426] **FIG. 400** shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in **FIG. 399**.

[0427] **FIG. 401** shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO19630 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA23336-2861".

[0428] **FIG. 402** shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in **FIG. 401**.

[0429] **FIG. 403** shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO203 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA30862-1396".

[0430] **FIG. 404** shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in **FIG. 403**.

[0431] **FIG. 405** shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO204 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA30871-1157".

[0432] **FIG. 406** shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in **FIG. 405**.

[0433] **FIG. 407** shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO210 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA32279-1131".

[0434] **FIG. 408** shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in **FIG. 407**.

[0435] **FIG. 409** shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO223 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA33206-1165".

[0436] **FIG. 410** shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in **FIG. 409**.

[0437] **FIG. 411** shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO247 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA35673-1201".

[0438] **FIG. 412** shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in **FIG. 411**.

[0439] **FIG. 413** shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO358 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA47361-1154-2".

[0440] **FIG. 414** shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in **FIG. 413**.

[0441] **FIG. 415** shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO724 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA49631-1328".

[0442] **FIG. 416** shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in **FIG. 415**.

[0443] **FIG. 417** shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO868 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA52594-1270".

[0444] **FIG. 418** shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in **FIG. 417**.

[0445] **FIG. 419** shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO740 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA55800-1263".

[0446] **FIG. 420** shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in **FIG. 419**.

[0447] **FIG. 421** shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO1478 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA56531-1648".

[0448] **FIG. 422** shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in **FIG. 421**.

[0449] **FIG. 423** shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO162 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA56965-1356".

[0450] **FIG. 424** shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in **FIG. 423**.

[0451] **FIG. 425** shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO828 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA57037-1444".

[0452] **FIG. 426** shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in **FIG. 425**.

[0453] **FIG. 427** shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO819 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA57695-1340".

[0454] **FIG. 428** shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in **FIG. 427**.

[0455] **FIG. 429** shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO813 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA57834-1339".

[0456] **FIG. 430** shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in **FIG. 429**.

[0457] **FIG. 431** shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO1194 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA57841-1522".

[0458] **FIG. 432** shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in **FIG. 431**.

[0459] **FIG. 433** shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO887 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA58130".

[0460] **FIG. 434** shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in **FIG. 433**.

[0461] **FIG. 435** shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA58847-1383".

[0462] **FIG. 436** shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in **FIG. 435**.

[0463] **FIG. 437** shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO1029 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA59493-1420".

[0464] **FIG. 438** shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in **FIG. 437**.

[0465] **FIG. 439** shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO1190 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA59586-1520".

[0466] **FIG. 440** shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in **FIG. 439**.

[0467] **FIG. 441** shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO4334 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA59608-2577".

[0468] **FIG. 442** shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in **FIG. 441**.

[0469] **FIG. 443** shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO1155 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA59849-1504".

[0470] **FIG. 444** shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in **FIG. 443**.

[0471] **FIG. 445** shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO1157 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA60292-1506".

[0472] **FIG. 446** shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in **FIG. 445**.

[0473] **FIG. 447** shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO1122 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA62377-1381-1".

[0474] **FIG. 448** shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in **FIG. 447**.

[0475] **FIG. 449** shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO1183 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA62880-1513".

[0476] **FIG. 450** shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in **FIG. 449**.

[0477] **FIG. 451** shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO1337 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA66672-1586".

[0478] **FIG. 452** shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in **FIG. 451**.

[0479] **FIG. 453** shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO1480 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA67962-1649".

[0480] **FIG. 454** shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in **FIG. 453**.

[0481] **FIG. 455** shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO19645 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA69555-2867".

[0482] **FIG. 456** shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in **FIG. 455**.

[0483] **FIG. 457** shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO9782 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA71162-2764".

[0484] **FIG. 458** shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in **FIG. 457**.

[0485] **FIG. 459** shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO1419 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA71290-1630".

[0486] **FIG. 460** shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in **FIG. 459**.

[0487] **FIG. 461** shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO1575 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA76401-1683".

[0488] **FIG. 462** shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in **FIG. 461**.

[0489] **FIG. 463** shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1567 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA76541-1675".

[0490] **FIG. 464** shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in **FIG. 463**.

[0491] **FIG. 465** shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1891 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA76788-2526".

[0492] **FIG. 466** shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in **FIG. 465**.

[0493] **FIG. 467** shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO1889 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA77623-2524".

[0494] **FIG. 468** shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in **FIG. 467**.

[0495] **FIG. 469** shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1785 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA80136-2503".

[0496] **FIG. 470** shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in **FIG. 469**.

[0497] **FIG. 471** shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO6003 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA83568-2692".

[0498] **FIG. 472** shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in **FIG. 471**.

[0499] **FIG. 473** shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO4333 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA84210-2576".

[0500] **FIG. 474** shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in **FIG. 473**.

[0501] **FIG. 475** shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO4356 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA86576-2595".

[0502] **FIG. 476** shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in **FIG. 475**.

[0503] **FIG. 477** shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO4352 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA87976-2593".

[0504] **FIG. 478** shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in **FIG. 477**.

[0505] **FIG. 479** shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO4354 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA92256-2596".

[0506] **FIG. 480** shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in **FIG. 479**.

[0507] **FIG. 481** shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO4369 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA92289-2598".

[0508] **FIG. 482** shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in **FIG. 481**.

[0509] **FIG. 483** shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO6030 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA96850-2705".

[0510] **FIG. 484** shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in **FIG. 483**.

[0511] **FIG. 485** shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO4433 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA96855-2629".

[0512] **FIG. 486** shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in **FIG. 485**.

[0513] **FIG. 487** shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO4424 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA96857-2636".

[0514] **FIG. 488** shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in **FIG. 487**.

[0515] **FIG. 489** shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO6017 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA96860-2700".

[0516] **FIG. 490** shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in **FIG. 489**.

[0517] **FIG. 491** shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO19563 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA96861-2844".

[0518] **FIG. 492** shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in **FIG. 491**.

[0519] **FIG. 493** shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO6015 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA96866-2698".

[0520] **FIG. 494** shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in **FIG. 493**.

[0521] **FIG. 495** shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO5779 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA96870-2676".

[0522] **FIG. 496** shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in **FIG. 495**.

[0523] **FIG. 497** shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO5776 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA96872-2674".

[0524] **FIG. 498** shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in **FIG. 497**.

[0525] **FIG. 499** shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO4430 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA96878-2626".

[0526] **FIG. 500** shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in **FIG. 499**.

[0527] **FIG. 501** shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO4421 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA96879-2619".

[0528] **FIG. 502** shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in **FIG. 501**.

[0529] **FIG. 503** shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO4499 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA96889-2641".

[0530] **FIG. 504** shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in **FIG. 503**.

[0531] **FIG. 505** shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO4423 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA96893-2621".

[0532] **FIG. 506** shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in **FIG. 505**.

[0533] **FIG. 507** shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO5998 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA96897-2688".

[0534] **FIG. 508** shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in **FIG. 507**.

[0535] **FIG. 509** shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO4501 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA98564-2643".

[0536] **FIG. 510** shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in **FIG. 509**.

[0537] **FIG. 511** shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO6240 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA107443-2718".

[0538] **FIG. 512** shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in **FIG. 511**.

[0539] **FIG. 513** shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO6245 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA107786-2723".

[0540] **FIG. 514** shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in **FIG. 513**.

[0541] **FIG. 515** shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO6175 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA108682-2712".

[0542] **FIG. 516** shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in **FIG. 515**.

[0543] **FIG. 517** shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO9742 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA108684-2761".

[0544] **FIG. 518** shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in **FIG. 517**.

[0545] **FIG. 519** shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO7179 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA108701-2749".

[0546] **FIG. 520** shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in **FIG. 519**.

[0547] **FIG. 521** shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO6239 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA108720-2717".

[0548] **FIG. 522** shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in **FIG. 521**.

[0549] **FIG. 523** shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO6493 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA108726-2729".

[0550] **FIG. 524** shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in **FIG. 523**.

[0551] **FIGS. 525A-525B** show a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO9741 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA108728-2760".

[0552] **FIG. 526** shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in **FIGS. 525A-525B**.

[0553] **FIG. 527** shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO9822 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA108738-2767".

[0554] **FIG. 528** shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in **FIG. 527**.

[0555] **FIG. 529** shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO6244 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA108743-2722".

[0556] **FIG. 530** shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in **FIG. 529**.

[0557] **FIG. 531** shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO9740 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA108758-2759".

[0558] **FIG. 532** shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in **FIG. 531**.

[0559] **FIG. 533** shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO9739 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA108765-2758".

[0560] **FIG. 534** shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in **FIG. 533**.

[0561] **FIG. 535** shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO7177 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA108783-2747".

[0562] **FIG. 536** shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in **FIG. 535**.

[0563] **FIG. 537** shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO7178 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA108789-2748".

[0564] **FIG. 538** shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in **FIG. 537**.

[0565] **FIG. 539** shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO6246 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA108806-2724".

[0566] **FIG. 540** shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in **FIG. 539**.

[0567] **FIG. 541** shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO6241 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA108936-2719".

[0568] **FIG. 542** shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in **FIG. 541**.

[0569] **FIG. 543** shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO9835 cDNA, wherein SEQ ID NO:543 is a clone designated herein as "DNA119510-2771".

[0570] **FIG. 544** shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in **FIG. 543**.

[0571] **FIG. 545** shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO9857 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA119517-2778".

[0572] **FIG. 546** shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in **FIG. 545**.

[0573] **FIG. 547** shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO7436 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA119535-2756".

[0574] **FIG. 548** shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in **FIG. 547**.

[0575] **FIG. 549** shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO9856 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA119537-2777".

[0576] **FIG. 550** shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in **FIG. 549**.

[0577] **FIG. 551** shows a nucleotide sequence (SEQ ID NO:551) of a native sequence PRO19605 cDNA, wherein SEQ ID NO:551 is a clone designated herein as "DNA119714-2851".

[0578] **FIG. 552** shows the amino acid sequence (SEQ ID NO:552) derived from the coding sequence of SEQ ID NO:551 shown in **FIG. 551**.

[0579] **FIG. 553** shows a nucleotide sequence (SEQ ID NO:553) of a native sequence PRO9859 cDNA, wherein SEQ ID NO:553 is a clone designated herein as "DNA125170-2780".

[0580] **FIG. 554** shows the amino acid sequence (SEQ ID NO:554) derived from the coding sequence of SEQ ID NO:553 shown in **FIG. 553**.

[0581] **FIG. 555** shows a nucleotide sequence (SEQ ID NO:555) of a native sequence PRO12970 cDNA, wherein SEQ ID NO:555 is a clone designated herein as "DNA129594-2841".

[0582] **FIG. 556** shows the amino acid sequence (SEQ ID NO:556) derived from the coding sequence of SEQ ID NO:555 shown in **FIG. 555**.

[0583] **FIG. 557** shows a nucleotide sequence (SEQ ID NO:557) of a native sequence PRO19626 cDNA, wherein SEQ ID NO:557 is a clone designated herein as "DNA129793-2857".

[0584] **FIG. 558** shows the amino acid sequence (SEQ ID NO:558) derived from the coding sequence of SEQ ID NO:557 shown in **FIG. 557**.

[0585] **FIG. 559** shows a nucleotide sequence (SEQ ID NO:559) of a native sequence PRO9833 cDNA, wherein SEQ ID NO:559 is a clone designated herein as "DNA130809-2769".

[0586] **FIG. 560** shows the amino acid sequence (SEQ ID NO:560) derived from the coding sequence of SEQ ID NO:559 shown in **FIG. 559**.

[0587] **FIG. 561** shows a nucleotide sequence (SEQ ID NO:561) of a native sequence PRO19670 cDNA, wherein SEQ ID NO:561 is a clone designated herein as "DNA131639-2874".

[0588] **FIG. 562** shows the amino acid sequence (SEQ ID NO:562) derived from the coding sequence of SEQ ID NO:561 shown in **FIG. 561**.

[0589] **FIG. 563** shows a nucleotide sequence (SEQ ID NO:563) of a native sequence PRO19624 cDNA, wherein SEQ ID NO:563 is a clone designated herein as "DNA131649-2855".

[0590] **FIG. 564** shows the amino acid sequence (SEQ ID NO:564) derived from the coding sequence of SEQ ID NO:563 shown in **FIG. 563**.

[0591] **FIG. 565** shows a nucleotide sequence (SEQ ID NO:565) of a native sequence PRO19680 cDNA, wherein SEQ ID NO:565 is a clone designated herein as "DNA131652-2876".

[0592] **FIG. 566** shows the amino acid sequence (SEQ ID NO:566) derived from the coding sequence of SEQ ID NO:565 shown in **FIG. 565**.

[0593] **FIG. 567** shows a nucleotide sequence (SEQ ID NO:567) of a native sequence PRO19675 cDNA, wherein SEQ ID NO:567 is a clone designated herein as "DNA131658-2875".

[0594] **FIG. 568** shows the amino acid sequence (SEQ ID NO:568) derived from the coding sequence of SEQ ID NO:567 shown in **FIG. 567**.

[0595] **FIG. 569** shows a nucleotide sequence (SEQ ID NO:569) of a native sequence PRO9834 cDNA, wherein SEQ ID NO:569 is a clone designated herein as "DNA132162-2770".

[0596] **FIG. 570** shows the amino acid sequence (SEQ ID NO:570) derived from the coding sequence of SEQ ID NO:569 shown in **FIG. 569**.

[0597] **FIG. 571** shows a nucleotide sequence (SEQ ID NO:571) of a native sequence PRO9744 cDNA, wherein SEQ ID NO:571 is a clone designated herein as "DNA136110-2763".

[0598] **FIG. 572** shows the amino acid sequence (SEQ ID NO:572) derived from the coding sequence of SEQ ID NO:571 shown in **FIG. 571**.

[0599] **FIG. 573** shows a nucleotide sequence (SEQ ID NO:573) of a native sequence PRO19644 cDNA, wherein SEQ ID NO:573 is a clone designated herein as "DNA139592-2866".

[0600] **FIG. 574** shows the amino acid sequence (SEQ ID NO:574) derived from the coding sequence of SEQ ID NO:573 shown in **FIG. 573**.

[0601] **FIG. 575** shows a nucleotide sequence (SEQ ID NO:575) of a native sequence PRO19625 cDNA, wherein SEQ ID NO:575 is a clone designated herein as "DNA139608-2856".

[0602] **FIG. 576** shows the amino acid sequence (SEQ ID NO:576) derived from the coding sequence of SEQ ID NO:575 shown in **FIG. 575**.

[0603] **FIG. 577** shows a nucleotide sequence (SEQ ID NO:577) of a native sequence PRO19597 cDNA, wherein SEQ ID NO:577 is a clone designated herein as "DNA143292-2848".

[0604] **FIG. 578** shows the amino acid sequence (SEQ ID NO:578) derived from the coding sequence of SEQ ID NO:577 shown in **FIG. 577**.

[0605] **FIG. 579** shows a nucleotide sequence (SEQ ID NO:579) of a native sequence PRO16090 cDNA, wherein SEQ ID NO:579 is a clone designated herein as "DNA144844-2843".

[0606] **FIG. 580** shows the amino acid sequence (SEQ ID NO:580) derived from the coding sequence of SEQ ID NO:579 shown in **FIG. 579**.

[0607] **FIG. 581** shows a nucleotide sequence (SEQ ID NO:581) of a native sequence PRO19576 cDNA, wherein SEQ ID NO:581 is a clone designated herein as "DNA144857-2845".

[0608] **FIG. 582** shows the amino acid sequence (SEQ ID NO:582) derived from the coding sequence of SEQ ID NO:581 shown in **FIG. 581**.

[0609] **FIG. 583** shows a nucleotide sequence (SEQ ID NO:583) of a native sequence PRO19646 cDNA, wherein SEQ ID NO:583 is a clone designated herein as "DNA145841-2868".

[0610] **FIG. 584** shows the amino acid sequence (SEQ ID NO:584) derived from the coding sequence of SEQ ID NO:583 shown in **FIG. 583**.

[0611] **FIG. 585** shows a nucleotide sequence (SEQ ID NO:585) of a native sequence PRO19814 cDNA, wherein SEQ ID NO:585 is a clone designated herein as "DNA148004-2882".

[0612] **FIG. 586** shows the amino acid sequence (SEQ ID NO:586) derived from the coding sequence of SEQ ID NO:585 shown in **FIG. 585**.

[0613] **FIG. 587** shows a nucleotide sequence (SEQ ID NO:587) of a native sequence PRO19669 cDNA, wherein SEQ ID NO:587 is a clone designated herein as "DNA149893-2873".

[0614] **FIG. 588** shows the amino acid sequence (SEQ ID NO:588) derived from the coding sequence of SEQ ID NO:587 shown in **FIG. 587**.

[0615] **FIG. 589** shows a nucleotide sequence (SEQ ID NO:589) of a native sequence PRO19818 cDNA, wherein SEQ ID NO:589 is a clone designated herein as "DNA149930-2884".

[0616] **FIG. 590** shows the amino acid sequence (SEQ ID NO:590) derived from the coding sequence of SEQ ID NO:589 shown in **FIG. 589**.

[0617] **FIG. 591** shows a nucleotide sequence (SEQ ID NO:591) of a native sequence PRO20088 cDNA, wherein SEQ ID NO:591 is a clone designated herein as "DNA150157-2898".

[0618] **FIG. 592** shows the amino acid sequence (SEQ ID NO:592) derived from the coding sequence of SEQ ID NO:591 shown in **FIG. 591**.

[0619] **FIG. 593** shows a nucleotide sequence (SEQ ID NO:593) of a native sequence PRO16089 cDNA, wherein SEQ ID NO:593 is a clone designated herein as "DNA150163-2842".

[0620] **FIG. 594** shows the amino acid sequence (SEQ ID NO:594) derived from the coding sequence of SEQ ID NO:593 shown in **FIG. 593**.

[0621] **FIG. 595** shows a nucleotide sequence (SEQ ID NO:595) of a native sequence PRO20025 cDNA, wherein SEQ ID NO:595 is a clone designated herein as "DNA153579-2894".

[0622] **FIG. 596** shows the amino acid sequence (SEQ ID NO:596) derived from the coding sequence of SEQ ID NO:595 shown in **FIG. 595**.

[0623] **FIG. 597** shows a nucleotide sequence (SEQ ID NO:597) of a native sequence PRO20040 cDNA, wherein SEQ ID NO:597 is a clone designated herein as "DNA164625-2890".

[0624] **FIG. 598** shows the amino acid sequence (SEQ ID NO:598) derived from the coding sequence of SEQ ID NO:597 shown in **FIG. 597**.

[0625] **FIG. 599** shows a nucleotide sequence (SEQ ID NO:599) of a native sequence PRO791 cDNA, wherein SEQ ID NO:599 is a clone designated herein as "DNA57838-1337".

[0626] **FIG. 600** shows the amino acid sequence (SEQ ID NO:600) derived from the coding sequence of SEQ ID NO:599 shown in **FIG. 599**.

[0627] **FIG. 601** shows a nucleotide sequence (SEQ ID NO:601) of a native sequence PRO1131 cDNA, wherein SEQ ID NO:601 is a clone designated herein as "DNA59777-1480".

[0628] **FIG. 602** shows the amino acid sequence (SEQ ID NO:602) derived from the coding sequence of SEQ ID NO:601 shown in **FIG. 601**.

[0629] **FIG. 603** shows a nucleotide sequence (SEQ ID NO:603) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:603 is a clone designated herein as "DNA66675-1587".

[0630] **FIG. 604** shows the amino acid sequence (SEQ ID NO:604) derived from the coding sequence of SEQ ID NO:603 shown in **FIG. 603**.

[0631] **FIG. 605** shows a nucleotide sequence (SEQ ID NO:605) of a native sequence PRO1760 cDNA, wherein SEQ ID NO:605 is a clone designated herein as "DNA76532-1702".

[0632] **FIG. 606** shows the amino acid sequence (SEQ ID NO:606) derived from the coding sequence of SEQ ID NO:605 shown in **FIG. 605**.

[0633] **FIG. 607** shows a nucleotide sequence (SEQ ID NO:607) of a native sequence PRO6029 cDNA, wherein SEQ ID NO:607 is a clone designated herein as "DNA105849-2704".

[0634] **FIG. 608** shows the amino acid sequence (SEQ ID NO:608) derived from the coding sequence of SEQ ID NO:607 shown in **FIG. 607**.

[0635] **FIG. 609** shows a nucleotide sequence (SEQ ID NO:609) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:609 is a clone designated herein as "DNA83500-2506".

[0636] **FIG. 610** shows the amino acid sequence (SEQ ID NO:610) derived from the coding sequence of SEQ ID NO:609 shown in **FIG. 609**.

DETAILED DESCRIPTION OF THE
PREFERRED EMBODIMENTS

[0637] I. Definitions

[0638] The terms “PRO polypeptide” and “PRO” as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms “PRO/number polypeptide” and “PRO/number” wherein the term “number” is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term “PRO polypeptide” refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the “PRO polypeptide” refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term “PRO polypeptide” also includes variants of the PRO/number polypeptides disclosed herein.

[0639] A “native sequence PRO polypeptide” comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term “native sequence PRO polypeptide” specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (e.g., an extracellular domain sequence), naturally-occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

[0640] The PRO polypeptide “extracellular domain” or “ECD” refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino

acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

[0641] The approximate location of the “signal peptides” of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., *Prot. Eng.* 10:1-6 (1997) and von Heinje et al., *Nucl. Acids. Res.* 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

[0642] “PRO polypeptide variant” means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a

PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

[0643] "Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0644] In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

[0645] where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B,

and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X," "Y" and "Z" each represent different hypothetical amino acid residues.

[0646] Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

[0647] Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropoff for final gapped alignment=25 and scoring matrix=BLOSUM62.

[0648] In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A

that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

[0649] where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

[0650] "PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

[0651] Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alter-

natively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

[0652] "Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

[0653] In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

[0654] where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

[0655] Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as

described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., *Methods in Enzymology* 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span=1, overlap fraction=0.125, word threshold (T)=11, and scoring matrix=BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

[0656] Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., *Nucleic Acids Res.* 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, Md. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask=yes, strand=all, expected occurrences=10, minimum low complexity length=15/5, multi-pass e-value=0.01, constant for multi-pass=25, dropout for final gapped alignment=25 and scoring matrix=BLOSUM62.

[0657] In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

[0658] where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

[0659] In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, prefer-

ably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

[0660] "Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide in situ within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

[0661] An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

[0662] The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

[0663] Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

[0664] The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO mono-

clonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptidic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term “monoclonal antibody” as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

[0665] “Stringency” of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., *Current Protocols in Molecular Biology*, Wiley Interscience Publishers, (1995).

[0666] “Stringent conditions” or “high stringency conditions”, as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50° C.; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42° C.; or (3) employ 50% formamide, 5× SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5× Denhardt’s solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42° C., with washes at 42° C. in 0.2× SSC (sodium chloride/sodium citrate) and 50% formamide at 55° C., followed by a high-stringency wash consisting of 0.1× SSC containing EDTA at 55° C.

[0667] “Moderately stringent conditions” may be identified as described by Sambrook et al., *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and % SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37° C. in a solution comprising: 20% formamide, 5× SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5× Denhardt’s solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1× SSC at about 37-50° C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

[0668] The term “epitope tagged” when used herein refers to a chimeric polypeptide comprising a PRO polypeptide

fused to a “tag polypeptide”. The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

[0669] As used herein, the term “immunoadhesin” designates antibody-like molecules which combine the binding specificity of a heterologous protein (an “adhesin”) with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is “heterologous”), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

[0670] “Active” or “activity” for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein “biological” activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an “immunological” activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

[0671] The term “antagonist” is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term “agonist” is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

[0672] “Treatment” refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

[0673] “Chronic” administration refers to administration of the agent(s) in a continuous mode as opposed to an acute

mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

[0674] "Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

[0675] Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

[0676] "Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are non-toxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEENTM, polyethylene glycol (PEG), and PLURONICSTM.

[0677] "Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., *Protein Eng.* 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

[0678] Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

[0679] "Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0680] The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or

more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0681] The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

[0682] Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

[0683] "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

[0684] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same polypeptide chain (V_H-V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

[0685] An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

[0686] An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

[0687] The word “label” when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a “labeled” antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

[0688] By “solid phase” is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of

discrete particles, such as those described in U.S. Pat. No. 4,275,149.

[0689] A “liposome” is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

[0690] A “small molecule” is defined herein to have a molecular weight below about 500 Daltons.

[0691] An “effective amount” of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An “effective amount” may be determined empirically and in a routine manner, in relation to the stated purpose.

Table 1

```

/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define _M -8 /* value of a match with a stop */

int _day[26][26] = {
/* A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
/* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
/* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
/* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ {_M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
/* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
/* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
#define MX          4       /* save if there's at least MX-1 bases since last jmp */

#define DMAT        3       /* value of matching bases */
#define DMIS        0       /* penalty for mismatched bases */
#define DINS0       8       /* penalty for a gap */
#define DINS1       1       /* penalty per base */
#define PINS0       8       /* penalty for a gap */
#define PINS1       4       /* penalty per residue */

struct jmp {
    short          n[MAXJMP];      /* size of jmp (neg for dely) */
    unsigned short x[MAXJMP];      /* base no. of jmp in seq x */
};
/* limits seq to 2^16 -1 */

struct diag {
    int            score;          /* score at last jmp */
    long           offset;         /* offset of prev block */
    short          jmp;           /* current jmp index */
    struct jmp     jp;            /* list of jmps */
};

struct path {
    int            spc;            /* number of leading spaces */
    short          n[JMPS];        /* size of jmp (gap) */
    int            x[JMPS];        /* loc of jmp (last elem before gap) */
};

char              *ofile;         /* output file name */
char              *namex[2];      /* seq names: getseqs() */
char              *prog;          /* prog name for err msgs */
char              *seqx[2];       /* seqs: getseqs() */
int               dmax;           /* best diag: nw() */
int               dmax0;          /* final diag */
int               dna;            /* set if dna: main() */
int               endgaps;        /* set if penalizing end gaps */
int               gapx, gapy;      /* total gaps in seqs */
int               len0, len1;      /* seq lens */
int               ngapx, ngapy;    /* total size of gaps */
int               smax;           /* max score: nw() */
int               *xbm;           /* bitmap for matching */
long              offset;         /* current offset in jmp file */
struct diag       *dx;            /* holds diagonals */
struct path       pp[2];          /* holds path for seqs */

char              *calloc(), *malloc(), *index(), *strcpy();
char              *getseq(), *g_calloc();

```

main

Table 1 (cont')

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
* When scores are equal, we prefer mismatches to any gap, prefer
* a new gap to extending an ongoing gap, and prefer a gap in seqx
* to a gap in seq y.
*/
nw()
{
    char          *px, *py;          /* seqs and ptrs */
    int           *ndely, *dely;      /* keep track of dely */
    int           ndelx, delx;        /* keep track of delx */
    int           *tmp;              /* for swapping row0, row1 */
    int           mis;               /* score for each type */
    int           ins0, ins1;         /* insertion penalties */
    register      id;                /* diagonal index */
    register      ij;               /* jmp index */
    register      *col0, *col1;       /* score for curr, last row */
    register      xx, yy;            /* index into seqs */

    dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

    ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
    dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
    col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
    col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
    ins0 = (dna)? DINS0 : PINS0;
    ins1 = (dna)? DINS1 : PINS1;

    smax = -10000;
    if (cndgaps) {
        for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
            col0[yy] = dely[yy] = col0[yy-1] - ins1;
            ndely[yy] = yy;
        }
        col0[0] = 0;          /* Waterman Bull Math Biol 84 */
    }
    else
        for (yy = 1; yy <= len1; yy++)
            dely[yy] = -ins0;

    /* fill in match matrix
    */
    for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
        /* initialize first entry in col
        */
        if (cndgaps) {
            if (xx == 1)
                col1[0] = delx = -(ins0+ins1);
            else
                col1[0] = delx = col0[0] - ins1;
            ndelx = xx;
        }
        else {
            col1[0] = 0;
            delx = -ins0;
            ndelx = 0;
        }
    }
}

```

Table 1 (cont')**...nw**

```

for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
    mis = col0[yy-1];
    if (dna)
        mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
    else
        mis += _day[*px-'A'][*py-'A'];

    /* update penalty for del in x seq;
     * favor new del over ongong del
     * ignore MAXGAP if weighting endgaps
     */
    if (endgaps || ndely[yy] < MAXGAP) {
        if (col0[yy] - ins0 >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else {
            dely[yy] -= ins1;
            ndely[yy]++;
        }
    } else {
        if (col0[yy] - (ins0+ins1) >= dely[yy]) {
            dely[yy] = col0[yy] - (ins0+ins1);
            ndely[yy] = 1;
        } else
            ndely[yy]++;
    }

    /* update penalty for del in y seq;
     * favor new del over ongong del
     */
    if (endgaps || ndelx < MAXGAP) {
        if (col1[yy-1] - ins0 >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else {
            delx -= ins1;
            ndelx++;
        }
    } else {
        if (col1[yy-1] - (ins0+ins1) >= delx) {
            delx = col1[yy-1] - (ins0+ins1);
            ndelx = 1;
        } else
            ndelx++;
    }

    /* pick the maximum score; we're favoring
     * mis over any del and delx over dely
     */

```

Table 1 (cont')

...nw

```

id = xx - yy + len1 - 1;
if (mis >= delx && mis >= dely[yy])
    col1[yy] = mis;
else if (delx >= dely[yy]) {
    col1[yy] = delx;
    ij = dx[id].ijmp;
    if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
    && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
        dx[id].ijmp++;
        if (++ij >= MAXJMP) {
            writejumps(id);
            ij = dx[id].ijmp = 0;
            dx[id].offset = offset;
            offset += sizeof(struct jmp) + sizeof(offset);
        }
        dx[id].jp.n[ij] = ndelx;
        dx[id].jp.x[ij] = xx;
        dx[id].score = delx;
    }
    else {
        col1[yy] = dely[yy];
        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
            dx[id].ijmp++;
            if (++ij >= MAXJMP) {
                writejumps(id);
                ij = dx[id].ijmp = 0;
                dx[id].offset = offset;
                offset += sizeof(struct jmp) + sizeof(offset);
            }
            dx[id].jp.n[ij] = -ndely[yy];
            dx[id].jp.x[ij] = xx;
            dx[id].score = dely[yy];
        }
        if (xx == lcn0 && yy < lcn1) {
            /* last col
            */
            if (endgaps)
                col1[yy] -= ins0+ins1*(len1-yy);
            if (col1[yy] > smax) {
                smax = col1[yy];
                dmax = id;
            }
        }
    }
    if (endgaps && xx < len0)
        col1[yy-1] -= ins0+ins1*(len0-xx);
    if (col1[yy-1] > smax) {
        smax = col1[yy-1];
        dmax = id;
    }
    tmp = col0; col0 = col1; col1 = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);
}

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC      3
#define P_LINE  256    /* maximum output line */
#define P_SPC    3      /* space between name or num and seq */

extern _day[26][26];
int olen;              /* set output line length */
FILE *fx;              /* output file */

print()
{
    int lx, ly, firstgap, lastgap;    /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
        fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
    olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
        pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
        pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
        lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
        lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

```

print

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)
    int      lx, ly;          /* "core" (minus endgaps) */
    int      firstgap, lastgap; /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
    char     outx[32];
    double   pct;
    register n0, n1;
    register char *p0, *p1;

    /* get total matches, score
     */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
        if (siz0) {
            p1++;
            n1++;
            siz0--;
        }
        else if (siz1) {
            p0++;
            n0++;
            siz1--;
        }
        else {
            if (xbm[*p0-'A']&xbm[*p1-'A'])
                nm++;
            if (n0++ == pp[0].x[i0])
                siz0 = pp[0].n[i0++];
            if (n1++ == pp[1].x[i1])
                siz1 = pp[1].n[i1++];
            p0++;
            p1++;
        }
    }

    /* pct homology:
     * if penalizing endgaps, base is the shorter seq
     * else, knock off overhangs and take shorter core
     */
    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
    pct = 100.*((double)nm)/((double)lx);
    fprintf(fx, "\n");
    fprintf(fx, "<%d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
}

```

getmat

Table 1 (cont')

```

fprintf(fx, "<gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)",
        ngapx, (dna)? "base":"residue", (ngapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
            ngapy, (dna)? "base":"residue", (ngapy == 1)? "" : "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
            lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
    else
        fprintf(fx, "<endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(namex[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr_align

Table 1 (cont')

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
         * do we have more of this sequence?
         */
        if (!*ps[i])
            continue;

        more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
        }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
        }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
            po[i]++;
            ps[i]++;

            /*
             * are we at next gap for this seq?
             */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                 * we need to merge all gaps
                 * at this location
                 */
                siz[i] = pp[i].n[ij[i]]++;
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]]++;
            }
            ni[i]++;
        }
    }
    if (++nn == olen || !more && nn) {
        dumpblock();
        for (i = 0; i < 2; i++)
            po[i] = out[i];
        nn = 0;
    }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
    register i;

    for (i = 0; i < 2; i++)
        *po[i]-- = '\0';
}

```

...pr_align

dumpblock

Table 1 (cont')

...dumpblock

```

(void) putc('\n', fx);
for (i = 0; i < 2; i++) {
    if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' '))
        if (i == 0)
            nums(i);
        if (i == 0 && *out[1])
            stars();
        putline(i);
        if (i == 0 && *out[1])
            fprintf(fx, star);
        if (i == 1)
            nums(i);
    }
}

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)
int    ix;    /* index in out[] holding seq line */
{
    char    nline[P_LINE];
    register    i, j;
    register char    *pn, *px, *py;

    for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
        *pn = ' ';
    for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
        if (*py == ' ' || *py == '-')
            *pn = ' ';
        else {
            if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                j = (i < 0)? -i : i;
                for (px = pn; j /= 10, px--)
                    *px = j%10 + '0';
                if (i < 0)
                    *px = '-';
            }
            else
                *pn = ' ';
            i++;
        }
    }
    *pn = '\0';
    nc[ix] = i;
    for (pn = nline; *pn; pn++)
        (void) putc(*pn, fx);
    (void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)
int    ix;
{

```

nums

putline

Table 1 (cont')**...putline**

```

int          i;
register char *px;

for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
    (void) putc(*px, fx);
for (; i < lmax+P_SPC; i++)
    (void) putc(' ', fx);

/* these count from 1:
 * ni[] is current element (from 1)
 * nc[] is number at start of current line
 */
for (px = out[ix]; *px; px++)
    (void) putc(*px&0x7F, fx);
(void) putc('\n', fx);
}

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()
{
    int          i;
    register char *p0, *p1, cx, *px;

    if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
        return;
    px = star;
    for (i = lmax+P_SPC; i; i--)
        *px++ = ' ';

    for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++){
        if (isalpha(*p0) && isalpha(*p1)) {
            if (xbm[*p0-'A']&xbm[*p1-'A'])
                cx = '*';
            nm++;
        }
        else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
            cx = '.';
        else
            cx = ' ';
    }
    else
        cx = ' ';
    *px++ = cx;
}
*px++ = '\n';
*px = '\0';
}

```

stars

Table 1 (cont')

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)
    char    *pn;    /* file name (may be path) */
{
    register char    *px, *py;

    py = 0;
    for (px = pn; *px; px++)
        if (*px == '/')
            py = px + 1;
    if (py)
        (void) strcpy(pn, py);
    return(strlen(pn));
}
```

stripname

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_alloc() -- calloc() with error checkin
 * readjumps() -- get the good jumps, from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";          /* tmp file for jumps */
FILE    *fj;

int      cleanup();                          /* cleanup tmp file */
long     lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i)
    int    i;
{
    if (fj)
        (void) unlink(jname);
    exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char     *
getseq(file, len)
    char    *file;    /* file name */
    int     *len;     /* seq len */
{
    char      line[1024], *pseq;
    register char *px, *py;
    int       natgc, tlen;
    FILE      *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';

```

cleanup

getseq

Table 1 (cont')

```

py = pseq + 4;
*len = tlen;
rewind(fp);

while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

char *
g_calloc(msg, nx, sz)
char *msg;          /* program, calling routine */
int nx, sz;          /* number and size of elements */
{
    char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
            fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
}

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
{
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

    if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
        }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
        while (1) {
            for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;

```

...getseq

g_calloc

readjmps

Table 1 (cont')**...readjumps**

```

    if (j < 0 && dx[dmax].offset && fj) {
        (void) lseek(fd, dx[dmax].offset, 0);
        (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
        (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
        dx[dmax].ijmp = MAXJMP-1;
    }
    else
        break;
}
if (i >= JMPS) {
    fprintf(stderr, "%s: too many gaps in alignment\n", prog);
    cleanup(1);
}
if (j >= 0) {
    siz = dx[dmax].jp.n[j];
    xx = dx[dmax].jp.x[j];
    dmax += siz;
    if (siz < 0) { /* gap in second seq */
        pp[1].n[i1] = -siz;
        xx += siz;
        /* id = xx - yy + len1 - 1 */
        /*
        pp[1].x[i1] = xx - dmax + len1 - 1;
        gapy++;
        ngapy -= siz;
        */
        /* ignore MAXGAP when doing endgaps */
        siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
        i1++;
    }
    else if (siz > 0) { /* gap in first seq */
        pp[0].n[i0] = siz;
        pp[0].x[i0] = xx;
        gapx++;
        ngapx += siz;
        /* ignore MAXGAP when doing endgaps */
        siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
        i0++;
    }
}
else
    break;
}

/* reverse the order of jumps */
/*
for (j = 0, i0--; j < i0; j++, i0--) {
    i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
    i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
}
for (j = 0, i1--; j < i1; j++, i1--) {
    i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
    i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
}
if (fd >= 0)
    (void) close(fd);
if (fj) {
    (void) unlink(jname);
    fj = 0;
    offset = 0;
}
}

```

Table 1 (cont')

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejumps(ix)
{
    int ix;

    char *mktemp();

    if (!fj) {
        if (mktemp(jname) < 0) {
            fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
            cleanup(1);
        }
        if (((fj = fopen(jname, "w")) == 0) {
            fprintf(stderr, "%s: can't write %s\n", prog, jname);
            exit(1);
        }
    }
    (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
    (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}
```

writejumps

TABLE 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 15 = 33.3%

[0692]

TABLE 3

PRO	XXXXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity = (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) = 5 divided by 10 = 50%

[0693]

TABLE 4

PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 6 divided by 14 = 42.9%

[0694]

TABLE 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity = (the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) = 4 divided by 12 = 33.3%

[0695] II. Compositions and Methods of the Invention

[0696] A. Full-Length PRO Polypeptides

[0697] The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

[0698] As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual

nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

[0699] B. PRO Polypeptide Variants

[0700] In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

[0701] Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative mutations set forth, for instance, in U.S. Pat. No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

[0702] PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

[0703] PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by poly-

merase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

[0704] In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

TABLE 6

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu

[0705] Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

[0706] (1) hydrophobic: norleucine, met, ala, val, leu, ile;

[0707] (2) neutral hydrophilic: cys, ser, thr;

[0708] (3) acidic: asp, glu;

[0709] (4) basic: asn, gin, his, lys, arg;

[0710] (5) residues that influence chain orientation: gly, pro; and

[0711] (6) aromatic: trp, tyr, phe.

[0712] Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

[0713] The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., *Nucl. Acids Res.*, 13:4331 (1986); Zoller et al., *Nucl. Acids Res.*, 10:6487 (1987)], cassette mutagenesis [Wells et al., *Gene*, 34:315 (1985)], restriction selection mutagenesis [Wells et al., *Philos. Trans. R. Soc. London SerA*, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

[0714] Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, *Science*, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, *The Proteins*, (W. H. Freeman & Co., N.Y.); Choithia, *J. Mol. Biol.*, 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

[0715] C. Modifications of PRO

[0716] Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C-terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis-(diazocetyl)-2-phenylethane, glutaraldehyde, N-hydroxy-succinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidyl-propionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

[0717] Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T. E. Creighton, *Proteins: Structure and Molecular Properties*, W. H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

[0718] Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means),

and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

[0719] Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

[0720] Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published Sep. 11, 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

[0721] Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge et al., *Anal. Biochem.* 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., *Meth. Enzymol.*, 138:350 (1987).

[0722] Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Pat. Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

[0723] The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

[0724] In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9,3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., *Protein Engineering*, 3(6):547-

553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., *Science*, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

[0725] In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also U.S. Pat. No. 5,428,130 issued Jun. 27, 1995.

[0726] D. Preparation of PRO

[0727] The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., *Solid-Phase Peptide Synthesis*, W. H. Freeman Co., San Francisco, Calif. (1969); Merrifield, *J. Am. Chem. Soc.*, 85:2149-2154 (1963)]. In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, Calif.) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

[0728] 1. Isolation of DNA Encoding PRO

[0729] DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

[0730] Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., *PCR Primer: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, 1995)].

[0731] The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ^{32}P -labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

[0732] Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

[0733] Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

[0734] 2. Selection and Transformation of Host Cells

[0735] Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in *Mammalian Cell Biotechnology: a Practical Approach*, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

[0736] Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., *Gene*, 23:315 (1983) and WO 89/05859 published Jun. 29, 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, *Virology*, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Pat. No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., *J. Bact.*, 130:946 (1977) and Hsiao et al., *Proc. Natl. Acad. Sci. (USA)*, 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene,

polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., *Methods in Enzymology*, 185:527-537 (1990) and Mansour et al., *Nature*, 336:348-352 (1988).

[0737] Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as Escherichia, e.g., *E. coli*, Enterobacter, Erwinia, Klebsiella, Proteus, Salmonella, e.g., *Salmonella typhimurium*, Serratia, e.g., *Serratia marcescans*, and Shigella, as well as Bacilli such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published Apr. 12, 1989), Pseudomonas such as *P. aeruginosa*, and Streptomyces. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype tonA ; *E. coli* W3110 strain 9E4, which has the complete genotype tonA ptr3; *E. coli* W3110 strain 27C7 (ATCC 55,244), which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169degP ompT kan^r; *E. coli* W3110 strain 37D6, which has the complete genotype tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant degP deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Pat. No. 4,946,783 issued Aug. 7, 1990. Alternatively, in vitro methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

[0738] In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, *Nature*, 290: 140 [1981]; EP 139,383 published May 2, 1985); Kluyveromyces hosts (U.S. Pat. No. 4,943,529; Fleer et al., *Bio/Technology*, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., *J. Bacteriol.*, 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., *Bio/Technology*, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., *J. Basic Microbiol.*, 28:265-278 [1988]); Candida; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., *Proc. Natl. Acad. Sci. USA*, 76:5259-5263 [1979]); Schwanniomycetes such as *Schwanniomycetes occidentalis* (EP 394,538 published Oct. 31, 1990); and filamentous fungi such as, e.g., Neurospora, Penicillium, Tolypocladium (WO 91/00357 published Jan. 10, 1991), and Aspergillus hosts such as *A. nidulans* (Balance et al., *Biochem. Biophys. Res. Commun.*, 112:284-289

[1983]; Tilburn et al., *Gene*, 26:205-221 [1983]; Yelton et al., *Proc. Natl. Acad. Sci. USA*, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, *EMBO J.*, 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, *The Biochemistry of Methylophilic Yeasts*, 269 (1982).

[0739] Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen. Virol.*, 36:59 (1977)); Chinese hamster ovary cells/DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, *Biol. Reprod.*, 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL 51). The selection of the appropriate host cell is deemed to be within the skill in the art.

[0740] 3. Selection and Use of a Replicable Vector

[0741] The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

[0742] The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Pat. No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published Apr. 4, 1990), or the signal described in WO 90/13646 published Nov. 15, 1990. In mammalian cell expression, mammalian signal sequences

may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

[0743] Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

[0744] Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

[0745] An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., *Proc. Natl. Acad. Sci. USA*, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., *Nature*, 282:39 (1979); Kingsman et al., *Gene*, 7:141 (1979); Tschemper et al., *Gene*, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, *Genetics*, 85:12 (1977)].

[0746] Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., *Nature*, 275:615 (1978); Goeddel et al., *Nature*, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, *Nucleic Acids Res.*, 8:4057 (1980); EP 36,776], and hybrid promoters such as the *tac* promoter [deBoer et al., *Proc. Natl. Acad. Sci. USA*, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

[0747] Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., *J. Biol. Chem.*, 255:2073 (1980)] or other glycolytic enzymes [Hess et al., *J. Adv. Enzyme Reg.*, 7:149 (1968); Holland, *Biochemistry*, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

[0748] Other yeast promoters, which are inducible promoters having the additional advantage of transcription

controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

[0749] PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published Jul. 5, 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

[0750] Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

[0751] Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

[0752] Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., *Nature*, 293:620-625 (1981); Mantei et al., *Nature*, 281:40-46 (1979); EP 117,060; and EP 117,058.

[0753] 4. Detecting Gene Amplification/Expression

[0754] Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, *Proc. Natl. Acad. Sci. USA*, 77:5201-5205 (1980)], dot blotting (DNA analysis), or in situ hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

[0755] Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

[0756] 5. Purification of Polypeptide

[0757] Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

[0758] It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, *Methods in Enzymology*, 182 (1990); Scopes, *Protein Purification: Principles and Practice*, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

[0759] E. Uses for PRO

[0760] Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

[0761] The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases.

Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

[0762] Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

[0763] Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (*Cancer Res.* 48:2659, 1988) and van der Krol et al. (*BioTechniques* 6:958, 1988).

[0764] Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable in vivo (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

[0765] Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increase affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

[0766] Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either in vivo or ex vivo. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retro-

virus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

[0767] Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

[0768] Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

[0769] Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

[0770] The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

[0771] Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as in situ hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

[0772] When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein

binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

[0773] Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

[0774] Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, *Cell*, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., *Cell*, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knock-

out animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

[0775] Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve in vivo synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes in vivo. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik et al., *Proc. Natl. Acad. Sci. USA* 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

[0776] There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells in vitro, or in vivo in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells in vitro include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred in vivo gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., *Trends in Biotechnology* 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., *J. Biol. Chem.* 262, 4429-4432 (1987); and Wagner et al., *Proc. Natl. Acad. Sci. USA* 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., *Science* 256, 808-813 (1992).

[0777] The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

[0778] The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

[0779] The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

[0780] The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (*Remington's Pharmaceutical Sciences* 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, PLURONICS™ or PEG.

[0781] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

[0782] Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

[0783] The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

[0784] Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

[0785] When in vivo administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage

amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μ g/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

[0786] Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-(rhIFN-), interleukin-2, and MN rgp120. Johnson et al., *Nat. Med.*, 2:795-799 (1996); Yasuda, *Biomed. Ther.*, 27:1221-1223 (1993); Hora et al., *BioTechnology*, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in *Vaccine Design: The Subunit and Adjuvant Approach*, Powell and Newman, eds. (Plenum Press: New York, 1995), pp.439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

[0787] The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), *Biodegradable Polymers as Drug Delivery Systems* (Marcel Dekker: New York, 1990), pp. 1-41.

[0788] This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

[0789] The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

[0790] All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

[0791] In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction

mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

[0792] If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, *Nature (London)*, 340:245-246 (1989); Chien et al., *Proc. Natl. Acad. Sci. USA*, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, *Proc. Natl. Acad. Sci. USA*, 89:5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-lacZ reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

[0793] Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the

reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

[0794] To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., *Current Protocols in Immun.*, 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

[0795] As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

[0796] In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

[0797] More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain anti-

bodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

[0798] Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix—see Lee et al., *Nucl. Acids Res.*, 6:3073 (1979); Cooney et al., *Science*, 241: 456 (1988); Dervan et al., *Science*, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the PRO polypeptide (antisense—Okano, *Neurochem.*, 56:560 (1991); *Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression* (CRC Press: Boca Raton, Fla., 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

[0799] Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

[0800] Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, *Current Biology*, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published Sep. 18, 1997).

[0801] Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, supra.

[0802] These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

[0803] Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

[0804] F. Anti-PRO Antibodies

[0805] The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

[0806] 1. Polyclonal Antibodies

[0807] The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

[0808] 2. Monoclonal Antibodies

[0809] The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature* 256:495(1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro.

[0810] The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp.59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine

phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

[0811] Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, Calif. and the American Type Culture Collection, Manassas, Va. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, *J. Immunol.*, 133:3001 (1984); Brodeur et al., *Monoclonal Antibody Production Techniques and Applications*, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

[0812] The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an in vitro binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, *Anal. Biochem.*, 107:220 (1980).

[0813] After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, *supra*]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown in vivo as ascites in a mammal.

[0814] The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

[0815] The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Pat. No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Pat. No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide.

Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

[0816] The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

[0817] In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

[0818] 3. Human and Humanized Antibodies

[0819] The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525(1986); Riechmann et al., *Nature*, 332:323-329(1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

[0820] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact

human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[0821] Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.* 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p.77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *Bio/technology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild et al., *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

[0822] The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

[0823] 4. Bispecific Antibodies

[0824] Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

[0825] Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published May 13, 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

[0826] Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The

fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., *Methods in Enzymology*, 121:210 (1986).

[0827] According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

[0828] Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using chemical linkage. Brennan et al., *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

[0829] Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

[0830] Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by

gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994). Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

[0831] Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

[0832] 5. Heteroconjugate Antibodies

[0833] Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Pat. No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared in vitro using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Pat. No. 4,676,980.

[0834] 6. Effector Function Engineering

[0835] It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp. Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with

enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*. 3: 219-230 (1989).

[0836] 7. Immunoconjugates

[0837] The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

[0838] Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re . Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimide HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl)hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethyl-enediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, aricin immunotoxin can be prepared as described in Vitetta et al., *Science*, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionuclide to the antibody. See WO94/11026.

[0839] In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionuclide).

[0840] 8. Immunoliposomes

[0841] The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., *Proc. Natl. Acad. Sci. USA*, 82: 3688 (1985); Hwang et al., *Proc. Natl. Acad. Sci. USA*, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556.

[0842] Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid compo-

sition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., *J. Biol. Chem.*, 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., *J. National Cancer Inst.*, 81(19): 1484 (1989).

[0843] 9. Pharmaceutical Compositions of Antibodies

[0844] Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

[0845] If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., *Proc. Natl. Acad. Sci. USA*, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

[0846] The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nano-capsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, supra.

[0847] The formulations to be used for in vivo administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

[0848] Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT™

(injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37° C., resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S—S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

[0849] G. Uses for anti-PRO Antibodies

[0850] The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, e.g., detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

[0851] Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

[0852] The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

[0853] All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

[0854] Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, Va.

Example 1

Extracellular Domain Homology Screening to
Identify Novel Polypeptides and cDNA Encoding
Therefor

[0855] The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (e.g., Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, Calif.). The search was performed using the computer program BLAST or BLAST-2 (Altschul et al., *Methods in Enzymology*, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Wash.).

[0856] Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

[0857] Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5 kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., *Current Protocols in Molecular Biology*, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

[0858] The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, Calif. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is

a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

Example 2

Isolation of cDNA clones by Amylase Screening

[0859] 1. Preparation of Oligo dT Primed cDNA Library

[0860] mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, Calif. (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, Md. (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linked cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

[0861] 2. Preparation of Random Primed cDNA Library

[0862] A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was sized to 500-1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

[0863] 3. Transformation and Detection

[0864] DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37° C. for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37° C.). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, e.g. CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

[0865] The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

[0866] The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha,

ura3-52, leu2-3, leu2-112, his3-11, his3-15, MAL⁺, SUC⁺, GAL⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in sec71, sec72, sec62, with truncated sec71 being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

[0867] Transformation was performed based on the protocol outlined by Gietz et al., *Nucl. Acid. Res.*, 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30° C. The YEPD broth was prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 207 (1994). The overnight culture was then diluted to about 2×10⁶ cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1×10⁷ cells/ml (approx. OD₆₀₀=0.4-0.5).

[0868] The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

[0869] Transformation took place by mixing the prepared cells (100 μ l) with freshly denatured single stranded salmon testes DNA (Lofstrand Labs, Gaithersburg, Md.) and transforming DNA (1 μ g, vol.<10 μ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li₂OOCCH₃, pH 7.5) was added. This mixture was gently mixed and incubated at 30° C. while agitating for 30 minutes. The cells were then heat shocked at 42° C. for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

[0870] Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

[0871] The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser et al., *Methods in Yeast Genetics*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y., p. 208-210 (1994). Transformants were grown at 30° C. for 2-3 days.

[0872] The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely et al.,

Anal. Biochem., 172:176-179(1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

[0873] The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

[0874] 4. Isolation of DNA by PCR Amplification

[0875] When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μ l) was used as a template for the PCR reaction in a 25 μ l volume containing: 0.5 μ l KlenTaq (Clontech, Palo Alto, Calif.); 4.0 μ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μ l Kentaq buffer (Clontech); 0.25 μ l forward oligo 1; 0.25 μ l reverse oligo 2; 12.5 μ l distilled water. The sequence of the forward oligonucleotide 1 was:

[0876] 5'-TGTAACGACGGCCAGTTAAATA-GACCTGCAATTATTAATCT-3' (SEQ ID NO:611)

[0877] The sequence of reverse oligonucleotide 2 was:

[0878] 5'-CAGGAAACAGCTATGACCACCTG-CACACCTGCAAATCCATT-3' (SEQ ID NO:612)

[0879] PCR was then performed as follows:

a.	Denature	92° C., 5 minutes
b. 3 cycles of	Denature	92° C., 30 seconds
	Anneal	59° C., 30 seconds
	Extend	72° C., 60 seconds
c. 3 cycles of	Denature	92° C., 30 seconds
	Anneal	57° C., 30 seconds
	Extend	72° C., 60 seconds
d. 25 cycles of	Denature	92° C., 30 seconds
	Anneal	55° C., 30 seconds
	Extend	72° C., 60 seconds
e.	Hold	4° C.

[0880] The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

[0881] Following the PCR, an aliquot of the reaction (5 μ l) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook et al., supra. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, Calif.).

Example 3

Isolation of cDNA Clones Using Signal Algorithm Analysis

[0882] Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, Calif.) upon ESTs as well as clustered and assembled EST fragments from public (e.g., GenBank) and/or private (LIFESQ®, Incyte Pharmaceuticals, Inc., Palo Alto, Calif.) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

Example 4

Isolation of cDNA Clones Encoding Human PRO Polypeptides

[0883] Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, Va. 20110-2209, USA (ATCC) as shown in Table 7 below.

TABLE 7

Material	ATCC Dep. No.	Deposit Date
DNA16435-1208	209930	Jun. 2, 1998
DNA23318-1211	209787	Apr. 21, 1998
DNA23322-1393	203400	Oct. 27, 1998
DNA23334-1392	209918	Jun. 2, 1998
DNA26843-1389	203099	Aug. 4, 1998
DNA26844-1394	209926	Jun. 2, 1998
DNA30867-1335	209807	Apr. 28, 1998
DNA33470-1175	209398	Oct. 17, 1997
DNA34436-1238	209523	Dec. 10, 1997
DNA35557-1137	209255	Sep. 16, 1997
DNA35599-1168	209373	Oct. 16, 1997
DNA35668-1171	209371	Oct. 16, 1997
DNA36992-1168	209382	Oct. 16, 1997
DNA39423-1182	209387	Oct. 17, 1997
DNA39427-1179	209395	Oct. 17, 1997
DNA39510-1181	209392	Oct. 17, 1997
DNA39518-1247	209529	Dec. 10, 1997
DNA39975-1210	209783	Apr. 21, 1998
DNA39976-1215	209524	Dec. 10, 1997
DNA39979-1213	209789	Apr. 21, 1998
DNA40594-1233	209617	Feb. 5, 1998
DNA40603-1232	209486	Nov. 21, 1997
DNA40604-1187	209394	Oct. 17, 1997
DNA40625-1189	209788	Apr. 21, 1998

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA41225-1217	209491	Nov. 21, 1997
DNA41379-1236	209488	Nov. 21, 1997
DNA41386-1316	209703	Mar. 26, 1998
DNA44161-1434	209907	May 27, 1998
DNA44179-1362	209851	May 6, 1998
DNA44192-1246	209531	Dec. 10, 1997
DNA44694-1500	203114	Aug. 11, 1998
DNA45234-1277	209654	Mar. 5, 1998
DNA45409-2511	203579	Jan. 12, 1999
DNA45415-1318	209810	Apr. 28, 1998
DNA45417-1432	209910	May 27, 1998
DNA45493-1349	209805	Apr. 28, 1998
DNA46776-1284	209721	Mar. 31, 1998
DNA48296-1292	209668	Mar. 11, 1998
DNA48306-1291	209911	May 27, 1998
DNA48328-1355	209843	May 6, 1998
DNA48329-1290	209785	Apr. 21, 1998
DNA48334-1435	209924	Jun. 2, 1998
DNA49141-1431	203003	Jun. 23, 1998
DNA49624-1279	209655	Mar. 5, 1998
DNA49647-1398	209919	Jun. 2, 1998
DNA49819-1439	209931	Jun. 2, 1998
DNA50911-1288	209714	Mar. 31, 1998
DNA50914-1289	209722	Mar. 31, 1998
DNA50919-1361	209848	May 6, 1998
DNA50980-1286	209717	Mar. 31, 1998
DNA52185-1370	209861	May 14, 1998
DNA53906-1368	209747	Apr. 7, 1998
DNA53912-1457	209870	May 14, 1998
DNA53913-1490	203162	Aug. 25, 1998
DNA53977-1371	209862	May 14, 1998
DNA53978-1443	209983	Jun. 16, 1998
DNA53996-1442	209921	Jun. 2, 1998
DNA54002-1367	209754	Apr. 7, 1998
DNA55737-1345	209753	Apr. 7, 1998
DNA56050-1455	203011	Jun. 23, 1998
DNA56052-1454	203026	Jun. 23, 1998
DNA56107-1415	203405	Oct. 27, 1998
DNA56110-1437	203113	Aug. 11, 1998
DNA56406-1704	203478	Nov. 17, 1998
DNA56409-1377	209882	May 20, 1998
DNA56410-1414	209923	Jun. 2, 1998
DNA56436-1448	209902	May 27, 1998
DNA56529-1647	203293	Sep. 29, 1998
DNA56855-1447	203004	Jun. 23, 1998
DNA56859-1445	203019	Jun. 23, 1998
DNA56860-1510	209952	Jun. 9, 1998
DNA56865-1491	203022	Jun. 23, 1998
DNA56868-1478	203024	Jun. 23, 1998
DNA56869-1545	203161	Aug. 25, 1998
DNA56870-1492	209925	Jun. 2, 1998
DNA57039-1402	209777	Apr. 14, 1998
DNA57253-1382	209867	May 14, 1998
DNA57254-1477	203289	Sep. 29, 1998
DNA57699-1412	203020	Jun. 23, 1998
DNA57704-1452	209953	Jun. 9, 1998
DNA57710-1451	203048	Jul. 1, 1998
DNA57827-1493	203045	Jul. 1, 1998
DNA57844-1410	203010	Jun. 23, 1998
DNA58723-1588	203133	Aug. 18, 1998
DNA58727-1474	203171	Sep. 1, 1998
DNA58730-1607	203221	Sep. 15, 1998
DNA58732-1650	203290	Sep. 29, 1998
DNA58737-1473	203136	Aug. 18, 1998
DNA58743-1609	203154	Aug. 25, 1998
DNA58747-1384	209868	May 14, 1998
DNA58828-1519	203172	Sep. 1, 1998
DNA58846-1409	209957	Jun. 9, 1998
DNA58848-1472	209955	Jun. 9, 1998
DNA58849-1494	209958	Jun. 9, 1998
DNA58850-1495	209956	Jun. 9, 1998
DNA58852-1637	203271	Sep. 22, 1998
DNA58853-1423	203016	Jun. 23, 1998
DNA58855-1422	203018	Jun. 23, 1998

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA59211-1450	209960	Jun. 9, 1998
DNA59212-1627	203245	Sep. 9, 1998
DNA59213-1487	209959	Jun. 9, 1998
DNA59219-1613	203220	Sep. 15, 1998
DNA59497-1496	209941	Jun. 4, 1998
DNA59602-1436	203051	Jul. 1, 1998
DNA59603-1419	209944	Jun. 9, 1998
DNA59605-1418	203005	Jun. 23, 1998
DNA59607-1497	209946	Jun. 9, 1998
DNA59610-1556	209990	Jun. 16, 1998
DNA59612-1466	209947	Jun. 9, 1998
DNA59613-1417	203007	Jun. 23, 1998
DNA59616-1465	209991	Jun. 16, 1998
DNA59619-1464	203041	Jul. 1, 1998
DNA59625-1498	209992	Jun. 16, 1998
DNA59817-1703	203470	Nov. 17, 1998
DNA59827-1426	203089	Aug. 4, 1998
DNA59828-1608	203158	Aug. 25, 1998
DNA59837-2545	203658	Feb. 9, 1999
DNA59844-2542	203650	Feb. 9, 1999
DNA59853-1505	209985	Jun. 16, 1998
DNA59854-1459	209974	Jun. 16, 1998
DNA59855-1485	209987	Jun. 16, 1998
DNA60278-1530	203170	Sep. 1, 1998
DNA60283-1484	203043	Jul. 1, 1998
DNA60608-1577	203126	Aug. 18, 1998
DNA60611-1524	203175	Sep. 1, 1998
DNA60619-1482	209993	Jun. 16, 1998
DNA60625-1507	209975	Jun. 16, 1998
DNA60629-1481	209979	Jun. 16, 1998
DNA60740-1615	203456	Nov. 3, 1998
DNA61608-1606	203239	Sep. 9, 1998
DNA61755-1554	203112	Aug. 11, 1998
DNA62809-1531	203237	Sep. 9, 1998
DNA62812-1594	203248	Sep. 9, 1998
DNA62813-2544	203655	Feb. 9, 1999
DNA62845-1684	203361	Oct. 20, 1998
DNA64849-1604	203468	Nov. 17, 1998
DNA64852-1589	203127	Aug. 18, 1998
DNA64863-1573	203251	Sep. 9, 1998
DNA64881-1602	203240	Sep. 9, 1998
DNA64902-1667	203317	Oct. 6, 1998
DNA64952-1568	203222	Sep. 15, 1998
DNA65403-1565	203230	Sep. 15, 1998
DNA65413-1534	203234	Sep. 15, 1998
DNA65423-1595	203227	Sep. 15, 1998
DNA66304-1546	203321	Oct. 6, 1998
DNA66308-1537	203159	Aug. 25, 1998
DNA66511-1563	203228	Sep. 15, 1998
DNA66512-1564	203218	Sep. 15, 1998
DNA66519-1535	203236	Sep. 15, 1998
DNA66521-1583	203225	Sep. 15, 1998
DNA66658-1584	203229	Sep. 15, 1998
DNA66660-1585	203279	Sep. 22, 1998
DNA66669-1597	203272	Sep. 22, 1998
DNA66674-1599	203281	Sep. 22, 1998
DNA68836-1656	203455	Nov. 3, 1998
DNA68862-2546	203652	Feb. 9, 1999
DNA68866-1644	203283	Sep. 22, 1998
DNA68869-1610	203164	Aug. 25, 1998
DNA68871-1638	203280	Sep. 22, 1998
DNA68879-1631	203274	Sep. 22, 1998
DNA68880-1676	203319	Oct. 6, 1998
DNA68882-1677	203318	Oct. 6, 1998
DNA68883-1691	203535	Dec. 15, 1998
DNA68885-1678	203311	Oct. 6, 1998
DNA71180-1655	203403	Oct. 27, 1998
DNA71184-1634	203266	Sep. 22, 1998
DNA71213-1659	203401	Oct. 27, 1998
DNA71234-1651	203402	Oct. 27, 1998
DNA71269-1621	203284	Sep. 22, 1998
DNA71277-1636	203285	Sep. 22, 1998
DNA71286-1687	203357	Oct. 20, 1998
DNA71883-1660	203475	Nov. 17, 1998

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA73401-1633	203273	Sep. 22, 1998
DNA73492-1671	203324	Oct. 6, 1998
DNA73730-1679	203320	Oct. 6, 1998
DNA73734-1680	203363	Oct. 20, 1998
DNA73735-1681	203356	Oct. 20, 1998
DNA73742-1662	203316	Oct. 6, 1998
DNA73746-1654	203411	Oct. 27, 1998
DNA73760-1672	203314	Oct. 6, 1998
DNA76393-1664	203323	Oct. 6, 1998
DNA76398-1699	203474	Nov. 17, 1998
DNA76399-1700	203472	Nov. 17, 1998
DNA76522-2500	203469	Nov. 17, 1998
DNA76533-1689	203410	Oct. 27, 1998
DNA77303-2502	203479	Nov. 17, 1998
DNA77626-1705	203536	Dec. 15, 1998
DNA77648-1688	203408	Oct. 27, 1998
DNA81754-2532	203542	Dec. 15, 1998
DNA81757-2512	203543	Dec. 15, 1998
DNA82302-2529	203534	Dec. 15, 1998
DNA82340-2530	203547	Dec. 22, 1998
DNA87991-2540	203656	Feb. 9, 1999
DNA92238-2539	203602	Jan. 20, 1999
DNA115291-2681	PTA-202	Jun. 8, 1999
DNA23336-2861	PTA-1673	Apr. 11, 2000
DNA30862-1396	209920	Jun. 2, 1998
DNA30871-1157	209380	Oct. 16, 1997
DNA32279-1131	209259	Sep. 16, 1997
DNA33206-1165	209372	Oct. 16, 1997
DNA35673-1201	209418	Oct. 28, 1997
DNA47361-1154-2	209431	Nov. 7, 1997
DNA49631-1328	209806	Apr. 28, 1998
DNA52594-1270	209679	Mar. 17, 1998
DNA55800-1263	209680	Mar. 17, 1998
DNA56531-1648	203286	Sep. 29, 1998
DNA56965-1356	209842	May 6, 1998
DNA57037-1444	209903	May 27, 1998
DNA57695-1340	203006	Jun. 23, 1998
DNA57834-1339	209954	Jun. 9, 1998
DNA57841-1522	203458	Nov. 3, 1998
DNA58847-1383	209879	May 20, 1998
DNA59493-1420	203050	Jul. 1, 1998
DNA59586-1520	203288	Sep. 29, 1998
DNA59608-2577	203870	Mar. 23, 1999
DNA59849-1504	209986	Jun. 16, 1998
DNA60292-1506	203540	Dec. 15, 1998
DNA62377-1381-1	203552	Dec. 22, 1998
DNA62880-1513	203097	Aug. 4, 1998
DNA66672-1586	203265	Sep. 22, 1998
DNA67962-1649	203291	Sep. 29, 1998
DNA69555-2867	PTA-1632	Apr. 4, 2000
DNA71162-2764	PTA-860	Oct. 19, 1999
DNA71290-1630	203275	Sep. 22, 1998
DNA76401-1683	203360	Oct. 20, 1998
DNA76541-1675	203409	Oct. 27, 1998
DNA76788-2526	203551	Dec. 22, 1998
DNA77623-2524	203546	Dec. 22, 1998
DNA80136-2503	203541	Dec. 15, 1998
DNA83568-2692	PTA-386	Jul. 20, 1999
DNA84210-2576	203818	Mar. 2, 1999
DNA86576-2595	203868	Mar. 23, 1999
DNA87976-2593	203888	Mar. 30, 1999
DNA92256-2596	203891	Mar. 30, 1999
DNA92289-2598	PTA-131	May 25, 1999
DNA96850-2705	PTA-479	Aug. 3, 1999
DNA96855-2629	PTA-18	May 4, 1999
DNA96857-2636	PTA-17	May 4, 1999
DNA96860-2700	PTA-478	Aug. 3, 1999
DNA96861-2844	PTA-1436	Mar. 2, 2000
DNA96866-2698	PTA-491	Aug. 3, 1999
DNA96870-2676	PTA-254	Jun. 22, 1999
DNA96872-2674	PTA-550	Aug. 17, 1999
DNA96878-2626	PTA-23	May 4, 1999
DNA96879-2619	203967	Apr. 27, 1999
DNA96889-2641	PTA-119	May 25, 1999

TABLE 7-continued

Material	ATCC Dep. No.	Deposit Date
DNA96893-2621	PTA-12	May 4, 1999
DNA96897-2688	PTA-379	Jul. 20, 1999
DNA98564-2643	PTA-125	May 25, 1999
DNA107443-2718	PTA-490	Aug. 3, 1999
DNA107786-2723	PTA-474	Aug. 3, 1999
DNA108682-2712	PTA-486	Aug. 3, 1999
DNA108684-2761	PTA-653	Sep. 14, 1999
DNA108701-2749	PTA-554	Aug. 17, 1999
DNA108720-2717	PTA-511	Aug. 10, 1999
DNA108726-2729	PTA-514	Aug. 10, 1999
DNA108728-2760	PTA-654	Sep. 14, 1999
DNA108738-2767	PTA-862	Oct. 19, 1999
DNA108743-2722	PTA-508	Aug. 10, 1999
DNA108758-2759	PTA-655	Sep. 14, 1999
DNA108765-2758	PTA-657	Sep. 14, 1999
DNA108783-2747	PTA-616	Aug. 31, 1999
DNA108789-2748	PTA-547	Aug. 17, 1999
DNA108806-2724	PTA-610	Aug. 31, 1999
DNA108936-2719	PTA-519	Aug. 10, 1999
DNA119510-2771	PTA-947	Nov. 9, 1999
DNA119517-2778	PTA-951	Nov. 16, 1999
DNA119535-2756	PTA-613	Aug. 31, 1999
DNA119537-2777	PTA-956	Nov. 16, 1999
DNA119714-2851	PTA-1537	Mar. 21, 2000
DNA125170-2780	PTA-953	Nov. 16, 1999
DNA129594-2841	PTA-1481	Mar. 14, 2000
DNA129793-2857	PTA-1733	Apr. 18, 2000
DNA130809-2769	PTA-949	Nov. 9, 1999
DNA131639-2874	PTA-1784	Apr. 25, 2000
DNA131649-2855	PTA-1482	Mar. 14, 2000
DNA131652-2876	PTA-1628	Apr. 4, 2000
DNA131658-2875	PTA-1671	Apr. 11, 2000
DNA132162-2770	PTA-950	Nov. 9, 1999
DNA136110-2763	PTA-652	Sep. 14, 1999
DNA139592-2866	PTA-1587	Mar. 28, 2000
DNA139608-2856	PTA-1581	Mar. 28, 2000
DNA143292-2848	PTA-1778	Apr. 25, 2000
DNA144844-2843	PTA-1536	Mar. 21, 2000
DNA144857-2845	PTA-1589	Mar. 28, 2000
DNA145841-2868	PTA-1678	Apr. 11, 2000
DNA148004-2882	PTA-1779	Apr. 25, 2000
DNA149893-2873	PTA-1672	Apr. 11, 2000
DNA149930-2884	PTA-1668	Apr. 11, 2000
DNA150157-2898	PTA-1777	Apr. 25, 2000
DNA150163-2842	PTA-1533	Mar. 21, 2000
DNA153579-2894	PTA-1729	Apr. 18, 2000
DNA164625-2890	PTA-1535	Mar. 21, 2000
DNA57838-1337	203014	Jun. 23, 1998
DNA59777-1480	203111	Aug. 11, 1998
DNA66675-1587	203282	Sep. 22, 1998
DNA76532-1702	203473	Nov. 17, 1998
DNA105849-2704	PTA-473	Aug. 3, 1999
DNA83500-2506	203391	Oct. 29, 1998

[0884] These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to

35 USC §122 and the Commissioner's rules pursuant thereto (including 37 CFR §1.14 with particular reference to 886 OG 638).

[0885] The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

Example 5

Use of PRO as a Hybridization Probe

[0886] The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

[0887] DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

[0888] Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5× SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2× Denhardt's solution, and 10% dextran sulfate at 42° C. for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1× SSC and 0.1% SDS at 42° C.

[0889] DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

Example 6

Expression of PRO in *E. coli*

[0890] This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

[0891] The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., *Gene*, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

[0892] The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

[0893] Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

[0894] After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

[0895] PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA (tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30° C. with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate.2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30° C. with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

[0896] *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4° C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4° C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

[0897] The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is

stirred gently at 4° C. for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

[0898] Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

[0899] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 7

Expression of PRO in Mammalian Cells

[0900] This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

[0901] The vector, pRK5 (see EP 307,247, published Mar. 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

[0902] In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 µg pRK5-PRO DNA is mixed with about 1 µg DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 µl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl₂. To this mixture is added, dropwise, 500 µl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO₄, and a precipitate is allowed to form for 10 minutes at 25° C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37° C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

[0903] Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 µCi/ml

^{35}S -cysteine and 200 $\mu\text{Ci/ml}$ ^{35}S -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

[0904] In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Sompariyac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μg pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 $\mu\text{g/ml}$ bovine insulin and 0.1 $\mu\text{g/ml}$ bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

[0905] In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

[0906] Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

[0907] PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

[0908] Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form. Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit

3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

[0909] Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Qiagen), Dosper® or Eugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

[0910] The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37° C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Pat. No. 5,122,469, issued Jun. 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33° C., and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μm filter. The filtrate was either stored at 4° C. or immediately loaded onto columns for purification.

[0911] For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 mL/min. at 4° C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80° C.

[0912] Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column

(Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

[0913] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 8

Expression of PRO in Yeast

[0914] The following method describes recombinant expression of PRO in yeast.

[0915] First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

[0916] Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

[0917] Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

[0918] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 9

Expression of PRO in Baculovirus-Infected Insect Cells

[0919] The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

[0920] The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers

complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

[0921] Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28° C., the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., *Baculovirus expression vectors: A Laboratory Manual*, Oxford: Oxford University Press (1994).

[0922] Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μ m filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₁₀ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed against loading buffer.

[0923] Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

[0924] Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

Example 10

Preparation of Antibodies that Bind PRO

[0925] This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

[0926] Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

[0927] Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and

injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, Mont.) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

[0928] After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63Ag.U.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

[0929] The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

[0930] The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

Example 11

Purification of PRO Polypeptides Using Specific Antibodies

[0931] Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

[0932] Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

[0933] Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

[0934] A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

Example 12

Drug Screening

[0935] This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

[0936] Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

[0937] Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on Sep. 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide

test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

[0938] This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

Example 13

Rational Drug Design

[0939] The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (i.e., a PRO polypeptide) or of small molecules with which they interact, e.g., agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide in vivo (c.f., Hodgson, *Bio/Technology*, 9: 19-21 (1991)).

[0940] In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda et al., *J. Biochem.*, 113:742-746 (1993).

[0941] It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

[0942] By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid

sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

Example 14

Identification of PRO Polypeptides That Stimulate TNF- α Release In Human Blood (Assay 128)

[0943] This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- α release would be beneficial. Specifically, 200 μ L of human blood supplemented with 50 mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300 μ L of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37° C. for 6 hours. The samples are then centrifuged and 50 μ L of plasma is collected from each well and tested for the presence of TNF- α by ELISA assay. A positive in the assay is a higher amount of TNF- α in the PRO polypeptide treated samples as compared to the negative control samples.

[0944] The following PRO polypeptides tested positive in this assay:

[0945] PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567, and PRO4333.

Example 15

Promotion of Chondrocyte Redifferentiation (Assay 129)

[0946] This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

[0947] Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 μ g/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 μ L of the same media without serum and 100 μ L of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 μ L/well. After 5 days at 37° C., 22 μ L of media containing 100 μ g/ml Hoechst 33342 and 50 μ g/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37° C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the >50% of the PRO polypeptide treated

cells are differentiated (compared to the background obtained by the negative control).

[0948] PRO6029 polypeptide tested positive in this assay.

Example 16

Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

[0949] Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

[0950] The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on Mar. 31, 2000 and which is herein incorporated by reference.

[0951] In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient ("matched colon control") were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective

relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

[0952] In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues listed above were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues as compared to a non-cancerous human tissue control. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

TABLE 8

Molecule	is overexpressed in:	as compared to:
PRO276	lung tumor	universal normal control
PRO284	colon tumor	universal normal control
PRO284	lung tumor	universal normal control
PRO284	breast tumor	universal normal control
PRO193	colon tumor	universal normal control
PRO193	lung tumor	universal normal control
PRO193	breast tumor	universal normal control
PRO193	prostate tumor	universal normal control
PRO190	colon tumor	universal normal control
PRO190	lung tumor	universal normal control
PRO190	breast tumor	universal normal control
PRO180	colon tumor	universal normal control
PRO180	lung tumor	universal normal control
PRO180	breast tumor	universal normal control
PRO194	colon tumor	universal normal control
PRO194	lung tumor	universal normal control
PRO194	breast tumor	universal normal control
PRO194	cervical tumor	universal normal control
PRO218	colon tumor	universal normal control
PRO218	lung tumor	universal normal control
PRO260	colon tumor	universal normal control
PRO260	lung tumor	universal normal control
PRO260	breast tumor	universal normal control
PRO260	rectal tumor	universal normal control
PRO233	colon tumor	universal normal control
PRO233	lung tumor	universal normal control
PRO233	breast tumor	universal normal control
PRO234	colon tumor	universal normal control
PRO234	lung tumor	universal normal control
PRO234	breast tumor	universal normal control
PRO234	liver tumor	universal normal control
PRO236	colon tumor	universal normal control
PRO236	lung tumor	universal normal control
PRO236	breast tumor	universal normal control
PRO244	colon tumor	universal normal control
PRO244	lung tumor	universal normal control
PRO262	colon tumor	universal normal control
PRO262	lung tumor	universal normal control
PRO262	breast tumor	universal normal control
PRO271	colon tumor	universal normal control
PRO271	lung tumor	universal normal control
PRO268	colon tumor	universal normal control
PRO268	lung tumor	universal normal control
PRO268	breast tumor	universal normal control
PRO270	colon tumor	universal normal control
PRO270	lung tumor	universal normal control
PRO270	breast tumor	universal normal control
PRO270	liver tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO537	breast tumor	universal normal control
PRO545	lung tumor	universal normal control
PRO545	breast tumor	universal normal control
PRO718	lung tumor	universal normal control
PRO718	breast tumor	universal normal control
PRO872	lung tumor	universal normal control
PRO872	breast tumor	universal normal control
PRO872	liver tumor	universal normal control
PRO704	colon tumor	universal normal control
PRO704	lung tumor	universal normal control
PRO704	breast tumor	universal normal control
PRO705	lung tumor	universal normal control
PRO705	breast tumor	universal normal control
PRO871	lung tumor	universal normal control
PRO871	breast tumor	universal normal control
PRO871	liver tumor	universal normal control
PRO702	lung tumor	universal normal control
PRO944	colon tumor	universal normal control
PRO944	lung tumor	universal normal control
PRO944	rectal tumor	universal normal control
PRO739	lung tumor	universal normal control
PRO739	breast tumor	universal normal control
PRO739	prostate tumor	universal normal control
PRO941	colon tumor	universal normal control
PRO941	lung tumor	universal normal control
PRO941	breast tumor	universal normal control
PRO941	rectal tumor	universal normal control
PRO1082	lung tumor	universal normal control
PRO1082	breast tumor	universal normal control
PRO1133	colon tumor	universal normal control
PRO1133	lung tumor	universal normal control
PRO983	colon tumor	universal normal control
PRO983	lung tumor	universal normal control
PRO983	breast tumor	universal normal control
PRO784	colon tumor	universal normal control
PRO784	lung tumor	universal normal control
PRO784	breast tumor	universal normal control
PRO784	prostate tumor	universal normal control
PRO783	colon tumor	universal normal control
PRO783	lung tumor	universal normal control
PRO783	breast tumor	universal normal control
PRO783	liver tumor	universal normal control
PRO940	colon tumor	universal normal control
PRO940	lung tumor	universal normal control
PRO940	breast tumor	universal normal control
PRO768	colon tumor	universal normal control
PRO768	lung tumor	universal normal control
PRO768	breast tumor	universal normal control
PRO1079	colon tumor	universal normal control
PRO1079	lung tumor	universal normal control
PRO1079	breast tumor	universal normal control
PRO1079	rectal tumor	universal normal control
PRO1078	colon tumor	universal normal control
PRO1078	lung tumor	universal normal control
PRO1018	colon tumor	universal normal control
PRO1018	lung tumor	universal normal control
PRO1018	breast tumor	universal normal control
PRO793	colon tumor	universal normal control
PRO793	lung tumor	universal normal control
PRO793	breast tumor	universal normal control
PRO793	rectal tumor	universal normal control
PRO1773	colon tumor	universal normal control
PRO1773	lung tumor	universal normal control
PRO1773	prostate tumor	universal normal control
PRO1014	lung tumor	universal normal control
PRO1014	breast tumor	universal normal control
PRO1013	colon tumor	universal normal control
PRO1013	lung tumor	universal normal control
PRO1013	breast tumor	universal normal control
PRO1013	liver tumor	universal normal control
PRO937	colon tumor	universal normal control
PRO937	lung tumor	universal normal control
PRO937	breast tumor	universal normal control
PRO937	cervical tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO1757	breast tumor	universal normal control
PRO1757	prostate tumor	universal normal control
PRO1758	lung tumor	universal normal control
PRO1781	colon tumor	universal normal control
PRO1781	lung tumor	universal normal control
PRO1781	breast tumor	universal normal control
PRO1606	lung tumor	universal normal control
PRO1606	breast tumor	universal normal control
PRO1784	colon tumor	universal normal control
PRO1784	lung tumor	universal normal control
PRO1784	breast tumor	universal normal control
PRO1774	colon tumor	universal normal control
PRO1774	lung tumor	universal normal control
PRO1774	breast tumor	universal normal control
PRO1605	colon tumor	universal normal control
PRO1605	lung tumor	universal normal control
PRO1605	prostate tumor	universal normal control
PRO1928	colon tumor	universal normal control
PRO1928	lung tumor	universal normal control
PRO1928	cervical tumor	universal normal control
PRO1865	lung tumor	universal normal control
PRO1865	liver tumor	universal normal control
PRO1925	lung tumor	universal normal control
PRO1926	liver tumor	universal normal control
PRO2630	colon tumor	universal normal control
PRO2630	lung tumor	universal normal control
PRO2630	breast tumor	universal normal control
PRO2630	liver tumor	universal normal control
PRO3443	colon tumor	universal normal control
PRO3443	lung tumor	universal normal control
PRO3443	breast tumor	universal normal control
PRO3301	colon tumor	universal normal control
PRO3301	lung tumor	universal normal control
PRO3301	breast tumor	universal normal control
PRO3301	rectal tumor	universal normal control
PRO3442	colon tumor	universal normal control
PRO3442	lung tumor	universal normal control
PRO3442	rectal tumor	universal normal control
PRO4978	colon tumor	universal normal control
PRO4978	lung tumor	universal normal control
PRO4978	breast tumor	universal normal control
PRO4978	rectal tumor	universal normal control
PRO5801	colon tumor	universal normal control
PRO5801	breast tumor	universal normal control
PRO19630	colon tumor	universal normal control
PRO203	colon tumor	universal normal control
PRO204	colon tumor	universal normal control
PRO204	lung tumor	universal normal control
PRO204	breast tumor	universal normal control
PRO204	prostate tumor	universal normal control
PRO210	colon tumor	universal normal control
PRO210	lung tumor	universal normal control
PRO223	lung tumor	universal normal control
PRO223	breast tumor	universal normal control
PRO247	colon tumor	universal normal control
PRO247	lung tumor	universal normal control
PRO247	breast	universal normal control
PRO358	lung tumor	universal normal control
PRO358	breast tumor	universal normal control
PRO358	prostate tumor	universal normal control
PRO724	lung tumor	universal normal control
PRO868	colon tumor	universal normal control
PRO868	lung tumor	universal normal control
PRO868	prostate tumor	universal normal control
PRO868	rectal tumor	universal normal control
PRO740	colon tumor	universal normal control
PRO1478	colon tumor	universal normal control
PRO1478	lung tumor	universal normal control
PRO162	colon tumor	universal normal control
PRO162	lung tumor	universal normal control
PRO162	breast tumor	universal normal control
PRO828	colon tumor	universal normal control
PRO828	lung tumor	universal normal control
PRO828	breast tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO828	cervical tumor	universal normal control
PRO828	liver tumor	universal normal control
PRO819	lung tumor	universal normal control
PRO819	breast tumor	universal normal control
PRO819	rectal tumor	universal normal control
PRO813	colon tumor	universal normal control
PRO813	lung tumor	universal normal control
PRO813	breast tumor	universal normal control
PRO813	prostate tumor	universal normal control
PRO1194	colon tumor	universal normal control
PRO1194	lung tumor	universal normal control
PRO1194	breast tumor	universal normal control
PRO887	colon tumor	universal normal control
PRO887	lung tumor	universal normal control
PRO887	rectal tumor	universal normal control
PRO1071	colon tumor	universal normal control
PRO1071	lung tumor	universal normal control
PRO1071	breast tumor	universal normal control
PRO1029	colon tumor	universal normal control
PRO1029	lung tumor	universal normal control
PRO1029	breast tumor	universal normal control
PRO1190	lung tumor	universal normal control
PRO1190	breast tumor	universal normal control
PRO4334	lung tumor	universal normal control
PRO1155	colon tumor	universal normal control
PRO1155	lung tumor	universal normal control
PRO1157	breast tumor	universal normal control
PRO1157	cervical tumor	universal normal control
PRO1122	lung tumor	universal normal control
PRO1122	breast tumor	universal normal control
PRO1183	colon tumor	universal normal control
PRO1183	lung tumor	universal normal control
PRO1183	breast tumor	universal normal control
PRO1337	colon tumor	universal normal control
PRO1337	lung tumor	universal normal control
PRO1337	breast tumor	universal normal control
PRO1480	colon tumor	universal normal control
PRO1480	lung tumor	universal normal control
PRO1480	breast tumor	universal normal control
PRO19645	colon tumor	universal normal control
PRO9782	colon tumor	universal normal control
PRO1419	colon tumor	universal normal control
PRO1575	colon tumor	universal normal control
PRO1575	lung tumor	universal normal control
PRO1567	colon tumor	universal normal control
PRO1567	lung tumor	universal normal control
PRO1567	breast tumor	universal normal control
PRO1891	colon tumor	universal normal control
PRO1889	colon tumor	universal normal control
PRO1889	lung tumor	universal normal control
PRO1785	lung tumor	universal normal control
PRO1785	prostate tumor	universal normal control
PRO6003	colon tumor	universal normal control
PRO4333	colon tumor	universal normal control
PRO4356	colon tumor	universal normal control
PRO4352	colon tumor	universal normal control
PRO4354	colon tumor	universal normal control
PRO4354	lung tumor	universal normal control
PRO4354	prostate tumor	universal normal control
PRO4369	colon tumor	universal normal control
PRO6030	colon tumor	universal normal control
PRO4433	colon tumor	universal normal control
PRO4424	colon tumor	universal normal control
PRO4424	breast tumor	universal normal control
PRO6017	colon tumor	universal normal control
PRO19563	colon tumor	universal normal control
PRO6015	colon tumor	universal normal control
PRO5779	colon tumor	universal normal control
PRO5776	colon tumor	universal normal control
PRO4430	lung tumor	universal normal control
PRO4421	colon tumor	universal normal control
PRO4499	colon tumor	universal normal control
PRO4423	colon tumor	universal normal control
PRO5998	colon tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO5998	lung tumor	universal normal control
PRO4501	colon tumor	universal normal control
PRO6240	colon tumor	universal normal control
PRO6245	colon tumor	universal normal control
PRO6175	colon tumor	universal normal control
PRO9742	colon tumor	universal normal control
PRO7179	colon tumor	universal normal control
PRO6239	colon tumor	universal normal control
PRO6493	colon tumor	universal normal control
PRO9741	colon tumor	universal normal control
PRO9822	colon tumor	universal normal control
PRO6244	colon tumor	universal normal control
PRO9740	colon tumor	universal normal control
PRO9739	colon tumor	universal normal control
PRO7177	colon tumor	universal normal control
PRO7178	colon tumor	universal normal control
PRO6246	colon tumor	universal normal control
PRO6241	colon tumor	universal normal control
PRO9835	colon tumor	universal normal control
PRO9857	colon tumor	universal normal control
PRO7436	colon tumor	universal normal control
PRO9856	colon tumor	universal normal control
PRO19605	colon tumor	universal normal control
PRO9859	colon tumor	universal normal control
PRO12970	colon tumor	universal normal control
PRO19626	colon tumor	universal normal control
PRO9883	colon tumor	universal normal control
PRO19670	colon tumor	universal normal control
PRO19624	colon tumor	universal normal control
PRO19680	colon tumor	universal normal control
PRO19675	colon tumor	universal normal control

TABLE 8-continued

Molecule	is overexpressed in:	as compared to:
PRO9834	colon tumor	universal normal control
PRO9744	colon tumor	universal normal control
PRO19644	colon tumor	universal normal control
PRO19625	colon tumor	universal normal control
PRO19597	colon tumor	universal normal control
PRO16090	colon tumor	universal normal control
PRO19576	colon tumor	universal normal control
PRO19646	colon tumor	universal normal control
PRO19814	colon tumor	universal normal control
PRO19669	colon tumor	universal normal control
PRO19818	colon tumor	universal normal control
PRO20088	colon tumor	universal normal control
PRO16089	colon tumor	universal normal control
PRO20025	colon tumor	universal normal control
PRO20040	colon tumor	universal normal control
PRO1760	adrenal tumor	universal normal control
PRO1760	breast tumor	universal normal control
PRO1760	cervical tumor	universal normal control
PRO1760	colon tumor	universal normal control
PRO1760	liver tumor	universal normal control
PRO1760	lung tumor	universal normal control
PRO1760	prostate tumor	universal normal control
PRO1760	rectal tumor	universal normal control
PRO6029	adrenal tumor	universal normal control
PRO6029	colon tumor	universal normal control
PRO6029	prostate tumor	universal normal control
PRO1801	colon tumor	universal normal control
PRO1801	lung tumor	universal normal control

[0953]

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (<http://seqdata.uspto.gov/sequence.html?DocID=20030036123>). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID

NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID

NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418), **FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472), **FIG. 474** (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548), **FIG. 550** (SEQ ID NO:550), **FIG. 552** (SEQ ID NO:552), **FIG. 554** (SEQ ID NO:554), **FIG. 556** (SEQ ID NO:556), **FIG. 558** (SEQ ID NO:558), **FIG. 560** (SEQ ID NO:560), **FIG. 562** (SEQ ID NO:562), **FIG. 564** (SEQ ID NO:564), **FIG. 566** (SEQ ID NO:566), **FIG. 568** (SEQ ID NO:568), **FIG. 570** (SEQ ID NO:570), **FIG. 572** (SEQ ID NO:572), **FIG. 574** (SEQ ID NO:574), **FIG. 576** (SEQ ID NO:576), **FIG. 578** (SEQ ID NO:578), **FIG. 580** (SEQ ID NO:580), **FIG. 582** (SEQ ID NO:582), **FIG. 584** (SEQ ID NO:584), **FIG. 586** (SEQ ID NO:586), **FIG. 588** (SEQ ID NO:588), **FIG. 590** (SEQ ID NO:590), **FIG. 592** (SEQ ID NO:592), **FIG. 594** (SEQ ID NO:594), **FIG. 596** (SEQ ID NO:596), **FIG. 598** (SEQ ID NO:598), **FIG. 600** (SEQ ID NO:600), **FIG. 602** (SEQ ID NO:602), **FIG. 604** (SEQ ID NO:604), **FIG. 606** (SEQ ID NO:606), **FIG. 608** (SEQ ID NO:608), and **FIG. 610** (SEQ ID NO:610).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in **FIG. 1** (SEQ ID NO:1), **FIG. 3** (SEQ ID NO:3), **FIG. 5** (SEQ ID NO:5), **FIG. 7** (SEQ ID NO:7), **FIG. 9** (SEQ ID NO:9), **FIG. 11** (SEQ ID NO:11), **FIG. 13** (SEQ ID NO:13), **FIG. 15** (SEQ ID NO:15), **FIG. 17** (SEQ ID NO:17), **FIG. 19** (SEQ ID NO:19), **FIG. 21** (SEQ ID NO:21), **FIG. 23** (SEQ ID NO:23), **FIG. 25** (SEQ ID NO:25), **FIG. 27** (SEQ ID

(SEQ ID NO:537), **FIG. 539** (SEQ ID NO:539), **FIG. 541** (SEQ ID NO:541), **FIG. 543** (SEQ ID NO:543), **FIG. 545** (SEQ ID NO:545), **FIG. 547** (SEQ ID NO:547), **FIG. 549** (SEQ ID NO:549), **FIG. 551** (SEQ ID NO:551), **FIG. 553** (SEQ ID NO:553), **FIG. 555** (SEQ ID NO:555), **FIG. 557** (SEQ ID NO:557), **FIG. 559** (SEQ ID NO:559), **FIG. 561** (SEQ ID NO:561), **FIG. 563** (SEQ ID NO:563), **FIG. 565** (SEQ ID NO:565), **FIG. 567** (SEQ ID NO:567), **FIG. 569** (SEQ ID NO:569), **FIG. 571** (SEQ ID NO:571), **FIG. 573** (SEQ ID NO:573), **FIG. 575** (SEQ ID NO:575), **FIG. 577** (SEQ ID NO:577), **FIG. 579** (SEQ ID NO:579), **FIG. 581** (SEQ ID NO:581), **FIG. 583** (SEQ ID NO:583), **FIG. 585** (SEQ ID NO:585), **FIG. 587** (SEQ ID NO:587), **FIG. 589** (SEQ ID NO:589), **FIG. 591** (SEQ ID NO:591), **FIG. 593** (SEQ ID NO:593), **FIG. 595** (SEQ ID NO:595), **FIG. 597** (SEQ ID NO:597), **FIG. 599** (SEQ ID NO:599), **FIG. 601** (SEQ ID NO:601), **FIG. 603** (SEQ ID NO:603), **FIG. 605** (SEQ ID NO:605), **FIG. 607** (SEQ ID NO:607), and **FIG. 609** (SEQ ID NO:609).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in **FIG. 1** (SEQ ID NO:1), **FIG. 3** (SEQ ID NO:3), **FIG. 5** (SEQ ID NO:5), **FIG. 7** (SEQ ID NO:7), **FIG. 9** (SEQ ID NO:9), **FIG. 11** (SEQ ID NO:11), **FIG. 13** (SEQ ID NO:13), **FIG. 15** (SEQ ID NO:15), **FIG. 17** (SEQ ID NO:17), **FIG. 19** (SEQ ID NO:19), **FIG. 21** (SEQ ID NO:21), **FIG. 23** (SEQ ID NO:23), **FIG. 25** (SEQ ID NO:25), **FIG. 27** (SEQ ID NO:27), **FIG. 29** (SEQ ID NO:29), **FIG. 31** (SEQ ID NO:31), **FIG. 33** (SEQ ID NO:33), **FIG. 35** (SEQ ID NO:35), **FIG. 37** (SEQ ID NO:37), **FIG. 39** (SEQ ID NO:39), **FIG. 41** (SEQ ID NO:41), **FIG. 43** (SEQ ID NO:43), **FIG. 45** (SEQ ID NO:45), **FIG. 47** (SEQ ID NO:47), **FIG. 49** (SEQ ID NO:49), **FIG. 51** (SEQ ID NO:51), **FIG. 53** (SEQ ID NO:53), **FIG. 55** (SEQ ID NO:55), **FIG. 57** (SEQ ID NO:57), **FIG. 59** (SEQ ID NO:59), **FIG. 61** (SEQ ID NO:61), **FIG. 63** (SEQ ID NO:63), **FIG. 65** (SEQ ID NO:65), **FIG. 67** (SEQ ID NO:67), **FIG. 69** (SEQ ID NO:69), **FIG. 71** (SEQ ID NO:71), **FIG. 73** (SEQ ID NO:73), **FIGS. 75A-75B** (SEQ ID NO:75), **FIG. 77** (SEQ ID NO:77), **FIG. 79** (SEQ ID NO:79), **FIG. 81** (SEQ ID NO:81), **FIG. 83** (SEQ ID NO:83), **FIG. 85** (SEQ ID NO:85), **FIG. 87** (SEQ ID NO:87), **FIG. 89** (SEQ ID NO:89), **FIG. 91** (SEQ ID NO:91), **FIG. 93** (SEQ ID NO:93), **FIG. 95** (SEQ ID NO:95), **FIG. 97** (SEQ ID NO:97), **FIG. 99** (SEQ ID NO:99), **FIG. 101** (SEQ ID NO:101), **FIG. 103** (SEQ ID NO:103), **FIG. 105** (SEQ ID NO:105), **FIG. 107** (SEQ ID NO:107), **FIG. 109** (SEQ ID NO:109), **FIG. 111** (SEQ ID NO:111), **FIG. 113** (SEQ ID NO:113), **FIG. 115** (SEQ ID NO:115), **FIG. 117** (SEQ ID NO:117), **FIG. 119** (SEQ ID NO:119), **FIG. 121** (SEQ ID NO:121), **FIG. 123** (SEQ ID NO:123), **FIG. 125** (SEQ ID NO:125), **FIG. 127** (SEQ ID NO:127), **FIG. 129** (SEQ ID NO:129), **FIG. 131** (SEQ ID NO:131), **FIG. 133** (SEQ ID NO:133), **FIG. 135** (SEQ ID NO:135), **FIG. 137** (SEQ ID NO:137), **FIG. 139** (SEQ ID NO:139), **FIG. 141** (SEQ ID NO:141), **FIG. 143** (SEQ ID NO:143), **FIG. 145** (SEQ ID NO:145), **FIG. 147** (SEQ ID NO:147), **FIG. 149** (SEQ ID NO:149), **FIG. 151** (SEQ ID NO:151), **FIG. 153** (SEQ ID NO:153), **FIG. 155** (SEQ ID NO:155), **FIG. 157** (SEQ ID NO:157), **FIG. 159** (SEQ ID NO:159), **FIG. 161** (SEQ ID NO:161), **FIG. 163** (SEQ ID NO:163), **FIG. 165** (SEQ ID NO:165), **FIG. 167** (SEQ ID NO:167), **FIG. 169** (SEQ ID

NO:169), **FIG. 171** (SEQ ID NO:171), **FIG. 173** (SEQ ID NO:173), **FIG. 175** (SEQ ID NO:175), **FIG. 177** (SEQ ID NO:177), **FIG. 179** (SEQ ID NO:179), **FIG. 181** (SEQ ID NO:181), **FIG. 183** (SEQ ID NO:183), **FIG. 185** (SEQ ID NO:185), **FIG. 187** (SEQ ID NO:187), **FIG. 189** (SEQ ID NO:189), **FIG. 191** (SEQ ID NO:191), **FIG. 193** (SEQ ID NO:193), **FIG. 195** (SEQ ID NO:195), **FIG. 197** (SEQ ID NO:197), **FIG. 199** (SEQ ID NO:199), **FIG. 201** (SEQ ID NO:201), **FIG. 203** (SEQ ID NO:203), **FIG. 205** (SEQ ID NO:205), **FIG. 207** (SEQ ID NO:207), **FIG. 209** (SEQ ID NO:209), **FIG. 211** (SEQ ID NO:211), **FIG. 213** (SEQ ID NO:213), **FIG. 215** (SEQ ID NO:215), **FIG. 217** (SEQ ID NO:217), **FIG. 219** (SEQ ID NO:219), **FIG. 221** (SEQ ID NO:221), **FIG. 223** (SEQ ID NO:223), **FIG. 225** (SEQ ID NO:225), **FIG. 227** (SEQ ID NO:227), **FIG. 229** (SEQ ID NO:229), **FIG. 231** (SEQ ID NO:231), **FIG. 233** (SEQ ID NO:233), **FIG. 235** (SEQ ID NO:235), **FIG. 237** (SEQ ID NO:237), **FIG. 239** (SEQ ID NO:239), **FIG. 241** (SEQ ID NO:241), **FIG. 243** (SEQ ID NO:243), **FIG. 245** (SEQ ID NO:245), **FIG. 247** (SEQ ID NO:247), **FIG. 249** (SEQ ID NO:249), **FIG. 251** (SEQ ID NO:251), **FIG. 253** (SEQ ID NO:253), **FIG. 255** (SEQ ID NO:255), **FIG. 257** (SEQ ID NO:257), **FIG. 259** (SEQ ID NO:259), **FIG. 261** (SEQ ID NO:261), **FIG. 263** (SEQ ID NO:263), **FIG. 265** (SEQ ID NO:265), **FIG. 267** (SEQ ID NO:267), **FIG. 269** (SEQ ID NO:269), **FIG. 271** (SEQ ID NO:271), **FIG. 273** (SEQ ID NO:273), **FIG. 275** (SEQ ID NO:275), **FIG. 277** (SEQ ID NO:277), **FIG. 279** (SEQ ID NO:279), **FIG. 281** (SEQ ID NO:281), **FIG. 283** (SEQ ID NO:283), **FIG. 285** (SEQ ID NO:285), **FIG. 287** (SEQ ID NO:287), **FIGS. 289A-289B** (SEQ ID NO:289), **FIG. 291** (SEQ ID NO:291), **FIG. 293** (SEQ ID NO:293), **FIG. 295** (SEQ ID NO:295), **FIG. 297** (SEQ ID NO:297), **FIG. 299** (SEQ ID NO:299), **FIG. 301** (SEQ ID NO:301), **FIG. 303** (SEQ ID NO:303), **FIG. 305** (SEQ ID NO:305), **FIG. 307** (SEQ ID NO:307), **FIG. 309** (SEQ ID NO:309), **FIGS. 311A-311B** (SEQ ID NO:311), **FIG. 313** (SEQ ID NO:313), **FIG. 315** (SEQ ID NO:315), **FIG. 317** (SEQ ID NO:317), **FIG. 319** (SEQ ID NO:319), **FIG. 321** (SEQ ID NO:321), **FIG. 323** (SEQ ID NO:323), **FIG. 325** (SEQ ID NO:325), **FIG. 327** (SEQ ID NO:327), **FIG. 329** (SEQ ID NO:329), **FIG. 331** (SEQ ID NO:331), **FIG. 333** (SEQ ID NO:333), **FIG. 335** (SEQ ID NO:335), **FIG. 337** (SEQ ID NO:337), **FIG. 339** (SEQ ID NO:339), **FIG. 341** (SEQ ID NO:341), **FIG. 343** (SEQ ID NO:343), **FIG. 345** (SEQ ID NO:345), **FIG. 347** (SEQ ID NO:347), **FIG. 349** (SEQ ID NO:349), **FIGS. 351A-351B** (SEQ ID NO:351), **FIG. 353** (SEQ ID NO:353), **FIG. 355** (SEQ ID NO:355), **FIG. 357** (SEQ ID NO:357), **FIG. 359** (SEQ ID NO:359), **FIG. 361** (SEQ ID NO:361), **FIG. 363** (SEQ ID NO:363), **FIG. 365** (SEQ ID NO:365), **FIG. 367** (SEQ ID NO:367), **FIG. 369** (SEQ ID NO:369), **FIG. 371** (SEQ ID NO:371), **FIG. 373** (SEQ ID NO:373), **FIG. 375** (SEQ ID NO:375), **FIG. 377** (SEQ ID NO:377), **FIG. 379** (SEQ ID NO:379), **FIG. 381** (SEQ ID NO:381), **FIG. 383** (SEQ ID NO:383), **FIG. 385** (SEQ ID NO:385), **FIG. 387** (SEQ ID NO:387), **FIG. 389** (SEQ ID NO:389), **FIG. 391** (SEQ ID NO:391), **FIG. 393** (SEQ ID NO:393), **FIG. 395** (SEQ ID NO:395), **FIG. 397** (SEQ ID NO:397), **FIG. 399** (SEQ ID NO:399), **FIG. 401** (SEQ ID NO:401), **FIG. 403** (SEQ ID NO:403), **FIG. 405** (SEQ ID NO:405), **FIG. 407** (SEQ ID NO:407), **FIG. 409** (SEQ ID NO:409), **FIG. 411** (SEQ ID NO:411), **FIG. 413** (SEQ ID NO:413), **FIG. 415** (SEQ ID NO:415), **FIG. 417** (SEQ ID NO:417), **FIG. 419** (SEQ ID NO:419), **FIG. 421** (SEQ ID NO:421), **FIG. 423** (SEQ ID

NO:423), **FIG. 425** (SEQ ID NO:425), **FIG. 427** (SEQ ID NO:427), **FIG. 429** (SEQ ID NO:429), **FIG. 431** (SEQ ID NO:431), **FIG. 433** (SEQ ID NO:433), **FIG. 435** (SEQ ID NO:435), **FIG. 437** (SEQ ID NO:437), **FIG. 439** (SEQ ID NO:439), **FIG. 441** (SEQ ID NO:441), **FIG. 443** (SEQ ID NO:443), **FIG. 445** (SEQ ID NO:445), **FIG. 447** (SEQ ID NO:447), **FIG. 449** (SEQ ID NO:449), **FIG. 451** (SEQ ID NO:451), **FIG. 453** (SEQ ID NO:453), **FIG. 455** (SEQ ID NO:455), **FIG. 457** (SEQ ID NO:457), **FIG. 459** (SEQ ID NO:459), **FIG. 461** (SEQ ID NO:461), **FIG. 463** (SEQ ID NO:463), **FIG. 465** (SEQ ID NO:465), **FIG. 467** (SEQ ID NO:467), **FIG. 469** (SEQ ID NO:469), **FIG. 471** (SEQ ID NO:471), **FIG. 473** (SEQ ID NO:473), **FIG. 475** (SEQ ID NO:475), **FIG. 477** (SEQ ID NO:477), **FIG. 479** (SEQ ID NO:479), **FIG. 481** (SEQ ID NO:481), **FIG. 483** (SEQ ID NO:483), **FIG. 485** (SEQ ID NO:485), **FIG. 487** (SEQ ID NO:487), **FIG. 489** (SEQ ID NO:489), **FIG. 491** (SEQ ID NO:491), **FIG. 493** (SEQ ID NO:493), **FIG. 495** (SEQ ID NO:495), **FIG. 497** (SEQ ID NO:497), **FIG. 499** (SEQ ID NO:499), **FIG. 501** (SEQ ID NO:501), **FIG. 503** (SEQ ID NO:503), **FIG. 505** (SEQ ID NO:505), **FIG. 507** (SEQ ID NO:507), **FIG. 509** (SEQ ID NO:509), **FIG. 511** (SEQ ID NO:511), **FIG. 513** (SEQ ID NO:513), **FIG. 515** (SEQ ID NO:515), **FIG. 517** (SEQ ID NO:517), **FIG. 519** (SEQ ID NO:519), **FIG. 521** (SEQ ID NO:521), **FIG. 523** (SEQ ID NO:523), **FIGS. 525A-525B** (SEQ ID NO:525), **FIG. 527** (SEQ ID NO:527), **FIG. 529** (SEQ ID NO:529), **FIG. 531** (SEQ ID NO:531), **FIG. 533** (SEQ ID NO:533), **FIG. 535** (SEQ ID NO:535), **FIG. 537** (SEQ ID NO:537), **FIG. 539** (SEQ ID NO:539), **FIG. 541** (SEQ ID NO:541), **FIG. 543** (SEQ ID NO:543), **FIG. 545** (SEQ ID NO:545), **FIG. 547** (SEQ ID NO:547), **FIG. 549** (SEQ ID NO:549), **FIG. 551** (SEQ ID NO:551), **FIG. 553** (SEQ ID NO:553), **FIG. 555** (SEQ ID NO:555), **FIG. 557** (SEQ ID NO:557), **FIG. 559** (SEQ ID NO:559), **FIG. 561** (SEQ ID NO:561), **FIG. 563** (SEQ ID NO:563), **FIG. 565** (SEQ ID NO:565), **FIG. 567** (SEQ ID NO:567), **FIG. 569** (SEQ ID NO:569), **FIG. 571** (SEQ ID NO:571), **FIG. 573** (SEQ ID NO:573), **FIG. 575** (SEQ ID NO:575), **FIG. 577** (SEQ ID NO:577), **FIG. 579** (SEQ ID NO:579), **FIG. 581** (SEQ ID NO:581), **FIG. 583** (SEQ ID NO:583), **FIG. 585** (SEQ ID NO:585), **FIG. 587** (SEQ ID NO:587), **FIG. 589** (SEQ ID NO:589), **FIG. 591** (SEQ ID NO:591), **FIG. 593** (SEQ ID NO:593), **FIG. 595** (SEQ ID NO:595), **FIG. 597** (SEQ ID NO:597), **FIG. 599** (SEQ ID NO:599), **FIG. 601** (SEQ ID NO:601), **FIG. 603** (SEQ ID NO:603), **FIG. 605** (SEQ ID NO:605), **FIG. 607** (SEQ ID NO:607), and **FIG. 609** (SEQ ID NO:609).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of claim 1.

6. A host cell comprising the vector of claim 5.

7. The host cell of claim 6, wherein said cell is a CHO cell.

8. The host cell of claim 6, wherein said cell is an *E. coli*.

9. The host cell of claim 6, wherein said cell is a yeast cell.

10. A process for producing a PRO polypeptide comprising culturing the host cell of claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6**

(SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID

NO:262), FIG. 264 (SEQ ID NO:264), FIG. 266 (SEQ ID NO:266), FIG. 268 (SEQ ID NO:268), FIG. 270 (SEQ ID NO:270), FIG. 272 (SEQ ID NO:272), FIG. 274 (SEQ ID NO:274), FIG. 276 (SEQ ID NO:276), FIG. 278 (SEQ ID NO:278), FIG. 280 (SEQ ID NO:280), FIG. 282 (SEQ ID NO:282), FIG. 284 (SEQ ID NO:284), FIG. 286 (SEQ ID NO:286), FIG. 288 (SEQ ID NO:288), FIG. 290 (SEQ ID NO:290), FIG. 292 (SEQ ID NO:292), FIG. 294 (SEQ ID NO:294), FIG. 296 (SEQ ID NO:296), FIG. 298 (SEQ ID NO:298), FIG. 300 (SEQ ID NO:300), FIG. 302 (SEQ ID NO:302), FIG. 304 (SEQ ID NO:304), FIG. 306 (SEQ ID NO:306), FIG. 308 (SEQ ID NO:308), FIG. 310 (SEQ ID NO:310), FIG. 312 (SEQ ID NO:312), FIG. 314 (SEQ ID NO:314), FIG. 316 (SEQ ID NO:316), FIG. 318 (SEQ ID NO:318), FIG. 320 (SEQ ID NO:320), FIG. 322 (SEQ ID NO:322), FIG. 324 (SEQ ID NO:324), FIG. 326 (SEQ ID NO:326), FIG. 328 (SEQ ID NO:328), FIG. 330 (SEQ ID NO:330), FIG. 332 (SEQ ID NO:332), FIG. 334 (SEQ ID NO:334), FIG. 336 (SEQ ID NO:336), FIG. 338 (SEQ ID NO:338), FIG. 340 (SEQ ID NO:340), FIG. 342 (SEQ ID NO:342), FIG. 344 (SEQ ID NO:344), FIG. 346 (SEQ ID NO:346), FIG. 348 (SEQ ID NO:348), FIG. 350 (SEQ ID NO:350), FIG. 352 (SEQ ID NO:352), FIG. 354 (SEQ ID NO:354), FIG. 356 (SEQ ID NO:356), FIG. 358 (SEQ ID NO:358), FIG. 360 (SEQ ID NO:360), FIG. 362 (SEQ ID NO:362), FIG. 364 (SEQ ID NO:364), FIG. 366 (SEQ ID NO:366), FIG. 368 (SEQ ID NO:368), FIG. 370 (SEQ ID NO:370), FIG. 372 (SEQ ID NO:372), FIG. 374 (SEQ ID NO:374), FIG. 376 (SEQ ID NO:376), FIG. 378 (SEQ ID NO:378), FIG. 380 (SEQ ID NO:380), FIG. 382 (SEQ ID NO:382), FIG. 384 (SEQ ID NO:384), FIG. 386 (SEQ ID NO:386), FIG. 388 (SEQ ID NO:388), FIG. 390 (SEQ ID NO:390), FIG. 392 (SEQ ID NO:392), FIG. 394 (SEQ ID NO:394), FIG. 396 (SEQ ID NO:396), FIG. 398 (SEQ ID NO:398), FIG. 400 (SEQ ID NO:400), FIG. 402 (SEQ ID NO:402), FIG. 404 (SEQ ID NO:404), FIG. 406 (SEQ ID NO:406), FIG. 408 (SEQ ID NO:408), FIG. 410 (SEQ ID NO:410), FIG. 412 (SEQ ID NO:412), FIG. 414 (SEQ ID NO:414), FIG. 416 (SEQ ID NO:416), FIG. 418 (SEQ ID NO:418), FIG. 420 (SEQ ID NO:420), FIG. 422 (SEQ ID NO:422), FIG. 424 (SEQ ID NO:424), FIG. 426 (SEQ ID NO:426), FIG. 428 (SEQ ID NO:428), FIG. 430 (SEQ ID NO:430), FIG. 432 (SEQ ID NO:432), FIG. 434 (SEQ ID NO:434), FIG. 436 (SEQ ID NO:436), FIG. 438 (SEQ ID NO:438), FIG. 440 (SEQ ID NO:440), FIG. 442 (SEQ ID NO:442), FIG. 444 (SEQ ID NO:444), FIG. 446 (SEQ ID NO:446), FIG. 448 (SEQ ID NO:448), FIG. 450 (SEQ ID NO:450), FIG. 452 (SEQ ID NO:452), FIG. 454 (SEQ ID NO:454), FIG. 456 (SEQ ID NO:456), FIG. 458 (SEQ ID NO:458), FIG. 460 (SEQ ID NO:460), FIG. 462 (SEQ ID NO:462), FIG. 464 (SEQ ID NO:464), FIG. 466 (SEQ ID NO:466), FIG. 468 (SEQ ID NO:468), FIG. 470 (SEQ ID NO:470), FIG. 472 (SEQ ID NO:472), FIG. 474 (SEQ ID NO:474), FIG. 476 (SEQ ID NO:476), FIG. 478 (SEQ ID NO:478), FIG. 480 (SEQ ID NO:480), FIG. 482 (SEQ ID NO:482), FIG. 484 (SEQ ID NO:484), FIG. 486 (SEQ ID NO:486), FIG. 488 (SEQ ID NO:488), FIG. 490 (SEQ ID NO:490), FIG. 492 (SEQ ID NO:492), FIG. 494 (SEQ ID NO:494), FIG. 496 (SEQ ID NO:496), FIG. 498 (SEQ ID NO:498), FIG. 500 (SEQ ID NO:500), FIG. 502 (SEQ ID NO:502), FIG. 504 (SEQ ID NO:504), FIG. 506 (SEQ ID NO:506), FIG. 508 (SEQ ID NO:508), FIG. 510 (SEQ ID NO:510), FIG. 512 (SEQ ID NO:512), FIG. 514 (SEQ ID NO:514), FIG. 516 (SEQ ID NO:516), FIG. 518 (SEQ ID

NO:518), FIG. 520 (SEQ ID NO:520), FIG. 522 (SEQ ID NO:522), FIG. 524 (SEQ ID NO:524), FIG. 526 (SEQ ID NO:526), FIG. 528 (SEQ ID NO:528), FIG. 530 (SEQ ID NO:530), FIG. 532 (SEQ ID NO:532), FIG. 534 (SEQ ID NO:534), FIG. 536 (SEQ ID NO:536), FIG. 538 (SEQ ID NO:538), FIG. 540 (SEQ ID NO:540), FIG. 542 (SEQ ID NO:542), FIG. 544 (SEQ ID NO:544), FIG. 546 (SEQ ID NO:546), FIG. 548 (SEQ ID NO:548), FIG. 550 (SEQ ID NO:550), FIG. 552 (SEQ ID NO:552), FIG. 554 (SEQ ID NO:554), FIG. 556 (SEQ ID NO:556), FIG. 558 (SEQ ID NO:558), FIG. 560 (SEQ ID NO:560), FIG. 562 (SEQ ID NO:562), FIG. 564 (SEQ ID NO:564), FIG. 566 (SEQ ID NO:566), FIG. 568 (SEQ ID NO:568), FIG. 570 (SEQ ID NO:570), FIG. 572 (SEQ ID NO:572), FIG. 574 (SEQ ID NO:574), FIG. 576 (SEQ ID NO:576), FIG. 578 (SEQ ID NO:578), FIG. 580 (SEQ ID NO:580), FIG. 582 (SEQ ID NO:582), FIG. 584 (SEQ ID NO:584), FIG. 586 (SEQ ID NO:586), FIG. 588 (SEQ ID NO:588), FIG. 590 (SEQ ID NO:590), FIG. 592 (SEQ ID NO:592), FIG. 594 (SEQ ID NO:594), FIG. 596 (SEQ ID NO:596), FIG. 598 (SEQ ID NO:598), FIG. 600 (SEQ ID NO:600), FIG. 602 (SEQ ID NO:602), FIG. 604 (SEQ ID NO:604), FIG. 606 (SEQ ID NO:606), FIG. 608 (SEQ ID NO:608), and FIG. 610 (SEQ ID NO:610).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

16. An antibody which specifically binds to a polypeptide according to claim 11.

17. The antibody of claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in FIG. 2 (SEQ ID NO:2), FIG. 4 (SEQ ID NO:4), FIG. 6 (SEQ ID NO:6), FIG. 8 (SEQ ID NO:8), FIG. 10 (SEQ ID NO:10), FIG. 12 (SEQ ID NO:12), FIG. 14 (SEQ ID NO:14), FIG. 16 (SEQ ID NO:16), FIG. 18 (SEQ ID NO:18), FIG. 20 (SEQ ID NO:20), FIG. 22 (SEQ ID NO:22), FIG. 24 (SEQ ID NO:24), FIG. 26 (SEQ ID NO:26), FIG. 28 (SEQ ID NO:28), FIG. 30 (SEQ ID NO:30), FIG. 32 (SEQ ID NO:32), FIG. 34 (SEQ ID NO:34), FIG. 36 (SEQ ID NO:36), FIG. 38 (SEQ ID NO:38), FIG. 40 (SEQ ID NO:40), FIG. 42 (SEQ ID NO:42), FIG. 44 (SEQ ID NO:44), FIG. 46 (SEQ ID NO:46), FIG. 48 (SEQ ID NO:48), FIG. 50 (SEQ ID NO:50), FIG. 52 (SEQ ID NO:52), FIG. 54 (SEQ ID NO:54), FIG. 56 (SEQ ID NO:56), FIG. 58 (SEQ ID NO:58), FIG. 60 (SEQ ID NO:60), FIG. 62 (SEQ ID NO:62), FIG. 64 (SEQ ID NO:64), FIG. 66 (SEQ ID NO:66), FIG. 68 (SEQ ID NO:68), FIG. 70 (SEQ ID NO:70), FIG. 72 (SEQ ID NO:72), FIG. 74 (SEQ ID NO:74), FIG. 76 (SEQ ID NO:76), FIG.

ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548), **FIG. 550** (SEQ ID NO:550), **FIG. 552** (SEQ ID NO:552), **FIG. 554** (SEQ ID NO:554), **FIG. 556** (SEQ ID NO:556), **FIG. 558** (SEQ ID NO:558), **FIG. 560** (SEQ ID NO:560), **FIG. 562** (SEQ ID NO:562), **FIG. 564** (SEQ ID NO:564), **FIG. 566** (SEQ ID NO:566), **FIG. 568** (SEQ ID NO:568), **FIG. 570** (SEQ ID NO:570), **FIG. 572** (SEQ ID NO:572), **FIG. 574** (SEQ ID NO:574), **FIG. 576** (SEQ ID NO:576), **FIG. 578** (SEQ ID NO:578), **FIG. 580** (SEQ ID NO:580), **FIG. 582** (SEQ ID NO:582), **FIG. 584** (SEQ ID NO:584), **FIG. 586** (SEQ ID NO:586), **FIG. 588** (SEQ ID NO:588), **FIG. 590** (SEQ ID NO:590), **FIG. 592** (SEQ ID NO:592), **FIG. 594** (SEQ ID NO:594), **FIG. 596** (SEQ ID NO:596), **FIG. 598** (SEQ ID NO:598), **FIG. 600** (SEQ ID NO:600), **FIG. 602** (SEQ ID NO:602), **FIG. 604** (SEQ ID NO:604), **FIG. 606** (SEQ ID NO:606), **FIG. 608** (SEQ ID NO:608), or **FIG. 610** (SEQ ID NO:610), lacking its associated signal peptide;

- (b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160**

(SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID NO:262), **FIG. 264** (SEQ ID NO:264), **FIG. 266** (SEQ ID NO:266), **FIG. 268** (SEQ ID NO:268), **FIG. 270** (SEQ ID NO:270), **FIG. 272** (SEQ ID NO:272), **FIG. 274** (SEQ ID NO:274), **FIG. 276** (SEQ ID NO:276), **FIG. 278** (SEQ ID NO:278), **FIG. 280** (SEQ ID NO:280), **FIG. 282** (SEQ ID NO:282), **FIG. 284** (SEQ ID NO:284), **FIG. 286** (SEQ ID NO:286), **FIG. 288** (SEQ ID NO:288), **FIG. 290** (SEQ ID NO:290), **FIG. 292** (SEQ ID NO:292), **FIG. 294** (SEQ ID NO:294), **FIG. 296** (SEQ ID NO:296), **FIG. 298** (SEQ ID NO:298), **FIG. 300** (SEQ ID NO:300), **FIG. 302** (SEQ ID NO:302), **FIG. 304** (SEQ ID NO:304), **FIG. 306** (SEQ ID NO:306), **FIG. 308** (SEQ ID NO:308), **FIG. 310** (SEQ ID NO:310), **FIG. 312** (SEQ ID NO:312), **FIG. 314** (SEQ ID NO:314), **FIG. 316** (SEQ ID NO:316), **FIG. 318** (SEQ ID NO:318), **FIG. 320** (SEQ ID NO:320), **FIG. 322** (SEQ ID NO:322), **FIG. 324** (SEQ ID NO:324), **FIG. 326** (SEQ ID NO:326), **FIG. 328** (SEQ ID NO:328), **FIG. 330** (SEQ ID NO:330), **FIG. 332** (SEQ ID NO:332), **FIG. 334** (SEQ ID NO:334), **FIG. 336** (SEQ ID NO:336), **FIG. 338** (SEQ ID NO:338), **FIG. 340** (SEQ ID NO:340), **FIG. 342** (SEQ ID NO:342), **FIG. 344** (SEQ ID NO:344), **FIG. 346** (SEQ ID NO:346), **FIG. 348** (SEQ ID NO:348), **FIG. 350** (SEQ ID NO:350), **FIG. 352** (SEQ ID NO:352), **FIG. 354** (SEQ ID NO:354), **FIG. 356** (SEQ ID NO:356), **FIG. 358** (SEQ ID NO:358), **FIG. 360** (SEQ ID NO:360), **FIG. 362** (SEQ ID NO:362), **FIG. 364** (SEQ ID NO:364), **FIG. 366** (SEQ ID NO:366), **FIG. 368** (SEQ ID NO:368), **FIG. 370** (SEQ ID NO:370), **FIG. 372** (SEQ ID NO:372), **FIG. 374** (SEQ ID NO:374), **FIG. 376** (SEQ ID NO:376), **FIG. 378** (SEQ ID NO:378), **FIG. 380** (SEQ ID NO:380), **FIG. 382** (SEQ ID NO:382), **FIG. 384** (SEQ ID NO:384), **FIG. 386** (SEQ ID NO:386), **FIG. 388** (SEQ ID NO:388), **FIG. 390** (SEQ

ID NO:390), **FIG. 392** (SEQ ID NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418), **FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472), **FIG. 474** (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548), **FIG. 550** (SEQ ID NO:550), **FIG. 552** (SEQ ID NO:552), **FIG. 554** (SEQ ID NO:554), **FIG. 556** (SEQ ID NO:556), **FIG. 558** (SEQ ID NO:558), **FIG. 560** (SEQ ID NO:560), **FIG. 562** (SEQ ID NO:562), **FIG. 564** (SEQ ID NO:564), **FIG. 566** (SEQ ID NO:566), **FIG. 568** (SEQ ID NO:568), **FIG. 570** (SEQ ID NO:570), **FIG. 572** (SEQ ID NO:572), **FIG. 574** (SEQ ID NO:574), **FIG. 576** (SEQ ID NO:576), **FIG. 578** (SEQ ID NO:578), **FIG. 580** (SEQ ID NO:580), **FIG. 582** (SEQ ID NO:582), **FIG. 584** (SEQ ID NO:584), **FIG. 586** (SEQ ID NO:586), **FIG. 588** (SEQ ID NO:588), **FIG. 590** (SEQ ID NO:590), **FIG. 592** (SEQ ID NO:592), **FIG. 594** (SEQ ID NO:594), **FIG. 596** (SEQ ID NO:596), **FIG. 598** (SEQ ID NO:598), **FIG. 600** (SEQ ID NO:600), **FIG. 602** (SEQ ID NO:602), **FIG. 604** (SEQ ID NO:604), **FIG. 606** (SEQ ID NO:606), **FIG. 608** (SEQ ID NO:608), or **FIG. 610** (SEQ ID NO:610), with its associated signal peptide; or

(c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID

NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID

NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID NO:262), **FIG. 264** (SEQ ID NO:264), **FIG. 266** (SEQ ID NO:266), **FIG. 268** (SEQ ID NO:268), **FIG. 270** (SEQ ID NO:270), **FIG. 272** (SEQ ID NO:272), **FIG. 274** (SEQ ID NO:274), **FIG. 276** (SEQ ID NO:276), **FIG. 278** (SEQ ID NO:278), **FIG. 280** (SEQ ID NO:280), **FIG. 282** (SEQ ID NO:282), **FIG. 284** (SEQ ID NO:284), **FIG. 286** (SEQ ID NO:286), **FIG. 288** (SEQ ID NO:288), **FIG. 290** (SEQ ID NO:290), **FIG. 292** (SEQ ID NO:292), **FIG. 294** (SEQ ID NO:294), **FIG. 296** (SEQ ID NO:296), **FIG. 298** (SEQ ID NO:298), **FIG. 300** (SEQ ID NO:300), **FIG. 302** (SEQ ID NO:302), **FIG. 304** (SEQ ID NO:304), **FIG. 306** (SEQ ID NO:306), **FIG. 308** (SEQ ID NO:308), **FIG. 310** (SEQ ID NO:310), **FIG. 312** (SEQ ID NO:312), **FIG. 314** (SEQ ID NO:314), **FIG. 316** (SEQ ID NO:316), **FIG. 318** (SEQ ID NO:318), **FIG. 320** (SEQ ID NO:320), **FIG. 322** (SEQ ID NO:322), **FIG. 324** (SEQ ID NO:324), **FIG. 326** (SEQ ID NO:326), **FIG. 328** (SEQ ID NO:328), **FIG. 330** (SEQ ID NO:330), **FIG. 332** (SEQ ID NO:332), **FIG. 334** (SEQ ID NO:334), **FIG. 336** (SEQ ID NO:336), **FIG. 338** (SEQ ID NO:338), **FIG. 340** (SEQ ID NO:340), **FIG. 342** (SEQ ID NO:342), **FIG. 344** (SEQ ID NO:344), **FIG. 346** (SEQ ID NO:346), **FIG. 348** (SEQ ID NO:348), **FIG. 350** (SEQ ID NO:350), **FIG. 352** (SEQ ID NO:352), **FIG. 354** (SEQ ID NO:354), **FIG. 356** (SEQ ID NO:356), **FIG. 358** (SEQ ID NO:358), **FIG. 360** (SEQ ID NO:360), **FIG. 362** (SEQ ID NO:362), **FIG. 364** (SEQ ID NO:364), **FIG. 366** (SEQ ID NO:366), **FIG. 368** (SEQ ID NO:368), **FIG. 370** (SEQ ID NO:370), **FIG. 372** (SEQ ID NO:372), **FIG. 374** (SEQ ID NO:374), **FIG. 376** (SEQ ID NO:376), **FIG. 378** (SEQ ID NO:378), **FIG. 380** (SEQ ID NO:380), **FIG. 382** (SEQ ID NO:382), **FIG. 384** (SEQ ID NO:384), **FIG. 386** (SEQ ID NO:386), **FIG. 388** (SEQ ID NO:388), **FIG. 390** (SEQ ID NO:390), **FIG. 392** (SEQ ID NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418), **FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472),

FIG. 474 (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548), **FIG. 550** (SEQ ID NO:550), **FIG. 552** (SEQ ID NO:552), **FIG. 554** (SEQ ID NO:554), **FIG. 556** (SEQ ID NO:556), **FIG. 558** (SEQ ID NO:558), **FIG. 560** (SEQ ID NO:560), **FIG. 562** (SEQ ID NO:562), **FIG. 564** (SEQ ID NO:564), **FIG. 566** (SEQ ID NO:566), **FIG. 568** (SEQ ID NO:568), **FIG. 570** (SEQ ID NO:570), **FIG. 572** (SEQ ID NO:572), **FIG. 574** (SEQ ID NO:574), **FIG. 576** (SEQ ID NO:576), **FIG. 578** (SEQ ID NO:578), **FIG. 580** (SEQ ID NO:580), **FIG. 582** (SEQ ID NO:582), **FIG. 584** (SEQ ID NO:584), **FIG. 586** (SEQ ID NO:586), **FIG. 588** (SEQ ID NO:588), **FIG. 590** (SEQ ID NO:590), **FIG. 592** (SEQ ID NO:592), **FIG. 594** (SEQ ID NO:594), **FIG. 596** (SEQ ID NO:596), **FIG. 598** (SEQ ID NO:598), **FIG. 600** (SEQ ID NO:600), **FIG. 602** (SEQ ID NO:602), **FIG. 604** (SEQ ID NO:604), **FIG. 606** (SEQ ID NO:606), **FIG. 608** (SEQ ID NO:608), or **FIG. 610** (SEQ ID NO:610), lacking its associated signal peptide.

19. An isolated polypeptide having at least 80% amino acid sequence identity to:

- (a) an amino acid sequence of the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86**

(SEQ ID NO:548), **FIG. 550** (SEQ ID NO:550), **FIG. 552** (SEQ ID NO:552), **FIG. 554** (SEQ ID NO:554), **FIG. 556** (SEQ ID NO:556), **FIG. 558** (SEQ ID NO:558), **FIG. 560** (SEQ ID NO:560), **FIG. 562** (SEQ ID NO:562), **FIG. 564** (SEQ ID NO:564), **FIG. 566** (SEQ ID NO:566), **FIG. 568** (SEQ ID NO:568), **FIG. 570** (SEQ ID NO:570), **FIG. 572** (SEQ ID NO:572), **FIG. 574** (SEQ ID NO:574), **FIG. 576** (SEQ ID NO:576), **FIG. 578** (SEQ ID NO:578), **FIG. 580** (SEQ ID NO:580), **FIG. 582** (SEQ ID NO:582), **FIG. 584** (SEQ ID NO:584), **FIG. 586** (SEQ ID NO:586), **FIG. 588** (SEQ ID NO:588), **FIG. 590** (SEQ ID NO:590), **FIG. 592** (SEQ ID NO:592), **FIG. 594** (SEQ ID NO:594), **FIG. 596** (SEQ ID NO:596), **FIG. 598** (SEQ ID NO:598), **FIG. 600** (SEQ ID NO:600), **FIG. 602** (SEQ ID NO:602), **FIG. 604** (SEQ ID NO:604), **FIG. 606** (SEQ ID NO:606), **FIG. 608** (SEQ ID NO:608), or **FIG. 610** (SEQ ID NO:610), lacking its associated signal peptide;

- (b) an amino acid sequence of an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12** (SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ

ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250), **FIG. 252** (SEQ ID NO:252), **FIG. 254** (SEQ ID NO:254), **FIG. 256** (SEQ ID NO:256), **FIG. 258** (SEQ ID NO:258), **FIG. 260** (SEQ ID NO:260), **FIG. 262** (SEQ ID NO:262), **FIG. 264** (SEQ ID NO:264), **FIG. 266** (SEQ ID NO:266), **FIG. 268** (SEQ ID NO:268), **FIG. 270** (SEQ ID NO:270), **FIG. 272** (SEQ ID NO:272), **FIG. 274** (SEQ ID NO:274), **FIG. 276** (SEQ ID NO:276), **FIG. 278** (SEQ ID NO:278), **FIG. 280** (SEQ ID NO:280), **FIG. 282** (SEQ ID NO:282), **FIG. 284** (SEQ ID NO:284), **FIG. 286** (SEQ ID NO:286), **FIG. 288** (SEQ ID NO:288), **FIG. 290** (SEQ ID NO:290), **FIG. 292** (SEQ ID NO:292), **FIG. 294** (SEQ ID NO:294), **FIG. 296** (SEQ ID NO:296), **FIG. 298** (SEQ ID NO:298), **FIG. 300** (SEQ ID NO:300), **FIG. 302** (SEQ ID NO:302), **FIG. 304** (SEQ ID NO:304), **FIG. 306** (SEQ ID NO:306), **FIG. 308** (SEQ ID NO:308), **FIG. 310** (SEQ ID NO:310), **FIG. 312** (SEQ ID NO:312), **FIG. 314** (SEQ ID NO:314), **FIG. 316** (SEQ ID NO:316), **FIG. 318** (SEQ ID NO:318), **FIG. 320** (SEQ ID NO:320), **FIG. 322** (SEQ ID NO:322), **FIG. 324** (SEQ ID NO:324), **FIG. 326** (SEQ ID NO:326), **FIG. 328** (SEQ ID NO:328), **FIG. 330** (SEQ ID NO:330), **FIG. 332** (SEQ ID NO:332), **FIG. 334** (SEQ ID NO:334), **FIG. 336** (SEQ ID NO:336), **FIG. 338** (SEQ ID NO:338), **FIG. 340** (SEQ ID NO:340), **FIG. 342** (SEQ ID NO:342), **FIG. 344** (SEQ ID NO:344), **FIG. 346** (SEQ ID NO:346), **FIG. 348** (SEQ ID NO:348), **FIG. 350** (SEQ ID NO:350), **FIG. 352** (SEQ ID NO:352), **FIG. 354** (SEQ ID NO:354), **FIG. 356** (SEQ ID NO:356), **FIG. 358** (SEQ ID NO:358), **FIG. 360** (SEQ ID NO:360), **FIG. 362** (SEQ ID NO:362), **FIG. 364** (SEQ ID NO:364), **FIG. 366** (SEQ ID NO:366), **FIG. 368** (SEQ ID NO:368), **FIG. 370** (SEQ ID NO:370), **FIG. 372** (SEQ ID NO:372), **FIG. 374** (SEQ ID NO:374), **FIG. 376** (SEQ ID NO:376), **FIG. 378** (SEQ ID NO:378), **FIG. 380** (SEQ ID NO:380), **FIG. 382** (SEQ ID NO:382), **FIG. 384** (SEQ ID NO:384), **FIG. 386** (SEQ ID NO:386), **FIG. 388** (SEQ ID NO:388), **FIG. 390** (SEQ ID NO:390), **FIG. 392** (SEQ ID NO:392), **FIG. 394** (SEQ ID NO:394), **FIG. 396** (SEQ ID NO:396), **FIG. 398** (SEQ ID

NO:398), **FIG. 400** (SEQ ID NO:400), **FIG. 402** (SEQ ID NO:402), **FIG. 404** (SEQ ID NO:404), **FIG. 406** (SEQ ID NO:406), **FIG. 408** (SEQ ID NO:408), **FIG. 410** (SEQ ID NO:410), **FIG. 412** (SEQ ID NO:412), **FIG. 414** (SEQ ID NO:414), **FIG. 416** (SEQ ID NO:416), **FIG. 418** (SEQ ID NO:418), **FIG. 420** (SEQ ID NO:420), **FIG. 422** (SEQ ID NO:422), **FIG. 424** (SEQ ID NO:424), **FIG. 426** (SEQ ID NO:426), **FIG. 428** (SEQ ID NO:428), **FIG. 430** (SEQ ID NO:430), **FIG. 432** (SEQ ID NO:432), **FIG. 434** (SEQ ID NO:434), **FIG. 436** (SEQ ID NO:436), **FIG. 438** (SEQ ID NO:438), **FIG. 440** (SEQ ID NO:440), **FIG. 442** (SEQ ID NO:442), **FIG. 444** (SEQ ID NO:444), **FIG. 446** (SEQ ID NO:446), **FIG. 448** (SEQ ID NO:448), **FIG. 450** (SEQ ID NO:450), **FIG. 452** (SEQ ID NO:452), **FIG. 454** (SEQ ID NO:454), **FIG. 456** (SEQ ID NO:456), **FIG. 458** (SEQ ID NO:458), **FIG. 460** (SEQ ID NO:460), **FIG. 462** (SEQ ID NO:462), **FIG. 464** (SEQ ID NO:464), **FIG. 466** (SEQ ID NO:466), **FIG. 468** (SEQ ID NO:468), **FIG. 470** (SEQ ID NO:470), **FIG. 472** (SEQ ID NO:472), **FIG. 474** (SEQ ID NO:474), **FIG. 476** (SEQ ID NO:476), **FIG. 478** (SEQ ID NO:478), **FIG. 480** (SEQ ID NO:480), **FIG. 482** (SEQ ID NO:482), **FIG. 484** (SEQ ID NO:484), **FIG. 486** (SEQ ID NO:486), **FIG. 488** (SEQ ID NO:488), **FIG. 490** (SEQ ID NO:490), **FIG. 492** (SEQ ID NO:492), **FIG. 494** (SEQ ID NO:494), **FIG. 496** (SEQ ID NO:496), **FIG. 498** (SEQ ID NO:498), **FIG. 500** (SEQ ID NO:500), **FIG. 502** (SEQ ID NO:502), **FIG. 504** (SEQ ID NO:504), **FIG. 506** (SEQ ID NO:506), **FIG. 508** (SEQ ID NO:508), **FIG. 510** (SEQ ID NO:510), **FIG. 512** (SEQ ID NO:512), **FIG. 514** (SEQ ID NO:514), **FIG. 516** (SEQ ID NO:516), **FIG. 518** (SEQ ID NO:518), **FIG. 520** (SEQ ID NO:520), **FIG. 522** (SEQ ID NO:522), **FIG. 524** (SEQ ID NO:524), **FIG. 526** (SEQ ID NO:526), **FIG. 528** (SEQ ID NO:528), **FIG. 530** (SEQ ID NO:530), **FIG. 532** (SEQ ID NO:532), **FIG. 534** (SEQ ID NO:534), **FIG. 536** (SEQ ID NO:536), **FIG. 538** (SEQ ID NO:538), **FIG. 540** (SEQ ID NO:540), **FIG. 542** (SEQ ID NO:542), **FIG. 544** (SEQ ID NO:544), **FIG. 546** (SEQ ID NO:546), **FIG. 548** (SEQ ID NO:548), **FIG. 550** (SEQ ID NO:550), **FIG. 552** (SEQ ID NO:552), **FIG. 554** (SEQ ID NO:554), **FIG. 556** (SEQ ID NO:556), **FIG. 558** (SEQ ID NO:558), **FIG. 560** (SEQ ID NO:560), **FIG. 562** (SEQ ID NO:562), **FIG. 564** (SEQ ID NO:564), **FIG. 566** (SEQ ID NO:566), **FIG. 568** (SEQ ID NO:568), **FIG. 570** (SEQ ID NO:570), **FIG. 572** (SEQ ID NO:572), **FIG. 574** (SEQ ID NO:574), **FIG. 576** (SEQ ID NO:576), **FIG. 578** (SEQ ID NO:578), **FIG. 580** (SEQ ID NO:580), **FIG. 582** (SEQ ID NO:582), **FIG. 584** (SEQ ID NO:584), **FIG. 586** (SEQ ID NO:586), **FIG. 588** (SEQ ID NO:588), **FIG. 590** (SEQ ID NO:590), **FIG. 592** (SEQ ID NO:592), **FIG. 594** (SEQ ID NO:594), **FIG. 596** (SEQ ID NO:596), **FIG. 598** (SEQ ID NO:598), **FIG. 600** (SEQ ID NO:600), **FIG. 602** (SEQ ID NO:602), **FIG. 604** (SEQ ID NO:604), **FIG. 606** (SEQ ID NO:606), **FIG. 608** (SEQ ID NO:608), or **FIG. 610** (SEQ ID NO:610), with its associated signal peptide; or

- (c) an amino acid sequence of an extracellular domain of the polypeptide shown in **FIG. 2** (SEQ ID NO:2), **FIG. 4** (SEQ ID NO:4), **FIG. 6** (SEQ ID NO:6), **FIG. 8** (SEQ ID NO:8), **FIG. 10** (SEQ ID NO:10), **FIG. 12**

(SEQ ID NO:12), **FIG. 14** (SEQ ID NO:14), **FIG. 16** (SEQ ID NO:16), **FIG. 18** (SEQ ID NO:18), **FIG. 20** (SEQ ID NO:20), **FIG. 22** (SEQ ID NO:22), **FIG. 24** (SEQ ID NO:24), **FIG. 26** (SEQ ID NO:26), **FIG. 28** (SEQ ID NO:28), **FIG. 30** (SEQ ID NO:30), **FIG. 32** (SEQ ID NO:32), **FIG. 34** (SEQ ID NO:34), **FIG. 36** (SEQ ID NO:36), **FIG. 38** (SEQ ID NO:38), **FIG. 40** (SEQ ID NO:40), **FIG. 42** (SEQ ID NO:42), **FIG. 44** (SEQ ID NO:44), **FIG. 46** (SEQ ID NO:46), **FIG. 48** (SEQ ID NO:48), **FIG. 50** (SEQ ID NO:50), **FIG. 52** (SEQ ID NO:52), **FIG. 54** (SEQ ID NO:54), **FIG. 56** (SEQ ID NO:56), **FIG. 58** (SEQ ID NO:58), **FIG. 60** (SEQ ID NO:60), **FIG. 62** (SEQ ID NO:62), **FIG. 64** (SEQ ID NO:64), **FIG. 66** (SEQ ID NO:66), **FIG. 68** (SEQ ID NO:68), **FIG. 70** (SEQ ID NO:70), **FIG. 72** (SEQ ID NO:72), **FIG. 74** (SEQ ID NO:74), **FIG. 76** (SEQ ID NO:76), **FIG. 78** (SEQ ID NO:78), **FIG. 80** (SEQ ID NO:80), **FIG. 82** (SEQ ID NO:82), **FIG. 84** (SEQ ID NO:84), **FIG. 86** (SEQ ID NO:86), **FIG. 88** (SEQ ID NO:88), **FIG. 90** (SEQ ID NO:90), **FIG. 92** (SEQ ID NO:92), **FIG. 94** (SEQ ID NO:94), **FIG. 96** (SEQ ID NO:96), **FIG. 98** (SEQ ID NO:98), **FIG. 100** (SEQ ID NO:100), **FIG. 102** (SEQ ID NO:102), **FIG. 104** (SEQ ID NO:104), **FIG. 106** (SEQ ID NO:106), **FIG. 108** (SEQ ID NO:108), **FIG. 110** (SEQ ID NO:110), **FIG. 112** (SEQ ID NO:112), **FIG. 114** (SEQ ID NO:114), **FIG. 116** (SEQ ID NO:116), **FIG. 118** (SEQ ID NO:118), **FIG. 120** (SEQ ID NO:120), **FIG. 122** (SEQ ID NO:122), **FIG. 124** (SEQ ID NO:124), **FIG. 126** (SEQ ID NO:126), **FIG. 128** (SEQ ID NO:128), **FIG. 130** (SEQ ID NO:130), **FIG. 132** (SEQ ID NO:132), **FIG. 134** (SEQ ID NO:134), **FIG. 136** (SEQ ID NO:136), **FIG. 138** (SEQ ID NO:138), **FIG. 140** (SEQ ID NO:140), **FIG. 142** (SEQ ID NO:142), **FIG. 144** (SEQ ID NO:144), **FIG. 146** (SEQ ID NO:146), **FIG. 148** (SEQ ID NO:148), **FIG. 150** (SEQ ID NO:150), **FIG. 152** (SEQ ID NO:152), **FIG. 154** (SEQ ID NO:154), **FIG. 156** (SEQ ID NO:156), **FIG. 158** (SEQ ID NO:158), **FIG. 160** (SEQ ID NO:160), **FIG. 162** (SEQ ID NO:162), **FIG. 164** (SEQ ID NO:164), **FIG. 166** (SEQ ID NO:166), **FIG. 168** (SEQ ID NO:168), **FIG. 170** (SEQ ID NO:170), **FIG. 172** (SEQ ID NO:172), **FIG. 174** (SEQ ID NO:174), **FIG. 176** (SEQ ID NO:176), **FIG. 178** (SEQ ID NO:178), **FIG. 180** (SEQ ID NO:180), **FIG. 182** (SEQ ID NO:182), **FIG. 184** (SEQ ID NO:184), **FIG. 186** (SEQ ID NO:186), **FIG. 188** (SEQ ID NO:188), **FIG. 190** (SEQ ID NO:190), **FIG. 192** (SEQ ID NO:192), **FIG. 194** (SEQ ID NO:194), **FIG. 196** (SEQ ID NO:196), **FIG. 198** (SEQ ID NO:198), **FIG. 200** (SEQ ID NO:200), **FIG. 202** (SEQ ID NO:202), **FIG. 204** (SEQ ID NO:204), **FIG. 206** (SEQ ID NO:206), **FIG. 208** (SEQ ID NO:208), **FIG. 210** (SEQ ID NO:210), **FIG. 212** (SEQ ID NO:212), **FIG. 214** (SEQ ID NO:214), **FIG. 216** (SEQ ID NO:216), **FIG. 218** (SEQ ID NO:218), **FIG. 220** (SEQ ID NO:220), **FIG. 222** (SEQ ID NO:222), **FIG. 224** (SEQ ID NO:224), **FIG. 226** (SEQ ID NO:226), **FIG. 228** (SEQ ID NO:228), **FIG. 230** (SEQ ID NO:230), **FIG. 232** (SEQ ID NO:232), **FIG. 234** (SEQ ID NO:234), **FIG. 236** (SEQ ID NO:236), **FIG. 238** (SEQ ID NO:238), **FIG. 240** (SEQ ID NO:240), **FIG. 242** (SEQ ID NO:242), **FIG. 244** (SEQ ID NO:244), **FIG. 246** (SEQ ID NO:246), **FIG. 248** (SEQ ID NO:248), **FIG. 250** (SEQ ID NO:250),

FIG. 252 (SEQ ID NO:252), FIG. 254 (SEQ ID NO:254), FIG. 256 (SEQ ID NO:256), FIG. 258 (SEQ ID NO:258), FIG. 260 (SEQ ID NO:260), FIG. 262 (SEQ ID NO:262), FIG. 264 (SEQ ID NO:264), FIG. 266 (SEQ ID NO:266), FIG. 268 (SEQ ID NO:268), FIG. 270 (SEQ ID NO:270), FIG. 272 (SEQ ID NO:272), FIG. 274 (SEQ ID NO:274), FIG. 276 (SEQ ID NO:276), FIG. 278 (SEQ ID NO:278), FIG. 280 (SEQ ID NO:280), FIG. 282 (SEQ ID NO:282), FIG. 284 (SEQ ID NO:284), FIG. 286 (SEQ ID NO:286), FIG. 288 (SEQ ID NO:288), FIG. 290 (SEQ ID NO:290), FIG. 292 (SEQ ID NO:292), FIG. 294 (SEQ ID NO:294), FIG. 296 (SEQ ID NO:296), FIG. 298 (SEQ ID NO:298), FIG. 300 (SEQ ID NO:300), FIG. 302 (SEQ ID NO:302), FIG. 304 (SEQ ID NO:304), FIG. 306 (SEQ ID NO:306), FIG. 308 (SEQ ID NO:308), FIG. 310 (SEQ ID NO:310), FIG. 312 (SEQ ID NO:312), FIG. 314 (SEQ ID NO:314), FIG. 316 (SEQ ID NO:316), FIG. 318 (SEQ ID NO:318), FIG. 320 (SEQ ID NO:320), FIG. 322 (SEQ ID NO:322), FIG. 324 (SEQ ID NO:324), FIG. 326 (SEQ ID NO:326), FIG. 328 (SEQ ID NO:328), FIG. 330 (SEQ ID NO:330), FIG. 332 (SEQ ID NO:332), FIG. 334 (SEQ ID NO:334), FIG. 336 (SEQ ID NO:336), FIG. 338 (SEQ ID NO:338), FIG. 340 (SEQ ID NO:340), FIG. 342 (SEQ ID NO:342), FIG. 344 (SEQ ID NO:344), FIG. 346 (SEQ ID NO:346), FIG. 348 (SEQ ID NO:348), FIG. 350 (SEQ ID NO:350), FIG. 352 (SEQ ID NO:352), FIG. 354 (SEQ ID NO:354), FIG. 356 (SEQ ID NO:356), FIG. 358 (SEQ ID NO:358), FIG. 360 (SEQ ID NO:360), FIG. 362 (SEQ ID NO:362), FIG. 364 (SEQ ID NO:364), FIG. 366 (SEQ ID NO:366), FIG. 368 (SEQ ID NO:368), FIG. 370 (SEQ ID NO:370), FIG. 372 (SEQ ID NO:372), FIG. 374 (SEQ ID NO:374), FIG. 376 (SEQ ID NO:376), FIG. 378 (SEQ ID NO:378), FIG. 380 (SEQ ID NO:380), FIG. 382 (SEQ ID NO:382), FIG. 384 (SEQ ID NO:384), FIG. 386 (SEQ ID NO:386), FIG. 388 (SEQ ID NO:388), FIG. 390 (SEQ ID NO:390), FIG. 392 (SEQ ID NO:392), FIG. 394 (SEQ ID NO:394), FIG. 396 (SEQ ID NO:396), FIG. 398 (SEQ ID NO:398), FIG. 400 (SEQ ID NO:400), FIG. 402 (SEQ ID NO:402), FIG. 404 (SEQ ID NO:404), FIG. 406 (SEQ ID NO:406), FIG. 408 (SEQ ID NO:408), FIG. 410 (SEQ ID NO:410), FIG. 412 (SEQ ID NO:412), FIG. 414 (SEQ ID NO:414), FIG. 416 (SEQ ID NO:416), FIG. 418 (SEQ ID NO:418), FIG. 420 (SEQ ID NO:420), FIG. 422 (SEQ ID NO:422), FIG. 424 (SEQ ID NO:424), FIG. 426 (SEQ ID NO:426), FIG. 428 (SEQ ID NO:428), FIG. 430 (SEQ ID NO:430), FIG. 432 (SEQ ID NO:432), FIG. 434 (SEQ ID NO:434), FIG. 436 (SEQ ID NO:436), FIG. 438 (SEQ ID NO:438), FIG. 440 (SEQ ID NO:440), FIG. 442 (SEQ ID NO:442), FIG. 444 (SEQ ID NO:444), FIG. 446 (SEQ ID NO:446), FIG. 448 (SEQ ID NO:448), FIG. 450 (SEQ ID NO:450), FIG. 452 (SEQ ID NO:452), FIG. 454 (SEQ ID NO:454), FIG. 456 (SEQ ID NO:456), FIG. 458 (SEQ ID NO:458), FIG. 460 (SEQ ID NO:460), FIG. 462 (SEQ ID NO:462), FIG. 464 (SEQ ID NO:464), FIG. 466 (SEQ ID NO:466), FIG. 468 (SEQ ID NO:468), FIG. 470 (SEQ ID NO:470), FIG. 472 (SEQ ID NO:472), FIG. 474 (SEQ ID NO:474), FIG. 476 (SEQ ID NO:476), FIG. 478

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20. A method for stimulating the release of TNF- α from human blood, said method comprising contacting said blood with a PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333 polypeptide, wherein the release of TNF- α from said blood is stimulated.

21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO6029 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

22. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

23. The method of claim 22, wherein said tumor is adrenal tumor, lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

24. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

专利名称(译)	分泌的和跨膜的多肽和编码它们的核酸		
公开(公告)号	US20030036123A1	公开(公告)日	2003-02-20
申请号	US10/180551	申请日	2002-06-25
[标]申请(专利权)人(译)	健泰科生物技术公司		
申请(专利权)人(译)	基因泰克, INC.		
当前申请(专利权)人(译)	基因泰克, INC.		
[标]发明人	BAKER KEVIN P CHEN JIAN DESNOYERS LUC GODDARD AUDREY GODOWSKI PAUL J GURNEY AUSTIN L PAN JAMES SMITH VICTORIA WATANABE COLIN K WOOD WILLIAM I ZHANG ZEMIN		
发明人	BAKER, KEVIN P. CHEN, JIAN DESNOYERS, LUC GODDARD, AUDREY GODOWSKI, PAUL J. GURNEY, AUSTIN L. PAN, JAMES SMITH, VICTORIA WATANABE, COLIN K. WOOD, WILLIAM I. ZHANG, ZEMIN		
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摘要(译)

本发明涉及新的多肽和编码这些多肽的核酸分子。本文还提供了包含那些核酸序列的载体和宿主细胞，包含与异源多肽序列融合的本发明多肽的嵌合多肽分子，与本发明多肽结合的抗体和产生本发明多肽的方法发明。

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