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(54) 【発明の名称】 歯周疾患の診断、治療、およびモニタリングのためのアクチノバチルス・アクチノミセテムコミタンス抗原の同定

(57) 【要約】

アクチノバチルス・アクチノミセテムコミタンスに起因する疾病の検出、予防、改善、および治療のための、抗体、ポリペプチド、およびポリヌクレオチドが提供される。

【特許請求の範囲】

【請求項 1】

以下からなる群から選択されるアミノ酸配列の少なくとも 5 個の連続するアミノ酸を含有する精製免疫原性ポリペプチド：配列番号 2、配列番号 4、配列番号 6、配列番号 8、配列番号 10、配列番号 12、配列番号 14、配列番号 16、配列番号 18、配列番号 20、配列番号 22、配列番号 24、配列番号 26、配列番号 28、配列番号 30、配列番号 32、配列番号 34、配列番号 36、配列番号 38、配列番号 40、配列番号 42、配列番号 44、配列番号 46、配列番号 48、配列番号 50、配列番号 52、配列番号 54、配列番号 56、配列番号 58、配列番号 60、配列番号 62、配列番号 64、配列番号 66、配列番号 68、配列番号 70、配列番号 72、配列番号 74、配列番号 76、配列番号 78、配列番号 80、配列番号 82、配列番号 84、配列番号 86、配列番号 88、配列番号 90、配列番号 92、配列番号 94、配列番号 96、配列番号 98、配列番号 100、配列番号 102、配列番号 103、配列番号 104、配列番号 105、配列番号 107、配列番号 109、配列番号 110、配列番号 111、配列番号 112、配列番号 113、配列番号 114、配列番号 116、配列番号 118、配列番号 120、配列番号 122、配列番号 124、配列番号 126、配列番号 128、配列番号 130、配列番号 132、配列番号 134、配列番号 136、配列番号 138、配列番号 140、配列番号 142、配列番号 144、配列番号 146、配列番号 148、配列番号 150、配列番号 152、配列番号 154、配列番号 156、配列番号 158、配列番号 160、配列番号 162、配列番号 164、配列番号 166、配列番号 168、配列番号 170、配列番号 172、配列番号 174、配列番号 176、配列番号 178、配列番号 180、配列番号 182、配列番号 184、配列番号 186、配列番号 188、配列番号 190、配列番号 192、配列番号 194、配列番号 196、配列番号 198、配列番号 200、配列番号 202、配列番号 204、配列番号 206、配列番号 208、配列番号 210、配列番号 212、配列番号 214、配列番号 216、配列番号 218、配列番号 220、配列番号 222、および配列番号 224。

【請求項 2】

以下からなる群から選択されるアミノ酸配列を含有する精製ポリペプチド：配列番号 2、配列番号 4、配列番号 6、配列番号 8、配列番号 10、配列番号 12、配列番号 14、配列番号 16、配列番号 18、配列番号 20、配列番号 22、配列番号 24、配列番号 26、配列番号 28、配列番号 30、配列番号 32、配列番号 34、配列番号 36、配列番号 38、配列番号 40、配列番号 42、配列番号 44、配列番号 46、配列番号 48、配列番号 50、配列番号 52、配列番号 54、配列番号 56、配列番号 58、配列番号 60、配列番号 62、配列番号 64、配列番号 66、配列番号 68、配列番号 70、配列番号 72、配列番号 74、配列番号 76、配列番号 78、配列番号 80、配列番号 82、配列番号 84、配列番号 86、配列番号 88、配列番号 90、配列番号 92、配列番号 94、配列番号 96、配列番号 98、配列番号 100、配列番号 102、配列番号 103、配列番号 104、配列番号 105、配列番号 107、配列番号 109、配列番号 110、配列番号 111、配列番号 112、配列番号 113、配列番号 114、配列番号 116、配列番号 118、配列番号 120、配列番号 122、配列番号 124、配列番号 126、配列番号 128、配列番号 130、配列番号 132、配列番号 134、配列番号 136、配列番号 138、配列番号 140、配列番号 142、配列番号 144、配列番号 146、配列番号 148、配列番号 150、配列番号 152、配列番号 154、配列番号 156、配列番号 158、配列番号 160、配列番号 162、配列番号 164、配列番号 166、配列番号 168、配列番号 170、配列番号 172、配列番号 174、配列番号 176、配列番号 178、配列番号 180、配列番号 182、配列番号 184、配列番号 186、配列番号 188、配列番号 190、配列番号 192、配列番号 194、配列番号 196、配列番号 198、配列番号 200、配列番号 202、配列番号 204、配列番号 206、配列番号 208、配列番号 210、配列番号 212、配列番号 214、配列番号 216、配列番号 218、配列番号 220、配列番号 222、および配列番号 224。

【請求項 3】

請求項 1 記載のポリペプチドをコードする配列を含有する精製ポリヌクレオチド。

【請求項 4】

以下からなる群から選択される配列の少なくとも約 15 個の連続した核酸を含有する精製ポリヌクレオチド、またはその縮重変異体：配列番号 1、配列番号 3、配列番号 5、配列番号 7、配列番号 9、配列番号 11、配列番号 13、配列番号 15、配列番号 17、配列番号 19、配列番号 21、配列番号 23、配列番号 25、配列番号 27、配列番号 29、配列番号 31、配列番号 33

、配列番号35、配列番号37、配列番号39、配列番号41、配列番号43、配列番号45、配列番号47、配列番号49、配列番号51、配列番号53、配列番号55、配列番号57、配列番号59、配列番号61、配列番号63、配列番号65、配列番号67、配列番号69、配列番号71、配列番号73、配列番号75、配列番号77、配列番号79、配列番号81、配列番号83、配列番号85、配列番号87、配列番号89、配列番号91、配列番号93、配列番号95、配列番号97、配列番号99、配列番号101、配列番号106、配列番号108、配列番号115、配列番号117、配列番号119、配列番号121、配列番号123、配列番号125、配列番号127、配列番号129、配列番号131、配列番号133、配列番号135、配列番号137、配列番号139、配列番号141、配列番号143、配列番号145、配列番号147、配列番号149、配列番号151、配列番号153、配列番号155、配列番号157、配列番号159、配列番号161、配列番号163、配列番号165、配列番号167、配列番号169、配列番号171、配列番号173、配列番号175、配列番号177、配列番号179、配列番号181、配列番号183、配列番号185、配列番号187、配列番号189、配列番号191、配列番号193、配列番号195、配列番号197、配列番号199、配列番号201、配列番号203、配列番号205、配列番号207、配列番号209、配列番号211、配列番号213、配列番号215、配列番号217、配列番号219、配列番号221、および配列番号223。

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【請求項5】

以下のヌクレオチド配列を含有する精製ポリヌクレオチド、またはその縮重変異体：配列番号1、配列番号3、配列番号5、配列番号7、配列番号9、配列番号11、配列番号13、配列番号15、配列番号17、配列番号19、配列番号21、配列番号23、配列番号25、配列番号27、配列番号29、配列番号31、配列番号33、配列番号35、配列番号37、配列番号39、配列番号41、配列番号43、配列番号45、配列番号47、配列番号49、配列番号51、配列番号53、配列番号55、配列番号57、配列番号59、配列番号61、配列番号63、配列番号65、配列番号67、配列番号69、配列番号71、配列番号73、配列番号75、配列番号77、配列番号79、配列番号81、配列番号83、配列番号85、配列番号87、配列番号89、配列番号91、配列番号93、配列番号95、配列番号97、配列番号99、配列番号101、配列番号106、配列番号108、配列番号115、配列番号117、配列番号119、配列番号121、配列番号123、配列番号125、配列番号127、配列番号129、配列番号131、配列番号133、配列番号135、配列番号137、配列番号139、配列番号141、配列番号143、配列番号145、配列番号147、配列番号149、配列番号151、配列番号153、配列番号155、配列番号157、配列番号159、配列番号161、配列番号163、配列番号165、配列番号167、配列番号169、配列番号171、配列番号173、配列番号175、配列番号177、配列番号179、配列番号181、配列番号183、配列番号185、配列番号187、配列番号189、配列番号191、配列番号193、配列番号195、配列番号197、配列番号199、配列番号201、配列番号203、配列番号205、配列番号207、配列番号209、配列番号211、配列番号213、配列番号215、配列番号217、配列番号219、配列番号221、および配列番号223。

【請求項6】

発現制御配列に動作可能なように連結された請求項4記載のポリヌクレオチドを含有する発現ベクター。

【請求項7】

請求項6記載のベクターを含有する培養細胞。

【請求項8】

ポリヌクレオチドが発現制御配列に動作可能なように連結されている、請求項4記載のポリヌクレオチドを含有する培養細胞。

【請求項9】

請求項1記載のポリペプチドに特異的に結合する抗体またはそのフラグメント。

【請求項10】

フラグメントがFabおよびF(ab')₂からなる群から選択される、請求項9記載の抗体またはそのフラグメント。

【請求項11】

抗体がモノクローナル抗体またはポリクローナル抗体である、請求項9記載の抗体。

【請求項12】

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請求項 9 記載の抗体および医薬的に許容されるキャリアーを含有する組成物。

【請求項 13】

A.アクチノミセテムコミタンスに起因する疾病を治療、改善、または予防する方法であって、請求項 9 記載の抗体またはそのフラグメントを動物に投与し、それによって A.アクチノミセテムコミタンスに起因する疾病を治療、改善、または予防することを含む上記方法。

【請求項 14】

疾病が局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、抗療性成人歯周炎、心内膜炎、甲状腺腫瘍、尿路感染症、脳腫瘍、および椎骨髄炎からなる群から選択される、請求項 13 記載の方法。

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【請求項 15】

試験サンプル中の A.アクチノミセテムコミタンスまたは A.アクチノミセテムコミタンス抗原の存在を検出する方法であって、

試験サンプルを、A.アクチノミセテムコミタンスまたは A.アクチノミセテムコミタンス抗原に特異的に結合する請求項 9 記載の抗体と、抗体と A.アクチノミセテムコミタンスまたは A.アクチノミセテムコミタンス抗原との間の免疫複合体の生成が可能な条件下で接触させ；そして

免疫複合体を検出する、ことを含み、ここで、免疫複合体の検出は試験サンプル中の A.アクチノミセテムコミタンスまたは A.アクチノミセテムコミタンス抗原の存在を示す、上記方法。

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【請求項 16】

A.アクチノミセテムコミタンス抗原が動物感染の際にインビボで発現される、請求項 15 記載の方法。

【請求項 17】

請求項 1 記載のポリペプチドおよび医薬的に許容されるキャリアーを含有する医薬組成物。

【請求項 18】

動物に請求項 1 記載の精製ポリペプチドを投与して免疫応答を誘発することを含む、免疫応答を誘発する方法。

【請求項 19】

A.アクチノミセテムコミタンスに起因する疾病または感染を治療、予防、または改善する方法であって、請求項 1 記載の精製ポリペプチドを動物に投与して疾病または感染を治療、予防、または改善することを含む上記方法。

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【請求項 20】

疾病が、局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、抗療性成人歯周炎、心内膜炎、甲状腺腫瘍、尿路感染症、脳腫瘍、および椎骨髄炎からなる群から選択される、請求項 19 記載の方法。

【請求項 21】

請求項 4 記載のポリヌクレオチドおよび医薬的に許容されるキャリアーを含有する組成物。

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【請求項 22】

ポリヌクレオチドが DNA である、請求項 21 記載の組成物。

【請求項 23】

ポリヌクレオチドがプラスミド中に存在する、請求項 21 記載の組成物。

【請求項 24】

請求項 4 記載の精製ポリヌクレオチドを動物に投与して免疫応答を誘発することを含む、免疫応答を誘発する方法。

【請求項 25】

A.アクチノミセテムコミタンスに起因する疾病または感染を治療、予防、または改善する方法であって、請求項 4 記載の精製ポリヌクレオチドを動物に投与して、疾病または感

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染を治療、予防、または改善する上記方法。

【請求項 26】

疾病が局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、抗療性成人歯周炎、心内膜炎、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎からなる群から選択される、請求項 25 記載の方法。

【請求項 27】

試験サンプル中の第 1 の A.アクチノミセテムコミタンス・ポリヌクレオチドの存在を同定する方法であって、

第 1 のポリヌクレオチドを含有する疑いのある試験サンプルを第 2 のポリヌクレオチドとハイブリダイゼーション条件下で接触させ、ここで、第 2 のポリヌクレオチドは請求項 4 記載のポリヌクレオチドであり；そして

ハイブリダイズした第 1 および第 2 のポリヌクレオチドの複合体を検出する、ことを含み、ここで、ハイブリダイズした第 1 および第 2 のポリヌクレオチドの存在は試験サンプル中の第 1 のポリヌクレオチドの存在を示す、上記方法。

【発明の詳細な説明】

【技術分野】

【0001】

政府の権利

本発明は国立保健研究所 (National Institutes of Health) (国立歯／頭蓋顔面研究所 (National Institute for Dental and Craniofacial Research、NIDCR)) による助成金番号 R01 DE 13523 下での政府の援助によるものである。政府は本発明において一定の権利を有する。

【0002】

技術分野

本発明はアクチノバチルス・アクチノミセテムコミタンス (*Actinobacillus actinomycetemcomitans*) に起因する疾病の診断、治療、予防、および改善のための方法および組成物を提供する。

【背景技術】

【0003】

発明の背景

アクチノバチルス・アクチノミセテムコミタンス (Aa) は、早期発症型歯周炎 (例えば、局所性および汎発性歯周炎、局所性および汎発性若年性歯周炎、および急速進行性または抗療性成人歯周炎等) の主要な原因微生物である。現在、これらの疾病の診断は、通常、疾病の発症後長時間を経て、支持する骨格および組織のかかなりの損傷が起こってから、X線分析によってなされる。歯の喪失は破壊性歯周疾患の最も有害な影響である。米国の国民調査により、局所性若年性歯周炎の罹患率は 0.53%、汎発性若年性歯周炎では 0.13% であることが明かとなった (Loe および Brown、J. Periodontol. 62:608-616 (1991))。多くの研究からの知見により、早期発症型疾患は他の先進国でも同様であり、発展途上国ではより頻度が高いという結論が裏付けてられている (Loe および Brown、J. Periodontol. 62:608-616 (1991))。従って、早期発症型歯周炎、局所性および汎発性若年性歯周炎、および急速進行性または抗療性成人歯周炎の早期診断法が当該分野で必要とされている。更に、一般に成人集団の半数以上が罹患している非常に一般的な症状である、ある種の成人歯周炎は、Aa によって起こると考えられる。また、Aa は口腔外疾患、例えば心内膜炎、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎 (vertebral osteomyelitis) を引き起こしうる。

【0004】

Aa 誘導型歯周炎の治療には、抗生物質療法、外科療法、および機械的治療法があるが、予防の方法はない。テトラサイクリンは早期発症型歯周炎の治療に広範に使用されてきた

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。しかしながら、テトラサイクリンへの耐性を獲得する株の懸念、並びに他の病原微生物の過剰増殖の可能性が残っている。これらの疾病の発生があるとすれば、Aaの安全なワクチンが必要とされる。ワクチンは例えば多価ワクチンであってもよい。歯周疾患の制御は、最近注目されている全身性疾患（例えば虚血性心疾患）のリスク因子としての歯周感染症の役割の可能性の点からも非常に重要である。

【0005】

ほとんどの人はその歯垢の正常なメンバーとしてAaを有するが、これは通常、疾病の原因とならない。しかしながら、Aaが疾病の原因となる時、宿主は著しい免疫応答を開始し、これは当然無駄に終わるが、それはおそらく免疫応答が誤ったAa抗原に向けられるためである。最も好適な歯周疾患治療を提供するためには、正確な診断を行い、最適な治療を実施し、そして治療に対する患者の反応をモニタリングすることが必要である。

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【0006】

現在、Aaの標準的な微生物学的試験は、歯垢中のAaの存在のみを検出するものであり、疾病の活性を特異的に同定するものではない。この理由から、これらの試験は、予測的な価値が低い。Aaは健康な個体の歯垢中にも一般的に見られるので、これらの試験の適用の有用性は、一定の疾病の臨床的兆候を示す人、例えば25才未満の進行性付着器官（attachment）喪失および骨喪失患者、約25－35才の相対的に短時間で付着器官および骨が急速破壊される（急速進行性歯周炎）患者、および厳密な治療にも関わらず付着器官を喪失し続ける（抗療性歯周炎）患者に限定される。

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【0007】

歯垢中のAaの存在を同定するためにDNAプローブ技術が開発されているが、この技術は歯垢群集の正常な一部分であるAaと実際の疾病過程に関与するAaを識別することができない。従って、これらのDNAプローブは疾病過程に関与するAaを同定しない。

【0008】

従って、Aaに起因する疾病の診断、モニタリング、治療、予防、または改善の方法が当該分野で必要とされている。

【発明の開示】

【課題を解決するための手段】

【0009】

発明の概要

本発明の目的は、Aaに起因する疾病の治療、改善、および予防のための方法および組成物を提供することである。本発明のこの目的および他の目的は、下記の態様の1またはそれ以上によって提供される。

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【0010】

本発明の1つの態様は、以下からなる群から選択されるアミノ酸配列の少なくとも5個の連続するアミノ酸を含有する精製免疫原性ポリペプチドを提供する：配列番号2、配列番号4、配列番号6、配列番号8、配列番号10、配列番号12、配列番号14、配列番号16、配列番号18、配列番号20、配列番号22、配列番号24、配列番号26、配列番号28、配列番号30、配列番号32、配列番号34、配列番号36、配列番号38、配列番号40、配列番号42、配列番号44、配列番号46、配列番号48、配列番号50、配列番号52、配列番号54、配列番号56、配列番号58、配列番号60、配列番号62、配列番号64、配列番号66、配列番号68、配列番号70、配列番号72、配列番号74、配列番号76、配列番号78、配列番号80、配列番号82、配列番号84、配列番号86、配列番号88、配列番号90、配列番号92、配列番号94、配列番号96、配列番号98、配列番号100、配列番号102、配列番号103、配列番号104、配列番号105、配列番号107、配列番号109、配列番号110、配列番号111、配列番号112、配列番号113、配列番号114、配列番号116、配列番号118、配列番号120、配列番号122、配列番号124、配列番号126、配列番号128、配列番号130、配列番号132、配列番号134、配列番号136、配列番号138、配列番号140、配列番号142、配列番号144、配列番号146、配列番号148、配列番号150、配列番号152、配列番号154、配列番号156、配列番号158、配列番号160、配列番号162、配列番号164、配列番号166、配列番号168、配列番号170、配列番号172、配列番号174、配

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列番号176、配列番号178、配列番号180、配列番号182、配列番号184、配列番号186、配列番号188、配列番号190、配列番号192、配列番号194、配列番号196、配列番号198、配列番号200、配列番号202、配列番号204、配列番号206、配列番号208、配列番号210、配列番号212、配列番号214、配列番号216、配列番号218、配列番号220、配列番号222、配列番号224、配列番号226、配列番号228、配列番号230、配列番号232、および配列番号234（“ポリペプチド配列番号”）。これらのポリペプチド配列のそれぞれを集合的に“ポリペプチド配列番号”と呼び、合わせて一群として表すが、これらの配列のそれぞれは、個別に考慮し特許請求することができる。

【0011】

本発明の別の態様は、“ポリペプチド配列番号”からなる群から選択されるアミノ酸配列を含有する精製ポリペプチドを提供する。 10

【0012】

本発明の更に別の態様は、“ポリペプチド配列番号”をコードする配列を含有する精製ポリヌクレオチドを提供する。

【0013】

本発明の更に別の態様は、以下からなる群から選択される配列の少なくとも約15個の連続する核酸を含有する精製ポリヌクレオチドを提供する：配列番号1、配列番号3、配列番号5、配列番号7、配列番号9、配列番号11、配列番号13、配列番号15、配列番号17、配列番号19、配列番号21、配列番号23、配列番号25、配列番号27、配列番号29、配列番号31、配列番号33、配列番号35、配列番号37、配列番号39、配列番号41、配列番号43、配列番号45、配列番号47、配列番号49、配列番号51、配列番号53、配列番号55、配列番号57、配列番号59、配列番号61、配列番号63、配列番号65、配列番号67、配列番号69、配列番号71、配列番号73、配列番号75、配列番号77、配列番号79、配列番号81、配列番号83、配列番号85、配列番号87、配列番号89、配列番号91、配列番号93、配列番号95、配列番号97、配列番号99、配列番号101、配列番号106、配列番号108、配列番号115、配列番号117、配列番号119、配列番号121、配列番号123、配列番号125、配列番号127、配列番号129、配列番号131、配列番号133、配列番号135、配列番号137、配列番号139、配列番号141、配列番号143、配列番号145、配列番号147、配列番号149、配列番号151、配列番号153、配列番号155、配列番号157、配列番号159、配列番号161、配列番号163、配列番号165、配列番号167、配列番号169、配列番号171、配列番号173、配列番号175、配列番号177、配列番号179、配列番号181、配列番号183、配列番号185、配列番号187、配列番号189、配列番号191、配列番号193、配列番号195、配列番号197、配列番号199、配列番号201、配列番号203、配列番号205、配列番号207、配列番号209、配列番号211、配列番号213、配列番号215、配列番号217、配列番号219、配列番号221、配列番号223、配列番号225、配列番号227、配列番号229、配列番号231、および配列番号233（“ポリヌクレオチド配列番号”）。これらのポリヌクレオチド配列のそれぞれを集合的に“ポリヌクレオチド配列番号”と呼び、合わせて一群として表すが、これらの配列はそれぞれ個別に考慮し特許請求することができる。 20 30

【0014】

本発明の別の態様は、“ポリヌクレオチド配列番号”のヌクレオチド配列またはそれらの縮重変異体を含有する精製ポリヌクレオチドを提供する。 40

【0015】

本発明の別の態様は、発現制御配列に動作可能なように連結された“ポリヌクレオチド配列番号”を含有する発現ベクターを提供する。ベクターは培養細胞中に存在してもよい。

【0016】

本発明の更に別の態様は、“ポリペプチド配列番号”のポリペプチドに特異的に結合する抗体またはそのフラグメントを提供する。抗体フラグメントは、例えばFabまたはF(ab')₂フラグメントであってもよい。抗体はモノクローナル抗体またはポリクローナル抗体であってもよい。抗体は医薬的に許容されるキャリアーと共に医薬組成物中に存在してもよい。

【0017】

本発明の更に別の態様は、A.アクチノミセテムコミタンスに起因する疾病の治療、改善、または予防の方法を提供する。方法は本発明の抗体またはそのフラグメントを動物に投与することを含む。それによって、A.アクチノミセテムコミタンスに起因する疾病の治療、改善、または予防する。A.アクチノミセテムコミタンスに起因する疾病は以下からなる群から選択することができる：局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、抗療性成人歯周炎、心内膜炎（endocarditis）、甲状腺膿瘍、尿路感染症、脳膿瘍、および椎骨髄炎。

【0018】

本発明の更に別の態様は、試験サンプル中のA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原の存在を検出する方法を提供する。方法は、試験サンプルとA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原に特異的に結合する本発明の抗体を、抗体とA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原との間の免疫複合体の生成が可能な条件下で接触させ、そして免疫複合体を検出することを含む。免疫複合体の検出は、試験サンプル中のA.アクチノミセテムコミタンスまたはA.アクチノミセテムコミタンス抗原の存在を示す。検出されるA.アクチノミセテムコミタンス抗原は、動物の感染の際にインビボで発現される抗原であってもよい。

【0019】

本発明の別の態様は、本発明のポリペプチドを医薬的に許容されるキャリアーと共に含有する医薬組成物を提供する。

【0020】

本発明の更に別の態様は、免疫応答を誘発する方法を提供する。方法は本発明のポリペプチドを動物に投与して免疫応答を誘発することを含む。

【0021】

本発明の更に別の態様は、A.アクチノミセテムコミタンスに起因する疾病または感染の治療、予防、または改善の方法を提供する。方法は本発明のポリペプチドを動物に投与して疾病または感染を治療、予防、または改善することを含む。

【0022】

本発明の更に別の態様は、本発明のポリヌクレオチドおよび医薬的に許容されるキャリアーを含有する組成物を提供する。ポリヌクレオチドはDNAであってもよい。ポリヌクレオチドはプラスミド中に存在してもよい。

【0023】

本発明の別の方法は、免疫応答を誘発する方法を提供し、方法は本発明の精製ポリヌクレオチドを動物に投与して免疫応答を誘発することを含む。本発明の更に別の態様は、A.アクチノミセテムコミタンスに起因する疾病または感染の治療、予防、または改善の方法を提供する。方法は本発明の精製ポリヌクレオチドを動物に投与して疾病または感染を治療、予防、または改善することを含む。

【0024】

本発明の更に別の態様は、第1のA.アクチノミセテムコミタンス・ポリヌクレオチドの存在を同定する方法を提供する。この方法は、ハイブリダイゼーション条件下で第1のA.アクチノミセテムコミタンス・ポリヌクレオチドを含有する疑いのある試験サンプルを第2のポリヌクレオチドと接触させることを含み、ここで第2のポリヌクレオチドは本発明のポリヌクレオチドである。ハイブリダイズした第1および第2のポリヌクレオチドの複合体を検出する。ハイブリダイズした第1および第2ポリヌクレオチド複合体の存在は、試験サンプル中の第1のポリヌクレオチドの存在を示す。

【発明を実施するための最良の形態】

【0025】

発明の詳細な説明ポリヌクレオチドおよびポリペプチドの同定法

微生物が疾病を誘発する能力にとって重要なヌクレオチド配列を同定する方法を、早期

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発症型歯周炎（例えば、局所性思春期前歯周炎、汎発性思春期前歯周炎、局所性若年性歯周炎、汎発性若年性歯周炎、急速進行性成人歯周炎、および抗療性成人歯周炎等）の主要な原因微生物であるAaに適用する。Aaはまた、心内膜炎、甲状腺腫瘍、尿路感染症、脳腫瘍、および椎骨髄炎も引き起こしうる。本発明のポリヌクレオチドおよびポリペプチド配列を同定するのに使用される方法は、インビボ誘導型抗原法（in vivo induced antigen technology; IVIAT）と呼ばれる（Handfieldら、Trends Microbiol. 336:336-339（2000）；国際特許公開WO 01/11081参照）。

【0026】

簡単には、IVIATは、インビボおよびインビトロでAaによって発現されるAa抗原に対する抗体のサンプルを得、インビトロで増殖させたAaの細胞または細胞抽出物に抗体を吸収させることを含む。使用できる抗体のサンプルの例は、Aaに感染したことがある、または感染している患者由来の血清である。未吸収の抗体を単離し、これを使用してAa DNAの発現ライブラリーを探索する。反応性クローンを単離し、クローニングしたフラグメントの配列を確認する。 10

【0027】

IVIATを使用して、Aaが動物（特にヒト）において実際に疾病を引き起こすことに携わる場合にのみ発現されるAaのポリヌクレオチドを同定した。通常、感染の際にAaによる毒性遺伝子の刺激を引き起こす重要な環境シグナルは、細菌を実験室で増殖させた場合は見られない。従って、診断およびワクチン戦略のための最も優れた標的の多くは未知であった。IVIAT方法論を使用して、ヒト宿主におけるAaの増殖の際には特異的に刺激されるが、日常的な実験室での増殖の際には刺激されないポリヌクレオチドを同定した。これらのポリヌクレオチド、および対応するポリペプチドおよび抗体は、例えば感染の初期段階にある被験体の同定および治療への反応のモニタリングのためのAaの診断試験の開発、および疑いのある動物におけるAaに起因する疾病を予防または治療するためのワクチンまたは治療の開発に有用である。 20

【0028】

IVIATによって同定される抗原は、Aaに起因する疾病（例えば歯周疾患）に関して、予測的な価値が非常に高い。Aaの診断試験は、母親が歯周炎の病歴を有する小児をスクリーニングして、小児がその疾病に罹患しやすい傾向を有するかどうかを確認するような適用に有用でありうる。思春期前の歯周炎に関係することが知られている疾病には以下がある：パピヨン・ルフェーブル症候群（PLS）、低ホスファターゼ血症、好中球減少症、白血球付着欠損症（leukocyte adhesion deficiency; LAD）、チェディアック・ヒガシ症候群、ダウン症候群、白血病、ヒスチオサイトーシスX、早期発症型I型糖尿病、および先端疼痛症。これらの疾病を有する小児はAa試験の候補者である。更に、歯周炎の傾向がより低い他の思春期前小児にもAa診断試験は有益であり、これは、他の予測方法、または既知のリスク因子がないためである。 30

【0029】

ポリペプチド

本発明の精製ポリペプチドは、完全長のポリペプチドまたはポリペプチドのフラグメントのいずれであってもよい。例えば本発明のポリペプチドのフラグメントは、本発明のポリペプチドの約5、10、25、50、100、または200アミノ酸を含有してもよい。本発明のポリペプチドの例には以下に示すものがある：配列番号2、配列番号4、配列番号6、配列番号8、配列番号10、配列番号12、配列番号14、配列番号16、配列番号18、配列番号20、配列番号22、配列番号24、配列番号26、配列番号28、配列番号30、配列番号32、配列番号34、配列番号36、配列番号38、配列番号40、配列番号42、配列番号44、配列番号46、配列番号48、配列番号50、配列番号52、配列番号54、配列番号56、配列番号58、配列番号60、配列番号62、配列番号64、配列番号66、配列番号68、配列番号70、配列番号72、配列番号74、配列番号76、配列番号78、配列番号80、配列番号82、配列番号84、配列番号86、配列番号88、配列番号90、配列番号92、配列番号94、配列番号96、配列番号98、配列番号100、配列番号102、配列番号103、配列番号104、配列番号105、配列番号107、配列番 40 50

号109、配列番号110、配列番号111、配列番号112、配列番号113、配列番号114、配列番号116、配列番号118、配列番号120、配列番号122、配列番号124、配列番号126、配列番号128、配列番号130、配列番号132、配列番号134、配列番号136、配列番号138、配列番号140、配列番号142、配列番号144、配列番号146、配列番号148、配列番号150、配列番号152、配列番号154、配列番号156、配列番号158、配列番号160、配列番号162、配列番号164、配列番号166、配列番号168、配列番号170、配列番号172、配列番号174、配列番号176、配列番号178、配列番号180、配列番号182、配列番号184、配列番号186、配列番号188、配列番号190、配列番号192、配列番号194、配列番号196、配列番号198、配列番号200、配列番号202、配列番号204、配列番号206、配列番号208、配列番号210、配列番号212、配列番号214、配列番号216、配列番号218、配列番号220、配列番号222、配列番号224、配列番号226、配列番号228、配列番号230、配列番号232、および配列番号234。これらのポリペプチドを“ポリペプチド配列番号”と呼ぶ。ポリペプチド配列番号に示すポリペプチド配列と少なくとも約75、または約90、96、98、もしくは99%の同一性を示す相同アミノ酸配列もAaポリペプチドである。相同なアミノ酸配列は生体活性を保持し、すなわち生体機能的に同等である。

【0030】

配列同一性のパーセンテージは当該分野で認識される意味を持ち、2つのポリペプチドまたはポリヌクレオチド配列間の同一性を測定するための多くの方法がある。例えば以下を参照されたい：Lesk編，Computational Molecular Biology, Oxford University Press, New York, (1988)；Smith編，Biocomputing: Informatics And Genome Projects, Academic Press, New York, (1993)；GriffinおよびGriffin編，Computer Analysis Of Sequence Data, Part I, Humana Press, New Jersey, (1994)；von Heinje, Sequence Analysis In Molecular Biology, Academic Press, (1987)；そして、GribskovおよびDevereux編，Sequence Analysis Primer, M Stockton Press, New York, (1991)。ポリヌクレオチドまたはポリペプチドをアラインメントする方法は以下のようなコンピュータプログラムにコーディングされている：GCGプログラムパッケージ（Devereuxら，Nuc. Acids Res. 12:387 (1984)）、BLASTP、BLASTN、FASTA（Atschul ら，J. Molec. Biol. 215:403 (1990)）、およびBestfitプログラム（Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711）（これはSmithおよびWatermanの局所相同性アルゴリズムを使用する（Adv. App. Math., 2:482-489 (1981)））。例えば、FASTAアルゴリズムを使用するコンピュータプログラムALIGNを、ギャップオープンペナルティー12、ギャップ伸長ペナルティー2のアフィンギャップサーチと共に使用できる。

【0031】

配列アラインメントプログラムを使用して、特定の配列が例えば参照配列と約95%の同一性を有するかどうかを確認する場合、同一性のパーセンテージが参照ポリヌクレオチドの完全長にわたって計算されるように、そして同一性のギャップが参照ポリヌクレオチド中のヌクレオチド総数の5%までとなるように、パラメーターを設定する。

【0032】

ポリペプチド配列番号に示すポリペプチド変異体およびそのフラグメントも本発明に含まれる。変異体は、保存的置換および／または修飾においてのみ、ポリペプチド配列番号またはそのフラグメントと異なるポリペプチドであり、そのためポリペプチドの抗原性は元のポリペプチドと実質的に同じである。一般に変異体の同定は、本発明のポリペプチド配列の1つを修飾し、修飾されたポリペプチドの抗原性を、例えば免疫組織化学的アッセイ、酵素結合免疫吸着アッセイ（ELISA）、ラジオイムノアッセイ（RIA）、またはウェスタンブロットアッセイを使用して評価することによって行うことができる。本発明のポリペプチドは少なくとも1、5、10、25、50、または100個の保存的アミノ酸置換を含むことができる。

【0033】

保存的置換は、アミノ酸が同様の特性を有する別のアミノ酸で置換され、そのためペ

チド化学分野の当業者によってポリペプチドの2次構造およびハイドロパシー特性が実質的に変化しないことが予期されるものである。一般に、以下のアミノ酸群は保存的变化を示す：(1) ala、pro、gly、glu、asp、gln、asn、ser、thr；(2) cys、ser、tyr、thr；(3) val、ile、leu、met、ala、phe；(4) lys、arg、his；および(5) phe、tyr、trp、his。

【0034】

変異体は更に(または代わりに)、例えばポリペプチドの抗原性、2次構造、およびハイドロパシー特性に最小限の影響しか与えないアミノ酸の欠失または添加によって修飾することもできる。例えばポリペプチドをタンパク質のN-末端でシグナル(またはリーダー)配列にコンジュゲートさせることができ、これは翻訳時に、または翻訳後にタンパク質を移動させる。また、ポリペプチドを、ポリペプチドの合成、精製、もしくは同定を容易にするため(例えばポリHis)、または固体支持体へのポリペプチドの結合を向上するために、リンカーまたは他の配列にコンジュゲートさせることもできる。例えばポリペプチドを免疫グロブリンのFc領域にコンジュゲートさせることができる。

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【0035】

本発明のポリペプチドはポリペプチド配列番号に示すポリペプチドの少なくとも約5、10、25、50、100、または200アミノ酸の生体機能的同等物を更に含んでもよい。ポリペプチドがアッセイ(例えば免疫組織化学的アッセイ、ELISA、RIA、またはウェスタンブロットアッセイ)において本発明のポリペプチドと実質的に同じように反応し、例えば元のポリペプチドの90-110%の活性を有する場合、これは生物学的同等物である。ある態様では、アッセイは競合アッセイであり、ここでは、生物学的に同等であるポリペプチドは、本発明のポリペプチドの対応する反応性抗原または抗体への結合を約80、95、99、または100%低下させる能力を有する。

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【0036】

本発明のポリペプチドは、Aaに対して反応性を有する抗体によって認識される抗原を含むことができる。抗原は1またはそれ以上のエピトープ(または抗原決定基)を含むことができる。エピトープは直鎖エピトープ、連続エピトープ(sequential epitope)、またはコンフォメーションエピトープであってもよい。本発明のポリペプチド内のエピトープはいくつかの方法によって同定できる。例えば米国特許第4,554,101号；JamesonおよびWolfe, CABIOS 4:181-186 (1988)参照。例えば、本発明のポリペプチドを単離およびスクリーニングすることができる。合わせると全ポリペプチド配列を網羅するような一連の短鎖ペプチドを、タンパク分解による開裂によって調製することができる。例えば100量体ポリペプチドフラグメントから出発して、ELISAで認識されるエピトープの存在について各フラグメントを試験できる。例えばELISAアッセイで、Aaポリペプチド(例えば100量体ポリペプチドフラグメント)を固体支持体(例えばプラスチック製のマルチウェルプレートのウェル)に結合させる。抗体集団を標識し、固体支持体に添加し、非特異的吸収が阻害されるような条件下で未標識の抗原に結合させ、未結合の抗体および他のタンパク質を洗浄除去する。抗体結合を、例えば無色の基質を着色された反応生成物に変換する反応によって検出する。次いで、同定された100量体から次第に小さくした重複するフラグメントを試験し、興味のエピトープのマッピングを行う。

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【0037】

本発明のポリペプチドは組換え技術によって生成することができる。本発明のポリペプチドをコードするポリヌクレオチドを組換え発現ベクターに導入することができ、これを当業界で周知の技術を使用して好適な発現宿主細胞系で発現させることができる。種々の細菌、酵母、植物、哺乳動物、および昆虫発現系が当業界で利用されており、それらの発現系のいずれを使用してもよい。必要により、ポリペプチドをコードするポリヌクレオチドを、細胞を使用しない翻訳系において翻訳することができる。また、ポリペプチドは化学的に合成することもできる。

【0038】

必要により、ポリペプチドを融合タンパク質として生成することができ、これは他のア

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ミノ酸配列（例えばアミノ酸リンカーまたはシグナル配列）、並びにタンパク質の精製に有用なリガンド（例えばグルタチオン-S-トランスフェラーゼ、ヒスチジンタグ、およびブドウ球菌プロテインA（staphylococcal protein A））を含むこともできる。融合タンパク質中には2個以上の本発明のポリペプチドが存在してもよい。

【0039】

ポリヌクレオチド

本発明のポリヌクレオチドは、微生物ゲノム全体より少ないものを含有し、1本鎖または2本鎖のDNAまたはRNAであってもよい。ポリヌクレオチドは他の成分（例えばタンパク質および脂質）が含有されないように精製することができる。本発明のポリヌクレオチドは上記のポリペプチドをコードする。本発明のポリヌクレオチドは他のヌクレオチド配列、例えばリンカーをコードする配列、シグナル配列、異種シグナル配列、TMR転写停止配列、膜貫通ドメイン、またはタンパク質精製に有用なリガンド、例えばグルタチオン-S-トランスフェラーゼ、ヒスチジンタグ、およびブドウ球菌プロテインAを含むこともできる。

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【0040】

本発明のポリヌクレオチドは、配列番号1、配列番号3、配列番号5、配列番号7、配列番号9、配列番号11、配列番号13、配列番号15、配列番号17、配列番号19、配列番号21、配列番号23、配列番号25、配列番号27、配列番号29、配列番号31、配列番号33、配列番号35、配列番号37、配列番号39、配列番号41、配列番号43、配列番号45、配列番号47、配列番号49、配列番号51、配列番号53、配列番号55、配列番号57、配列番号59、配列番号61、配列番号63、配列番号65、配列番号67、配列番号69、配列番号71、配列番号73、配列番号75、配列番号77、配列番号79、配列番号81、配列番号83、配列番号85、配列番号87、配列番号89、配列番号91、配列番号93、配列番号95、配列番号97、配列番号99、配列番号101、配列番号106、配列番号108、配列番号115、配列番号117、配列番号119、配列番号121、配列番号123、配列番号125、配列番号127、配列番号129、配列番号131、配列番号133、配列番号135、配列番号137、配列番号139、配列番号141、配列番号143、配列番号145、配列番号147、配列番号149、配列番号151、配列番号153、配列番号155、配列番号157、配列番号159、配列番号161、配列番号163、配列番号165、配列番号167、配列番号169、配列番号171、配列番号173、配列番号175、配列番号177、配列番号179、配列番号181、配列番号183、配列番号185、配列番号187、配列番号189、配列番号191、配列番号193、配列番号195、配列番号197、配列番号199、配列番号201、配列番号203、配列番号205、配列番号207、配列番号209、配列番号211、配列番号213、配列番号215、配列番号217、配列番号219、配列番号221、配列番号223、配列番号225、配列番号227、配列番号229、配列番号231、および配列番号233で示される。これらのポリヌクレオチドを“ポリヌクレオチド配列番号”と呼ぶ。

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【0041】

本発明のポリペプチドをコードする縮重ヌクレオチド配列、並びにポリヌクレオチド配列番号に示すヌクレオチド配列と少なくとも約75%、または約90、96、98、もしくは99%の同一性を有する相同ヌクレオチド配列およびそれらの相補体も本発明のポリヌクレオチドである。配列同一性のパーセンテージを“ポリペプチド”の項に記載するように算出できる。縮重ヌクレオチド配列は、ポリペプチド配列番号に示すポリペプチドまたはそのフラグメントをコードするポリヌクレオチドであるが、遺伝子コードの縮重により、ポリヌクレオチド配列番号に示される配列と核酸配列が異なる。相補DNA（cDNA）分子、種間相同体、および生体機能的AaポリペプチドをコードするAaポリヌクレオチドの変異体もAaポリヌクレオチドである。本発明のポリヌクレオチドはポリヌクレオチド配列番号に示す核酸配列の約5、10、15、50、100、または200ヌクレオチドを含有することができる。

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【0042】

本発明のポリヌクレオチドは、例えば、感染した個体由来の生体サンプル、例えば歯垢、唾液、歯肉滲出液、痰、血液、血清、血漿、尿、便、脳脊髄液、羊水、創傷滲出液、ま

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たは組織中に存在する核酸配列から単離できる。ポリヌクレオチドは、例えば自動合成装置を使用して、実験室で合成することもできる。PCRのような増幅法を使用して、ポリペプチドをコードするゲノムDNAまたはcDNAのいずれかからポリヌクレオチドを増幅することができる。

【0043】

本発明のポリヌクレオチドは天然に存在するポリペプチドのコーディング配列を含んでもよく、または天然には存在しない変更された配列をコードしてもよい。必要により、発現制御要素を含む発現ベクター中にポリヌクレオチドをクローニングすることができ、それらの要素には、例えば複製開始点、プロモーター、エンハンサー、または宿主細胞において本発明のポリヌクレオチドの発現を誘導する他の要素がある。発現ベクターは、例えばプラスミド（例えばpBR322、pUC、またはColE1）またはアデノウィルスベクター（例えばアデノウィルスII型ベクターまたはV型ベクター）であってもよい。必要により他のベクターを使用することができ、それらには、限定される訳ではないが、シンドビスウィルス、シミアンウィルス40、アルファウィルスベクター、ポックスウィルスベクター、およびサイトメガロウィルスおよびレトロウィルスベクター、例えばマウス肉腫ウィルス、マウス乳腺癌ウィルス、マウスモロニー白血病ウィルス、およびラウス肉腫ウィルス等が含まれる。ミニクロモソーム、例えばMCおよびMC1、バクテリオファージ、ファージミド、人工酵母染色体、人工細菌染色体、ウィルス粒子、ウィルス様粒子、コスミド（入ファージのcos部位を挿入したプラスミド）、およびレプリコン（細胞中でそれら独自の制御下で複製する能力を有する遺伝要素）を使用することもできる。

【0044】

発現制御配列に動作可能なように連結されたポリヌクレオチドの調製および宿主細胞でのそれらの発現の方法は当該分野で周知である。例えば米国特許第4,366,246号を参照されたい。本発明のポリヌクレオチドは、ポリヌクレオチドの転写および／または翻訳を指示する1またはそれ以上の発現制御要素に隣接して配置されている場合、動作可能なように連結されている。

【0045】

本発明のポリヌクレオチドを含有するベクターを、例えば細菌、酵母、昆虫、または哺乳動物細胞に形質転換し、本発明のポリペプチドを細胞培養液中で発現させ、そこから単離することができる。当該分野で可能な方法のいずれかを使用して、宿主細胞にポリヌクレオチドを導入することができる。これらには、限定されるわけではないが、裸の、またはカプセルに封入された核酸でのトランスフェクション、細胞融合、プロトプラスト融合、ウィルス感染、およびエレクトロポレーション等がある。

【0046】

本発明のポリヌクレオチドを、例えばプローブまたはプライマー（例えばPCRプライマー）として使用し、サンプル（例えば生体サンプル）中のAaポリヌクレオチドの存在を検出することができる。それらのプローブおよびプライマーがAaポリヌクレオチド配列に特異的にハイブリダイズする能力により、それらを使用して所定のサンプル中の相補配列の存在を検出することが可能となる。本発明のポリヌクレオチドプローブおよびプライマーを、サンプル（例えば生体サンプル（例えば歯垢、唾液、歯肉滲出液、痰、血液、尿、便、脳脊髄液、羊水、創傷滲出液、または組織））中の相補配列にハイブリダイズさせることができる。サンプル由来のポリヌクレオチドを、例えばゲル電気泳動もしくは他のサイズ分離法に適用するか、またはサイズ分離を行わずに固定化することができる。ポリヌクレオチドプローブまたはプライマーを標識することができる。好適な標識、およびプローブおよびプライマーを標識する方法は当業界で周知であり、それらには、例えば、ニックトランスレーションまたはキナーゼによって導入する放射線標識、ビオチン標識、蛍光標識、化学発光標識、生物発光標識、金属キレート剤標識、および酵素標識がある。サンプル由来のポリヌクレオチドを、好適なストリンジェンシーのハイブリダイゼーション条件下でプローブまたはプライマーと接触させる。

【0047】

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用途によって、種々のハイブリダイゼーション条件を使用して、プローブまたはプライマーの標的配列に対する選択性を種々の程度にすることができる。高度の選択性を必要とする用途では、相対的にストリンジェントな条件（例えば低塩および／または高温条件、例えば約0.02 Mから約0.15 Mの塩濃度で、約50℃から約70℃の温度）が使用される。より低い選択性が必要とされる適用では、より低いストリンジェンシーのハイブリダイゼーション条件を使用できる。例えば約0.14 Mから約0.9 Mの塩濃度で約20℃から約55℃の温度範囲である。プローブまたはプライマーおよび試験サンプル由来の相補ポリヌクレオチドを含有するハイブリッド複合体の存在は、サンプル中のAaまたはAaポリヌクレオチド配列の存在を示す。

【0048】

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抗体

本発明の抗体は、本発明のAaポリペプチドまたはそのフラグメントに特異的かつ安定に結合する抗体分子である。本発明の抗体はポリクローナル抗体、モノクローナル抗体、1本鎖抗体（scFv）、または抗体のフラグメントであってもよい。抗体のフラグメントは無傷の抗体の抗原結合部位または可変領域を含む無傷の抗体の一部であり、この部分は無傷の抗体のFc領域の定常領域重鎖ドメインを含まない。抗体フラグメントの例にはFab、Fab'、Fab'-SH、F(ab')₂、およびF_vフラグメントがある。

【0049】

本発明の抗体は、例えばIgG、IgM、IgA、IgD、およびIgEを含むいずれのクラスの抗体であってもよい。抗体またはそのフラグメントは本発明のポリペプチドのエピトープに結合する。抗体は、好適な実験動物においてインビボで生成するか、または組換えDNA技術を使用してインビトロで生成できる。抗体を調製および特性決定する方法は当該分野で周知である。例えば以下を参照されたい：Methods Mol. Biol. 80:23-37 (1998)；Dean, Methods Mol. Biol. 32:361-79 (1994)；Baileg, Methods Mol. Biol. 32:381-88 (1994)；Gullick, Methods Mol. Biol. 32:389-99 (1994)；Drenckhahnら Methods Cell. Biol. 37:7-56 (1993)；Morrison, Ann. Rev. Immunol. 10:239-65 (1992)；Wrightら Crit. Rev. Immunol. 12:125-68 (1992)。例えば、ポリクローナル抗体の生成は、本発明のポリペプチドを動物（例えばヒトもしくは他の霊長類、マウス、ラット、ウサギ、モルモット、ヤギ、ブタ、ウシ、ヒツジ、ロバ、またはウマ）に投与することによって行ってもよい。免疫化した動物からの血清を回収し、例えば硫酸アンモニウムによる沈殿、次いでクロマトグラフィー（例えばアフィニティークロマトグラフィー）によって、抗体を血漿から精製する。ポリクローナル抗体を生成および加工する技術は当該分野で周知である。

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【0050】

更に、本発明のポリペプチド上に存在するエピトープに対するモノクローナル抗体も容易に生成できる。例えば本発明のポリペプチドで免疫化した哺乳動物（例えばマウス）由来の正常B細胞を、例えばHAT感受性マウス骨髄腫細胞と融合させてハイブリドーマを生成することができる。Aa特異的抗体を生成するハイブリドーマは、RIAまたはELISAを使用して同定し、半流動寒天中でクローニングするか、または限界希釈によって単離することができる。Aa特異的抗体を生成するクローンを、更なるラウンドのスクリーニングによって単離する。モノクローナル抗体の特異性に関するスクリーニングは、標準的な技術、例えば本発明のポリペプチドをマイクロタイタープレートに結合させ、ELISAアッセイによってモノクローナル抗体の結合を測定することによって行うことができる。モノクローナル抗体の生成および加工の技術は当該分野で周知である。例えばKohlerおよびMilstein, Nature, 256:495 (1975)を参照されたい。モノクローナル抗体の特定のアイソタイプの調製は、異なるアイソタイプのモノクローナル抗体を分泌する親ハイブリドーマから直接、初めの融合体からの選択によって、または二次的に行うことができ、これは同胞選択法（sib selection technique）を使用してクラススイッチ変異体を単離することによって行う。Steplewskiら., P.N.A.S. U.S.A. 82:8653 1985；Spriaら, J. Immunolog. Meth. 74:307, 1984参照。本発明のモノクローナル抗体は組換えモノクローナル抗体であってもよい。例えば米国特許第4,474,893号；米国特許第4,816,567号参照。本発明の抗体は化学的

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に構築することもできる。例えば米国特許第4,676,980号参照。

【0051】

本発明の抗体はキメラ（例えば米国特許第5,482,856号参照）、ヒト化（例えばJonesら, Nature 321:522 (1986); Reichmannら, Nature 332:323 (1988); Presta, Curr. Op. Struct. Biol. 2:593 (1992)参照）、またはヒト抗体であってもよい。ヒト抗体は、例えば直接不死化、ファージディスプレイ、トランスジェニックマウス、またはトリメラ（Trimer）法によって生成することができる。例えばReisenerら, Trends Biotechnol. 16:242-246 (1998)参照。

【0052】

Aa抗原に対する抗体（モノクローナル抗体およびポリクローナル抗体のいずれも）は、サンプル（例えばAa感染したヒト由来の血清サンプル）中のAaまたはAa抗原の存在を検出するのに特に有用である。AaまたはAa抗原に関する免疫アッセイは1つの抗体、またはいくつかの抗体を利用することができる。AaまたはAa抗原に関する免疫アッセイは、例えば以下を使用することができる：Aaエピトープ（単数）に対するモノクローナル抗体（単数）、1つのAaポリペプチドのエピトープ（複数）に対するモノクローナル抗体（複数）の組み合わせ、異なるAaポリペプチド（複数）のエピトープ（複数）に対するモノクローナル抗体（複数）、同じAa抗原（単数）に対するポリクローナル抗体（複数）、異なるAa抗原（複数）に対するポリクローナル抗体（複数）、またはモノクローナルおよびポリクローナル抗体の組み合わせ。免疫アッセイのプロトコールは、例えば競合、直接反応、またはサンドイッチ型アッセイ（例えば標識した抗体を使用する）に基づくものであってもよい。本発明の抗体は、当該分野で周知の型の標識、例えば蛍光、化学発光、放射能、酵素、コロイド金属、放射性同位元素、および生体発光標識で標識することができる。

【0053】

本発明の抗体またはそのフラグメントを支持体に結合させ、AaまたはAa抗原の存在を検出することができる。支持体には、例えばガラス、ポリスチレン、ポリプロピレン、ポリエチレン、デキストラン、ナイロン、アミラーゼ、天然および修飾セルロース、ポリアクリルアミド、アガロース、およびマグネタイトがある。

【0054】

本発明のポリクローナルまたはモノクローナル抗体は、更に免疫アフィニティーカラムによるAa生体またはAa抗原の単離に使用することができる。抗体がその免疫選択活性を保持するように、例えば吸収または共有結合によって固体支持体に抗体を固定化することができる。必要により、スパーサー基を含有させて、抗体の抗原結合部位を利用可能な状態に保持することができる。その後、固定化した抗体を使用してサンプル由来のAa生体またはAa抗原を結合させることができるが、それらのサンプルは例えば唾液、歯垢、歯肉滲出液、痰、血液、尿、便、脳脊髄液、羊水、創傷滲出液、または組織を含む生体サンプルである。結合したAa生体またはAa抗原を、カラムマトリクスから（例えばpH変化によって）回収する。

【0055】

本発明の抗体を免疫局在化の研究に使用し、種々の細胞事象または生理学的状態の際の本発明のポリペプチドの存在および分布を分析することもできる。抗体を使用して、受動免疫に関係する分子の同定および非タンパク質抗原の生合成に関係する分子の同定を行うこともできる。それらの分子の同定はワクチンの開発に有用でありうる。本発明の抗体（例えばモノクローナル抗体および1本鎖抗体を含む）を使用して、Aaに起因する疾病の回復の経過をモニタリングすることができる。動物由来の試験サンプル中のAaタンパク質に対するAa抗体の増加または減少を測定することによって、障害を改善することを目的とする特定の治療計画が有効かどうかを確認することができる。抗体は、例えば直接結合アッセイ（例えばRIA、ELISA、またはウェスタンブロットアッセイ）を使用して検出および／または定量することができる。

【0056】

Aaに感染している疑いのある動物由来の試験サンプルを得ることにより、本発明の抗体

をAa感染の診断法に使用することができる。試験サンプルを、抗体－抗原複合体（すなわち免疫複合体）の生成が可能な条件下で、本発明の抗体と接触させる。抗体－抗原複合体の量は、当該分野で周知の方法によって測定できる。コントロールサンプルで生成されたものよりレベルが高ければ、Aa感染を示している。あるいはまた、本発明のポリペプチドを試験サンプルと接触させることができる。陽性生体サンプル中のAa抗体は、好適な条件下で抗原－抗体複合体を生成する。抗体－抗原複合体の量は、当該分野で周知の方法によって測定できる。

【0057】

Aaに起因する疾病の治療、改善、または予防の方法

本発明のポリペプチド、ポリヌクレオチド、および抗体を使用して、Aaに起因する疾病（例えば早期発症型歯周炎（例えば局所性および汎発性思春期前歯周炎、局所性および汎発性若年性歯周炎、および急速進行性または抗療性成人歯周炎、心内膜炎、甲状腺腫瘍、尿路感染症、脳腫瘍、および椎骨髄炎を含む）を治療、改善、または予防することができる。 10

【0058】

例えば本発明のモノクローナル抗体のような抗体またはそのフラグメントを動物（例えばヒト）に投与することができる。本発明のある態様では、抗体またはそのフラグメントを、医薬的に許容されるキャリアーを含む医薬組成物で動物に投与する。医薬組成物は治療的有效量の抗体またはそのフラグメントを含有する。治療的有效量は、被験体においてAa感染の症状を改善する、またはAa生体の量を低減するのに有効な量である。 20

【0059】

本発明のポリペプチドまたはポリヌクレオチドを使用して、宿主において免疫応答を誘発することができる。免疫原性ポリペプチドまたはポリヌクレオチドは、動物において免疫応答を誘導する能力のある本発明のポリペプチドまたはポリヌクレオチドである。本発明の免疫原性ポリペプチドまたはポリヌクレオチドは、動物の免疫系を感作するのに特に有用であり、その結果として免疫応答が起こり、これによってAa感染の影響が改善または予防される。動物モデルにおける免疫応答の誘発は、例えば最適な投与量または投与経路を決定するのに有用でありうる。免疫応答の誘発は、Aaに起因する疾病または感染を治療、予防、または改善するのに有用でありうる。免疫応答には体液性免疫応答もしくは細胞介在型免疫応答、またはそれらの組み合わせがある。免疫応答は、例えばディフェンシンの生成の促進による、全身性宿主応答の促進を含んでもよい。 30

【0060】

動物によるAaに対する抗体価の生成は、感染からの防御および感染のクリアランスに重要でありうる。ポリペプチドまたはポリヌクレオチドをデリバリーした後の抗体の検出および／または定量を使用して、抗体価の誘発に特に有効なエピトープを同定することができる。Aaに対する強い抗体反応に関与するエピトープは、異なる長さのAaポリペプチドに対する抗体を誘発させることによって同定できる。その後、特定のポリペプチドエピトープによって誘発される抗体を、例えばELISAアッセイを使用して試験し、いずれのポリペプチドが強い反応の生成に最も有効なエピトープを含有するかを確認できる。次いで、これらのエピトープまたはエピトープをコードするポリヌクレオチドを含有するポリペプチドまたは融合タンパク質を構築し、強い抗体反応を誘発するために使用できる。 40

【0061】

本発明のポリペプチド、ポリヌクレオチド、または抗体を、哺乳動物（例えばマウス、ウサギ、モルモット、マカク、ヒヒ、チンパンジー、ヒト、ウシ、ヒツジ、ブタ、ウマ、イヌ、ネコ）またはニワトリもしくはアヒルのような動物に投与して、インビボにおいて抗体を誘発することができる。ポリヌクレオチドの注射は構築および修飾の簡易化に実用上、有益である。更に、ポリヌクレオチドの注射によって、宿主におけるポリペプチドの合成が起こる。従って、ポリペプチドは天然の翻訳後修飾、構造、およびコンフォメーションで宿主免疫系に存在する。ポリヌクレオチドは“裸DNA”として被験体に送達することができる。 50

【0062】

ポリヌクレオチド、ポリペプチド、または抗体の投与は当該分野で知られるいずれの方法によってもよく、例えば、筋肉内、静脈内、肺内、筋肉内、皮内、腹膜内、または皮下注射、エアロゾル、鼻腔内、輸液ポンプ、坐薬、粘膜、局所、および経口（生物学的弾道銃（biological ballistic gun；“遺伝子銃”）を使用する注射を含む）が挙げられる。ポリヌクレオチド、ポリペプチド、または抗体は経口投与のためのタンパク質キャリアを伴うことができる。投与方法を併用して免疫応答を誘発することもできる。抗体を約0.5mgから約200mgの日用量で投与することができる。本発明のある態様では、抗体を約20から約100mgの日用量で投与する。

【0063】

治療に使用するための医薬的に許容されるキャリアおよび希釈剤は当該分野で周知であり、例えばレミントンの薬学（Remington's Pharmaceutical Sciences, Mack Publishing社（A.R. Gennaro編（1985））に記載されている。キャリアそのものは宿主に有害な抗体の生成を誘導すべきではない。それらのキャリアには、限定されるわけではないが、大型で代謝が遅い巨大分子（例えばタンパク質、多糖、例えばラテックス機能性化セファロース、アガロース、セルロース、セルロースビーズなど）、ポリ乳酸、ポリグリコール酸、重合アミノ酸（例えばポリグルタミン酸、ポリリジンなど）、アミノ酸コポリマー、ペプチド、リピトイド、および不活性無毒性ウィルス粒子または細菌細胞等が含まれる。リボソーム、ヒドロゲル、シクロデキストリン、生分解性ナノカプセル、および生物接着性剤（bioadhesive）も本発明の組成物のキャリアとして使用できる。

【0064】

医薬的に許容される塩も本発明の組成物に使用することができ、それらは例えば、金属塩（例えば塩酸塩、臭化水素酸塩、リン酸塩、または硫酸塩）、並びに有機酸の塩（例えば酢酸塩、プロピオン酸塩、マロン酸塩、または安息香酸塩）である。特に有用なタンパク質基質は、血清アルブミン、キーホールリンペットヘモシアニン、免疫グロブリン分子、サイログロブリン、オボアルブミン、破傷風トキソイド、および当業者に周知の他のタンパク質である。本発明の組成物は液体または添加剤、例えば水、食塩水、リン酸バッファ液、リンガー液、ハンクス液、グルコース、グリセロール、デキストロース、マロデキストリン、エタノールなど（単独で、または組み合わせで）、並びに基質、例えば湿潤剤、乳化剤、浸透圧調整剤、界面活性剤、またはpH調整剤を含有することもできる。更なる活性剤、例えば殺菌剤を使用することもできる。

【0065】

必要により、リンパ球に対する免疫原性提示を向上する共刺激分子（例えばB7-1またはB7-2）、またはサイトカイン（MIP1 α 、GM-CSF、IL-2、およびIL-12）を本発明の組成物に含有させることができる。必要により、アジュバントを組成物に含有させることもできる。アジュバントは特異的免疫応答を非特異的に増加させるために使用できる物質である。一般に、本発明のアジュバントおよびポリペプチドは混合した後に免疫系に提示するか、または別々に、しかし動物の同じ部位に提示する。アジュバントは、例えば以下を含有することができる：オイルアジュバント（例えばフロイントの完全および不完全アジュバント）金属塩（例えばAlK(SO₄)₂；AlNa(SO₄)₂、AlNH₄(SO₄)、シリカ、アラム、Al(OH)₃、およびCa₃(PO₄)₂）、ポリヌクレオチド（すなわちPolyicおよびポリAU酸）、およびある種の天然物質（例えば結核菌（Mycobacterium tuberculosis）由来のワックスD、並びにコリネバクテリウム・パルヴム（Corynebacterium parvum）、百日咳菌（Bordetella pertussis）、およびブルセラ菌属のメンバーに見られる物質）。使用できるアジュバントには、限定される訳ではないが以下がある：MF59-0、水酸化アルミニウム、N-アセチルムラミール-L-トレオニル-D-イソグルタミン（thr-MDP）、N-アセチルムラミール-L-アラニル-D-イソグルタミン（CGP 11637、ノル-MDPとも呼ばれる）、N-アセチルムラミール-L-アラニル-D-イソグルタミニル-L-アラニン-2-(1'-2'-ジパルミトイル-sn-グリセロ-3-ヒドロキシホスホリルオキシ)-エチルアミン（CGP 19835A、MTP-PEと呼ばれる）、およびRIBIで、細菌から抽出された3つの成分、モノ

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ホスホリルリピッドA、トレハロースジミコレート、および細胞壁骨格（MPL+TDM+CWS）を2%スクアレン／ツイーン80エマルジョンに混合して含有するもの。

【0066】

本発明の組成物は、経口錠剤、バッカル錠、トローチ、カプセル、エリキシル、懸濁液、シロップ、オブラート、注射用製剤、マウスウォッシュ、歯磨き粉などに調製することができる。それらの組成物および製剤中の1またはそれ以上の本発明のポリペプチド、ポリヌクレオチド、または抗体のパーセンテージは単位重量の0.1%から60%で様々でありうる。

【0067】

ポリペプチドまたはポリヌクレオチドの投与によって動物における免疫応答を誘発することができ、これは少なくとも1週間、1ヶ月、3ヶ月、6ヶ月、1年、またはそれ以上の間持続する。必要により、初期注射後1ヶ月、3ヶ月、6ヶ月、1年、またはそれ以上の時点でポリペプチドまたはポリヌクレオチドを1回以上追加注射し、動物における免疫応答を保持することができる。必要により、共刺激分子またはアジュバントを組成物の前、後、または共に与えてもよい。

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【0068】

ポリペプチド、ポリヌクレオチド、またはそれらを組み合わせたものを含有する本発明の組成物を、使用される特定の組成物に適合する方法で、ELISA等により検出される免疫応答を誘発するのに有効な量で投与する。ポリヌクレオチドを大型哺乳動物（例えばヒヒ、チンパンジー、またはヒト）に、1ng/kg、10ng/kg、100ng/kg、1000ng/kg、0.001mg/kg、0.1mg/kg、または0.5 mg/kgの用量で筋肉内注射することができる。ポリペプチドを大型哺乳動物（例えばヒト）に、0.01、0.05、0.5、0.75、1.0、1.5、2.0、2.5、5、または10mg/kgの用量で筋肉内注射することができる。

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【0069】

ポリペプチド、ポリヌクレオチド、もしくは抗体、またはその組み合わせをAaに感染していない動物、またはAa感染した動物のいずれにも投与できる。組成物中のポリヌクレオチド、ポリペプチド、または抗体の特定の用量は多くの因子に依存し、それらには、限定されるわけではないが、組成物を投与する哺乳動物の種、年齢、性別、併用する医薬品、一般的な状態、および組成物の投与方法等が含まれる。本発明の組成物の有効量は、日常

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【0070】

本発明の方法に使用する原料はキットの形態であってもよい。キットは方法に使用される1またはそれ以上の要素を含むことができる。例えば、キットは容器内に本発明の抗体を含み、別の容器内にAaポリペプチドを含むことができる。キットおよび容器にラベルを付け、キットは容器内の要素の使用説明書を含む。キットの成分は、例えば液体または凍結乾燥した形態であってもよい。

【0071】

本明細書に引用する全ての文献は、参照により本明細書に組み込まれる。

【配列表】

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SEQUENCE LISTING

<110> Handfield, Martin
Hillman, Jeffrey
Progulske-Fox, Ann

<120> Identification of Actinobacillus actinomycetemcomitans Antigens for
Use in the Diagnosis, Treatment, and Monitoring of Periodontal Diseases

<130> MBHB01-662B

<140>

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Gly	Asp	Val	Gln	Leu	Gly	Cys	Ile	Gly	Leu	Gly	Val	Thr	Glu	Pro	Ala	
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Pro	Gln	Ala	Val	Thr	Asp	Pro	Glu	Met	Asn	Val	Arg	Ile	Asn	Pro	His	
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 Leu Ala Glu Lys Leu Gly Thr Asp Ala Tyr Ala Leu Leu Glu Gln Met
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 35 40 45

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Pro Ile Lys Glu Thr Gly Thr Arg Leu Gly Glu Val Thr Ser Glu Val
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Ala Gln Gln Thr Gly Leu Ile Gln Gly Thr Pro Val Val Val Gly Gly
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Gly Asp Val Gln Leu Gly Cys Ile Gly Leu Gly Val Thr Glu Pro Ala
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Gln Ala Ala Val Ile Gly Gly Thr Phe Trp Gln Gln Val Val Asn Leu
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 Arg Leu Gly Asn Ser Phe Arg Val Phe Arg Glu His Ser Ala Pro Tyr
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 Ile Asp Leu Ser Gly Pro Lys Glu Glu Val Ser Ala Gln Leu Glu Ser
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 Val Met Ser Asp Glu Met Ile Ile Gly Asp Asp Glu Ala Phe Phe Leu
 65 70 75 80
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 His Pro Gly Val Leu Ala Leu Ala Thr Thr Leu Glu Ser Val Lys Leu
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 gaa ggc aaa atc gtg ttg gaa ttt tac aat tcc ggc aaa tta ccg tta 432
 Glu Gly Lys Ile Val Leu Glu Phe Tyr Asn Ser Gly Lys Leu Pro Leu
 130 135 140
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 Ala Leu Arg Pro Asn Met Ile Ile Gly Ala Leu Ser Phe Glu Val Leu
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 35 40 45

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His Pro Gly Val Leu Ala Leu Ala Thr Thr Leu Glu Ser Val Lys Leu
 85 90 95

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Leu Gly Leu Met Val His Val Thr Ala His Arg Ile Asp Pro Gly Trp
 115 120 125

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 130 135 140

Ala Leu Arg Pro Asn Met Ile Ile Gly Ala Leu Ser Phe Glu Val Leu
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aga tca aaa ata cat tta att gac ggc aag ctt cct ttc ggc aat gcc      96
Arg Ser Lys Ile His Leu Ile Asp Gly Lys Leu Pro Phe Gly Asn Ala
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Thr Glu Leu Gly Phe Val Gly Leu His Ala Met Arg Ile Gly Glu Trp
          35          40          45
ctg gag caa ccg tta tat ttg gtg gaa acc caa ccg aac gac aac cgc      192
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          50          55          60
acc tat ttt tct tta cgc gat caa ctg ccg ctg ccg caa gcg caa ttt      240
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Asn Leu Leu Ser Cys Gly Val Glu Leu Asn His Phe Tyr Gln Thr His
          85          90          95
caa ttc tgc gga aag tgc ggt gga aaa acc gag caa atg cag gag gaa      336
Gln Phe Cys Gly Lys Cys Gly Gly Lys Thr Glu Gln Met Gln Glu Glu
          100          105          110
tgg gcg gta aaa tgc cgt gcc tgc ggt ttt cat acc tat ccc gtc att      384
Trp Ala Val Lys Cys Arg Ala Cys Gly Phe His Thr Tyr Pro Val Ile
          115          120          125
tgc cct tcc att atc gtt gca gta cga cac gat tca caa atc ctg ctg      432
Cys Pro Ser Ile Ile Val Ala Val Arg His Asp Ser Gln Ile Leu Leu
          130          135          140
gca aat cat atg cgc cac aaa ggc ggc att tac acc acg ttg gcg ggt      480
Ala Asn His Met Arg His Lys Gly Gly Ile Tyr Thr Thr Leu Ala Gly
          145          150          155          160
ttt gtg gaa gta ggc gaa acc ttt gag gat gcg gta cat cgc gaa att      528
Phe Val Glu Val Gly Glu Thr Phe Glu Asp Ala Val His Arg Glu Ile
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Gln Trp Phe Asp Cys Asp Gln Pro Leu Pro Glu Leu Pro Pro His Gly
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Ala Asn His Met Arg His Lys Gly Gly Ile Tyr Thr Thr Leu Ala Gly
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Phe Val Glu Val Gly Glu Thr Phe Glu Asp Ala Val His Arg Glu Ile
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Trp Glu Glu Thr Gln Ile Lys Val Lys Asn Leu Arg Tyr Phe Asp Ser
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Gly Gln Leu His Pro Thr Ile Ala Gln Lys Ile Gly Leu Thr Gly Lys
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Ala Arg Ala Lys Glu Ile Ser Arg Phe Pro Ala Asn Arg Arg Asp Leu
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Ala Val Val Val Ala Asp Asn Ile Pro Ala Asn Asp Val Leu Glu Val
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Cys Arg Thr Ala Gly Gly Asp Lys Leu Thr Gln Ile Asn Leu Phe Asp
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50	55	60	
aat aac ggc aag aaa ttc gat cct aaa aat gct gct gat gtg agt gaa			240
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65	70	75	80
ttg ggt aaa agc atc gcc ttt gaa gtg ttt gag att aaa gaa aat aaa			288
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	85	90	95
gac tct cac tca gta ttt gaa tcc ggc gcc ggc att tgt tac ggc ttc			336
Asp Ser His Ser Val Phe Glu Ser Gly Ala Gly Ile Cys Tyr Gly Phe			
	100	105	110
aaa tat acc gat ggc gtc gcg ttc acc gat tct aca acc tat tat gta			384
Lys Tyr Thr Asp Gly Val Ala Phe Thr Asp Ser Thr Thr Tyr Tyr Val			
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gat aaa tcc aag cag caa tat tac gcc agt atc atc ggc gcc acc gta			432
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	145	150	155
att cag gat ccc gag tta gat aaa gaa gta aag tcg gaa gaa caa cga			528
Ile Gln Asp Pro Glu Leu Asp Lys Glu Val Lys Ser Glu Glu Gln Arg			
	165	170	175
aac ggt aaa acc ttg att aat aaa aat ttg caa aag agc aga gaa att			576
Asn Gly Lys Thr Leu Ile Asn Lys Asn Leu Gln Lys Ser Arg Glu Ile			
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Leu Gly Lys Ser Ile Ala Phe Glu Val Phe Glu Ile Lys Glu Asn Lys
85 90 95

Asp Ser His Ser Val Phe Glu Ser Gly Ala Gly Ile Cys Tyr Gly Phe
100 105 110

Lys Tyr Thr Asp Gly Val Ala Phe Thr Asp Ser Thr Thr Tyr Tyr Val
115 120 125

Asp Lys Ser Lys Gln Gln Tyr Tyr Ala Ser Ile Ile Gly Ala Thr Val
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Ser Ser Asp Val Glu Pro Lys Asn Val Gln Tyr Ala Pro Val Phe Asn
145 150 155 160

Ile Gln Asp Pro Glu Leu Asp Lys Glu Val Lys Ser Glu Glu Gln Arg
165 170 175

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Leu Ser Asn Val Val Cys Lys
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tgt tct tct aag gct cca caa atc aat caa gct cct tta gat aag cag 96
Cys Ser Ser Lys Ala Pro Gln Ile Asn Gln Ala Pro Leu Asp Lys Gln
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Thr Val Glu Ala Tyr Gln Ala Lys Val Tyr Ser Gly Asn Thr Val Ser

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  50              55              60

gct agt gat tgg gaa ccg aaa acc gtg att tat cgc gag cgt cag cca      240
Ala Ser Asp Ser Glu Pro Lys Thr Val Ile Tyr Arg Glu Arg Gln Pro
  65              70              75              80

aga ctg gtt gtg aca ccg agc att ggc tat tat cgc ggt tgg cac tgg      288
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<210> 15
<211> 403
<212> DNA
<213> Actinobacillus actinomycetemcomitans

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<220>
<221> CDS
<222> (1)..(402)

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<400> 15
cca aac tgg ttg cgc ccg caa gtc ggt gtc gtc ttg caa gat aat gtg      48
Pro Asn Trp Leu Arg Arg Gln Val Gly Val Val Leu Gln Asp Asn Val
 1              5              10              15

ttg ctt aat cga agt atc aga gag aat att gcg tta acc aat ccg gga      96

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Leu Leu Asn Arg Ser Ile Arg Glu Asn Ile Ala Leu Thr Asn Pro Gly
 20 25 30
 atg cca atg gaa aag gtt att gcc gcg gca aaa ctt gcg gga gcg cac 144
 Met Pro Met Glu Lys Val Ile Ala Ala Lys Leu Ala Gly Ala His
 35 40 45
 gat ttt att tct gaa tta aga gaa ggt tat aac acg gtt gtg ggg gaa 192
 Asp Phe Ile Ser Glu Leu Ser Arg Glu Gly Tyr Asn Thr Val Val Gly Glu
 50 55 60
 cag gga gcc ggt ttg tcc gga gga caa cgt caa cgg atc gcg ata gca 240
 Gln Gly Ala Gly Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala
 65 70 75 80
 agg gca cta gtc aat aac cca agg att ttg att ttt gat gaa gca acc 288
 Arg Ala Leu Val Asn Asn Pro Arg Ile Leu Ile Phe Asp Glu Ala Thr
 85 90 95
 agt gca ctt gat tac gaa tct gaa aat atc att atg cat aat atg cat 336
 Ser Ala Leu Asp Tyr Glu Ser Glu Asn Ile Ile Met His Asn Met His
 100 105 110
 aaa att tgc caa aat cgt act gtg ctt atc att gct cac cgc ctt tct 384
 Lys Ile Cys Gln Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser
 115 120 125
 act gta aaa aat gct gat c 403
 Thr Val Lys Asn Ala Asp
 130

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<210> 16
 <211> 134
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 16

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Pro Asn Trp Leu Arg Arg Gln Val Gly Val Val Leu Gln Asp Asn Val
 1 5 10 15
 Leu Leu Asn Arg Ser Ile Arg Glu Asn Ile Ala Leu Thr Asn Pro Gly
 20 25 30
 Met Pro Met Glu Lys Val Ile Ala Ala Ala Lys Leu Ala Gly Ala His
 35 40 45
 Asp Phe Ile Ser Glu Leu Arg Glu Gly Tyr Asn Thr Val Val Gly Glu
 50 55 60
 Gln Gly Ala Gly Leu Ser Gly Gly Gln Arg Gln Arg Ile Ala Ile Ala
 65 70 75 80
 Arg Ala Leu Val Asn Asn Pro Arg Ile Leu Ile Phe Asp Glu Ala Thr
 85 90 95

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Ser Ala Leu Asp Tyr Glu Ser Glu Asn Ile Ile Met His Asn Met His
 100 105 110

Lys Ile Cys Gln Asn Arg Thr Val Leu Ile Ile Ala His Arg Leu Ser
 115 120 125

Thr Val Lys Asn Ala Asp
 130

<210> 17
 <211> 374
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(372)

<400> 17
 cac cgt tta ccg gaa atg att aac caa att cgc ggt ggc aaa agt gct 48
 His Arg Leu Pro Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ala
 1 5 10 15
 gtg gtg gat att agt ttc ccg gaa atc gaa aaa ttc gac cgg ttg ccg 96
 Val Val Asp Ile Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro
 20 25 30
 gaa ccg cgc gca gaa ggc ccg act gcc ttt gtt tct atc atg gaa ggc 144
 Glu Pro Arg Ala Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly
 35 40 45
 tgt aat aaa tac tgt act tac tgc gtg gtg cct tat acc cgt ggc gag 192
 Cys Asn Lys Tyr Cys Thr Tyr Cys Val Val Pro Tyr Thr Arg Gly Glu
 50 55 60
 gaa gtt agc cgt ccg gtg gat gat att tta ttt gaa att gcc cag ttg 240
 Glu Val Ser Arg Pro Val Asp Asp Ile Leu Phe Glu Ile Ala Gln Leu
 65 70 75 80
 gcg gag caa ggc gtg cgc gaa gtg aat ttg ctc ggc cag aac gtg aac 288
 Ala Glu Gln Gly Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn
 85 90 95
 gcc tat cgt ggt ccg aca ttt gat ggc gat att tgc acc ttc gcc gaa 336
 Ala Tyr Arg Gly Pro Thr Phe Asp Gly Asp Ile Cys Thr Phe Ala Glu
 100 105 110
 ttg ttg cgt ttg gta gcg gcc att gac ggt atc gat cg 374
 Leu Leu Arg Leu Val Ala Ala Ile Asp Gly Ile Asp
 115 120

<210> 18
 <211> 124
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

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<400> 18

His Arg Leu Pro Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ala
 1 5 10 15

Val Val Asp Ile Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro
 20 25 30

Glu Pro Arg Ala Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly
 35 40 45

Cys Asn Lys Tyr Cys Thr Tyr Cys Val Val Pro Tyr Thr Arg Gly Glu
 50 55 60

Glu Val Ser Arg Pro Val Asp Asp Ile Leu Phe Glu Ile Ala Gln Leu
 65 70 75 80

Ala Glu Gln Gly Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn
 85 90 95

Ala Tyr Arg Gly Pro Thr Phe Asp Gly Asp Ile Cys Thr Phe Ala Glu
 100 105 110

Leu Leu Arg Leu Val Ala Ala Ile Asp Gly Ile Asp
 115 120

<210> 19

<211> 158

<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> (1)..(156)

<400> 19

cta agc gta ttc aac tac gcc cat ttg ccg agc cgt ttt gcc gga cag 48
 Leu Ser Val Phe Asn Tyr Ala His Leu Pro Ser Arg Phe Ala Gly Gln
 1 5 10 15

gcg aaa atc aag gat tgg cag ttg ccg aaa ccg gaa gcg aaa ctg gaa 96
 Ala Lys Ile Lys Asp Trp Gln Leu Pro Lys Pro Glu Ala Lys Leu Glu
 20 25 30

att ctg caa aaa acc atc gaa acg ctg gcc aac gcc ggt tac aaa ttt 144
 Ile Leu Gln Lys Thr Ile Glu Thr Leu Gly Asn Ala Gly Tyr Lys Phe
 35 40 45

atc gcc atg gat ca 158
 Ile Gly Met Asp
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<210> 20
 <211> 52
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 20

Leu Ser Val Phe Asn Tyr Ala His Leu Pro Ser Arg Phe Ala Gly Gln
 1 5 10 15

Ala Lys Ile Lys Asp Trp Gln Leu Pro Lys Pro Glu Ala Lys Leu Glu
 20 25 30

Ile Leu Gln Lys Thr Ile Glu Thr Leu Gly Asn Ala Gly Tyr Lys Phe
 35 40 45

Ile Gly Met Asp
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<210> 21
 <211> 1098
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(1095)

<400> 21
 aat cag atg aat aaa acc tta aaa att tca ttg ttt gcc atg att tcc 48
 Asn Gln Met Asn Lys Thr Leu Lys Ile Ser Leu Phe Ala Met Ile Ser
 1 5 10 15
 gcg tta gct ttt aat acc atg gca aat aca caa ccg tta gcc gtg ttg 96
 Ala Leu Ala Phe Asn Thr Met Ala Asn Thr Gln Pro Leu Ala Val Leu
 20 25 30
 gaa ccg cag gta aac tat caa cag tta ctc acc caa ccg cag gtg gtg 144
 Glu Pro Gln Val Asn Tyr Gln Gln Leu Leu Thr Gln Arg Gln Val Val
 35 40 45
 gat gat tta atc gcg cag gcg gtg aaa atc caa aat tca ccg gcg ccg 192
 Asp Asp Leu Ile Ala Gln Ala Val Lys Ile Gln Asn Ser Pro Ala Arg
 50 55 60
 gtg tcc aat gcg ggc ttt acc gca aaa ttg cca agc aac atg gaa cgc 240
 Val Ser Asn Ala Gly Phe Thr Ala Lys Leu Pro Ser Asn Met Glu Arg
 65 70 75 80
 att gcc gcg att ttg ttg gaa gcc tat gaa ttg gaa cct tac cgc gtt 288
 Ile Ala Ala Ile Leu Leu Glu Ala Tyr Glu Leu Glu Pro Tyr Arg Val
 85 90 95
 gat ttt ctg ttc ggc gca gca aat gcc aac att tac aac ggc aat acg 336
 Asp Phe Leu Phe Gly Ala Ala Asn Ala Asn Ile Tyr Asn Gly Asn Thr
 100 105 110

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gac aaa gcc atc gag ctt tac caa aaa gtg ctc acg gtg gcg cct gat 384
 Asp Lys Ala Ile Glu Leu Tyr Gln Lys Val Leu Thr Val Ala Pro Asp
 115 120 125

gat gtg aaa gca cat att tat tta acc gcg tgg aat cgt ttt aaa caa 432
 Asp Val Lys Ala His Ile Tyr Leu Thr Ala Trp Asn Arg Phe Lys Gln
 130 135 140

aac caa ggg gaa acc gac aaa tac ttc acc cgc tta aaa gcg ctg gca 480
 Asn Gln Gly Glu Thr Asp Lys Tyr Phe Thr Arg Leu Lys Ala Leu Ala
 145 150 155 160

ccg caa aaa gca gcg gaa ctg gag cag gtc ttc aag att att gat aac 528
 Pro Gln Lys Ala Ala Glu Leu Glu Gln Val Phe Lys Ile Ile Asp Asn
 165 170 175

gcc gca agc caa ccg att agc gat aaa ttg gcg aat aaa ttg ccg gcg 576
 Ala Ala Ser Gln Pro Ile Ser Asp Lys Leu Ala Asn Lys Leu Pro Ala
 180 185 190

gat tcc gcc att att acc ttg ggt tat gcg tta aat ccg gac ggc agt 624
 Asp Ser Ala Ile Ile Thr Leu Gly Tyr Ala Leu Asn Pro Asp Gly Ser
 195 200 205

atg cac gac att ttg att cag cgt ttg gaa aaa acc ttg gaa atc gcc 672
 Met His Asp Ile Leu Ile Gln Arg Leu Glu Lys Thr Leu Glu Ile Ala
 210 215 220

aaa caa aat cct gat gca ttg att att gtc acc ggc ggc atg ccg caa 720
 Lys Gln Asn Pro Asp Ala Leu Ile Ile Val Thr Gly Gly Met Pro Gln
 225 230 235 240

aat aat cgt acg gaa ggg gca tta atg aaa caa tgg ctg att aac aaa 768
 Asn Asn Arg Thr Glu Gly Ala Leu Met Lys Gln Trp Leu Ile Asn Lys
 245 250 255

ggc atc gat gcc aaa cgc att tat gcc gac aat tac gcc cgt tca acg 816
 Gly Ile Asp Ala Lys Arg Ile Tyr Ala Asp Asn Tyr Ala Arg Ser Thr
 260 265 270

gtg gaa aat gcg tta ttt tcc cgt tac gcc ttg gcg aaa cac cat atc 864
 Val Glu Asn Ala Leu Phe Ser Arg Tyr Ala Leu Ala Lys His His Ile
 275 280 285

aaa cac gcc tcc ctc atc agc tcc ggt agc cat gtg cgg cgc ggt cag 912
 Lys His Ala Ser Leu Ile Ser Ser Gly Ser His Val Arg Arg Gly Gln
 290 295 300

gcg ttg ttt gaa atc gcc gcc ttg gaa tcc ggt ccg caa aac atc aaa 960
 Ala Leu Phe Glu Ile Ala Ala Leu Glu Ser Gly Pro Gln Asn Ile Lys
 305 310 315 320

atc gaa acg gtg gcg gcg cta gac aaa ccg tta gac gaa tta caa aaa 1008
 Ile Glu Thr Val Ala Ala Leu Asp Lys Pro Leu Asp Glu Leu Gln Lys
 325 330 335

gtg agt gaa aaa gat tta ttg gga atc tat cgc gac agc ctg aaa acc 1056
 Val Ser Glu Lys Asp Leu Leu Gly Ile Tyr Arg Asp Ser Leu Lys Thr
 340 345 350

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atg ggc ttg cca atg ttt aat agc gga gca cta caa gat taa 1098
 Met Gly Leu Pro Met Phe Asn Ser Gly Ala Leu Gln Asp
 355 360 365

<210> 22
 <211> 365
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 22

Asn Gln Met Asn Lys Thr Leu Lys Ile Ser Leu Phe Ala Met Ile Ser
 1 5 10 15

Ala Leu Ala Phe Asn Thr Met Ala Asn Thr Gln Pro Leu Ala Val Leu
 20 25 30

Glu Pro Gln Val Asn Tyr Gln Gln Leu Leu Thr Gln Arg Gln Val Val
 35 40 45

Asp Asp Leu Ile Ala Gln Ala Val Lys Ile Gln Asn Ser Pro Ala Arg
 50 55 60

Val Ser Asn Ala Gly Phe Thr Ala Lys Leu Pro Ser Asn Met Glu Arg
 65 70 75 80

Ile Ala Ala Ile Leu Leu Glu Ala Tyr Gln Leu Glu Pro Tyr Arg Val
 85 90 95

Asp Phe Leu Phe Gly Ala Ala Asn Ala Asn Ile Tyr Asn Gly Asn Thr
 100 105 110

Asp Lys Ala Ile Glu Leu Tyr Gln Lys Val Leu Thr Val Ala Pro Asp
 115 120 125

Asp Val Lys Ala His Ile Tyr Leu Thr Ala Trp Asn Arg Phe Lys Gln
 130 135 140

Asn Gln Gly Glu Thr Asp Lys Tyr Phe Thr Arg Leu Lys Ala Leu Ala
 145 150 155 160

Pro Gln Lys Ala Ala Glu Leu Glu Gln Val Phe Lys Ile Ile Asp Asn
 165 170 175

Ala Ala Ser Gln Pro Ile Ser Asp Lys Leu Ala Asn Lys Leu Pro Ala
 180 185 190

Asp Ser Ala Ile Ile Thr Leu Gly Tyr Ala Leu Asn Pro Asp Gly Ser

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195 200 205

Met His Asp Ile Leu Ile Gln Arg Leu Glu Lys Thr Leu Glu Ile Ala
210 215 220

Lys Gln Asn Pro Asp Ala Leu Ile Ile Val Thr Gly Gly Met Pro Gln
225 230 235 240

Asn Asn Arg Thr Glu Gly Ala Leu Met Lys Gln Trp Leu Ile Asn Lys
245 250 255

Gly Ile Asp Ala Lys Arg Ile Tyr Ala Asp Asn Tyr Ala Arg Ser Thr
260 265 270

Val Glu Asn Ala Leu Phe Ser Arg Tyr Ala Leu Ala Lys His His Ile
275 280 285

Lys His Ala Ser Leu Ile Ser Ser Gly Ser His Val Arg Arg Gly Gln
290 295 300

Ala Leu Phe Glu Ile Ala Ala Leu Glu Ser Gly Pro Gln Asn Ile Lys
305 310 315 320

Ile Glu Thr Val Ala Ala Leu Asp Lys Pro Leu Asp Glu Leu Gln Lys
325 330 335

Val Ser Glu Lys Asp Leu Leu Gly Ile Tyr Arg Asp Ser Leu Lys Thr
340 345 350

Met Gly Leu Pro Met Phe Asn Ser Gly Ala Leu Gln Asp
355 360 365

<210> 23
<211> 134
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(132)

<400> 23
ttg gat caa ttc ccg tcc gac gtt tat caa ggc ggc gcg ggc act tcc
Leu Asp Gln Phe Pro Ser Asp Val Tyr Gln Gly Gly Ala Gly Thr Ser
1 5 10 15

gtc aac atg aat acg aac gaa gtg gtt gcg aat ctg gca ttg gaa att
Val Asn Met Asn Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Ile
20 25 30

48

96

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tta gga cac aaa aaa ggc gaa tat aat tat ttg gat cc 134
 Leu Gly His Lys Lys Gly Glu Tyr Asn Tyr Leu Asp
 35 40

<210> 24
 <211> 44
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 24

Leu Asp Gln Phe Pro Ser Asp Val Tyr Gln Gly Gly Ala Gly Thr Ser
 1 5 10 15

Val Asn Met Asn Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Ile
 20 25 30

Leu Gly His Lys Lys Gly Glu Tyr Asn Tyr Leu Asp
 35 40

<210> 25
 <211> 380
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(378)

<400> 25
 gat cgg aac agc ttc aaa ctg cgc ggc gaa ttg agc cac ggc aaa gac 48
 Asp Pro Asn Ser Phe Lys Leu Arg Gly Glu Leu Ser His Gly Lys Asp
 1 5 10 15

gtg gaa atc gac atg aac gtg att tta aac ggc aaa gtg cgg tta gga 96
 Val Glu Ile Asp Met Asn Val Ile Leu Asn Gly Lys Val Arg Leu Gly
 20 25 30

aat cgg gtg aaa atc ggt gca ggt tgt gtg ttg act aac tgc gac atc 144
 Asn Arg Val Lys Ile Gly Ala Gly Cys Val Leu Thr Asn Cys Asp Ile
 35 40 45

ggc gat gac gtg gaa atc aaa cgg tat tcc gtg ctg gaa gat gcc tcc 192
 Gly Asp Asp Val Glu Ile Lys Pro Tyr Ser Val Leu Glu Asp Ala Ser
 50 55 60

gta ggc gcc aat gcc gcc atc gga cgg ttc tcc cgc tta cgt cgg ggc 240
 Val Gly Ala Asn Ala Ala Ile Gly Pro Phe Ser Arg Leu Arg Pro Gly
 65 70 75 80

gcc gac ttg gcg gaa aac acc cac gtg ggc aat ttc gtg gaa atc aaa 288
 Ala Asp Leu Ala Glu Asn Thr His Val Gly Asn Phe Val Glu Ile Lys
 85 90 95

aaa gcg tac atc ggc aaa ggc tcc aaa gtg aac cac tta acc tat gtg 336
 Lys Ala Tyr Ile Gly Lys Gly Ser Lys Val Asn His Leu Thr Tyr Val
 100 105 110

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ggc gac gcg gaa atc ggc aaa gat tgt aac ata ggc gca ggc gt 380
 Gly Asp Ala Glu Ile Gly Lys Asp Cys Asn Ile Gly Ala Gly
 115 120 125

<210> 26
 <211> 126
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 26

Asp Pro Asn Ser Phe Lys Leu Arg Gly Glu Leu Ser His Gly Lys Asp
 1 5 10 15

Val Glu Ile Asp Met Asn Val Ile Leu Asn Gly Lys Val Arg Leu Gly
 20 25 30

Asn Arg Val Lys Ile Gly Ala Gly Cys Val Leu Thr Asn Cys Asp Ile
 35 40 45

Gly Asp Asp Val Glu Ile Lys Pro Tyr Ser Val Leu Glu Asp Ala Ser
 50 55 60

Val Gly Ala Asn Ala Ala Ile Gly Pro Phe Ser Arg Leu Arg Pro Gly
 65 70 75 80

Ala Asp Leu Ala Glu Asn Thr His Val Gly Asn Phe Val Glu Ile Lys
 85 90 95

Lys Ala Tyr Ile Gly Lys Gly Ser Lys Val Asn His Leu Thr Tyr Val
 100 105 110

Gly Asp Ala Glu Ile Gly Lys Asp Cys Asn Ile Gly Ala Gly
 115 120 125

<210> 27
 <211> 468
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(468)

<400> 27

att ggt cgc caa ctt gct cag ttg ctc aac atg gat ttt gta gat acc 48
 Ile Gly Arg Gln Leu Ala Gln Leu Leu Asn Met Asp Phe Val Asp Thr
 1 5 10 15

gac gca gaa att gaa gaa cgc gcc ggc gca gat att ggc tgg att ttt 96
 Asp Ala Glu Ile Glu Glu Arg Ala Gly Ala Asp Ile Gly Trp Ile Phe

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20	25	30	
gat gtt gag ggc gaa gcc ggt ttc cgt aaa aga gaa gaa cgt att att			144
Asp Val Glu Gly Glu Ala Gly Phe Arg Lys Arg Glu Glu Arg Ile Ile			
35	40	45	
aac gaa tta acg caa cgc caa ggc atc gtg tta tct acc ggc ggc ggt			192
Asn Glu Leu Thr Gln Arg Gln Gly Ile Val Leu Ser Thr Gly Gly Gly			
50	55	60	
gca gtg tta tct aag gac aat cga aac cag ctt gcc gcg cgc ggt att			240
Ala Val Leu Ser Lys Asp Asn Arg Asn Gln Leu Ala Ala Arg Gly Ile			
65	70	75	80
gtg att tat ctg gaa acc act gtt gaa aag caa tat caa cgc acc cag			288
Val Ile Tyr Leu Lys Thr Thr Val Glu Lys Gln Tyr Gln Arg Thr Gln			
85	90	95	
cgg gat aaa aag cgc ccg ctt ttg caa gat gtt gcc gat ccg cgt cag			336
Arg Asp Lys Lys Arg Pro Leu Leu Leu Asp Val Ala Asp Pro Arg Gln			
100	105	110	
gtg ttg gaa gat ttg gcg aaa atc cgc aat ccg ctg tat gaa gac gta			384
Val Leu Glu Asp Leu Ala Lys Ile Arg Asn Pro Leu Tyr Glu Asp Val			
115	120	125	
gca gac att acc ctc cct act gat gac caa agt gcc aag gta atg gca			432
Ala Asp Ile Thr Leu Pro Thr Asp Asp Gln Ser Ala Lys Val Met Ala			
130	135	140	
acg cag att atc gac ttg att gat aac tat aac ggt			468
Thr Gln Ile Ile Asp Leu Ile Asp Asn Tyr Asn Gly			
145	150	155	

<210> 28
 <211> 156
 <212> PRT
 <213> Actinobacillus actinomycescomitans

<400> 28

Ile Gly Arg Gln Leu Ala Gln Leu Leu Asn Met Asp Phe Val Asp Thr
1 5 10 15

Asp Ala Glu Ile Glu Glu Arg Ala Gly Ala Asp Ile Gly Trp Ile Phe
20 25 30

Asp Val Glu Gly Glu Ala Gly Phe Arg Lys Arg Glu Glu Arg Ile Ile
35 40 45

Asn Glu Leu Thr Gln Arg Gln Gly Ile Val Leu Ser Thr Gly Gly Gly
50 55 60

Ala Val Leu Ser Lys Asp Asn Arg Asn Gln Leu Ala Ala Arg Gly Ile
65 70 75 80

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Val Ile Tyr Leu Glu Thr Thr Val Glu Lys Gln Tyr Gln Arg Thr Gln
85 90 95

Arg Asp Lys Lys Arg Pro Leu Leu Gln Asp Val Ala Asp Pro Arg Gln
100 105 110

Val Leu Glu Asp Leu Ala Lys Ile Arg Asn Pro Leu Tyr Glu Asp Val
115 120 125

Ala Asp Ile Thr Leu Pro Thr Asp Asp Gln Ser Ala Lys Val Met Ala
130 135 140

Thr Gln Ile Ile Asp Leu Ile Asp Asn Tyr Asn Gly
145 150 155

<210> 29
<211> 307
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CBS
<222> (1)..(306)

<400> 29
gcc tcc cgc agt ggc gat gcc gat gag cgt gtc atg gat tcc aac gat 48
Ala Ser Arg Ser Gly Asp Ala Asp Glu Arg Val Met Asp Ser Asn Asp 20
1 5 10 15
tta gaa aaa gag cgc ggc atc act att tta gcg aaa aat act gcc att 96
Leu Glu Lys Glu Arg Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile 30
20 25 30
aac tgg aat agc tac cgt att aac att gta gac acc ccg ggg cac gcg 144
Asn Trp Asn Ser Tyr Arg Ile Asn Ile Val Asp Thr Pro Gly His Ala 45
35 40 45
gac ttc ggt ggc gaa gtg gaa cgc gta ctt tcc atg gtg gat tcc gta 192
Asp Phe Gly Gly Glu Val Glu Arg Val Leu Ser Met Val Asp Ser Val 60
50 55 60
tta ttg atg gtg gat gcc ttc gac ggc ccg atg ccg caa acc cgt ttt 240
Leu Leu Met Val Asp Ala Phe Asp Gly Pro Met Pro Gln Thr Arg Phe 80
65 70 75 80
gtt acg caa aaa gcc ttc tcc cac ggt tta aaa cct atc gta gtc atc 288
Val Thr Gln Lys Ala Phe Ser His Gly Leu Lys Pro Ile Val Val Ile 95
85 90 95
aat aaa gtt gac cgc ccg g 307
Asn Lys Val Asp Arg Pro 100

<210> 30

<211> 102
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

 <400> 30
 Ala Ser Arg Ser Gly Asp Ala Asp Glu Arg Val Met Asp Ser Asn Asp
 1 5 10 15

 Leu Glu Lys Glu Arg Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile
 20 25 30

 Asn Trp Asn Ser Tyr Arg Ile Asn Ile Val Asp Thr Pro Gly His Ala
 35 40 45

 Asp Phe Gly Gly Glu Val Glu Arg Val Leu Ser Met Val Asp Ser Val
 50 55 60

 Leu Leu Met Val Asp Ala Phe Asp Gly Pro Met Pro Gln Thr Arg Phe
 65 70 75 80

 Val Thr Gln Lys Ala Phe Ser His Gly Leu Lys Pro Ile Val Val Ile
 85 90 95

 Asn Lys Val Asp Arg Pro
 100

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<210> 31
 <211> 891
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(891)

 <220>
 <221> misc_feature
 <222> (182)..(182)
 <223> n is any nucleotide a, g, c, or t.

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<220>
 <221> misc_feature
 <222> (186)..(186)
 <223> n is any nucleotide a, g, c, or t.

<400> 31
 atg gct atc gta caa tcc aaa tct gcc cgc tac cgt tta tgg gtg acc 48
 Met Ala Ile Val Gln Ser Lys Ser Ala Arg Tyr Arg Leu Trp Val Thr
 1 5 10 15

 cat ttg ctg ctg att gca ttt att tgt ctg att att ttc cag tta ctg 96

30

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                260                265                270
cct att acc ctc gtg ttc tta ctg gca caa cgc tgg tta atc ggc gga      864
Pro Ile Thr Leu Val Phe Leu Leu Ala Gln Arg Trp Leu Ile Gly Gly
      275                280                285

tta acg gca ggt ggg gtn aar ggn tga      891
Leu Thr Ala Gly Gly Val Lys Gly
      290                295

<210> 32
<211> 296
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<220>
<221> misc_feature
<222> (182)..(182)
<223> n is any nucleotide a, g, c, or t.

<220>
<221> misc_feature
<222> (188)..(188)
<223> n is any nucleotide a, g, c, or t.

<400> 32

Met Ala Ile Val Gln Ser Lys Ser Ala Arg Tyr Arg Leu Trp Val Thr
1                5                10                15

His Leu Leu Leu Ile Ala Phe Ile Cys Leu Ile Ile Phe Pro Leu Leu
      20                25                30

Met Val Ile Gly Ile Ser Leu Arg Pro Gly Asn Leu Ala Leu Gly Asp
      35                40                45

Leu Ile Pro Lys Gln Ile Ser Trp Glu His Trp Gln Ala Ala Leu Gly
      50                55                60

Phe Tyr Val Val His Ala Asp Gly Ser Val Thr Pro Pro Pro Phe Pro
65                70                75                80

Val Leu Leu Trp Leu Trp Asn Ser Ile Lys Val Ala Thr Ile Thr Ser
      85                90                95

Val Gly Ile Val Val Met Ser Thr Thr Cys Ala Tyr Ala Phe Ala Arg
      100                105                110

Met Lys Phe Lys Gly Lys Lys Thr Ile Leu Gln Gly Met Leu Ile Phe
      115                120                125

Gln Met Phe Pro Ala Val Leu Ser Leu Val Ala Leu Tyr Ala Leu Phe

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130 135 140
 Asp Arg Leu Gly Gln Tyr Ile Pro Phe Leu Gly Leu Asn Thr His Gly
 145 150 155 160
 Gly Val Ile Phe Ala Tyr Leu Gly Gly Ile Ala Leu His Val Trp Thr
 165 170 175
 Ile Lys Gly Tyr Phe Glu Thr Ile Asp Gly Ser Leu Glu Glu Ala Ala
 180 185 190
 Ala Leu Asp Gly Ala Thr Pro Trp Gln Ala Phe Arg Leu Ile Leu Leu
 195 200 205
 Pro Leu Ser Val Pro Ile Leu Ala Val Val Phe Ile Leu Ser Phe Ile
 210 215 220
 Ala Ala Ile Thr Glu Val Pro Val Ala Ser Leu Leu Leu Arg Asp Val
 225 230 235 240
 Asn Ser Tyr Thr Leu Ala Val Gly Met Gln Gln Tyr Leu Tyr Pro Gln
 245 250 255
 Asn Tyr Leu Trp Gly Asp Phe Ala Ala Ala Ala Val Leu Ser Ala Ile
 260 265 270
 Pro Ile Thr Leu Val Phe Leu Leu Ala Gln Arg Trp Leu Ile Gly Gly
 275 280 285
 Leu Thr Ala Gly Gly Val Lys Gly
 290 295

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<210> 33
 <211> 323
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 <213> Actinobacillus actinomycetemcomitans

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 <222> (1)..(321)

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 Asn Val Tyr Gly Gly Thr Lys Ala Phe Val Lys Gln Phe Ser Leu Asn
 1 5 10 15
 cta cgt gcc gat ctt gcc gga acc aat att cgc gtt tcc aat gta gaa 96
 Leu Arg Ala Asp Leu Ala Gly Thr Asn Ile Arg Val Ser Asn Val Glu
 20 25 30

ccg gga ctg tgc ggc ggc acg gaa ttt tct aac gta cgt ttt aaa ggc 144
 Pro Gly Leu Cys Gly Gly Thr Glu Phe Ser Asn Val Arg Phe Lys Gly
 35 40 45

gat aac gcc cgc gcg gaa aaa ctc tac gaa aac gta caa tat gtt acg 192
 Asp Asn Ala Arg Ala Glu Lys Leu Tyr Glu Asn Val Gln Tyr Val Thr
 50 55 60

cca caa gat att gcc aat atc gtg ttg tgg ctc aat caa caa ccg gaa 240
 Pro Gln Asp Ile Ala Asn Ile Val Leu Trp Leu Asn Gln Gln Pro Glu
 65 70 75 80

cac gtc aac att aac cgc att gaa gtg atg ccg acg gcg caa acc ttc 288
 His Val Asn Ile Asn Arg Ile Glu Val Met Pro Thr Ala Gln Thr Phe
 85 90 95

gcc ccg ctt aat gta gca agg aat tta aat tta ga 323
 Ala Pro Leu Asn Val Ala Arg Asn Leu Asn Leu
 100 105

<210> 34
 <211> 107
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 34

Asn Val Tyr Gly Gly Thr Lys Ala Phe Val Lys Gln Phe Ser Leu Asn
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Leu Arg Ala Asp Leu Ala Gly Thr Asn Ile Arg Val Ser Asn Val Glu
 20 25 30

Pro Gly Leu Cys Gly Gly Thr Glu Phe Ser Asn Val Arg Phe Lys Gly
 35 40 45

Asp Asn Ala Arg Ala Glu Lys Leu Tyr Glu Asn Val Gln Tyr Val Thr
 50 55 60

Pro Gln Asp Ile Ala Asn Ile Val Leu Trp Leu Asn Gln Gln Pro Glu
 65 70 75 80

His Val Asn Ile Asn Arg Ile Glu Val Met Pro Thr Ala Gln Thr Phe
 85 90 95

Ala Pro Leu Asn Val Ala Arg Asn Leu Asn Leu
 100 105

<210> 35
 <211> 585
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

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<220>

<221> CDS

<222> (1)..(585)

<400> 35

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atg gcg gaa acg att tta aac ccg tat ttc ggg gaa ttc ggc gga atg      48
Met Ala Glu Thr Ile Leu Asn Pro Tyr Phe Gly Glu Phe Gly Gly Met
1           5           10           15

tat gtg ccg gaa att cta gtg ccg gtg ttg caa cag ttg gaa aaa gcg      96
Tyr Val Pro Glu Ile Leu Val Pro Val Leu Gln Gln Leu Glu Lys Ala
           20           25           30

ttt gta gaa gcc aag gcg gat cct gca ttt cag cgc gaa ttt cag gat      144
Phe Val Glu Ala Lys Ala Asp Pro Ala Phe Gln Arg Glu Phe Gln Asp
           35           40           45

tta ttg aaa aat tat gcc ggc aga ccc acc gca ctt acc ctt tgt cgc      192
Leu Leu Lys Asn Tyr Ala Gly Arg Pro Thr Ala Leu Thr Leu Cys Arg
           50           55           60

aat ctc acc aaa ggc acc aac gcc aaa atc tat tta aaa cgg gaa gat      240
Asn Leu Thr Lys Gly Thr Asn Ala Lys Ile Tyr Leu Lys Arg Glu Asp
           65           70           75           80

tta tta cac ggc ggc gca cat aaa acc aac cag gta tta ggt cag att      288
Leu Leu His Gly Gly Ala His Lys Thr Asn Gln Val Leu Gly Gln Ile
           85           90           95

ttg ctt gcc aaa cgc atg ggc aaa acc cgc att att gcc gaa acc ggc      336
Leu Leu Ala Lys Arg Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly
           100          105          110

gcg gga cag cac ggt gtc gcc act gct ctc gcc tgc gcc atg ttg gat      384
Ala Gly Gln His Gly Val Ala Thr Ala Leu Ala Cys Ala Met Leu Asp
           115          120          125

atg ccg tgc cgt gtt tat atg ggc gcg aaa gat gtg gaa cgc caa tcg      432
Met Pro Cys Arg Val Tyr Met Gly Ala Lys Asp Val Glu Arg Gln Ser
           130          135          140

ccg aat gtg ttt cgt atg cgt tta atg ggc acg gaa gtg gta ccg gtg      480
Pro Asn Val Phe Arg Met Arg Leu Met Gly Thr Glu Val Val Pro Val
           145          150          155          160

caa aaa ggt tcc tgt tct ttg aaa gac got tgc tgc gaa gcc atg cgt      528
Gln Lys Gly Ser Cys Ser Leu Lys Asp Ala Cys Cys Glu Ala Met Arg
           165          170          175

gac tgg tcg gca aat tat gaa aat acg cac tat ttg ctc ggc aca gcg      576
Asp Trp Ser Ala Asn Tyr Glu Asn Thr His Tyr Leu Leu Gly Thr Ala
           180          185          190

gca ggt ccg      585
Ala Gly Pro
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<210> 36

<211> 195

<212> PRT

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<213> Actinobacillus actinomycetemcomitans

<400> 36

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Tyr Val Pro Glu Ile Leu Val Pro Val Leu Gln Gln Leu Glu Lys Ala
20 25 30

Phe Val Glu Ala Lys Ala Asp Pro Ala Phe Gln Arg Glu Phe Gln Asp
35 40 45

Leu Leu Lys Asn Tyr Ala Gly Arg Pro Thr Ala Leu Thr Leu Cys Arg
50 55 60

Asn Leu Thr Lys Gly Thr Asn Ala Lys Ile Tyr Leu Lys Arg Glu Asp
65 70 75 80

Leu Leu His Gly Gly Ala His Lys Thr Asn Gln Val Leu Gly Gln Ile
85 90 95

Leu Leu Ala Lys Arg Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly
100 105 110

Ala Gly Gln His Gly Val Ala Thr Ala Leu Ala Cys Ala Met Leu Asp
115 120 125

Met Pro Cys Arg Val Tyr Met Gly Ala Lys Asp Val Glu Arg Gln Ser
130 135 140

Pro Asn Val Phe Arg Met Arg Leu Met Gly Thr Glu Val Val Pro Val
145 150 155 160

Gln Lys Gly Ser Cys Ser Leu Lys Asp Ala Cys Cys Glu Ala Met Arg
165 170 175

Asp Trp Ser Ala Asn Tyr Glu Asn Thr His Tyr Leu Leu Gly Thr Ala
180 185 190

Ala Gly Pro
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<210> 37

<211> 543

<212> DNA

<213> Actinobacillus actinomycetemcomitans

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<220>
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 <222> (1)..(543)

<400> 37
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 gta ctt att tac ccg gaa gag cac ctt aaa gtg gtt tgc gat ccg gtc 96
 Val Leu Ile Tyr Pro Glu Glu His Leu Lys Val Val Cys Asp Pro Val
 20 25 30
 gtg gaa gtc aat gac aac acg cgt aag att att gat aat atg ttt gat 144
 Val Glu Val Asn Asp Asn Thr Arg Lys Ile Ile Asp Asn Met Phe Asp
 35 40 45
 acc atg tat cag gaa ggc ggt atc ggc cta gcg gca ccg cag gtg gat 192
 Thr Met Tyr Gln Glu Gly Ile Ile Gly Leu Ala Ala Pro Gln Val Asp
 50 55 60
 att tta cag cgt att atc act att gat att gag ggt gac aaa caa aac 240
 Ile Leu Gln Arg Ile Ile Thr Ile Asp Ile Glu Gly Asp Lys Gln Asn
 65 70 75 80
 cag tta gtg ttg att aac cct gaa att ttg gaa tcg gaa ggt gaa acc 288
 Gln Leu Val Leu Ile Asn Pro Glu Ile Leu Glu Ser Glu Gly Glu Thr
 85 90 95
 gga att gaa gag ggt tgt ttg tcg att ccc gga ttt cgt gcg tta gtg 336
 Gly Ile Glu Glu Gly Cys Leu Ser Ile Pro Gly Phe Arg Ala Leu Val
 100 105 110
 cca cgt aaa gag aaa gtg act gta aaa gcg ctg gat cgt cat ggt aaa 384
 Pro Arg Lys Glu Lys Val Thr Val Lys Ala Leu Asp Arg His Gly Lys
 115 120 125
 gaa ttc acc tta aaa gcc gat ggt ctg ttg gca att tgt att cag cat 432
 Glu Phe Thr Leu Lys Ala Asp Gly Leu Leu Ala Ile Cys Ile Gln His
 130 135 140
 gaa att gat cat tta aac ggt att ctt ttt gtg gat tat ctc tct cca 480
 Glu Ile Asp His Leu Asn Gly Ile Leu Phe Val Asp Tyr Leu Ser Pro
 145 150 155 160
 ttg aaa cgt cag cgg att aaa gaa aag ctg att aaa atg aaa aag cag 528
 Leu Lys Arg Gln Arg Ile Lys Glu Lys Leu Ile Lys Met Lys Lys Gln
 165 170 175
 atg gaa aag caa aaa 543
 Met Glu Lys Gln Lys
 180

<210> 38
 <211> 181
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 38

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Val Leu Ile Tyr Pro Glu Glu His Leu Lys Val Val Cys Asp Pro Val
 20 25 30

Val Glu Val Asn Asp Asn Thr Arg Lys Ile Ile Asp Asn Met Phe Asp
 35 40 45

Thr Met Tyr Gln Glu Gly Gly Ile Gly Leu Ala Ala Pro Gln Val Asp
 50 55 60

Ile Leu Gln Arg Ile Ile Thr Ile Asp Ile Glu Gly Asp Lys Gln Asn
 65 70 75 80

Gln Leu Val Leu Ile Asn Pro Glu Ile Leu Glu Ser Glu Gly Glu Thr
 85 90 95

Gly Ile Glu Glu Gly Cys Leu Ser Ile Pro Gly Phe Arg Ala Leu Val
 100 105 110

Pro Arg Lys Glu Lys Val Thr Val Lys Ala Leu Asp Arg His Gly Lys
 115 120 125

Glu Phe Thr Leu Lys Ala Asp Gly Leu Leu Ala Ile Cys Ile Gln His
 130 135 140

Glu Ile Asp His Leu Asn Gly Ile Leu Phe Val Asp Tyr Leu Ser Pro
 145 150 155 160

Leu Lys Arg Gln Arg Ile Lys Glu Lys Leu Ile Lys Met Lys Lys Gln
 165 170 175

Met Glu Lys Gln Lys
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<210> 39
 <211> 353
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(351)

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 Arg Gly Val Thr Pro Glu Leu Phe Ala Asp Trp Leu Lys Gln Leu His
 1 5 10 15

48

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cag gcg ggc gta aaa gtg gtg ttg gac agc agt aac gcc gca ttg acc 96
 Gln Ala Gly Val Lys Val Val Leu Asp Ser Ser Asn Ala Ala Leu Thr
 20 25 30
 gcc ggc tta acg gcg caa cct tgg ttg gtt aaa ccg aat cat cgt gag 144
 Ala Gly Leu Thr Ala Gln Pro Trp Leu Val Lys Pro Asn His Arg Glu
 35 40 45
 ttg gaa gcc tgg att ggt cat gcg ctg ccg acc ttg gac gac att atc 192
 Leu Glu Ala Trp Ile Gly His Ala Leu Pro Thr Leu Asp Asp Ile Ile
 50 55 60
 gcg gcg gcg aaa aaa ctg aaa gca caa ggc att gct aac gtg att att 240
 Ala Ala Ala Lys Lys Leu Lys Ala Gln Gly Ile Ala Asn Val Ile Ile
 65 70 75 80
 tcc atg gcg gcc aac ggt tcc ttg tgg ttg agc gat aca gcc gtc gta 288
 Ser Met Gly Ala Asn Gly Ser Leu Trp Leu Ser Asp Thr Ala Val Val
 85 90 95
 cag gcg caa ccg ccg aaa tgc gaa aac gtg gtc agc acc gtg ggc gcg 336
 Gln Ala Gln Pro Pro Lys Cys Glu Asn Val Val Ser Thr Val Gly Ala
 100 105 110
 ggc gat tct atg gtg gc 353
 Gly Asp Ser Met Val
 115

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<210> 40
 <211> 117
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 <213> Actinobacillus actinomycetemcomitans

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<400> 40

Arg Gly Val Thr Pro Glu Leu Phe Ala Asp Trp Leu Lys Gln Leu His
 1 5 10 15

Gln Ala Gly Val Lys Val Val Leu Asp Ser Ser Asn Ala Ala Leu Thr
 20 25 30

Ala Gly Leu Thr Ala Gln Pro Trp Leu Val Lys Pro Asn His Arg Glu
 35 40 45

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Leu Glu Ala Trp Ile Gly His Ala Leu Pro Thr Leu Asp Asp Ile Ile
 50 55 60

Ala Ala Ala Lys Lys Leu Lys Ala Gln Gly Ile Ala Asn Val Ile Ile
 65 70 75 80

Ser Met Gly Ala Asn Gly Ser Leu Trp Leu Ser Asp Thr Ala Val Val
 85 90 95

Gln Ala Gln Pro Pro Lys Cys Glu Asn Val Val Ser Thr Val Gly Ala
 100 105 110

Gly Asp Ser Met Val
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<210> 41
 <211> 367
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(366)

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<400> 41
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 Met Lys Lys Trp Phe Met Leu Leu Leu Pro Leu Thr Phe Ile Gly Ser
 1 5 10 15
 ctt tgg gcg cag gaa gcg cct tcc ccc ttt ott gcc ggg gaa tta ccg 96
 Leu Trp Ala Gln Glu Ala Pro Ser Pro Phe Leu Ala Gly Glu Leu Pro
 20 25 30
 gca gcg caa aaa atc gaa aaa gtc tta agc gcc ggt aat ccg agt gat 144
 Ala Ala Lys Lys Ile Glu Lys Val Leu Ser Ala Gly Asn Pro Ser Asp
 35 40 45
 gcg tta ttg ctg gcc gcc gcg ccg caa aaa atg gtc gga ctg gcg gcc 192
 Ala Leu Leu Leu Ala Ala Pro Gln Lys Met Val Gly Leu Ala Gly
 50 55 60
 ttt aag atg gca tcc aaa ggc gcc aaa tta ttt cct gtg caa caa caa 240
 Phe Lys Met Ala Ser Lys Gly Gly Lys Leu Phe Pro Val Gln Gln Gln
 65 70 75 80
 gcg ttg ccg acc atc gcc aaa att gcc gga aag gcc agt acg ttt tcc 288
 Ala Leu Pro Thr Ile Gly Lys Ile Ala Gly Lys Gly Ser Thr Phe Ser
 85 90 95
 gcc gaa aaa atc gtg gcg ctt caa ccg aat ttg att att gat gtg gcc 336
 Ala Glu Lys Ile Val Ala Leu Gln Pro Asn Leu Ile Ile Asp Val Gly
 100 105 110
 aat gtg gcg ccg aat tac atc gat cag gca a 367
 Asn Val Ala Pro Asn Tyr Ile Asp Gln Ala
 115 120

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<210> 42
 <211> 122
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

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 1 5 10 15

Leu Trp Ala Gln Glu Ala Pro Ser Pro Phe Leu Ala Gly Glu Leu Pro
20 25 30

Ala Ala Gln Lys Ile Glu Lys Val Leu Ser Ala Gly Asn Pro Ser Asp
35 40 45

Ala Leu Leu Leu Ala Ala Ala Pro Gln Lys Met Val Gly Leu Ala Gly
50 55 60

Phe Lys Met Ala Ser Lys Gly Gly Lys Leu Phe Pro Val Gln Gln Gln
65 70 75 80

Ala Leu Pro Thr Ile Gly Lys Ile Ala Gly Lys Gly Ser Thr Phe Ser
85 90 95

Ala Glu Lys Ile Val Ala Leu Gln Pro Asn Leu Ile Ile Asp Val Gly
100 105 110

Asn Val Ala Pro Asn Tyr Ile Asp Gln Ala
115 120

<210> 43

<211> 4593

<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> (1)..(4593)

<400> 43

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Val Phe Lys Val Ile Trp Cys Lys Thr Ser Gln Thr Trp Ile Ala Val
1 5 10 15

tct gaa cta tct aaa gct ttt tcc ctt tct acc act aca gat ata cct 96
Ser Glu Leu Ser Lys Ala Phe Ser Leu Ser Thr Thr Thr Asp Ile Pro
20 25 30

aaa aaa act aaa ata ttc att gct gca gcc ccg tta tta ttt ctc tcc 144
Lys Lys Thr Lys Ile Phe Ile Ala Ala Ala Pro Leu Leu Phe Leu Ser
35 40 45

ttt aat acc aac gct tac att gct ata ggt tct gtt gaa aac aat tct 192
Phe Asn Thr Asn Ala Tyr Ile Ala Ile Gly Ser Val Glu Asn Asn Ser
50 55 60

gtg aaa tcc gag ggg gca gaa gcc tcc cca aac aag aga aag gga agc 240
Val Lys Ser Glu Gly Ala Glu Ala Ser Pro Asn Lys Arg Lys Gly Ser
65 70 75 80

caa gca tta aat tat tac aac ccc ggt agt aaa tca tat gat gat aaa 288
Gln Ala Leu Asn Tyr Tyr Asn Pro Gly Ser Lys Ser Tyr Asp Asp Lys

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85						90						95							
gac	aaa	ccg	agc	aat	cct	gaa	aga	aga	tac	agc	aat	ggg	gag	gca	tat	336			
Asp	Lys	Pro	Ser	Asn	Pro	Glu	Arg	Arg	Tyr	Ser	Asn	Gly	Glu	Ala	Tyr				
		100						105					110						
ggt	atc	gct	atc	ggt	aaa	aat	acc	gat	gtt	cgt	gac	tca	agt	aag	gat	384			
Gly	Ile	Ala	Ile	Gly	Lys	Asn	Thr	Asp	Val	Arg	Asp	Ser	Ser	Lys	Asp				
		115					120					125							
tca	aat	ggt	atc	gcc	tta	ggc	gat	tat	tct	aaa	gct	acc	ggt	ggg	ctt	432			
Ser	Asn	Gly	Ile	Ala	Leu	Gly	Asp	Tyr	Ser	Lys	Ala	Thr	Gly	Gly	Leu				
		130				135					140								
gcc	atg	gcc	tta	ggt	tca	ttt	tcc	aga	gca	gaa	aaa	aat	ggc	ggt	att	480	10		
Ala	Met	Ala	Leu	Gly	Ser	Phe	Ser	Arg	Ala	Glu	Lys	Asn	Gly	Gly	Ile				
		145				150					155				160				
gca	atc	ggt	ata	gct	tcc	aga	tca	tca	gga	att	aat	tct	ctt	gcg	atg	528			
Ala	Ile	Gly	Ile	Ala	Ser	Arg	Ser	Ser	Gly	Ile	Asn	Ser	Leu	Ala	Met				
				165					170					175					
atg	cgt	caa	tct	gca	gca	acc	ggg	gat	tat	tct	act	gcc	att	ggt	tct	576			
Met	Arg	Gln	Ser	Ala	Ala	Thr	Gly	Asp	Tyr	Ser	Thr	Ala	Ile	Gly	Ser				
		180						185					190						
gtc	gca	tgg	gct	gca	ggt	caa	tca	agc	ttc	gca	ctg	ggg	gct	tct	gct	624			
Val	Ala	Trp	Ala	Ala	Gly	Gln	Ser	Ser	Phe	Ala	Leu	Gly	Ala	Ser	Ala				
		195					200					205							
act	gct	aaa	ggc	aac	caa	tcc	att	gca	att	ggc	agc	ttg	gaa	caa	aaa	672	20		
Thr	Ala	Lys	Gly	Asn	Gln	Ser	Ile	Ala	Ile	Gly	Ser	Leu	Glu	Gln	Lys				
		210				215					220								
ata	tct	ccg	aat	ggt	tct	ggt	gtg	cca	atc	aca	aaa	tac	aac	ggg	tta	720			
Ile	Ser	Pro	Asn	Gly	Ser	Gly	Val	Pro	Ile	Thr	Lys	Tyr	Asn	Gly	Leu				
		225				230					235				240				
gac	aac	aca	caa	acc	aat	ggt	aac	cgt	tcc	atg	gca	ttg	ggt	acg	gca	768			
Asp	Asn	Thr	Gln	Thr	Asn	Gly	Asn	Arg	Ser	Met	Ala	Leu	Gly	Thr	Ala				
				245					250					255					
gct	aaa	acc	aat	ggt	gat	gat	tca	ttt	gct	att	ggt	tat	aaa	gca	cac	816			
Ala	Lys	Thr	Asn	Gly	Asp	Asp	Ser	Phe	Ala	Ile	Gly	Tyr	Lys	Ala	His				
			260					265					270						
acc	ggt	gag	ttt	aaa	gtg	gaa	cat	gac	aac	tat	cta	aaa	gag	aat	gtt	864			
Thr	Gly	Glu	Phe	Lys	Val	Glu	His	Asp	Asn	Tyr	Leu	Lys	Glu	Asn	Val		30		
		275					280					285							
acc	tct	ccg	gat	ctg	tct	aaa	aaa	gct	gat	aaa	gcc	att	gct	gtc	ggt	912			
Thr	Ser	Pro	Asp	Leu	Ser	Lys	Lys	Ala	Asp	Lys	Ala	Ile	Ala	Val	Gly				
		290				295					300								
acg	agt	gcc	ctt	gcg	caa	aaa	gaa	tct	gct	atc	gca	ttt	ggc	tac	caa	960			
Thr	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ser	Ala	Ile	Ala	Phe	Gly	Tyr	Gln				
		305				310				315					320				
gct	aat	gct	tcc	ggc	att	aat	gca	att	tct	ctt	ggc	gca	aat	gca	aaa	1008			
Ala	Asn	Ala	Ser	Gly	Ile	Asn	Ala	Ile	Ser	Leu	Gly	Ala	Asn	Ala	Lys				
				325					330						335				

gca tct caa gat aac gtt gta gca ata ggt aaa tat gct aca gcc act Ala Ser Gln Asp Asn Val Val Ala Ile Gly Lys Tyr Ala Thr Ala Thr 340 345 350	1056
gaa tct ggt tca atg gcc att ggt cag gga gct aaa tct acc ttt aaa Glu Ser Gly Ser Met Ala Ile Gly Gln Gly Ala Lys Ser Thr Phe Lys 355 360 365	1104
aac tca ttg gca tta ggt aca ggt acc att gtc aac agt gtc gat ggc Asn Ser Leu Ala Leu Gly Thr Gly Thr Ile Val Asn Ser Val Asp Gly 370 375 380	1152
ggg caa tct aaa ttt act gca caa aat tat gat gct aat aat ggt gtt Gly Gln Ser Lys Phe Thr Ala Gln Asn Tyr Asp Ala Asn Asn Gly Val 385 390 395 400	1200
gta gct gtt gca aac gcc ggt aaa gag cgt cga att att aat gtt gcc Val Ala Val Ala Asn Ala Gly Lys Glu Arg Arg Ile Ile Asn Val Ala 405 410 415	1248
ggt ggt cgt aat gat act gat gca gtg aat att gcc cag tta aaa ttc Gly Gly Arg Asn Asp Thr Asp Ala Val Asn Ile Ala Gln Leu Lys Phe 420 425 430	1296
gtg aat gat aac tta gcc aag tcc atc gca ggc gcc ggt tat aac ggc Val Asn Asp Asn Leu Ala Lys Ser Ile Ala Gly Ala Gly Tyr Asn Gly 435 440 445	1344
tat gaa aca gac gga cat act tac aaa gca ccg gta ttt agt att aaa Tyr Glu Thr Asp Gly His Thr Tyr Lys Ala Pro Val Phe Ser Ile Lys 450 455 460	1392
aat acc aac tat cac gat gtc aaa aca gct gtt gaa gcg gca caa acc Asn Thr Asn Tyr His Asp Val Lys Thr Ala Val Glu Ala Ala Gln Thr 465 470 475 480	1440
aat tat gta agt gta aat agc act aat aca gca gcc gat agt aat tac Asn Tyr Val Ser Val Asn Ser Thr Asn Thr Ala Ala Asp Ser Asn Tyr 485 490 495	1488
gac aat aaa ggg gct aaa gca gta ggt tct att gcg tta ggc gaa aaa Asp Asn Lys Gly Ala Lys Ala Val Gly Ser Ile Ala Leu Gly Glu Lys 500 505 510	1536
gcc aca aca gga acg gcg gca atg aac tct att gcc att ggt tta aac Ala Thr Thr Gly Thr Ala Ala Met Asn Ser Ile Ala Ile Gly Leu Asn 515 520 525	1584
agc aat gtt agc ggc caa aat acc gtt gca ttg ggt gcc aat atc acc Ser Asn Val Ser Gly Gln Asn Thr Val Ala Leu Gly Ala Asn Ile Thr 530 535 540	1632
gcg aca acc aac ggt tcc gtc att tta gga aat tcc tcc acc acg gaa Ala Thr Thr Asn Gly Ser Val Ile Leu Gly Asn Ser Ser Thr Thr Glu 545 550 555 560	1680
ggt tca cat cct gtt tca aat gtt agc agt gcg act gtt aac gga tat Gly Ser His Pro Val Ser Asn Val Ser Ser Ala Thr Val Asn Gly Tyr 565 570 575	1728

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acc tac tca ggt ttt acc ggc acg gta aaa gag tcg gga cat ttt gtg Thr Tyr Ser Gly Phe Thr Gly Thr Val Lys Glu Ser Gly His Phe Val 580 585 590	1776
agc att ggt tca aaa ggc aat gag cgt caa att aaa aat gtg gca gca Ser Ile Gly Ser Lys Gly Asn Glu Arg Gln Ile Lys Asn Val Ala Ala 595 600 605	1824
ggt aat gtt gcg gca aac tca acc gat gcc gtt aat ggc tct caa tta Gly Asn Val Ala Ala Asn Ser Thr Asp Ala Val Asn Gly Ser Gln Leu 610 615 620	1872
ttt gct gtc gcc agt cgt gta gaa caa ggt tgg caa atc act tcc ggc Phe Ala Val Ala Ser Arg Val Glu Gln Gly Trp Gln Ile Thr Ser Gly 625 630 635 640	1920
gta gaa aat ggt ggt act caa aat ggc gca gcc tca aca gca aca atc Val Glu Asn Gly Gly Thr Gln Asn Gly Ala Ala Ser Thr Ala Thr Ile 645 650 655	1968
aaa ccg agt aac caa gtg aag cta ctg gca gga aag aat tta gca gtc Lys Pro Ser Asn Gln Val Lys Leu Leu Ala Gly Lys Asn Leu Ala Val 660 665 670	2016
aaa caa aac ggc act aac ttc acc ttc tca acc caa gaa aat gtc acg Lys Gln Asn Gly Thr Asn Phe Thr Phe Ser Thr Gln Glu Asn Val Thr 675 680 685	2064
ttc act aat gtt acg acc caa gat cta act gca aca ggc aac acc act Phe Thr Asn Val Thr Thr Gln Asp Leu Thr Ala Thr Gly Asn Thr Thr 690 695 700	2112
ggt aag aac ttc agc gtt caa aat ggc gga acc atc aat atg gga aat Val Lys Asn Phe Ser Val Gln Asn Gly Gly Thr Ile Asn Met Gly Asn 705 710 715 720	2160
aat cgc att acc ggt gtc gct gaa ggc act caa gat gac gac gcg gtt Asn Arg Ile Thr Gly Val Ala Glu Gly Thr Gln Asp Asp Ala Val 725 730 735	2208
aac ttt aaa caa tta aaa agc ctt ctt ggt ggc tcc gca tca acg gaa Asn Phe Lys Gln Leu Lys Ser Leu Leu Gly Gly Ser Ala Ser Thr Glu 740 745 750	2256
att gtt gag aaa aaa gca gct caa gcc gga gat gaa aac ctg gcg gat Ile Val Glu Lys Lys Ala Ala Gln Ala Gly Asp Glu Asn Leu Ala Asp 755 760 765	2304
att agc gta gca aat ggt aaa aac gcc ggc gat atg ggt gcg aaa tac Ile Ser Val Ala Asn Gly Lys Asn Ala Gly Asp Met Gly Ala Lys Tyr 770 775 780	2352
gaa gta tct gta tcc aaa aaa gcc gta caa agt gcc gca aaa gaa gcg Glu Val Ser Val Ser Lys Lys Ala Val Gln Ser Ala Ala Lys Glu Ala 785 790 795 800	2400
ggt aaa gtg aca ggt tcg gca ccg att aat gta aac aaa aca gat gta Val Lys Val Thr Gly Ser Ala Pro Ile Asn Val Asn Lys Thr Asp Val 805 810 815	2448
aat ggc gtt gat act tat gcc gta acc ttt aat ggc aca gaa gcg gcg	2496

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Asn Gly Val Asp Thr Tyr Ala Val Thr Phe Asn Gly Thr Glu Ala Ala
 820 825 830
 aaa tct atc cca tta act tat aaa gct aac ggt agc ggt gat aaa acc 2544
 Lys Ser Ile Pro Leu Thr Tyr Lys Ala Asn Gly Ser Gly Asp Lys Thr
 835 840 845
 gtc atg ttg gat aaa gga tta aac ttt acc aat ggt atg atg aca acc 2592
 Val Met Leu Asp Lys Gly Leu Asn Phe Thr Asn Gly Met Met Thr Thr
 850 855 860
 gct tcc gtg gca aat gac ggt gtg gtg aaa tat gac gtc aat tta tcc 2640
 Ala Ser Val Ala Asn Asp Gly Val Val Lys Tyr Asp Val Asn Leu Ser
 865 870 875 880
 acc att aaa gta gaa gat ggc aag gct gcc gta gcc ggt aca ccg ggc 2688
 Thr Ile Lys Val Glu Asp Gly Lys Ala Val Ala Gly Thr Pro Gly
 885 890 895
 aca aat ggc gcc aac ggc act gat ggc aaa gat ggc gta gcg acg gtt 2736
 Thr Asn Gly Ala Asn Gly Thr Asp Gly Lys Asp Gly Val Ala Thr Val
 900 905 910
 aaa aat gtg gta gag gcg tta aat aat gcc gca tgg aca ata act gcc 2784
 Lys Asn Val Val Glu Ala Leu Asn Asn Ala Ala Trp Thr Ile Thr Ala
 915 920 925
 tct aaa tct gac ggc gaa gtc gtc agc aat gca tct aat tcc gtt aaa 2832
 Ser Lys Ser Asp Gly Glu Val Val Ser Asn Ala Ser Asn Ser Val Lys
 930 935 940
 aat ggg gat acg gtg act tat gat gcc ggc aaa aac atc aaa att act 2880
 Asn Gly Asp Thr Val Thr Tyr Asp Ala Gly Lys Asn Ile Lys Ile Thr
 945 950 955 960
 caa aga gat aaa aaa ttc tct ttt gcc acc aaa gat aat gtt gaa ttt 2928
 Gln Arg Asp Lys Lys Phe Ser Phe Ala Thr Lys Asp Asn Val Glu Phe
 965 970 975
 act tct gtg acc acg ggc aat acc aaa tta acc ggt aat ggt gta gaa 2976
 Thr Ser Val Thr Thr Gly Asn Thr Lys Leu Thr Gly Asn Gly Val Glu
 980 985 990
 atc acc aac ggc cct aaa ctt acc caa tca ggt gtg gat gca ggc ggt 3024
 Ile Thr Asn Gly Pro Lys Leu Thr Gln Ser Gly Val Asp Ala Gly Gly
 995 1000 1005
 aag aaa atc acc aat gta gca gat ggc gtt att gca got aac agc 3069
 Lys Lys Ile Thr Asn Val Ala Asp Gly Val Ile Ala Ala Asn Ser
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 Lys Asp Ala Val Asn Gly Gly Gln Leu Phe Ala Glu Thr Ala Lys
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 gcc aaa act acg gtt gag aaa ggt gat gat aat att caa atc aca 3159
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 Ser Glu Thr Ala Thr Asp Gly His Ile Asn Tyr Lys Val Ala Leu

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1055	1060	1065	
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acc att gat ggt aat aac ggc Thr Ile Asp Gly Asn Asn Gly 1085	tat att acc ggt tta Tyr Ile Thr Gly Leu 1090	acc aat aca Thr Asn Thr 1095	3294
agc tgg acg ggc gcg cca aca Ser Trp Thr Gly Ala Pro Thr 1100	acc ggt cgt gca gca Thr Gly Arg Ala Ala 1105	acg gaa gat Thr Glu Asp 1110	3339
caa tta tct ata gtc gat aaa Gln Leu Ser Ile Val Asp Lys 1115	aaa ttc gat aat aag Lys Phe Asp Asn Lys 1120	gtt tct tta Val Ser Leu 1125	3384
ggc ggt gac aac ggt agt aoc Gly Gly Ile Asp Asn Gly Ser Thr 1130	aca gag aaa tcc ttg Thr Glu Lys Ser Leu 1135	tct cac aac Ser His Asn 1140	3429
ggc gga atc aaa ttt aat atc Gly Gly Ile Lys Phe Asn Ile 1145	aaa ggc gga gac agc Lys Gly Gly Asp Ser 1150	caa aaa tat Gln Lys Tyr 1155	3474
gtg acg aca tca gga tcc ggc Val Thr Thr Ser Gly Ser Gly 1160	gat gat gtc acg gtg Asp Asp Val Thr Val 1165	gat ott gcc Asp Leu Ala 1170	3519
caa acc aca aaa aat aag atc Gln Thr Thr Lys Asn Lys Ile 1175	gac aat gcg gca gat Asp Asn Ala Ala Asp 1180	aaa gat ctc Lys Asp Leu 1185	3564
gcc aac att acc gat aat ggt Ala Asn Ile Thr Asp Asn Gly 1190	aaa aaa gtt att acc Lys Lys Val Ile Thr 1195	gct tta ggc Ala Leu Gly 1200	3609
gct gta gtg aaa gcg gct gat Ala Val Val Lys Ala Ala Asp 1205	tct acg att acg gta Ser Thr Ile Thr Val 1210	act gac gaa Thr Asp Glu 1215	3654
acc gat aat acg aca gga caa Thr Asp Asn Thr Thr Gly Gln 1220	aaa acc tac aaa atc Lys Thr Tyr Lys Ile 1225	aaa gcc aat Lys Ala Asn 1230	3699
att cca aca ccg gaa aaa aca Ile Pro Thr Pro Glu Lys Thr 1235	gca atg gct ccc ggc Ala Met Ala Pro Gly 1240	aac aat aca Asn Asn Thr 1245	3744
acc att gaa ggt gat ggc tca Thr Ile Glu Gly Asp Gly Ser 1250	gcc gcc aat ccg ttt Ala Ala Asn Pro Phe 1255	aaa gtg aat Lys Val Asn 1260	3789
ctg aaa gat gat tta gcg cta Leu Lys Asp Asp Leu Ala Leu 1265	ggc caa aaa gac gct Gly Gln Lys Asp Ala 1270	aac ggc gta Asn Gly Val 1275	3834
acc ggt aaa gat tct tcc att Thr Gly Lys Asp Ser Ser Ile 1280	aaa gtg aac ggc aaa Lys Val Asn Gly Lys 1285	gat ggc tcc Asp Gly Ser 1290	3879

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gcc ggt gtg aat gaa acc aat ccc aaa gac cgt tta atg gtg aat 4014 Ala Gly Val Asn Glu Thr Asn Pro Lys Asp Arg Leu Met Val Asn 1325 1330 1335	
aac gac gct gtt gca acc ctt aaa gac ggc tta aaa ttc gcc gga 4059 Asn Asp Ala Val Ala Thr Leu Lys Asp Gly Leu Lys Phe Ala Gly 1340 1345 1350	10
gat aac agc acc gaa gtc atc act aaa acc tta aat caa aaa ctg 4104 Asp Asn Ser Thr Glu Val Ile Thr Lys Thr Leu Asn Gln Lys Leu 1355 1360 1365	
gaa att gtg ggt ggt gca gat aaa sac aaa tta tct gac aac aat 4149 Glu Ile Val Gly Gly Ala Asp Lys Asn Lys Leu Ser Asp Asn Asn 1370 1375 1380	
atc ggc gta aat gcc aat aac ggc aaa ctg gaa gtg aaa tta gcc 4194 Ile Gly Val Asn Ala Asn Thr Asn Gly Lys Leu Glu Val Lys Leu Ala 1385 1390 1395	
aaa gag ttg aat gag tta acc agt gcg caa ttc aag aat ggc gac 4239 Lys Glu Leu Asn Glu Leu Thr Ser Ala Gln Phe Lys Asn Gly Asp 1400 1405 1410	20
aac aca acg gtt atc aat ggc aat ggc ata aca att acc ccg aaa 4284 Asn Thr Thr Val Ile Asn Gly Asn Gly Ile Thr Ile Thr Pro Lys 1415 1420 1425	
gat ccg aca aag gcg gtc agc tta acg gat aaa gga cta aac aat 4329 Asp Pro Thr Lys Ala Val Ser Leu Thr Asp Lys Gly Leu Asn Asn 1430 1435 1440	
ggt ggt aat caa att gtg aac att gac agc gga tta aaa caa gcc 4374 Gly Gly Asn Gln Ile Val Asn Ile Asp Ser Gly Leu Lys Gln Ala 1445 1450 1455	
gac ggt tca aca gtt gct tta aaa gac gcc tca ggt gat acc tta 4419 Asp Gly Ser Thr Val Ala Leu Lys Asp Ala Ser Gly Asp Thr Leu 1460 1465 1470	
aaa aat gcg gcg aat atc ggc gat tta caa aaa tcc att aac gac 4464 Lys Asn Ala Ala Asn Ile Gly Asp Leu Gln Lys Ser Ile Asn Asp 1475 1480 1485	
att acc gac gca agt aaa aac ggc ggc ttc ggt tta agc gat gac 4509 Ile Thr Asp Ala Ser Lys Asn Gly Gly Phe Gly Leu Ser Asp Asp 1490 1495 1500	
aat ggc gca acc gct aaa gcc aac tta ggt gaa acc cgt gaa agt 4554 Asn Gly Ala Thr Ala Lys Ala Asn Leu Gly Glu Thr Arg Glu Ser 1505 1510 1515	

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 20 25 30

Lys Lys Thr Lys Ile Phe Ile Ala Ala Ala Pro Leu Leu Phe Leu Ser
 35 40 45

Phe Asn Thr Asn Ala Tyr Ile Ala Ile Gly Ser Val Glu Asn Asn Ser
 50 55 60

Val Lys Ser Glu Gly Ala Glu Ala Ser Pro Asn Lys Arg Lys Gly Ser
 65 70 75 80

Gln Ala Leu Asn Tyr Tyr Asn Pro Gly Ser Lys Ser Tyr Asp Asp Lys
 85 90 95

Asp Lys Pro Ser Asn Pro Glu Arg Arg Tyr Ser Asn Gly Glu Ala Tyr
 100 105 110

Gly Ile Ala Ile Gly Lys Asn Thr Asp Val Arg Asp Ser Ser Lys Asp
 115 120 125

Ser Asn Gly Ile Ala Leu Gly Asp Tyr Ser Lys Ala Thr Gly Gly Leu
 130 135 140

Ala Met Ala Leu Gly Ser Phe Ser Arg Ala Glu Lys Asn Gly Gly Ile
 145 150 155 160

Ala Ile Gly Ile Ala Ser Arg Ser Ser Gly Ile Asn Ser Leu Ala Met
 165 170 175

Met Arg Gln Ser Ala Ala Thr Gly Asp Tyr Ser Thr Ala Ile Gly Ser
 180 185 190

Val Ala Trp Ala Ala Gly Gln Ser Ser Phe Ala Leu Gly Ala Ser Ala

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195	200	205
Thr Ala Lys Gly Asn Gln Ser Ile Ala Ile Gly Ser Leu Glu Gln Lys		
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Ile Ser Pro Asn Gly Ser Gly Val Pro Ile Thr Lys Tyr Asn Gly Leu		
225	230	235 240
Asp Asn Thr Gln Thr Asn Gly Asn Arg Ser Met Ala Leu Gly Thr Ala		
	245	250 255
Ala Lys Thr Asn Gly Asp Asp Ser Phe Ala Ile Gly Tyr Lys Ala His		
	260	265 270
Thr Gly Glu Phe Lys Val Glu His Asp Asn Tyr Leu Lys Glu Asn Val		
	275	280 285
Thr Ser Pro Asp Leu Ser Lys Lys Ala Asp Lys Ala Ile Ala Val Gly		
	290	295 300
Thr Ser Ala Leu Ala Gln Lys Glu Ser Ala Ile Ala Phe Gly Tyr Gln		
305	310	315 320
Ala Asn Ala Ser Gly Ile Asn Ala Ile Ser Leu Gly Ala Asn Ala Lys		
	325	330 335
Ala Ser Gln Asp Asn Val Val Ala Ile Gly Lys Tyr Ala Thr Ala Thr		
	340	345 350
Glu Ser Gly Ser Met Ala Ile Gly Gln Gly Ala Lys Ser Thr Phe Lys		
	355	360 365
Asn Ser Leu Ala Leu Gly Thr Gly Thr Ile Val Asn Ser Val Asp Gly		
	370	375 380
Gly Gln Ser Lys Phe Thr Ala Gln Asn Tyr Asp Ala Asn Asn Gly Val		
385	390	395 400
Val Ala Val Ala Asn Ala Gly Lys Glu Arg Arg Ile Ile Asn Val Ala		
	405	410 415
Gly Gly Arg Asn Asp Thr Asp Ala Val Asn Ile Ala Gln Leu Lys Phe		
	420	425 430
Val Asn Asp Asn Leu Ala Lys Ser Ile Ala Gly Ala Gly Tyr Asn Gly		
	435	440 445

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Tyr Glu Thr Asp Gly His Thr Tyr Lys Ala Pro Val Phe Ser Ile Lys
450 455 460

Asn Thr Asn Tyr His Asp Val Lys Thr Ala Val Glu Ala Ala Gln Thr
465 470 475 480

Asn Tyr Val Ser Val Asn Ser Thr Asn Thr Ala Ala Asp Ser Asn Tyr
485 490 495

Asp Asn Lys Gly Ala Lys Ala Val Gly Ser Ile Ala Leu Gly Glu Lys
500 505 510

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Ala Thr Thr Gly Thr Ala Ala Met Asn Ser Ile Ala Ile Gly Leu Asn
515 520 525

Ser Asn Val Ser Gly Gln Asn Thr Val Ala Leu Gly Ala Asn Ile Thr
530 535 540

Ala Thr Thr Asn Gly Ser Val Ile Leu Gly Asn Ser Ser Thr Thr Glu
545 550 555 560

Gly Ser His Pro Val Ser Asn Val Ser Ser Ala Thr Val Asn Gly Tyr
565 570 575

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Thr Tyr Ser Gly Phe Thr Gly Thr Val Lys Glu Ser Gly His Phe Val
580 585 590

Ser Ile Gly Ser Lys Gly Asn Glu Arg Gln Ile Lys Asn Val Ala Ala
595 600 605

Gly Asn Val Ala Ala Asn Ser Thr Asp Ala Val Asn Gly Ser Gln Leu
610 615 620

Phe Ala Val Ala Ser Arg Val Glu Gln Gly Trp Gln Ile Thr Ser Gly
625 630 635 640

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Val Glu Asn Gly Gly Thr Gln Asn Gly Ala Ala Ser Thr Ala Thr Ile
645 650 655

Lys Pro Ser Asn Gln Val Lys Leu Leu Ala Gly Lys Asn Leu Ala Val
660 665 670

Lys Gln Asn Gly Thr Asn Phe Thr Phe Ser Thr Gln Glu Asn Val Thr
675 680 685

Phe Thr Asn Val Thr Thr Gln Asp Leu Thr Ala Thr Gly Asn Thr Thr
690 695 700

Val Lys Asn Phe Ser Val Gln Asn Gly Gly Thr Ile Asn Met Gly Asn
705 710 715 720

Asn Arg Ile Thr Gly Val Ala Glu Gly Thr Gln Asp Asp Ala Val
725 730 735

Asn Phe Lys Gln Leu Lys Ser Leu Leu Gly Gly Ser Ala Ser Thr Glu
740 745 750

Ile Val Glu Lys Lys Ala Ala Gln Ala Gly Asp Glu Asn Leu Ala Asp
755 760 765

Ile Ser Val Ala Asn Gly Lys Asn Ala Gly Asp Met Gly Ala Lys Tyr
770 775 780

Glu Val Ser Val Ser Lys Lys Ala Val Gln Ser Ala Ala Lys Glu Ala
785 790 795 800

Val Lys Val Thr Gly Ser Ala Pro Ile Asn Val Asn Lys Thr Asp Val
805 810 815

Asn Gly Val Asp Thr Tyr Ala Val Thr Phe Asn Gly Thr Glu Ala Ala
820 825 830

Lys Ser Ile Pro Leu Thr Tyr Lys Ala Asn Gly Ser Gly Asp Lys Thr
835 840 845

Val Met Leu Asp Lys Gly Leu Asn Phe Thr Asn Gly Met Met Thr Thr
850 855 860

Ala Ser Val Ala Asn Asp Gly Val Val Lys Tyr Asp Val Asn Leu Ser
865 870 875 880

Thr Ile Lys Val Glu Asp Gly Lys Ala Ala Val Ala Gly Thr Pro Gly
885 890 895

Thr Asn Gly Ala Asn Gly Thr Asp Gly Lys Asp Gly Val Ala Thr Val
900 905 910

Lys Asn Val Val Glu Ala Leu Asn Asn Ala Ala Trp Thr Ile Thr Ala
915 920 925

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Ser Lys Ser Asp Gly Glu Val Val Ser Asn Ala Ser Asn Ser Val Lys
 930 935 940
 Asn Gly Asp Thr Val Thr Tyr Asp Ala Gly Lys Asn Ile Lys Ile Thr
 945 950 955 960
 Gln Arg Asp Lys Lys Phe Ser Phe Ala Thr Lys Asp Asn Val Glu Phe
 965 970 975
 Thr Ser Val Thr Thr Gly Asn Thr Lys Leu Thr Gly Asn Gly Val Glu
 980 985 990
 Ile Thr Asn Gly Pro Lys Leu Thr Gln Ser Gly Val Asp Ala Gly Gly
 995 1000 1005
 Lys Lys Ile Thr Asn Val Ala Asp Gly Val Ile Ala Ala Asn Ser
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 Lys Asp Ala Val Asn Gly Gly Gln Leu Phe Ala Glu Thr Ala Lys
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 Ala Lys Thr Thr Val Glu Lys Gly Asp Asp Asn Ile Gln Ile Thr
 1040 1045 1050
 Ser Glu Thr Ala Thr Asp Gly His Ile Asn Tyr Lys Val Ala Leu
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 Asn Pro Ser Leu Thr Val Gly Pro Arg Thr Asn Gly His Pro Ile
 1070 1075 1080
 Thr Ile Asp Gly Asn Asn Gly Tyr Ile Thr Gly Leu Thr Asn Thr
 1085 1090 1095
 Ser Trp Thr Gly Ala Pro Thr Thr Gly Arg Ala Ala Thr Glu Asp
 1100 1105 1110
 Gln Leu Ser Ile Val Asp Lys Lys Phe Asp Asn Lys Val Ser Leu
 1115 1120 1125
 Gly Gly Asp Asn Gly Ser Thr Thr Glu Lys Ser Leu Ser His Asn
 1130 1135 1140
 Gly Gly Ile Lys Phe Asn Ile Lys Gly Gly Asp Ser Gln Lys Tyr
 1145 1150 1155
 Val Thr Thr Ser Gly Ser Gly Asp Asp Val Thr Val Asp Leu Ala

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1160	1165	1170
Gln Thr Thr Lys Asn Lys Ile Asp Asn Ala Ala Asp Lys Asp Leu		
1175	1180	1185
Ala Asn Ile Thr Asp Asn Gly Lys Lys Val Ile Thr Ala Leu Gly		
1190	1195	1200
Ala Val Val Lys Ala Ala Asp Ser Thr Ile Thr Val Thr Asp Glu		
1205	1210	1215
Thr Asp Asn Thr Thr Gly Gln Lys Thr Tyr Lys Ile Lys Ala Asn		
1220	1225	1230
Ile Pro Thr Pro Glu Lys Thr Ala Met Ala Pro Gly Asn Asn Thr		
1235	1240	1245
Thr Ile Glu Gly Asp Gly Ser Ala Ala Asn Pro Phe Lys Val Asn		
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Leu Lys Asp Asp Leu Ala Leu Gly Gln Lys Asp Ala Asn Gly Val		
1265	1270	1275
Thr Gly Lys Asp Ser Ser Ile Lys Val Asn Gly Lys Asp Gly Ser		
1280	1285	1290
Gly Val Ala Ile Asn Gly Lys Asp Gly Ser Ile Ala Leu Asn Gly		
1295	1300	1305
Lys Asp Gly Ala Asn Pro Val Thr Ile Lys Thr Ala Gln Gly Pro		
1310	1315	1320
Ala Gly Val Asn Glu Thr Asn Pro Lys Asp Arg Leu Met Val Asn		
1325	1330	1335
Asn Asp Ala Val Ala Thr Leu Lys Asp Gly Leu Lys Phe Ala Gly		
1340	1345	1350
Asp Asn Ser Thr Glu Val Ile Thr Lys Thr Leu Asn Gln Lys Leu		
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Glu Ile Val Gly Gly Ala Asp Lys Asn Lys Leu Ser Asp Asn Asn		
1370	1375	1380
Ile Gly Val Asn Ala Asn Asn Gly Lys Leu Glu Val Lys Leu Ala		
1385	1390	1395

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Lys Glu Leu Asn Glu Leu Thr Ser Ala Gln Phe Lys Asn Gly Asp
1400 1405 1410

Asn Thr Thr Val Ile Asn Gly Asn Gly Ile Thr Ile Thr Pro Lys
1415 1420 1425

Asp Pro Thr Lys Ala Val Ser Leu Thr Asp Lys Gly Leu Asn Asn
1430 1435 1440

Gly Gly Asn Gln Ile Val Asn Ile Asp Ser Gly Leu Lys Gln Ala
1445 1450 1455

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Asp Gly Ser Thr Val Ala Leu Lys Asp Ala Ser Gly Asp Thr Leu
1460 1465 1470

Lys Asn Ala Ala Asn Ile Gly Asp Leu Gln Lys Ser Ile Asn Asp
1475 1480 1485

Ile Thr Asp Ala Ser Lys Asn Gly Gly Phe Gly Leu Ser Asp Asp
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Glu Arg Arg Trp Gln Cys Tyr Tyr Lys Ser Ser Tyr Arg
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cct tat tta tac ggt gta acc cgt agt gat ttg gaa aaa atc gtc atc 96
Pro Tyr Leu Tyr Gly Val Thr Arg Ser Asp Leu Glu Lys Ile Val Ile
20 25 30
atg ggc gtg tgg ttt gaa gac atg aaa acc ctc gcg ccc tac tgg caa 144
Met Gly Val Trp Phe Glu Asp Met Lys Thr Leu Ala Pro Tyr Trp Gln
35 40 45
atc acc ggc acg ccc acc ggt gtc aac ttt gac gaa cgc aac gcc atg 192

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Ile Thr Gly Thr Pro Thr Gly Val Asn Phe Asp Glu Arg Asn Ala Met
50          55          60
atc ggc aaa acc ctc gcc gaa cgc tta aac ctg aaa gtg ggc agt aag      240
Ile Gly Lys Thr Leu Ala Glu Arg Leu Asn Leu Lys Val Gly Ser Lys
65          70          75          80
ctg acc tta agc ctg aat tcg gta gat aaa cac cag ttt acg att aaa      288
Leu Thr Leu Ser Leu Asn Ser Val Asp Lys His Gln Phe Thr Ile Lys
85          90          95
gcc atc gtg gaa gcg ggc gac gcc acc gac aat atg ctc atc gtg agc      336
Ala Ile Val Glu Ala Gly Asp Ala Thr Asp Asn Met Leu Ile Val Ser
100         105         110
ctg gat ttc gcg caa aac tgg ctg gaa aaa gaa aac ttt gcc acc aat      384
Leu Asp Phe Ala Gln Asn Trp Leu Glu Lys Glu Asn Phe Ala Thr Asn
115         120         125
gcc ctg ctt aac gtg aaa aat gat cag ggg caa gtg gaa caa ttc gca      432
Ala Leu Leu Asn Val Lys Asn Asp Gln Gly Gln Val Glu Gln Phe Ala
130         135         140
cag caa ctt cag caa caa tat ccc gat ttg gat att cat ccg atc cgc      480
Gln Gln Leu Gln Gln Gln Tyr Pro Asp Leu Asp Ile His Pro Ile Arg
145         150         155         160
aaa gtc tcc gcc tcc gaa ggg caa att ctg gat aag att aaa ggc ttg      528
Lys Val Ser Ala Ser Glu Gly Gln Ile Leu Asp Lys Ile Lys Gly Leu
165         170         175
atg ggc ttg att tcc gtg gtg att ctg att tta gcc a      565
Met Gly Leu Ile Ser Val Val Ile Leu Ile Leu Ala
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Met Gly Val Trp Phe Glu Asp Met Lys Thr Leu Ala Pro Tyr Trp Gln
35        40        45

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Ile Thr Gly Thr Pro Thr Gly Val Asn Phe Asp Glu Arg Asn Ala Met
50          55          60

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Ile Gly Lys Thr Leu Ala Glu Arg Leu Asn Leu Lys Val Gly Ser Lys
65          70          75          80

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Leu Thr Leu Ser Leu Asn Ser Val Asp Lys His Gln Phe Thr Ile Lys
85 90 95

Ala Ile Val Glu Ala Gly Asp Ala Thr Asp Asn Met Leu Ile Val Ser
100 105 110

Leu Asp Phe Ala Gln Asn Trp Leu Glu Lys Glu Asn Phe Ala Thr Asn
115 120 125

Ala Leu Leu Asn Val Lys Asn Asp Gln Gly Gln Val Glu Gln Phe Ala
130 135 140

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Gln Gln Leu Gln Gln Gln Tyr Pro Asp Leu Asp Ile His Pro Ile Arg
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Met Gly Leu Ile Ser Val Val Ile Leu Ile Leu Ala
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caa aaa cgt cag gta aaa agt gcg gtt aaa aat cca agt gtt ttt aaa 96
Gln Lys Arg Gln Val Lys Ser Ala Val Lys Asn Pro Ser Val Phe Lys
20 25 30
ggg cgt ttc ggt ttc agc aaa gat caa ctt atg gaa gcc ttc cgt atg 144
Gly Arg Phe Gly Phe Ser Lys Asp Gln Leu Met Glu Ala Phe Arg Met
35 40 45
tcc gtc agt gcc att gta gcg cac aaa atg cgc tca ttg ctg acc atg 192
Ser Val Ser Ala Ile Val Ala His Lys Met Arg Ser Leu Leu Thr Met
50 55 60
ctg gga att atc atc ggg atc act tcc gtc gtt tcc gtg gtg gcg tta 240
Leu Gly Ile Ile Ile Gly Ile Thr Ser Val Val Ser Val Val Ala Leu
65 70 75 80
gga aat ggt tca caa caa aag att ttg gaa aat att cgc ggt atc ggc 288

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Gly Asn Gly Ser Gln Gln Lys Ile Leu Glu Asn Ile Arg Gly Ile Gly
85 90 95

aca aac aca atg acg att ttt aac ggt aat ggt ttc ggt gac cgt cgt 336
Thr Asn Thr Met Thr Ile Phe Asn Gly Asn Gly Phe Gly Asp Arg Arg
100 105 110

tca cgg cac att caa aac cta aaa atc agc gat gcc aat acg tta tcg 384
Ser Arg His Ile Gln Asn Leu Lys Ile Ser Asp Ala Asn Thr Leu Ser
115 120 125

aaa caa agt tat att caa agc gtt act cca aat acc tct tcc agc ggc 432
Lys Gln Ser Tyr Ile Gln Ser Val Thr Pro Asn Thr Ser Ser Ser Gly
130 135 140

att tta gtg gtc ggt aac aaa tcc ttc aca tcc gcc aat tta tat ggt 480
Ile Leu Val Val Gly Asn Lys Ser Phe Thr Ser Ala Asn Leu Tyr Gly
145 150 155 160

atc ggt gaa caa tat ttt gat gta gaa ggc ttg aag tta aaa cag ggc 528
Ile Gly Glu Gln Tyr Phe Asp Val Glu Gly Leu Lys Leu Lys Gln Gly
165 170 175

cgt tta tta acc gag gac gat gtg gat caa agc aac cag gtg gtc gtg 576
Arg Leu Leu Thr Glu Asp Asp Val Asp Gln Ser Asn Gln Val Val Val
180 185 190

ctg gac gaa agt gca aaa aaa gcc att ttt gcc aac gaa aat ccc ctt 624
Leu Asp Glu Ser Ala Lys Lys Ala Ile Phe Ala Asn Glu Asn Pro Leu
195 200 205

ggc aaa acg gtg att ttt aat aag cga cca ttt cgt gtc att gg 668
Gly Lys Thr Val Ile Phe Asn Lys Arg Pro Phe Arg Val Ile
210 215 220

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<210> 48
<211> 222
<212> PRT
<213> Actinobacillus actinomycetemcomitans

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<400> 48

Ala Asn Arg Ile Ile Glu Ile Lys Asp Gly Glu Ile Ile Ser Asp Thr
1 5 10 15

Gln Lys Arg Gln Val Lys Ser Ala Val Lys Asn Pro Ser Val Phe Lys
20 25 30

30

Gly Arg Phe Gly Phe Ser Lys Asp Gln Leu Met Glu Ala Phe Arg Met
35 40 45

Ser Val Ser Ala Ile Val Ala His Lys Met Arg Ser Leu Leu Thr Met
50 55 60

Leu Gly Ile Ile Ile Gly Ile Thr Ser Val Val Ser Val Val Ala Leu
65 70 75 80

Gly Asn Gly Ser Gln Gln Lys Ile Leu Glu Asn Ile Arg Gly Ile Gly
85 90 95

Thr Asn Thr Met Thr Ile Phe Asn Gly Asn Gly Phe Gly Asp Arg Arg
100 105 110

Ser Arg His Ile Gln Asn Leu Lys Ile Ser Asp Ala Asn Thr Leu Ser
115 120 125

Lys Gln Ser Tyr Ile Gln Ser Val Thr Pro Asn Thr Ser Ser Ser Gly
130 135 140

Ile Leu Val Val Gly Asn Lys Ser Phe Thr Ser Ala Asn Leu Tyr Gly
145 150 155 160

Ile Gly Glu Gln Tyr Phe Asp Val Glu Gly Leu Lys Leu Lys Gln Gly
165 170 175

Arg Leu Leu Thr Glu Asp Asp Val Asp Gln Ser Asn Gln Val Val Val
180 185 190

Leu Asp Glu Ser Ala Lys Lys Ala Ile Phe Ala Asn Glu Asn Pro Leu
195 200 205

Gly Lys Thr Val Ile Phe Asn Lys Arg Pro Phe Arg Val Ile
210 215 220

<210> 49

<211> 276

<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> (1)..(276)

<400> 49

atg aga atg cac aat cct cca cac ccg gga gaa ctg tta aaa gaa tat 48
Met Arg Met His Asn Pro Pro His Pro Gly Glu Leu Leu Lys Glu Tyr
1 5 10 15

att gat ggc gtg agt gtc acg aag gtt gcc caa aaa tta ggt gtt tcg 96
Ile Asp Gly Val Ser Val Thr Lys Val Ala Gln Lys Leu Gly Val Ser
20 25 30

cgt gtt acg ctt tcc cgc att ctt aat ggg aaa gca agt ata acg cct 144
Arg Val Thr Leu Ser Arg Ile Leu Asn Gly Lys Ala Ser Ile Thr Pro
35 40 45

gaa atg gct gtg cga tta agc gaa tta ttg aat acc aca aca ccg aaa 192

10

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Glu Met Ala Val Arg Leu Ser Glu Leu Leu Asn Thr Thr Thr Pro Lys
50 55 60

tta tgg ctg ggt atg caa gca gac tac gat tta tgg caa att gaa caa 240
Leu Trp Leu Gly Met Gln Ala Asp Tyr Asp Leu Trp Gln Ile Glu Gln
65 70 75 80

caa cac gcc gta ttc aac atc caa cca tta ttt aat 276
Gln His Ala Val Phe Asn Ile Gln Pro Leu Phe Asn
85 90

<210> 50
<211> 92
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 50

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Met Arg Met His Asn Pro Pro His Pro Gly Glu Leu Leu Lys Glu Tyr
1 5 10 15

Ile Asp Gly Val Ser Val Thr Lys Val Ala Gln Lys Leu Gly Val Ser
20 25 30

Arg Val Thr Leu Ser Arg Ile Leu Asn Gly Lys Ala Ser Ile Thr Pro
35 40 45

Glu Met Ala Val Arg Leu Ser Glu Leu Leu Asn Thr Thr Thr Pro Lys
50 55 60

20

Leu Trp Leu Gly Met Gln Ala Asp Tyr Asp Leu Trp Gln Ile Glu Gln
65 70 75 80

Gln His Ala Val Phe Asn Ile Gln Pro Leu Phe Asn
85 90

<210> 51
<211> 537
<212> DNA
<213> Actinobacillus actinomycetemcomitans

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<220>
<221> CDS
<222> (1)..(537)

<400> 51
caa cat aat ggt gta cta ggt cct tat atc ggt aaa ggc agt tta acc 48
Gln His Asn Gly Val Leu Gly Pro Tyr Ile Gly Lys Gly Ser Leu Thr
1 5 10 15

tta aaa tta ccg gct tac tgg gaa cta tca gga ttc cat caa tta acc 96
Leu Lys Leu Pro Ala Tyr Trp Glu Leu Ser Gly Phe His Gln Leu Thr
20 25 30

gat caa tgg gct atc cac tat agc tat aaa tat aca gaa tgg agt cgt 144
Asp Gln Trp Ala Ile His Tyr Ser Tyr Lys Tyr Thr Glu Trp Ser Arg
35 40 45

ttt aaa gaa tta cgc ggc aaa tat caa gat ggt tcc ggc tat gag gcc 192
Phe Lys Glu Leu Arg Gly Lys Tyr Gln Asp Gly Ser Gly Tyr Glu Ala
50 55 60

ttt acc aag aaa gag gaa tac aaa gac aac tcc cgt ttt gct att ggt 240
Phe Thr Lys Lys Glu Glu Tyr Lys Asp Asn Ser Arg Phe Ala Ile Gly
65 70 75 80

aca aca tat agc cta aat gat gct tta aca tta cgt gca ggt ttg gct 288
Thr Thr Tyr Ser Leu Asn Asp Ala Leu Thr Leu Arg Ala Gly Leu Ala
85 90 95

tac gat aaa gcc gcg agt aaa acg cat tta tot gcg tcc att cct gat 336
Tyr Asp Lys Ala Ala Ser Lys Thr His Leu Ser Ala Ser Ile Pro Asp
100 105 110

acc gac cgt atg tgg tat agt ata gga gcc acc tat aaa ttc acc ccg 384
Thr Asp Arg Met Trp Tyr Ser Ile Gly Ala Thr Tyr Lys Phe Thr Pro
115 120 125

aat tta tot gtt gat gtc ggc ttc gct cat tta cgt ggt aag aag aaa 432
Asn Leu Ser Val Asp Val Gly Phe Ala His Leu Arg Gly Lys Lys Lys
130 135 140

cat ttt gtt gag acc caa aat atc aag ggg tta ttg ctt gtt gag gcg 480
His Phe Val Glu Thr Gln Asn Ile Lys Gly Leu Leu Leu Val Glu Ala
145 150 155 160

gat tac acc act aaa gcc acc gct aac ctc tac ggt ttg aat cta aat 528
Asp Tyr Thr Thr Lys Ala Thr Ala Asn Leu Tyr Gly Leu Asn Leu Asn
165 170 175

tac cgt ttc 537
Tyr Arg Phe

<210> 52
<211> 179
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 52

Gln His Asn Gly Val Leu Gly Pro Tyr Ile Gly Lys Gly Ser Leu Thr
1 5 10 15

Leu Lys Leu Pro Ala Tyr Trp Glu Leu Ser Gly Phe His Gln Leu Thr
20 25 30

Asp Gln Trp Ala Ile His Tyr Ser Tyr Lys Tyr Thr Glu Trp Ser Arg
35 40 45

Phe Lys Glu Leu Arg Gly Lys Tyr Gln Asp Gly Ser Gly Tyr Glu Ala

10

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50 55 60
 Phe Thr Lys Lys Glu Glu Tyr Lys Asp Asn Ser Arg Phe Ala Ile Gly
 65 70 75 80
 Thr Thr Tyr Ser Leu Asn Asp Ala Leu Thr Leu Arg Ala Gly Leu Ala
 85 90 95
 Tyr Asp Lys Ala Ala Ser Lys Thr His Leu Ser Ala Ser Ile Pro Asp
 100 105 110
 Thr Asp Arg Met Trp Tyr Ser Ile Gly Ala Thr Tyr Lys Phe Thr Pro
 115 120 125
 Asn Leu Ser Val Asp Val Gly Phe Ala His Leu Arg Gly Lys Lys Lys
 130 135 140
 His Phe Val Glu Thr Gln Asn Ile Lys Gly Leu Leu Leu Val Glu Ala
 145 150 155 160
 Asp Tyr Thr Thr Lys Ala Thr Ala Asn Leu Tyr Gly Leu Asn Leu Asn
 165 170 175

Tyr Arg Phe

<210> 53
 <211> 548
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(546)

<400> 53
 gga cca agt gtc acc aag gac ggc att cac gcc aat gat aag aaa atc 48
 Gly Pro Ser Val Thr Lys Asp Gly Ile His Ala Asn Asp Lys Lys Ile
 1 5 10 15
 acc ggt gta aaa gac ggt gaa att tca gcc cat agt aaa gag gcg gtg 96
 Thr Gly Val Lys Asp Gly Glu Ile Ser Ala His Ser Lys Glu Ala Val
 20 25 30
 aac ggt agc caa tta cat caa acc aac caa aat gtg acg aat tta gcc 144
 Asn Gly Ser Gln Leu His Gln Thr Asn Gln Asn Val Thr Asn Leu Ala
 35 40 45
 aac aat gtg gac aaa ggg ctg aat ttc caa gga gac aat caa gaa gtc 192
 Asn Asn Val Asp Lys Gly Leu Asn Phe Gln Gly Asp Asn Gln Glu Val
 50 55 60

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aca gtt aat cgt aaa tta ggc gat caa ctt aac att cgc ggc ggt gcg 240
 Thr Val Asn Arg Lys Leu Gly Asp Gln Leu Asn Ile Arg Gly Gly Ala
 65 70 75 80

gat ccg aag aaa tta aca caa aat aat atc ggc gtg acc gca gat aaa 288
 Asp Pro Lys Lys Leu Thr Gln Asn Asn Ile Gly Val Thr Ala Asp Lys
 85 90 95

aac ggc acc atg acc gtt cag ctg gcg aag gaa gtt aat ctc ggc gca 336
 Asn Gly Thr Met Thr Val Gln Leu Ala Lys Glu Val Asn Leu Gly Ala
 100 105 110

gat ggc agc ctt act gta ggc aat acc acg gtc aat aac gac ggt gtt 384
 Asp Gly Ser Leu Thr Val Gly Asn Thr Thr Val Asn Asn Asp Gly Val
 115 120 125

acg att aaa gac ggt cca agc atg aca agc cac ggc atc aac gcc ggc 432
 Thr Ile Lys Asp Gly Pro Ser Met Thr Ser His Gly Ile Asn Ala Gly
 130 135 140

ggc aaa cga att gct aac gtt gcg aaa ggg aaa gca ccg acg gat gca 480
 Gly Lys Arg Ile Ala Asn Val Ala Lys Gly Lys Ala Pro Thr Asp Ala
 145 150 155 160

gta aat atg agt cag ctt caa gac gtc ggc agt gcc att aat aat cgc 528
 Val Asn Met Ser Gln Leu Gln Asp Val Gly Ser Ala Ile Asn Asn Arg
 165 170 175

att gat aac att gat aag cg 548
 Ile Asp Asn Ile Asp Lys
 180

<210> 54
 <211> 182
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 54

Gly Pro Ser Val Thr Lys Asp Gly Ile His Ala Asn Asp Lys Lys Ile
 1 5 10 15

Thr Gly Val Lys Asp Gly Glu Ile Ser Ala His Ser Lys Glu Ala Val
 20 25 30

Asn Gly Ser Gln Leu His Gln Thr Asn Gln Asn Val Thr Asn Leu Ala
 35 40 45

Asn Asn Val Asp Lys Gly Leu Asn Phe Gln Gly Asp Asn Gln Glu Val
 50 55 60

Thr Val Asn Arg Lys Leu Gly Asp Gln Leu Asn Ile Arg Gly Gly Ala
 65 70 75 80

Asp Pro Lys Lys Leu Thr Gln Asn Asn Ile Gly Val Thr Ala Asp Lys

10

20

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85 90 95
 Asn Gly Thr Met Thr Val Gln Leu Ala Lys Glu Val Asn Leu Gly Ala
 100 105 110
 Asp Gly Ser Leu Thr Val Gly Asn Thr Thr Val Asn Asn Asp Gly Val
 115 120 125
 Thr Ile Lys Asp Gly Pro Ser Met Thr Ser His Gly Ile Asn Ala Gly
 130 135 140
 Gly Lys Arg Ile Ala Asn Val Ala Lys Gly Lys Ala Pro Thr Asp Ala
 145 150 155 160
 Val Asn Met Ser Gln Leu Gln Asp Val Gly Ser Ala Ile Asn Asn Arg
 165 170 175
 Ile Asp Asn Ile Asp Lys
 180

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<210> 55
 <211> 168
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

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<220>
 <221> CDS
 <222> (1)..(168)

<400> 55
 atg gat cac ttt ccg ccg ctt tgg ctt ttt ccg tta aac agc tta atg 48
 Met Asp His Phe Pro Pro Leu Trp Leu Phe Arg Leu Asn Ser Leu Met
 1 5 10 15
 ctt ctt ttg ctg ctt ctt ccg ttg cat aaa cct gtt caa aat cca ccg 96
 Leu Leu Leu Leu Leu Leu Pro Leu His Lys Pro Val Gln Asn Pro Pro
 20 25 30
 tgc agt cag aac cgt caa tca ccg tac cca cct cga cac aac agc aaa 144
 Cys Ser Gln Asn Arg Gln Ser Pro Tyr Pro Pro Arg His Asn Ser Lys
 35 40 45
 ctt ttg ctt ctt ccg cct gac att 168
 Leu Leu Leu Leu Pro Pro Asp Ile
 50 55

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<210> 56
 <211> 56
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 56

Met Asp His Phe Pro Pro Leu Trp Leu Phe Arg Leu Asn Ser Leu Met
1 5 10 15

Leu Leu Leu Leu Leu Leu Pro Leu His Lys Pro Val Gln Asn Pro Pro
20 25 30

Cys Ser Gln Asn Arg Gln Ser Pro Tyr Pro Pro Arg His Asn Ser Lys
35 40 45

Leu Leu Leu Leu Pro Pro Asp Ile
50 55

<210> 57
<211> 492
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(492)

<400> 57
atg acg aac aaa cca aaa tcc ggg ctc tca ttt ttg tgg tta agt acg 48
Met Thr Asn Lys Pro Lys Ser Gly Leu Ser Phe Leu Trp Leu Ser Thr
1 5 10 15
ctg gca ttt atc gcc gat att ttt acc aaa tac tta atc gta agc cat 96
Leu Ala Phe Ile Ala Asp Ile Phe Thr Lys Tyr Leu Ile Val Ser His
20 25 30
ttt gaa tac ggc gaa agc gta aat atc ctg ccg att ttt aat ttg acc 144
Phe Glu Tyr Gly Glu Ser Val Asn Ile Leu Pro Ile Phe Asn Leu Thr
35 40 45
tat gtg ggt aac ttt ggc gcc gct ttt agt ttc ctg gcg gat cat gac 192
Tyr Val Gly Asn Phe Gly Ala Ala Phe Ser Phe Leu Ala Asp His Asp
50 55 60
ggg tgg caa aaa ttc ttt ttc ctt gcg ttg gca gtg ggg att tcc gcc 240
Gly Trp Gln Lys Phe Phe Phe Leu Ala Leu Ala Val Gly Ile Ser Ala
65 70 75 80
atg ttg gtt tat ttt tta atg aaa aat cgc cat gaa caa aaa ctg ctg 288
Met Leu Val Tyr Phe Leu Met Lys Asn Arg His Glu Gln Lys Leu Leu
85 90 95
aat gcc gcc tac gct ttg att atc ggc ggc gct ttg ggc aat gcg gcg 336
Asn Ala Ala Tyr Ala Leu Ile Ile Gly Gly Ala Leu Gly Asn Ala Ala
100 105 110
gat cgt ctg tat cac ggc tat gtg gtg gat ttt tta gat ttc tat tgg 384
Asp Arg Leu Tyr His Gly Tyr Val Val Asp Phe Leu Asp Phe Tyr Trp
115 120 125
cgg gat tgg cat tat ccc gtg ttt aac ctg gcg gat att gcc att tgt 432
Arg Asp Trp His Tyr Pro Val Phe Asn Leu Ala Asp Ile Ala Ile Cys
130 135 140

10

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gtg ggt gcc ggt ttg att gcc ttg gat gcg ttc aaa aac ggc aat aaa 480
 Val Gly Ala Gly Leu Ile Ala Leu Asp Ala Phe Lys Asn Gly Asn Lys
 145 150 155 160

cag gaa tgt aaa 492
 Gln Glu Cys Lys

<210> 58
 <211> 164
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 58

Met Thr Asn Lys Pro Lys Ser Gly Leu Ser Phe Leu Trp Leu Ser Thr
 1 5 10 15

Leu Ala Phe Ile Ala Asp Ile Phe Thr Lys Tyr Leu Ile Val Ser His
 20 25 30

Phe Glu Tyr Gly Glu Ser Val Asn Ile Leu Pro Ile Phe Asn Leu Thr
 35 40 45

Tyr Val Gly Asn Phe Gly Ala Ala Phe Ser Phe Leu Ala Asp His Asp
 50 55 60

Gly Trp Gln Lys Phe Phe Phe Leu Ala Leu Ala Val Gly Ile Ser Ala
 65 70 75 80

Met Leu Val Tyr Phe Leu Met Lys Asn Arg His Glu Gln Lys Leu Leu
 85 90 95

Asn Ala Ala Tyr Ala Leu Ile Ile Gly Gly Ala Leu Gly Asn Ala Ala
 100 105 110

Asp Arg Leu Tyr His Gly Tyr Val Val Asp Phe Leu Asp Phe Tyr Trp
 115 120 125

Arg Asp Trp His Tyr Pro Val Phe Asn Leu Ala Asp Ile Ala Ile Cys
 130 135 140

Val Gly Ala Gly Leu Ile Ala Leu Asp Ala Phe Lys Asn Gly Asn Lys
 145 150 155 160

Gln Glu Cys Lys

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<210> 59
 <211> 453
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(453)

<400> 59
 atg gct aaa ttg tat ttt tac tat tcc acc atg aat gca gga aaa tcc 48
 Met Ala Lys Leu Tyr Phe Tyr Tyr Ser Thr Met Asn Ala Gly Lys Ser
 1 5 10 15
 acc acc ttg ttg caa tct tcc tat aat tac cgc gaa cgt aac atg aac 96
 Thr Thr Leu Leu Gln Ser Ser Tyr Asn Tyr Arg Glu Arg Asn Met Asn
 20 25 30
 acg ctg gtt tat aca gcg gcg ata gac gat cgt ttc gcc gta ggg cag 144
 Thr Leu Val Tyr Thr Ala Ala Ile Asp Asp Arg Phe Gly Val Gly Gln
 35 40 45
 gtg act tcc cgc atc ggg att agc gaa cgg gcg aat acc ttt acc cgc 192
 Val Thr Ser Arg Ile Gly Ile Ser Glu Arg Ala Asn Thr Phe Thr Arg
 50 55 60
 aat acg aat ttg ttc gct gaa att gaa caa cat ctg gcg cag gag ccg 240
 Asn Thr Asn Leu Phe Ala Glu Ile Glu Gln His Leu Ala Gln Glu Pro
 65 70 75 80
 ctt cat tgt att ttg gtg gat gag gca cag ttt tta acc aaa gaa cag 288
 Leu His Cys Ile Leu Val Asp Glu Ala Gln Phe Leu Thr Lys Glu Gln
 85 90 95
 gtt tat caa ctg agc gat gtg gtg gat aaa cta cat att ccc gtg ttg 336
 Val Tyr Gln Leu Ser Asp Val Val Asp Lys Leu His Ile Pro Val Leu
 100 105 110
 tgc tac ggt ttg cgc acc gat ttc caa gcg gaa tta ttt gaa gcc agt 384
 Cys Tyr Gly Leu Arg Thr Asp Phe Gln Ala Glu Leu Phe Glu Gly Ser
 115 120 125
 cgc tat tta ctg gcg tgg gcg gat cag ctg gaa gaa ctc aaa acc att 432
 Arg Tyr Leu Leu Ala Trp Ala Asp Gln Leu Glu Glu Leu Lys Thr Ile
 130 135 140
 tgt tac tgc ggt cgc aaa gcc 453
 Cys Tyr Cys Gly Arg Lys Ala
 145 150

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<210> 60
 <211> 151
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 60

Met Ala Lys Leu Tyr Phe Tyr Tyr Ser Thr Met Asn Ala Gly Lys Ser
 1 5 10 15

Thr Thr Leu Leu Gln Ser Ser Tyr Asn Tyr Arg Glu Arg Asn Met Asn
20 25 30

Thr Leu Val Tyr Thr Ala Ala Ile Asp Asp Arg Phe Gly Val Gly Gln
35 40 45

Val Thr Ser Arg Ile Gly Ile Ser Glu Arg Ala Asn Thr Phe Thr Arg
50 55 60

Asn Thr Asn Leu Phe Ala Glu Ile Glu Gln His Leu Ala Gln Glu Pro
65 70 75 80

Leu His Cys Ile Leu Val Asp Glu Ala Gln Phe Leu Thr Lys Glu Gln
85 90 95

Val Tyr Gln Leu Ser Asp Val Val Asp Lys Leu His Ile Pro Val Leu
100 105 110

Cys Tyr Gly Leu Arg Thr Asp Phe Gln Ala Glu Leu Phe Glu Gly Ser
115 120 125

Arg Tyr Leu Leu Ala Trp Ala Asp Gln Leu Glu Glu Leu Lys Thr Ile
130 135 140

Cys Tyr Cys Gly Arg Lys Ala
145 150

<210> 61
<211> 643
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(642)

<400> 61
tat aac gaa aaa act tac gaa aat gac tta acc gca aaa gaa atc ttc 48
Tyr Asn Glu Lys Thr Tyr Glu Asn Asp Leu Thr Ala Lys Glu Ile Phe
1 5 10 15
gta act tat gta ttg aaa aac aaa ttg tta tgg tac atc gcc att gct 96
Val Thr Tyr Val Leu Lys Asn Lys Leu Leu Trp Tyr Ile Ala Ile Ala
20 25 30
aac gtg ttc gtt tac tta atc cgc tac ggc gta ttg aaa tgg tct ccg 144
Asn Val Phe Val Tyr Leu Ile Arg Tyr Gly Val Leu Lys Trp Ser Pro
35 40 45
gtt tac ttg agt gaa gtg aaa cac ttc aac atc aaa ggt acc gca tgg 192
Val Tyr Leu Ser Glu Val Lys His Phe Asn Ile Lys Gly Thr Ala Trp

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50 55 60
 gca tac acc att tat gaa ttg gcg gcc gtt ccg ggt aca tta ctt tgc 240
 Ala Tyr Thr Ile Tyr Glu Leu Ala Ala Val Pro Gly Thr Leu Leu Cys
 65 70 75 80
 ggt tgg gta tct gac cat gta ttc aaa ggt aaa cgt ggc tta acc ggt 288
 Gly Trp Val Ser Asp His Val Phe Lys Gly Lys Arg Gly Leu Thr Gly
 85 90 95
 ttc atc ttt atg att tta acc acc gca gcg gta gcc aca tac tgg atg 336
 Phe Ile Phe Met Ile Leu Thr Thr Ala Ala Val Ala Thr Tyr Trp Met
 100 105 110
 aac cct gca aca ccg gaa gct gag ctt gca aac tac agc gca tgg tat 384
 Asn Pro Ala Thr Pro Glu Ala Glu Leu Ala Asn Tyr Ser Ala Trp Tyr
 115 120 125
 gaa aac cca tac caa tta acc gac ttt att ttg atg acc tta atc ggt 432
 Glu Asn Pro Tyr Gln Leu Thr Asp Phe Ile Leu Met Thr Leu Ile Gly
 130 135 140
 ttc tta atc tac ggc cct gtg atg cta atc ggc ttg cac gcc ctt gaa 480
 Phe Leu Ile Tyr Gly Pro Val Met Leu Ile Gly Leu His Ala Leu Glu
 145 150 155 160
 ctt gca ccg aaa aaa gcg gca ggt acc gca gca ggt ttc acc ggt tta 528
 Leu Ala Pro Lys Lys Ala Ala Gly Thr Ala Ala Gly Phe Thr Gly Leu
 165 170 175
 ttc ggt tac tta ggc ggt acc gtg tct gca tca gca gtt atc ggt tgg 576
 Phe Gly Tyr Leu Gly Gly Thr Val Ser Ala Ser Ala Val Ile Gly Trp
 180 185 190
 gca gcc caa cac tac ggc tgg gac ggc ggt ttt tac gtg atg atc ggc 624
 Ala Ala Gln His Tyr Gly Trp Asp Gly Gly Phe Tyr Val Met Ile Gly
 195 200 205
 ggt ggt atc tta ccg gtc a 643
 Gly Gly Ile Leu Pro Val
 210

<210> 62
 <211> 214
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 62

Tyr Asn Glu Lys Thr Tyr Glu Asn Asp Leu Thr Ala Lys Glu Ile Phe
 1 5 10 15

Val Thr Tyr Val Leu Lys Asn Lys Leu Leu Trp Tyr Ile Ala Ile Ala
 20 25 30

Asn Val Phe Val Tyr Leu Ile Arg Tyr Gly Val Leu Lys Trp Ser Pro
 35 40 45

10

20

30

Val Tyr Leu Ser Glu Val Lys His Phe Asn Ile Lys Gly Thr Ala Trp
50 55 60

Ala Tyr Thr Ile Tyr Glu Leu Ala Ala Val Pro Gly Thr Leu Leu Cys
65 70 75 80

Gly Trp Val Ser Asp His Val Phe Lys Gly Lys Arg Gly Leu Thr Gly
85 90 95

Phe Ile Phe Met Ile Leu Thr Thr Ala Ala Val Ala Thr Tyr Trp Met
100 105 110

Asn Pro Ala Thr Pro Glu Ala Glu Leu Ala Asn Tyr Ser Ala Trp Tyr
115 120 125

Glu Asn Pro Tyr Gln Leu Thr Asp Phe Ile Leu Met Thr Leu Ile Gly
130 135 140

Phe Leu Ile Tyr Gly Pro Val Met Leu Ile Gly Leu His Ala Leu Glu
145 150 155 160

Leu Ala Pro Lys Lys Ala Ala Gly Thr Ala Ala Gly Phe Thr Gly Leu
165 170 175

Phe Gly Tyr Leu Gly Gly Thr Val Ser Ala Ser Ala Val Ile Gly Trp
180 185 190

Ala Ala Gln His Tyr Gly Trp Asp Gly Gly Phe Tyr Val Met Ile Gly
195 200 205

Gly Gly Ile Leu Pro Val
210

<210> 63
<211> 333
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(333)

<400> 63
gaa tgg gcg gga acg cct tat cgt atc ggc gga caa agt cgc agt ggc 48
Glu Trp Ala Gly Thr Pro Tyr Arg Ile Gly Gly Gln Ser Arg Ser Gly
1 5 10 15

gtg gat tgc tcc ggt ttc gtg caa acc acc ttt ttc gat cgc ttc ggc 96
Val Asp Cys Ser Gly Phe Val Gln Thr Thr Phe Phe Asp Arg Phe Gly

10

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30

20	25	30	
ata aaa ttg cgc cga caa acc aaa gat cag gca aat tac ggt cag tat			144
Ile Lys Leu Pro Arg Gln Thr Lys Asp Gln Ala Asn Tyr Gly Gln Tyr			
35	40	45	
att gaa aaa ggc gat att caa acc ggt gat ttg gtg ttc ttt aaa acc			192
Ile Glu Lys Gly Asp Ile Gln Thr Gly Asp Leu Val Phe Phe Lys Thr			
50	55	60	
ggt cgc ggt cct cat ggc tat cat gtg ggc att tat gtg aag gaa gac			240
Gly Arg Gly Pro His Gly Tyr His Val Gly Ile Tyr Val Lys Glu Asp			
65	70	75	80
aaa ttt ctg cac ggc tct act aag ggt ggc gtg att tat tcc tcg ttg			288
Lys Phe Leu His Ala Ser Thr Lys Gly Gly Val Ile Tyr Ser Ser Leu			
85	90	95	
aac agc gat tat tgg cgt aag gca tat tgg cag gca aga cga att			333
Asn Ser Asp Tyr Trp Arg Lys Ala Tyr Trp Gln Ala Arg Arg Ile			
100	105	110	

<210> 64
 <211> 111
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 64

Glu Trp Ala Gly Thr Pro Tyr Arg Ile Gly Gly Gln Ser Arg Ser Gly	
1	15

Val Asp Cys Ser Gly Phe Val Gln Thr Thr Phe Phe Asp Arg Phe Gly	
20	30

Ile Lys Leu Pro Arg Gln Thr Lys Asp Gln Ala Asn Tyr Gly Gln Tyr	
35	45

Ile Glu Lys Gly Asp Ile Gln Thr Gly Asp Leu Val Phe Phe Lys Thr	
50	60

Gly Arg Gly Pro His Gly Tyr His Val Gly Ile Tyr Val Lys Glu Asp	
65	80

Lys Phe Leu His Ala Ser Thr Lys Gly Gly Val Ile Tyr Ser Ser Leu	
85	95

Asn Ser Asp Tyr Trp Arg Lys Ala Tyr Trp Gln Ala Arg Arg Ile	
100	110

<210> 65
 <211> 423
 <212> DNA

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<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> (1)..(423)

<400> 65

atg aaa aaa cgt tgc aca tgg gcg gaa aac tca caa att tat cag gat 48
Met Lys Lys Arg Cys Thr Trp Ala Glu Asn Ser Gln Ile Tyr Gln Asp
1 5 10 15

tac cac gac aac gaa tgg ggt aaa cca caa ttt gat gat cgc aaa tta 96
Tyr His Asp Asn Glu Trp Gly Lys Pro Gln Phe Asp Asp Arg Lys Leu
20 25 30

ttt gaa aaa ctg tgt ctg gaa ggg cag caa gcg ggc ctg tcg tgg att 144
Phe Glu Lys Leu Cys Leu Glu Gly Gln Gln Ala Gly Leu Ser Trp Ile
35 40 45

acg gta tta aaa aaa cgg gaa gct tat cgg cag gcg ttt ttc cat ttt 192
Thr Val Leu Lys Lys Arg Glu Ala Tyr Arg Gln Ala Phe Phe His Phe
50 55 60

gat ccg cac aaa gtc gca gca atg act gat gcc gat atc gat cac tgt 240
Asp Pro His Lys Val Ala Ala Met Thr Asp Ala Asp Ile Asp His Cys
65 70 75 80

atg caa aat aca ggc tta att cgc cat cgc gct aaa tta cag gca atc 288
Met Gln Asn Thr Gly Leu Ile Arg His Arg Ala Lys Leu Gln Ala Ile
85 90 95

gtc acc aat gcg cgg gcg ttt ott gcc atg caa aag tgc ggt gaa aat 336
Val Thr Asn Ala Arg Ala Phe Leu Ala Met Gln Lys Cys Gly Glu Asn
100 105 110

ttc agt cat ttt att tgg tot ttc gtg aat cat cag ccg caa att cat 384
Phe Ser His Phe Ile Trp Ser Phe Val Asn His Gln Pro Gln Ile His
115 120 125

gac gtg ccc gag tta agc cat gtg ccg gcg caa acg gca 423
Asp Val Pro Glu Leu Ser His Val Pro Ala Gln Thr Ala
130 135 140

<210> 66

<211> 141

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 66

Met Lys Lys Arg Cys Thr Trp Ala Glu Asn Ser Gln Ile Tyr Gln Asp
1 5 10 15

Tyr His Asp Asn Glu Trp Gly Lys Pro Gln Phe Asp Asp Arg Lys Leu
20 25 30

Phe Glu Lys Leu Cys Leu Glu Gly Gln Gln Ala Gly Leu Ser Trp Ile
35 40 45

10

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Thr Val Leu Lys Lys Arg Glu Ala Tyr Arg Gln Ala Phe Phe His Phe
50 55 60

Asp Pro His Lys Val Ala Ala Met Thr Asp Ala Asp Ile Asp His Cys
65 70 75 80

Met Gln Asn Thr Gly Leu Ile Arg His Arg Ala Lys Leu Gln Ala Ile
85 90 95

Val Thr Asn Ala Arg Ala Phe Leu Ala Met Gln Lys Cys Gly Glu Asn
100 105 110

10

Phe Ser His Phe Ile Trp Ser Phe Val Asn His Gln Pro Gln Ile His
115 120 125

Asp Val Pro Glu Leu Ser His Val Pro Ala Gln Thr Ala
130 135 140

<210> 67
<211> 375
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(375)

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<400> 67
gac atc gtt aca ttt acc caa aaa cgc tgc ccg ttt aat cac atg acg 48
Asp Ile Val Thr Phe Thr Gln Lys Arg Cys Pro Phe Asn His Met Thr
1 5 10 15
gtg gcg tat caa aaa agt gcg gtc ata aat tgc ggc gga tat gag gat 96
Val Ala Tyr Gln Lys Ser Ala Val Ile Asn Cys Gly Gly Tyr Glu Asp
20 25 30
tta cag gaa gat tat tat ttg tgg atc aaa ctg gtg gcg caa ggg cag 144
Leu Gln Glu Asp Tyr Tyr Leu Trp Ile Lys Leu Val Ala Gln Gly Gln
35 40 45
cgc gta gca aat tta ccc gat att ttg gtc tat gcg cgc gtc ggc aac 192
Arg Val Ala Asn Leu Pro Asp Ile Leu Val Tyr Ala Arg Val Gly Asn
50 55 60
ggc atg gta ggg cga cgc cgt ggt tta aac caa gcc aaa gcg gaa tgg 240
Gly Met Val Gly Arg Arg Arg Gly Leu Asn Gln Ala Lys Ala Glu Trp
65 70 75 80
cgc tta ttt aag cta aaa cac cat ott ggc att cag gga ttt tta tcc 288
Arg Leu Phe Lys Leu Lys His His Leu Gly Ile Gln Gly Phe Leu Ser
85 90 95
ggg cta ttc act ttt gtc ctg cgt tcc ggt gcc aga tta ttg cag aca 336

30

Gly Leu Phe Thr Phe Val Leu Arg Ser Gly Ala Arg Leu Leu Pro Thr
 100 105 110

tca tta ctg aaa aac atc tat caa acc ttt tta aga aaa 375
 Ser Leu Leu Lys Asn Ile Tyr Gln Thr Phe Leu Arg Lys
 115 120 125

<210> 68
 <211> 125
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 68

Asp Ile Val Thr Phe Thr Gln Lys Arg Cys Pro Phe Asn His Met Thr
 1 5 10 15

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Val Ala Tyr Gln Lys Ser Ala Val Ile Asn Cys Gly Gly Tyr Glu Asp
 20 25 30

Leu Gln Glu Asp Tyr Tyr Leu Trp Ile Lys Leu Val Ala Gln Gly Gln
 35 40 45

Arg Val Ala Asn Leu Pro Asp Ile Leu Val Tyr Ala Arg Val Gly Asn
 50 55 60

Gly Met Val Gly Arg Arg Arg Gly Leu Asn Gln Ala Lys Ala Glu Trp
 65 70 75 80

20

Arg Leu Phe Lys Leu Lys His His Leu Gly Ile Gln Gly Phe Leu Ser
 85 90 95

Gly Leu Phe Thr Phe Val Leu Arg Ser Gly Ala Arg Leu Leu Pro Thr
 100 105 110

Ser Leu Leu Lys Asn Ile Tyr Gln Thr Phe Leu Arg Lys
 115 120 125

<210> 69
 <211> 1005
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

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<220>
 <221> CDS
 <222> (1)..(1005)

<400> 69
 tcc ggt aaa tcc gtc ggc gta aat acc atg att tta agc ctg ctt tac 48
 Ser Gly Lys Ser Val Gly Val Asn Thr Met Ile Leu Ser Leu Leu Tyr
 1 5 10 15

cgc gtt aaa cgc gaa gaa gtg aaa ttc atc atg att gac cgc aaa gtg Arg Val Lys Pro Glu Glu Val Lys Phe Ile Met Ile Asp Pro Lys Val 20 25 30	96
gtg gaa ttg tct att tat aat gat att cgc cat ctt tta acg gaa gtg Val Glu Leu Ser Ile Tyr Asn Asp Ile Pro His Leu Leu Thr Glu Val 35 40 45	144
gtc acg gac atg aaa aaa gcg gca aac gcg ttg cgc tgg tgt gta gac Val Thr Asp Met Lys Lys Ala Ala Asn Ala Leu Arg Trp Cys Val Asp 50 55 60	192
gaa atg gag cgc cgt tat caa tta ttg tct gct ttg cgc gtg cgt aat Glu Met Glu Arg Arg Tyr Gln Leu Leu Ser Ala Leu Arg Val Arg Asn 65 70 75 80	240
att gaa gga ttt aac gag aaa gtt gat gaa tat gag gcc tta aat atg Ile Glu Gly Phe Asn Glu Lys Val Asp Glu Tyr Glu Ala Leu Asn Met 85 90 95	288
ccg att ccg aac cgc tta tgg aag cgc ggc gat tcc atg gat act ttg Pro Ile Pro Asn Pro Leu Trp Lys Pro Gly Asp Ser Met Asp Thr Leu 100 105 110	336
ccg cca cca tta gaa aaa ctg agt tac att gtg gtg att gtg gat gaa Pro Pro Pro Leu Glu Lys Leu Ser Tyr Ile Val Val Ile Val Asp Glu 115 120 125	384
ttc gcc gat ttg atg atg gtg gca ggc aaa cag gtg gaa gag ctt atc Phe Ala Asp Leu Met Met Val Ala Gly Lys Gln Val Glu Glu Leu Ile 130 135 140	432
gca cgt ttg cgc caa aaa gcc cgt gcg gtg ggg att cac tta att ttg Ala Arg Leu Ala Gln Lys Ala Arg Ala Val Gly Ile His Leu Ile Leu 145 150 155 160	480
gca acc caa cgc cct tcc gta gat gtg att acc ggt ttg att aaa gcg Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Leu Ile Lys Ala 165 170 175	528
aac gta ccg agt cga att gcg ttt act gtg gcg act aaa att gac tcg Asn Val Pro Ser Arg Ile Ala Phe Thr Val Ala Thr Lys Ile Asp Ser 180 185 190	576
cgt act att ctt gat gca ggc ggt gcg gaa tcc tta ttg ggt aaa ggt Arg Thr Ile Leu Asp Ala Gly Gly Ala Glu Ser Leu Leu Gly Lys Gly 195 200 205	624
gat atg ctg tat tcc cca cag ggt tct acc gaa tta gtc cgt att cac Asp Met Leu Tyr Ser Pro Gln Gly Ser Thr Glu Leu Val Arg Ile His 210 215 220	672
ggt gcc ttt atg act gat gac gaa gtc gtg cgc gtg gta gat gat tgg Gly Ala Phe Met Thr Asp Asp Glu Val Val Arg Val Val Asp Asp Trp 225 230 235 240	720
aaa gca cgc ggt aaa ccg aat tac att gat ggt att tta gag ggt gat Lys Ala Arg Gly Lys Pro Asn Tyr Ile Asp Gly Ile Leu Glu Gly Asp 245 250 255	768
gaa gaa gat gcc ggt gcg gaa cgc tta agt gag cgt ggc ggc gaa acc	816

10

20

30

Glu Glu Asp Ala Gly Ala Glu Arg Leu Ser Glu Arg Gly Gly Glu Thr
 260 265 270
 gac ggg ttg ttt gat gaa gtg gta gag ttt gtg gtc agc aca ggc acc 864
 Asp Gly Leu Phe Asp Glu Val Val Glu Phe Val Val Ser Thr Gly Thr
 275 280 285
 acg tct att tct gcg att caa cgc cgt ttc cga gta ggc ttt aac cgt 912
 Thr Ser Ile Ser Ala Ile Gln Arg Arg Phe Arg Val Gly Phe Asn Arg
 290 295 300
 gcc gcc aat att atg gat cag ctg gaa gag cag ggc att gtt tcg ccg 960
 Ala Ala Asn Ile Met Asp Gln Leu Glu Glu Gln Gly Ile Val Ser Pro
 305 310 315 320
 gtg caa aac ggt aaa cgt gaa gtg ttg gcg cgc agt gcg gat tat 1005
 Val Gln Asn Gly Lys Arg Glu Val Leu Ala Arg Ser Ala Asp Tyr
 325 330 335

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<210> 70
 <211> 335
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 70

Ser Gly Lys Ser Val Gly Val Asn Thr Met Ile Leu Ser Leu Leu Tyr
 1 5 10 15

Arg Val Lys Pro Glu Glu Val Lys Phe Ile Met Ile Asp Pro Lys Val
 20 25 30

20

Val Glu Leu Ser Ile Tyr Asn Asp Ile Pro His Leu Leu Thr Glu Val
 35 40 45

Val Thr Asp Met Lys Lys Ala Ala Asn Ala Leu Arg Trp Cys Val Asp
 50 55 60

Glu Met Glu Arg Arg Tyr Gln Leu Leu Ser Ala Leu Arg Val Arg Asn
 65 70 75 80

Ile Glu Gly Phe Asn Glu Lys Val Asp Glu Tyr Glu Ala Leu Asn Met
 85 90 95

30

Pro Ile Pro Asn Pro Leu Trp Lys Pro Gly Asp Ser Met Asp Thr Leu
 100 105 110

Pro Pro Pro Leu Glu Lys Leu Ser Tyr Ile Val Val Ile Val Asp Glu
 115 120 125

Phe Ala Asp Leu Met Met Val Ala Gly Lys Gln Val Glu Glu Leu Ile
 130 135 140

Ala Arg Leu Ala Gln Lys Ala Arg Ala Val Gly Ile His Leu Ile Leu
145 150 155 160

Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Leu Ile Lys Ala
165 170 175

Asn Val Pro Ser Arg Ile Ala Phe Thr Val Ala Thr Lys Ile Asp Ser
180 185 190

Arg Thr Ile Leu Asp Ala Gly Gly Ala Glu Ser Leu Leu Gly Lys Gly
195 200 205

10

Asp Met Leu Tyr Ser Pro Gln Gly Ser Thr Glu Leu Val Arg Ile His
210 215 220

Gly Ala Phe Met Thr Asp Asp Glu Val Val Arg Val Val Asp Asp Trp
225 230 235 240

Lys Ala Arg Gly Lys Pro Asn Tyr Ile Asp Gly Ile Leu Glu Gly Asp
245 250 255

Glu Glu Asp Ala Gly Ala Glu Arg Leu Ser Glu Arg Gly Gly Glu Thr
260 265 270

20

Asp Gly Leu Phe Asp Glu Val Val Glu Phe Val Val Ser Thr Gly Thr
275 280 285

Thr Ser Ile Ser Ala Ile Gln Arg Arg Phe Arg Val Gly Phe Asn Arg
290 295 300

Ala Ala Asn Ile Met Asp Gln Leu Glu Glu Gln Gly Ile Val Ser Pro
305 310 315 320

Val Gln Asn Gly Lys Arg Glu Val Leu Ala Arg Ser Ala Asp Tyr
325 330 335

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<210> 71
<211> 426
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(426)

<400> 71
atg tcg cct aat tat cct tat att aaa aca ttg gtt ata ttt cct ctg

48

Met Ser Pro Asn Tyr Pro Tyr Ile Lys Thr Leu Val Ile Phe Pro Leu
 1 5 10 15
 ctt gct caa ctt atc ggc acc atc atc agc att tgt gtg gat gac aat 96
 Leu Ala Gln Leu Ile Gly Thr Ile Ile Ser Ile Cys Val Asp Asp Asn
 20 25 30
 act gac agt ttt ctc ggc act gcc gac gtg atc ctt ttt agt ctg tta 144
 Thr Asp Ser Phe Leu Gly Thr Ala Asp Val Ile Leu Phe Ser Leu Leu
 35 40 45
 tcg act ttt atc gtg gca acc gtg ccc gct ttt ttg att gca ctg tgg 192
 Ser Thr Phe Ile Val Ala Thr Val Pro Ala Phe Leu Ile Ala Leu Trp
 50 55 60
 aca aaa att tat cgc tat acg cgc tat aac atg atg gcg att gtg tta 240
 Thr Lys Ile Tyr Arg Tyr Thr Arg Tyr Asn Met Met Ala Ile Val Leu
 65 70 75 80
 atc tgc ctg att atc gct ttt tgt tat ggc aac gta gct agc ttt atc 288
 Ile Ser Leu Ile Ile Ala Phe Cys Tyr Gly Asn Val Ala Ser Phe Ile
 85 90 95
 tac atg acg ttc tct cag cca aac atg acg ttt ggt att tgg ctg cgt 336
 Tyr Met Thr Phe Ser Gln Pro Asn Met Thr Phe Gly Ile Trp Leu Arg
 100 105 110
 agc ggc ggc att gat atg gcg ttt tta ctg agt ttc ggc atg gcg ttg 384
 Ser Gly Gly Ile Asp Met Ala Phe Leu Leu Ser Phe Gly Met Ala Leu
 115 120 125
 tat tca gtt ctt gtc ttg cct ttg ttg tta ccg caa acc aga 426
 Tyr Ser Val Leu Val Leu Pro Leu Leu Leu Pro Gln Thr Arg
 130 135 140

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<210> 72
 <211> 142
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

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<400> 72

Met Ser Pro Asn Tyr Pro Tyr Ile Lys Thr Leu Val Ile Phe Pro Leu
 1 5 10 15
 Leu Ala Gln Leu Ile Gly Thr Ile Ile Ser Ile Cys Val Asp Asp Asn
 20 25 30
 Thr Asp Ser Phe Leu Gly Thr Ala Asp Val Ile Leu Phe Ser Leu Leu
 35 40 45
 Ser Thr Phe Ile Val Ala Thr Val Pro Ala Phe Leu Ile Ala Leu Trp
 50 55 60
 Thr Lys Ile Tyr Arg Tyr Thr Arg Tyr Asn Met Met Ala Ile Val Leu
 65 70 75 80

30

Ile Ser Leu Ile Ile Ala Phe Cys Tyr Gly Asn Val Ala Ser Phe Ile
85 90 95

Tyr Met Thr Phe Ser Gln Pro Asn Met Thr Phe Gly Ile Trp Leu Arg
100 105 110

Ser Gly Gly Ile Asp Met Ala Phe Leu Leu Ser Phe Gly Met Ala Leu
115 120 125

Tyr Ser Val Leu Val Leu Pro Leu Leu Leu Pro Gln Thr Arg
130 135 140

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<210> 73
<211> 600
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(600)

<400> 73
gta tct caa caa aac cgc tgc gga ttc cac cac gga ttc aat aat gaa 48
Val Ser Gln Gln Asn Arg Cys Gly Phe His His Gly Phe Asn Asn Glu
1 5 10 15
aga gga aaa ata atc atg ttg gca aga atg tta ttt caa tcc tgg cgt 96
Arg Gly Lys Ile Ile Met Leu Ala Arg Met Leu Phe Gln Ser Trp Arg
20 25 30
tat gat tta aag cgc aaa ctc ctc gcc att gtg acc att ttc ctc gct 144
Tyr Asp Leu Lys Arg Lys Leu Leu Ala Ile Val Thr Ile Phe Leu Ala
35 40 45
gcc gga tta att tcc gcc ttg ctt gcg gtg tcc atc gac atc gcc gac 192
Ala Gly Leu Ile Ser Ala Leu Leu Ala Val Ser Ile Asp Ile Gly Asp
50 55 60
aaa atg gcg aaa gag ctt aaa tcc tac gcc gcc aat att ctg gtg gag 240
Lys Met Ala Lys Glu Leu Lys Ser Tyr Gly Ala Asn Ile Leu Val Glu
65 70 75 80
ccc gcc agc agc gcc att ttg cct gat gaa gtg agc cgt aat aat tct 288
Pro Ala Ser Ser Ala Ile Leu Pro Asp Glu Val Ser Arg Asn Asn Ser
85 90 95
ctc gcc acg caa gat ttt ttg gac gaa aaa gaa ctg ccg aac att aaa 336
Leu Ala Thr Gln Asp Phe Leu Asp Glu Lys Glu Leu Pro Asn Ile Lys
100 105 110
gac att ttt tgg cgt aac aat att gta gcc ttc gcc ccg tta ctc agc 384
Asp Ile Phe Trp Arg Asn Asn Ile Val Gly Phe Ala Pro Leu Leu Ser
115 120 125
gca caa gtc aaa gcc gat gga cca aac gcc aag gcg caa gac atc gac 432

20

30

Ala Gln Val Lys Ala Asp Gly Pro Asn Gly Lys Ala Gln Asp Ile Asp
 130 135 140
 att ctc ggc acg ttt ttt gat cat caa atc gcc gtg ccg gat gaa gac 480
 Ile Leu Gly Thr Phe Phe Asp His Gln Ile Ala Val Pro Asp Glu Asp
 145 150 155 160
 gat tac cac acc ggg caa aaa atc atc aac cct tat tgg cag gtg gaa 528
 Asp Tyr His Thr Gly Gln Lys Ile Ile Asn Pro Tyr Trp Gln Val Glu
 165 170 175
 ggc gaa tgg gtg aac gat gcc acc gat gat ttc agc gaa cag gtt cct 576
 Gly Glu Trp Val Asn Asp Ala Thr Asp Asp Phe Ser Glu Gln Val Pro
 180 185 190
 gcg tta ctc ggc gca caa ctt gcc 600
 Ala Leu Leu Gly Ala Gln Leu Ala
 195 200

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<210> 74
 <211> 200
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 74

Val Ser Gln Gln Asn Arg Cys Gly Phe His His Gly Phe Asn Asn Glu
 1 5 10 15

Arg Gly Lys Ile Ile Met Leu Ala Arg Met Leu Phe Gln Ser Trp Arg
 20 25 30

20

Tyr Asp Leu Lys Arg Lys Leu Leu Ala Ile Val Thr Ile Phe Leu Ala
 35 40 45

Ala Gly Leu Ile Ser Ala Leu Leu Ala Val Ser Ile Asp Ile Gly Asp
 50 55 60

Lys Met Ala Lys Glu Leu Lys Ser Tyr Gly Ala Asn Ile Leu Val Glu
 65 70 75 80

Pro Ala Ser Ser Ala Ile Leu Pro Asp Glu Val Ser Arg Asn Asn Ser
 85 90 95

30

Leu Ala Thr Gln Asp Phe Leu Asp Glu Lys Glu Leu Pro Asn Ile Lys
 100 105 110

Asp Ile Phe Trp Arg Asn Asn Ile Val Gly Phe Ala Pro Leu Leu Ser
 115 120 125

Ala Gln Val Lys Ala Asp Gly Pro Asn Gly Lys Ala Gln Asp Ile Asp
 130 135 140

Ile Leu Gly Thr Phe Phe Asp His Gln Ile Ala Val Pro Asp Glu Asp
145 150 155 160

Asp Tyr His Thr Gly Gln Lys Ile Ile Asn Pro Tyr Trp Gln Val Glu
165 170 175

Gly Glu Trp Val Asn Asp Ala Thr Asp Asp Phe Ser Glu Gln Val Pro
180 185 190

Ala Leu Leu Gly Ala Gln Leu Ala
195 200

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<210> 75
<211> 603
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(603)

<400> 75
gaa cct cga atc act gca ttg cac caa gaa aat caa ggc aaa gcc agt 48
Glu Pro Arg Ile Thr Ala Leu His Gln Glu Asn Gln Gly Lys Ala Ser
1 5 10 15
gca ttg aat cat ggt tta acg gtt gcc aag gga aaa tac gtt gcc tgt 96
Ala Leu Asn His Gly Leu Thr Val Ala Lys Gly Lys Tyr Val Ala Cys
20 25 30
atc gac ggt gat gcg gta ttg gat tac tac gcg ctg gac tac atg gtt 144
Ile Asp Gly Asp Ala Val Leu Asp Tyr Tyr Ala Leu Asp Tyr Met Val
35 40 45
caa gcc tta gag caa gat ccg aaa tat gct gct acc aca ggt aat ccg 192
Gln Ala Leu Glu Gln Asp Pro Lys Tyr Ala Ala Thr Thr Gly Asn Pro
50 55 60
cgt gta cgt aac cgt agt act att ttg ggg cgt tta cag gta tcc gag 240
Arg Val Arg Asn Arg Ser Thr Ile Leu Gly Arg Leu Gln Val Ser Glu
65 70 75 80
ttc agc tcc atc atc ggt cta att aag cgg gca caa ggt cta atg gcc 288
Phe Ser Ser Ile Ile Gly Leu Ile Lys Arg Ala Gln Gly Leu Met Gly
85 90 95
aca atc ttt acc gtt tcc ggc gtg tgt tgt tta ttc cgt aaa gat gtc 336
Thr Ile Phe Thr Val Ser Gly Val Cys Cys Leu Phe Arg Lys Asp Val
100 105 110
atg gaa gaa atc ggt gga tgg agt act aac atg atc acc gaa gac att 384
Met Glu Glu Ile Gly Gly Trp Ser Thr Asn Met Ile Thr Glu Asp Ile
115 120 125
gat att agc tgg aaa att caa att gcc ggt tac aac atc atg tac gaa 432

20

30

Asp Ile Ser Trp Lys Ile Gln Ile Ala Gly Tyr Asn Ile Met Tyr Glu
 130 135 140
 cca cgc gca ctc tgc tgg gtg ctt atg ccg gaa agc ata aaa ggg ctt 480
 Pro Arg Ala Leu Cys Trp Val Leu Met Pro Glu Ser Ile Lys Gly Leu
 145 150 155 160
 tat aaa cag cgt ttg cgt tgg gca cca ggc ggt gcg gaa act atc atg 528
 Tyr Lys Gln Arg Leu Arg Trp Ala Gln Gly Gly Ala Glu Thr Ile Met
 165 170 175
 aag tat ttt tcg aaa ata tgg cat tgg cgg aat cgt cgc ttg tgg cca 576
 Lys Tyr Phe Ser Lys Ile Trp His Trp Arg Asn Arg Arg Leu Trp Pro
 180 185 190
 atg tat att gag tat ttt gct acc gtt 603
 Met Tyr Ile Glu Tyr Phe Ala Thr Val
 195 200

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<210> 76
 <211> 201
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 76

Glu Pro Arg Ile Thr Ala Leu His Gln Glu Asn Gln Gly Lys Ala Ser
 1 5 10 15

Ala Leu Asn His Gly Leu Thr Val Ala Lys Gly Lys Tyr Val Ala Cys
 20 25 30

20

Ile Asp Gly Asp Ala Val Leu Asp Tyr Tyr Ala Leu Asp Tyr Met Val
 35 40 45

Gln Ala Leu Glu Gln Asp Pro Lys Tyr Ala Ala Thr Thr Gly Asn Pro
 50 55 60

Arg Val Arg Asn Arg Ser Thr Ile Leu Gly Arg Leu Gln Val Ser Glu
 65 70 75 80

Phe Ser Ser Ile Ile Gly Leu Ile Lys Arg Ala Gln Gly Leu Met Gly
 85 90 95

30

Thr Ile Phe Thr Val Ser Gly Val Cys Cys Leu Phe Arg Lys Asp Val
 100 105 110

Met Glu Glu Ile Gly Gly Trp Ser Thr Asn Met Ile Thr Glu Asp Ile
 115 120 125

Asp Ile Ser Trp Lys Ile Gln Ile Ala Gly Tyr Asn Ile Met Tyr Glu
 130 135 140

Pro Arg Ala Leu Cys Trp Val Leu Met Pro Glu Ser Ile Lys Gly Leu
145 150 155 160

Tyr Lys Gln Arg Leu Arg Trp Ala Gln Gly Glu Thr Ile Met
165 170 175

Lys Tyr Phe Ser Lys Ile Trp His Trp Arg Asn Arg Arg Leu Trp Pro
180 185 190

Met Tyr Ile Glu Tyr Phe Ala Thr Val
195 200

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<210> 77
<211> 759
<212> DNA
<213> Actinobacillus actinomycetamcomitans

<220>
<221> CDS
<222> (1)..(759)

<400> 77
atg cga tat ttg aaa caa aca aca att tca ctg tta att ttg acc gca 48
Met Arg Tyr Leu Lys Gln Thr Thr Ile Ser Leu Leu Ile Leu Thr Ala
1 5 10 15
ctt tcc tcc tcc ttt gcc aat cag cac aag gcg aca acg cat aaa gcg 96
Leu Ser Ser Ser Phe Ala Asn Gln His Lys Ala Thr Thr His Lys Ala
20 25 30
aat gtt gcc cat acg cac gcc aaa ccg gag caa cac cac gca gaa tta 144
Asn Val Ala His Thr His Ala Lys Pro Glu Gln His His Ala Glu Leu
35 40 45
gaa cgg cta aaa cag cgt gca act ttt ctg cag tta gaa agc ctg ctg 192
Glu Arg Leu Lys Gln Arg Ala Thr Phe Leu Gln Leu Glu Ser Leu Leu
50 55 60
aaa agt gcg gtc aaa aat aac ggc gtt ttt atc aac caa act gta ttc 240
Lys Ser Ala Val Lys Asn Asn Gly Val Phe Ile Asn Gln Thr Val Phe
65 70 75 80
ctg aaa ctg att gag gat ttg aaa ggc tat ccg ttg caa aca gat gcc 288
Leu Lys Leu Ile Glu Asp Leu Lys Gly Tyr Pro Leu Gln Thr Asp Ala
85 90 95
ata gcg gct tat ttc gac gcc tgc att aaa agc gta aat cac gac aca 336
Ile Ala Ala Tyr Phe Asp Ala Cys Ile Lys Ser Val Asn His Asp Thr
100 105 110
tcg aag gga gaa gtt aag gcg cta aaa cag gac att gag caa ttt atc 384
Ser Lys Gly Glu Val Lys Ala Leu Lys Gln Asp Ile Glu Gln Phe Ile
115 120 125
gaa aag cat ccg act cat ttt cta cgg gaa aaa ttg gaa caa aga ctt 432

20

30

Glu Lys His Pro Thr His Phe Leu Arg Glu Lys Leu Glu Gln Arg Leu
 130 135 140
 ttt acc tta ttt atc aac acg gaa gat ctt gaa ggc tta gtt ggt tac 480
 Phe Thr Leu Phe Ile Asn Thr Glu Asp Leu Glu Gly Leu Val Gly Tyr
 145 150 155 160
 gcg caa cgg gtt aaa cgg aaa ggg ttg gaa gcc caa ctt gca gtg ttg 528
 Ala Gln Arg Val Lys Pro Lys Gly Leu Glu Ala Gln Leu Ala Val Leu
 165 170 175
 aat gcc gaa tat caa ctg ggg cgc aaa cgt gcc gaa tct gat aaa aat 576
 Asn Ala Glu Tyr Gln Leu Gly Arg Lys Arg Ala Glu Ser Asp Lys Asn
 180 185 190
 ccg aat gcg aat gtg tcg aaa atc atc gcc cgt tat gag caa ctt tgg 624
 Pro Asn Ala Asn Val Ser Lys Ile Ile Ala Arg Tyr Glu Gln Leu Trp
 195 200 205
 tta aac aat agt gaa ctg cca aac gat gcg cag cta cgg gca aaa tgg 672
 Leu Asn Asn Ser Glu Leu Pro Asn Asp Ala Gln Leu Arg Ala Lys Trp
 210 215 220
 tat tcc gac gcc gcc aga atg gca gaa aaa gtg tat caa aaa gct gag 720
 Tyr Ser Asp Gly Gly Arg Met Ala Glu Lys Val Tyr Gln Lys Ala Glu
 225 230 235 240
 aat ctc ttt atc aaa aac aat gta aaa ggc ttg gaa ttg 759
 Asn Leu Phe Ile Lys Asn Asn Val Lys Gly Leu Glu Leu
 245 250

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<210> 78
 <211> 253
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 78

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Met Arg Tyr Leu Lys Gln Thr Thr Ile Ser Leu Leu Ile Leu Thr Ala
 1 5 10 15
 Leu Ser Ser Ser Phe Ala Asn Gln His Lys Ala Thr Thr His Lys Ala
 20 25 30
 Asn Val Ala His Thr His Ala Lys Pro Glu Gln His His Ala Glu Leu
 35 40 45
 Glu Arg Leu Lys Gln Arg Ala Thr Phe Leu Gln Leu Glu Ser Leu Leu
 50 55 60
 Lys Ser Ala Val Lys Asn Asn Gly Val Phe Ile Asn Gln Thr Val Phe
 65 70 75 80
 Leu Lys Leu Ile Glu Asp Leu Lys Gly Tyr Pro Leu Gln Thr Asp Ala
 85 90 95

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Ile Ala Ala Tyr Phe Asp Ala Cys Ile Lys Ser Val Asn His Asp Thr
100 105 110

Ser Lys Gly Glu Val Lys Ala Leu Lys Gln Asp Ile Glu Gln Phe Ile
115 120 125

Glu Lys His Pro Thr His Phe Leu Arg Glu Lys Leu Glu Gln Arg Leu
130 135 140

Phe Thr Leu Phe Ile Asn Thr Glu Asp Leu Glu Gly Leu Val Gly Tyr
145 150 155 160

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Ala Gln Arg Val Lys Pro Lys Gly Leu Glu Ala Gln Leu Ala Val Leu
165 170 175

Asn Ala Glu Tyr Gln Leu Gly Arg Lys Arg Ala Glu Ser Asp Lys Asn
180 185 190

Pro Asn Ala Asn Val Ser Lys Ile Ile Ala Arg Tyr Glu Gln Leu Trp
195 200 205

Leu Asn Asn Ser Glu Leu Pro Asn Asp Ala Gln Leu Arg Ala Lys Trp
210 215 220

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Tyr Ser Asp Gly Gly Arg Met Ala Glu Lys Val Tyr Gln Lys Ala Glu
225 230 235 240

Asn Leu Phe Ile Lys Asn Asn Val Lys Gly Leu Glu Leu
245 250

<210> 79
<211> 624
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(624)

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<400> 79
gtc ggt caa tgg acg gag aaa ggt aac caa acg gaa aat cgc gat aat 48
Val Gly Gln Trp Thr Glu Lys Gly Asn Gln Thr Glu Asn Arg Asp Asn
1 5 10 15
tcc gat ccg tcc ggt tta ggt tgt act ctt ggt tgg ggc ttt gca tgg 96
Ser Asp Pro Ser Gly Leu Gly Cys Thr Leu Gly Trp Gly Phe Ala Trp
20 25 30
cca gca aac cgc cgc gtg ctt tat agc cgc gcc tct ttg gat att aac 144

Pro Ala Asn Arg Arg Val Leu Tyr Ser Arg Ala Ser Leu Asp Ile Asn
 35 40 45

ggt aat cct tgg gat aaa cac cgt caa ctg atc aaa tgg aac ggt aaa 192
 Gly Asn Pro Trp Asp Lys His Arg Gln Leu Ile Lys Trp Asn Gly Lys
 50 55 60

aac tgg aac tgg ttt gat att gcc gac tac ggc act caa cca cca ggt 240
 Asn Trp Asn Trp Phe Asp Ile Ala Asp Tyr Gly Thr Gln Pro Pro Gly
 65 70 75 80

tcc gat acc aga cca ttt atg atg tca gcc gaa ggt gtt gga cgc tta 288
 Ser Asp Thr Arg Pro Phe Met Met Ser Ala Glu Gly Val Gly Arg Leu
 85 90 95

ttt gcc gtt gat aaa att aat agc gga ccg ttc ccg gaa cac tat gaa 336
 Phe Ala Val Asp Lys Ile Asn Ser Gly Pro Phe Pro Glu His Tyr Glu
 100 105 110

ccg att gaa agt ccg att gat acg aat ccg ctt cat ccg aat gtg gta 384
 Pro Ile Glu Ser Pro Ile Asp Thr Asn Pro Leu His Pro Asn Val Val
 115 120 125

tca gat ccg acg gtg cgt att tac aaa gaa gat cgc gag ttt atc ggc 432
 Ser Asp Pro Thr Val Arg Ile Tyr Lys Glu Asp Arg Glu Phe Ile Gly
 130 135 140

tca aat aaa gaa tat ccg ttt gtg gca aca act tat cgt cta acc gaa 480
 Ser Asn Lys Glu Tyr Pro Phe Val Ala Thr Thr Tyr Arg Leu Thr Glu
 145 150 155 160

cat ttc cac agt tgg acc gcg caa tct gcc att aac atc atc gca caa 528
 His Phe His Ser Trp Thr Ala Gln Ser Ala Ile Asn Ile Ile Ala Gln
 165 170 175

ccg caa caa ttt gtg gaa atc ggt gaa aaa ttg gca gaa gaa aaa ggt 576
 Pro Gln Gln Phe Val Glu Ile Gly Glu Lys Leu Ala Glu Glu Lys Gly
 180 185 190

atc caa aaa ggc gat atg gta cgt att acc tcc aaa ccg ggc tat att 624
 Ile Gln Lys Gly Asp Met Val Arg Ile Thr Ser Lys Arg Gly Tyr Ile
 195 200 205

<210> 80
 <211> 208
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 80

Val Gly Gln Trp Thr Glu Lys Gly Asn Gln Thr Glu Asn Arg Asp Asn
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Ser Asp Pro Ser Gly Leu Gly Cys Thr Leu Gly Trp Gly Phe Ala Trp
 20 25 30

Pro Ala Asn Arg Arg Val Leu Tyr Ser Arg Ala Ser Leu Asp Ile Asn
 35 40 45

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Gly Asn Pro Trp Asp Lys His Arg Gln Leu Ile Lys Trp Asn Gly Lys
50 55 60

Asn Trp Asn Trp Phe Asp Ile Ala Asp Tyr Gly Thr Gln Pro Pro Gly
65 70 75 80

Ser Asp Thr Arg Pro Phe Met Met Ser Ala Glu Gly Val Gly Arg Leu
85 90 95

Phe Ala Val Asp Lys Ile Asn Ser Gly Pro Phe Pro Glu His Tyr Glu
100 105 110

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Pro Ile Glu Ser Pro Ile Asp Thr Asn Pro Leu His Pro Asn Val Val
115 120 125

Ser Asp Pro Thr Val Arg Ile Tyr Lys Glu Asp Arg Glu Phe Ile Gly
130 135 140

Ser Asn Lys Glu Tyr Pro Phe Val Ala Thr Thr Tyr Arg Leu Thr Glu
145 150 155 160

His Phe His Ser Trp Thr Ala Gln Ser Ala Ile Asn Ile Ile Ala Gln
165 170 175

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Pro Gln Gln Phe Val Glu Ile Gly Glu Lys Leu Ala Glu Glu Lys Gly
180 185 190

Ile Gln Lys Gly Asp Met Val Arg Ile Thr Ser Lys Arg Gly Tyr Ile
195 200 205

<210> 81
<211> 534
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(534)

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ile pro gly leu ile glu gly ala ser glu gly ala gly leu gly ile
1 5 10 15
cgc ttc ctg aaa cac ttg gaa cgt tgc cgc gtg ttg att cat ttg gtg 96
arg phe leu lys his leu glu arg cys arg val leu ile his leu val
20 25 30
gat atc aac cca att gat gat tcc aac ccg gcg gat aac gtg gcg att 144

Asp Ile Asn Pro Ile Asp Asp Ser Asn Pro Ala Asp Asn Val Ala Ile
 35 40 45
 atc gaa tcg gaa ttg ttc caa tac agc gag tcc ttg gcg gaa aaa ccg 192
 Ile Glu Ser Glu Leu Phe Gln Tyr Ser Glu Ser Leu Ala Glu Lys Pro
 50 55 60
 cgc tgg ctg gtg ttc aac aaa atc gat acg ctc agt gat gaa gaa gcc 240
 Arg Trp Leu Val Phe Asn Lys Ile Asp Thr Leu Ser Asp Glu Glu Ala
 65 70 75 80
 cat gcg cga gcg aaa gag atc acc gaa cgt ctg ggc cgg gag gaa ggt 288
 His Ala Arg Ala Lys Glu Ile Thr Glu Arg Leu Gly Arg Glu Glu Gly
 85 90 95
 tat tat tta att tcc gcc gcc acc ggt aaa aac gcc ccg caa ctg tgc 336
 Tyr Tyr Leu Ile Ser Ala Ala Thr Gly Lys Asn Ala Pro Gln Leu Cys
 100 105 110
 cgc gat att atg gac ttc ctg gaa gcc cac ccg cgc aaa aca gaa aaa 384
 Arg Asp Ile Met Asp Phe Leu Glu Ala His Pro Arg Lys Thr Glu Lys
 115 120 125
 acg ccg gta gaa aat gaa gaa gtc aaa ttc aaa tgg gaa gat tat cat 432
 Thr Pro Val Glu Asn Glu Glu Val Lys Phe Lys Trp Glu Asp Tyr His
 130 135 140
 cag gag caa ttg gaa aat gcc gat gtt gat gat gaa gag gat aat gac 480
 Gln Glu Gln Leu Glu Asn Ala Asp Val Asp Asp Glu Glu Asp Asn Asp
 145 150 155 160
 tgg gat gac tgg tcg gaa gac gat gaa gaa ggc gtg gaa att atc tat 528
 Trp Asp Asp Trp Ser Glu Asp Asp Glu Glu Gly Val Glu Ile Ile Tyr
 165 170 175
 aag cct 534
 Lys Pro

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<210> 82
 <211> 178
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 82

Ile Pro Gly Leu Ile Glu Gly Ala Ser Glu Gly Ala Gly Leu Gly Ile
 1 5 10 15
 Arg Phe Leu Lys His Leu Glu Arg Cys Arg Val Leu Ile His Leu Val
 20 25 30
 Asp Ile Asn Pro Ile Asp Asp Ser Asn Pro Ala Asp Asn Val Ala Ile
 35 40 45
 Ile Glu Ser Glu Leu Phe Gln Tyr Ser Glu Ser Leu Ala Glu Lys Pro
 50 55 60

30

Arg Trp Leu Val Phe Asn Lys Ile Asp Thr Leu Ser Asp Glu Glu Ala
65 70 75 80

His Ala Arg Ala Lys Glu Ile Thr Glu Arg Leu Gly Arg Glu Glu Gly
85 90 95

Tyr Tyr Leu Ile Ser Ala Ala Thr Gly Lys Asn Ala Pro Gln Leu Cys
100 105 110

Arg Asp Ile Met Asp Phe Leu Glu Ala His Pro Arg Lys Thr Glu Lys
115 120 125

10

Thr Pro Val Glu Asn Glu Glu Val Lys Phe Lys Trp Glu Asp Tyr His
130 135 140

Gln Glu Gln Leu Glu Asn Ala Asp Val Asp Asp Glu Glu Asp Asn Asp
145 150 155 160

Trp Asp Asp Trp Ser Glu Asp Asp Glu Glu Gly Val Glu Ile Ile Tyr
165 170 175

Lys Pro

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<210> 83
<211> 372
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(372)

<400> 83
atg tta acg gaa agt gcg gtc gtt att gag tac gaa tcc ggc aga gcc 48
Met Leu Thr Glu Ser Ala Val Val Ile Glu Tyr Glu Ser Gly Arg Ala
1 5 10 15
aaa gtg aaa tgc caa tca caa agc gca tgc ggc gct tgc gcg gca aaa 96
Lys Val Lys Cys Gln Ser Gln Ser Ala Cys Gly Ala Cys Ala Ala Lys
20 25 30
ccg gcg tgc ggt aat tct gcc ttg tcg gaa tta gcc agc agc ggc gcg 144
Pro Ala Cys Gly Asn Ser Ala Leu Ser Glu Leu Ala Ser Ser Gly Ala
35 40 45
cgc ggc gaa cat att ttc acc atc gag acc att acg cca ctg aaa atc 192
Arg Gly Glu His Ile Phe Thr Ile Glu Thr Ile Thr Pro Leu Lys Ile
50 55 60
ggg caa cgg gtg gaa atc ggt ttg tcc gaa cgt tcc tta atc aaa tcc 240

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Gly Gln Arg Val Glu Ile Gly Leu Ser Glu Arg Ser Leu Ile Lys Ser
 65 70 75 80
 gcc ttg ctc atg tat tgc gtg ccg cta ttt act tta tta ttc agc acg 288
 Ala Leu Leu Met Tyr Cys Val Pro Leu Phe Thr Leu Leu Phe Ser Thr
 85 90 95
 tta tta ttt gat tcg ctg ttt gcc cat gag ctc gtc agc gtc ttt ttt 336
 Leu Leu Phe Asp Ser Leu Phe Ala His Glu Leu Val Ser Val Phe Phe
 100 105 110
 atc ttc att tcc act gca ctt tct ttc ctt ggt gtg 372
 Ile Phe Ile Ser Thr Ala Leu Ser Phe Leu Gly Val
 115 120

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<210> 84
 <211> 124
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 84

Met Leu Thr Glu Ser Ala Val Val Ile Glu Tyr Glu Ser Gly Arg Ala
 1 5 10 15

Lys Val Lys Cys Gln Ser Gln Ser Ala Cys Gly Ala Cys Ala Ala Lys
 20 25 30

Pro Ala Cys Gly Asn Ser Ala Leu Ser Glu Leu Ala Ser Ser Gly Ala
 35 40 45

20

Arg Gly Glu His Ile Phe Thr Ile Glu Thr Ile Thr Pro Leu Lys Ile
 50 55 60

Gly Gln Arg Val Glu Ile Gly Leu Ser Glu Arg Ser Leu Ile Lys Ser
 65 70 75 80

Ala Leu Leu Met Tyr Cys Val Pro Leu Phe Thr Leu Leu Phe Ser Thr
 85 90 95

Leu Leu Phe Asp Ser Leu Phe Ala His Glu Leu Val Ser Val Phe Phe
 100 105 110

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Ile Phe Ile Ser Thr Ala Leu Ser Phe Leu Gly Val
 115 120

<210> 85
 <211> 629
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans
 <220>

<221> CDS

<222> (1)..(627)

<400> 85

att tct tcc ggt tcc tta ttg ctt gcc gtg ctt tat aaa cgc aat cgc 48
 Ile Ser Ser Gly Ser Leu Leu Leu Ala Val Leu Tyr Lys Arg Asn Arg
 1 5 10 15

aaa cgc gaa aaa aca agc gaa aac tgg att att cgc agt gct gcg atc 96
 Lys Pro Glu Lys Thr Ser Glu Asn Trp Ile Ile Arg Ser Ala Ala Ile
 20 25 30

tta gcg cct ggc acg gtg att atc ggt tta ttg ctg ttg att ttc cac 144
 Leu Ala Pro Gly Thr Val Ile Ile Gly Leu Leu Leu Ile Phe His
 35 40 45

ttg gcg cgc cct tgg acg ttc tgg tat ttg atg ttt aac tac cag ttc 192
 Leu Ala Arg Pro Trp Thr Phe Trp Tyr Leu Met Phe Asn Tyr Gln Phe
 50 55 60

aat tcc gtg atg tcc atg ggg gta ctg tta ttc caa atc tat atg gcg 240
 Asn Ser Val Met Ser Met Gly Val Leu Leu Phe Gln Ile Tyr Met Ala
 65 70 75 80

gcg gtt ctc ctc tgg att gcg att ctc ttt aaa aat gaa ctt gcc gcc 288
 Ala Val Leu Leu Trp Ile Ala Ile Leu Phe Lys Asn Glu Leu Ala Ala
 85 90 95

ttg ctc gat aga ttt tta cgc aaa tta aaa ttt atc gtg aaa tgg att 336
 Leu Leu Asp Arg Phe Leu Pro Lys Leu Lys Phe Ile Val Lys Trp Ile
 100 105 110

ttc gcc tgt gaa cgc att acc aac cgc ttg gaa ctg ttc ctg ttg ttc 384
 Phe Ala Cys Glu Arg Ile Thr Asn Pro Leu Glu Leu Phe Leu Leu Phe
 115 120 125

ctt gcg gtg ttg cta ggc gct tat acc ggt ttc tta ttg tcg gcg tta 432
 Leu Ala Val Leu Leu Gly Ala Tyr Thr Gly Phe Leu Leu Ser Ala Leu
 130 135 140

atc agc tac cgc atg cta aac aat ccc gta ttg cgc gca tta ttc ctc 480
 Ile Ser Tyr Pro Met Leu Asn Asn Pro Val Leu Pro Ala Leu Phe Leu
 145 150 155 160

gct tcg ggc acg tct tcc ggt atc gcg gcg gta ttc tta acc atc ctg 528
 Ala Ser Gly Thr Ser Ser Gly Ile Ala Ala Val Phe Leu Thr Ile Leu
 165 170 175

att gtg ggc aaa tta aaa ggg cat tcc gac gaa gtg aat ttc atg cat 576
 Ile Val Gly Lys Leu Lys Gly His Ser Asp Glu Val Asn Phe Met His
 180 185 190

aaa ttt gaa gtg cgc atc atg ctc gcc gaa ctc ttt tgc atc gcc tgc 624
 Lys Phe Glu Val Pro Ile Met Leu Ala Glu Leu Phe Cys Ile Gly Cys
 195 200 205

ttc tt 629
 Phe

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<210> 86
 <211> 209
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 86

Ile Ser Ser Gly Ser Leu Leu Leu Ala Val Leu Tyr Lys Arg Asn Arg
 1 5 10 15

Lys Pro Glu Lys Thr Ser Glu Asn Trp Ile Ile Arg Ser Ala Ala Ile
 20 25 30

Leu Ala Pro Gly Thr Val Ile Ile Gly Leu Leu Leu Leu Ile Phe His
 35 40 45

Leu Ala Arg Pro Trp Thr Phe Trp Tyr Leu Met Phe Asn Tyr Gln Phe
 50 55 60

Asn Ser Val Met Ser Met Gly Val Leu Leu Phe Gln Ile Tyr Met Ala
 65 70 75 80

Ala Val Leu Leu Trp Ile Ala Ile Leu Phe Lys Asn Glu Leu Ala Ala
 85 90 95

Leu Leu Asp Arg Phe Leu Pro Lys Leu Lys Phe Ile Val Lys Trp Ile
 100 105 110

Phe Ala Cys Glu Arg Ile Thr Asn Pro Leu Glu Leu Phe Leu Leu Phe
 115 120 125

Leu Ala Val Leu Leu Gly Ala Tyr Thr Gly Phe Leu Leu Ser Ala Leu
 130 135 140

Ile Ser Tyr Pro Met Leu Asn Asn Pro Val Leu Pro Ala Leu Phe Leu
 145 150 155 160

Ala Ser Gly Thr Ser Ser Gly Ile Ala Ala Val Phe Leu Thr Ile Leu
 165 170 175

Ile Val Gly Lys Leu Lys Gly His Ser Asp Glu Val Asn Phe Met His
 180 185 190

Lys Phe Glu Val Pro Ile Met Leu Ala Glu Leu Phe Cys Ile Gly Cys
 195 200 205

Phe

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<210> 87
 <211> 266
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(264)

<400> 87
 tgg gat gcc att gag aaa tgt att cag gaa tgg caa ccg gcg cgt att 48
 Trp Asp Ala Ile Glu Lys Cys Ile Gln Glu Trp Gln Pro Ala Arg Ile
 1 5 10 15
 gtg gtc ggt ttg cca ctg aat atg gat ggt acg gaa cag ccc tta acg 96
 Val Val Gly Leu Pro Leu Asn Met Asp Gly Thr Glu Gln Pro Leu Thr
 20 25 30
 ttg cgt gcc aaa aag ttt gct aag cgt ttg cac gga cgt ttt aac gtg 144
 Leu Arg Ala Lys Lys Phe Ala Lys Arg Leu His Gly Arg Phe Asn Val
 35 40 45
 ccg gtg gat tta cag gac gaa cgt ctt acc acc acc gaa gcg cgt agc 192
 Pro Val Asp Leu Gln Asp Glu Arg Leu Thr Thr Thr Glu Ala Arg Ser
 50 55 60
 gaa att ttc agt cgt ggt ggt tat cgc gcc tta aat aaa agc aaa gtg 240
 Glu Ile Phe Ser Arg Gly Gly Tyr Arg Ala Leu Asn Lys Ser Lys Val
 65 70 75 80
 gac ggc att tcc gcc tgt ttg att tt 266
 Asp Gly Ile Ser Ala Cys Leu Ile
 85

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<210> 88
 <211> 88
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 88

Trp Asp Ala Ile Glu Lys Cys Ile Gln Glu Trp Gln Pro Ala Arg Ile
 1 5 10 15
 Val Val Gly Leu Pro Leu Asn Met Asp Gly Thr Glu Gln Pro Leu Thr
 20 25 30
 Leu Arg Ala Lys Lys Phe Ala Lys Arg Leu His Gly Arg Phe Asn Val
 35 40 45
 Pro Val Asp Leu Gln Asp Glu Arg Leu Thr Thr Thr Glu Ala Arg Ser
 50 55 60
 Glu Ile Phe Ser Arg Gly Gly Tyr Arg Ala Leu Asn Lys Ser Lys Val

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65	70	75	80
Asp Gly Ile Ser Ala Cys Leu Ile			
85			
<210> 89			
<211> 567			
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<213> Actinobacillus actinomycetemcomitans			
<220>			
<221> CDS			
<222> (1)..(567)			
<400> 89			
caa caa gta aaa gcg ccg gga gaa gcc aaa tcc gac gta tgg caa ttg			48
Gln Gln Val Lys Ala Pro Gly Glu Ala Lys Ser Asp Val Trp Gln Leu			
1 5 10 15			
gta gaa ttc tcc aaa tat ttc acc acc gat gaa atg tgg ccg gcg gaa			96
Val Glu Phe Ser Lys Tyr Phe Thr Thr Asp Glu Met Trp Pro Ala Glu			
20 25 30			
att ctg gac aaa aat ccg gaa tac aaa ggc aaa acc tta tat gac gtg			144
Ile Leu Asp Lys Asn Pro Glu Tyr Lys Gly Lys Thr Leu Tyr Asp Val			
35 40 45			
tta tac cgc aac ggt caa gta gat aaa ttc ccg tta agc gaa ttg gcg			192
Leu Tyr Arg Asn Gly Gln Val Asp Lys Phe Pro Leu Ser Glu Leu Ala			
50 55 60			
gaa gga caa ttg aat gat gag tcc tat cac ttc ggt ttc tac ttg caa			240
Glu Gly Gln Leu Asn Asp Glu Ser Tyr His Phe Gly Phe Tyr Leu Gln			
65 70 75 80			
aaa ggc tta ttt gag gaa tac gcc tcc ttc ggt cgc ggt cac gga cat			288
Lys Gly Leu Phe Glu Glu Tyr Ala Ser Phe Gly Arg Gly His Gly His			
85 90 95			
gac ttg gca tgc ttc gat act tac cac aaa gca cgc ggt tta cgc tgg			336
Asp Leu Ala Ser Phe Asp Thr Tyr His Lys Ala Arg Gly Leu Arg Trp			
100 105 110			
ccg gtg gtg gac ggc aaa gaa acc tta tgg cgt tat cgc gaa ggc tac			384
Pro Val Val Asp Gly Lys Glu Thr Leu Trp Arg Tyr Arg Glu Gly Tyr			
115 120 125			
gac ccg tat gtc aaa gaa ggg gaa ggt gtg gcg ttc tac ggc tat ccg			432
Asp Pro Tyr Val Lys Glu Gly Glu Gly Val Ala Phe Tyr Gly Tyr Pro			
130 135 140			
gat aaa aaa gcg att att ctt gcc gtg cct tat gag ccg cct gcg gaa			480
Asp Lys Lys Ala Ile Ile Leu Ala Val Pro Tyr Glu Pro Pro Ala Glu			
145 150 155 160			
tca ccg gac gaa gaa tac gat ttg tgg tta tgt acc ggt cgc gtg ttg			528
Ser Pro Asp Glu Glu Tyr Asp Leu Trp Leu Cys Thr Gly Arg Val Leu			
165 170 175			

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gaa cac tgg cac acc ggc acc atg acc cgt cgt gta cca 567
 Glu His Trp His Thr Gly Thr Met Thr Arg Arg Val Pro
 180 185

<210> 90
 <211> 189
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 90

Gln Gln Val Lys Ala Pro Gly Glu Ala Lys Ser Asp Val Trp Gln Leu
 1 5 10 15

Val Glu Phe Ser Lys Tyr Phe Thr Thr Asp Glu Met Trp Pro Ala Glu
 20 25 30

Ile Leu Asp Lys Asn Pro Glu Tyr Lys Gly Lys Thr Leu Tyr Asp Val
 35 40 45

Leu Tyr Arg Asn Gly Gln Val Asp Lys Phe Pro Leu Ser Glu Leu Ala
 50 55 60

Glu Gly Gln Leu Asn Asp Glu Ser Tyr His Phe Gly Phe Tyr Leu Gln
 65 70 75 80

Lys Gly Leu Phe Glu Glu Tyr Ala Ser Phe Gly Arg Gly His Gly His
 85 90 95

Asp Leu Ala Ser Phe Asp Thr Tyr His Lys Ala Arg Gly Leu Arg Trp
 100 105 110

Pro Val Val Asp Gly Lys Glu Thr Leu Trp Arg Tyr Arg Glu Gly Tyr
 115 120 125

Asp Pro Tyr Val Lys Glu Gly Glu Gly Val Ala Phe Tyr Gly Tyr Pro
 130 135 140

Asp Lys Lys Ala Ile Ile Leu Ala Val Pro Tyr Glu Pro Pro Ala Glu
 145 150 155 160

Ser Pro Asp Glu Glu Tyr Asp Leu Trp Leu Cys Thr Gly Arg Val Leu
 165 170 175

Glu His Trp His Thr Gly Thr Met Thr Arg Arg Val Pro
 180 185

<210> 91

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<211> 563
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(561)

<400> 91
 ccg aaa cct ttc tat ttt tcc gct gaa aaa gat ggc att ggt gta gaa 48
 Pro Lys Pro Phe Tyr Phe Ser Ala Glu Lys Asp Gly Ile Gly Val Glu
 1 5 10 15
 att gcg ttg caa tgg aac gac ggt tac gcg gaa aac att tat tgt ttc 96
 Ile Ala Leu Gln Trp Asn Asp Gly Tyr Ala Glu Asn Ile Tyr Cys Phe
 20 25 30
 acc aac aac att ccg caa cgg gac ggc ggt acg cac tta gcc ggt ttc 144
 Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ala Gly Phe
 35 40 45
 cgt ggc gca atg acc cgc acc ttg aac aac tac atg gaa aac gaa ggc 192
 Arg Gly Ala Met Thr Arg Thr Leu Asn Asn Tyr Met Glu Asn Glu Gly
 50 55 60
 tac acc aag aaa tcc aaa gtg gcg act tcc ggt gat gat gcc cgt gaa 240
 Tyr Thr Lys Lys Ser Lys Val Ala Thr Ser Gly Asp Asp Ala Arg Glu
 65 70 75 80
 ggc ttg gtg gcg gtg att tcc gtg aaa gta ccg gat ccg aaa ttc tct 288
 Gly Leu Val Ala Val Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser
 85 90 95
 tct caa aca aaa gac aaa ctg gtt tcc tcc gaa gtg aaa agt gcg gtg 336
 Ser Gln Thr Lys Asp Lys Leu Val Ser Ser Glu Val Lys Ser Ala Val
 100 105 110
 gaa tcc ctg atg aac gaa tat tta caa acc tat ttg ttg gaa aac ccg 384
 Glu Ser Leu Met Asn Glu Tyr Leu Gln Thr Tyr Leu Leu Glu Asn Pro
 115 120 125
 aac gat gta aaa atc atc gtg acc aaa att att gat gcc gcg cgt gcc 432
 Asn Asp Val Lys Ile Ile Val Thr Lys Ile Ile Asp Ala Ala Arg Ala
 130 135 140
 cgt gaa gcc gcc cgc aaa gcc cgc gaa atg acc cgt cgt aaa ggc gcg 480
 Arg Glu Ala Ala Arg Lys Ala Arg Glu Met Thr Arg Arg Lys Gly Ala
 145 150 155 160
 ttg gat tta gcc gcc ttg ccg gcc aaa ttg gcg gat tgt cag gaa cgc 528
 Leu Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Gln Glu Arg
 165 170 175
 gat ccg gcg tta tcc gag ctt tac atc gtg gag gg 563
 Asp Pro Ala Leu Ser Glu Leu Tyr Ile Val Glu
 180 185

<210> 92
 <211> 187
 <212> PRT

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<213> Actinobacillus actinomycetemcomitans

<400> 92

Pro Lys Pro Phe Tyr Phe Ser Ala Glu Lys Asp Gly Ile Gly Val Glu
1 5 10 15

Ile Ala Leu Gln Trp Asn Asp Gly Tyr Ala Glu Asn Ile Tyr Cys Phe
20 25 30

Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ala Gly Phe
35 40 45

Arg Gly Ala Met Thr Arg Thr Leu Asn Asn Tyr Met Glu Asn Glu Gly
50 55 60

Tyr Thr Lys Lys Ser Lys Val Ala Thr Ser Gly Asp Asp Ala Arg Glu
65 70 75 80

Gly Leu Val Ala Val Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser
85 90 95

Ser Gln Thr Lys Asp Lys Leu Val Ser Ser Glu Val Lys Ser Ala Val
100 105 110

Glu Ser Leu Met Asn Glu Tyr Leu Gln Thr Tyr Leu Leu Glu Asn Pro
115 120 125

Asn Asp Val Lys Ile Ile Val Thr Lys Ile Ile Asp Ala Ala Arg Ala
130 135 140

Arg Glu Ala Ala Arg Lys Ala Arg Glu Met Thr Arg Arg Lys Gly Ala
145 150 155 160

Leu Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Gln Glu Arg
165 170 175

Asp Pro Ala Leu Ser Glu Leu Tyr Ile Val Glu
180 185

<210> 93

<211> 627

<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> (1)..(627)

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<400> 93
 aaa cag caa tta gcc gct gca ctt gcc cga caa gaa caa aaa caa att 48
 Lys Gln Gln Leu Ala Ala Ala Leu Ala Arg Gln Glu Gln Lys Gln Ile
 1 5 10 15
 atc gtt tta caa aaa aag tta acg tct ttg tct tcc cta tcc cca caa 96
 Ile Val Leu Gln Lys Lys Leu Thr Ser Leu Ser Ser Leu Ser Pro Gln
 20 25 30
 cgt ctt gcg caa caa att cgg act acc gaa aaa att ctg acc cgt att 144
 Arg Leu Ala Gln Gln Ile Arg Thr Thr Glu Lys Ile Leu Thr Arg Ile
 35 40 45
 ttt aaa aca gag aaa aat ctg aca ccc aaa ttt att gat tac ctg tat 192
 Phe Lys Thr Glu Lys Asn Leu Thr Pro Lys Phe Ile Asp Tyr Leu Tyr
 50 55 60
 ttt gag cca att gaa acg gct gat gac acc tta atg cag gaa atg aaa 240
 Phe Glu Pro Ile Glu Thr Ala Asp Asp Thr Leu Met Gln Glu Met Lys
 65 70 75 80
 aaa aat ctt ttg atc tct ttc ttg gca aat gaa cgc gct caa atc tat 288
 Lys Asn Leu Leu Ile Ser Phe Leu Ala Asn Glu Arg Ala Gln Ile Tyr
 85 90 95
 att aaa gac atg cca aac gct aat caa ttt gtt cag ctt tta aca gaa 336
 Ile Lys Asp Met Pro Asn Ala Asn Gln Phe Val Gln Leu Leu Thr Glu
 100 105 110
 aaa gga gca aag act acg caa ata tcc gta ttg gca gaa oct gct aaa 384
 Lys Gly Ala Lys Thr Thr Gln Ile Ser Val Leu Ala Glu Pro Ala Lys
 115 120 125
 acc att ttc cag cga atc cgc gaa caa atg tac caa gat ttt oct aat 432
 Thr Ile Phe Gln Arg Ile Arg Glu Gln Met Tyr Gln Asp Phe Pro Asn
 130 135 140
 aaa aaa cag ttt act atc act gaa aat cga gta agt gtt att gcc oct 480
 Lys Lys Gln Phe Thr Ile Thr Glu Asn Arg Val Ser Val Ile Ala Pro
 145 150 155 160
 tcc tcc gtt att aag cca cgc ctt gcc ttg gca gct gca att ttt gat 528
 Ser Ser Val Ile Lys Pro Arg Leu Ala Leu Ala Ala Ala Ile Phe Asp
 165 170 175
 cag cag ttt aaa ggg gtt gaa gtt gat gat ttt tct tac ttg gat caa 576
 Gln Gln Phe Lys Gly Val Glu Val Asp Asp Phe Ser Tyr Leu Asp Gln
 180 185 190
 ccg cgt gaa aat ttg caa cac aat aat gat aca acc cgt tat aaa acc 624
 Pro Arg Glu Asn Leu Gln His Asn Asn Asp Thr Thr Arg Tyr Lys Thr
 195 200 205
 ttt 627
 Phe

<210> 94
 <211> 209
 <212> PRT

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<213> Actinobacillus actinomycetemcomitans

<400> 94

Lys Gln Gln Leu Ala Ala Ala Leu Ala Arg Gln Glu Gln Lys Gln Ile
1 5 10 15

Ile Val Leu Gln Lys Lys Leu Thr Ser Leu Ser Ser Leu Ser Pro Gln
20 25 30

Arg Leu Ala Gln Gln Ile Arg Thr Thr Glu Lys Ile Leu Thr Arg Ile
35 40 45

Phe Lys Thr Glu Lys Asn Leu Thr Pro Lys Phe Ile Asp Tyr Leu Tyr
50 55 60

Phe Glu Pro Ile Glu Thr Ala Asp Asp Thr Leu Met Gln Glu Met Lys
65 70 75 80

Lys Asn Leu Leu Ile Ser Phe Leu Ala Asn Glu Arg Ala Gln Ile Tyr
85 90 95

Ile Lys Asp Met Pro Asn Ala Asn Gln Phe Val Gln Leu Leu Thr Glu
100 105 110

Lys Gly Ala Lys Thr Thr Gln Ile Ser Val Leu Ala Glu Pro Ala Lys
115 120 125

Thr Ile Phe Gln Arg Ile Arg Glu Gln Met Tyr Gln Asp Phe Pro Asn
130 135 140

Lys Lys Gln Phe Thr Ile Thr Glu Asn Arg Val Ser Val Ile Ala Pro
145 150 155 160

Ser Ser Val Ile Lys Pro Arg Leu Ala Leu Ala Ala Ala Ile Phe Asp
165 170 175

Gln Gln Phe Lys Gly Val Glu Val Asp Asp Phe Ser Tyr Leu Asp Gln
180 185 190

Pro Arg Glu Asn Leu Gln His Asn Asn Asp Thr Thr Arg Tyr Lys Thr
195 200 205

Phe

<210> 95

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<211> 270
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(270)

<400> 95
 tct gac aat acg caa tat ttt tgc ccg gcg gga tta agc gag gag cgt 48
 Ser Asp Asn Thr Gln Tyr Phe Cys Pro Ala Gly Leu Ser Glu Glu Arg
 1 5 10 15
 gaa cag gag ctc cgc cgt ttg gta aaa cag gcc tat gat gtg gtg gcc 96
 Glu Gln Glu Leu Arg Arg Leu Val Lys Gln Ala Tyr Asp Val Val Gly
 20 25 30
 tgt cgt ggt tgg agc cgt att gat gtg atg gcg gat gcg gaa gga aag 144
 Cys Arg Gly Trp Ser Arg Ile Asp Val Met Ala Asp Ala Glu Gly Lys
 35 40 45
 ttc cgt ttg gtg gaa gtt aat acc aac cct gcc atg acc agc cac agt 192
 Phe Arg Leu Val Glu Val Asn Thr Asn Pro Gly Met Thr Ser His Ser
 50 55 60
 tta ttc ccg aaa tcg gcg gca acg gtc gcc tat tct ttt gcg cag ttg 240
 Leu Phe Pro Lys Ser Ala Ala Thr Val Gly Tyr Ser Phe Ala Gln Leu
 65 70 75 80
 gtt gag aaa att tta gag ttg agc gcg gaa 270
 Val Glu Lys Ile Leu Glu Leu Ser Ala Glu
 85 90

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<210> 96
 <211> 90
 <212> FRT
 <213> Actinobacillus actinomycetemcomitans

<400> 96
 Ser Asp Asn Thr Gln Tyr Phe Cys Pro Ala Gly Leu Ser Glu Glu Arg
 1 5 10 15
 Glu Gln Glu Leu Arg Arg Leu Val Lys Gln Ala Tyr Asp Val Val Gly
 20 25 30
 Cys Arg Gly Trp Ser Arg Ile Asp Val Met Ala Asp Ala Glu Gly Lys
 35 40 45
 Phe Arg Leu Val Glu Val Asn Thr Asn Pro Gly Met Thr Ser His Ser
 50 55 60
 Leu Phe Pro Lys Ser Ala Ala Thr Val Gly Tyr Ser Phe Ala Gln Leu
 65 70 75 80

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Val Glu Lys Ile Leu Glu Leu Ser Ala Glu
85 90

<210> 97
<211> 379
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(378)

<400> 97
ggg gaa tat ttc ggt cct tat ccg aat gcc ggt gca gtg cgc gaa acc 48
Gly Glu Tyr Phe Gly Pro Tyr Pro Asn Ala Gly Ala Val Arg Glu Thr 10
1 5 10 15
ctg tct tta tta caa aaa ctg ttc ccc att cgg cag tgt gaa aac tcc 96
Leu Ser Leu Leu Gln Lys Leu Phe Pro Ile Arg Gln Cys Glu Asn Ser
20 25 30
gtg tat aac aac cgt tgc cgc ccc tgt ttg cag tat caa atc ggg cgt 144
Val Tyr Asn Asn Arg Ser Arg Pro Cys Leu Gln Tyr Gln Ile Gly Arg
35 40 45
tgt ctg gcg cct tgc gta aag ggc tat gtg acc gat gaa gcc tat gcg 192
Cys Leu Ala Pro Cys Val Lys Gly Tyr Val Thr Asp Glu Ala Tyr Ala
50 55 60
cag cag gtc aat ttc gcc cgc ttg ttt tta caa gga aaa gat caa cag 240
Gln Gln Val Asn Phe Ala Arg Leu Phe Leu Gln Gly Lys Asp Gln Gln 20
65 70 75 80
gtg ctg gat cat ttg gtg aag caa atg gaa cag gca agt cag caa ctg 288
Val Leu Asp His Leu Val Lys Gln Met Glu Gln Ala Ser Gln Gln Leu
85 90 95
aat ttt gaa gaa gcg gca cgc gtt cgt gat caa att cag gca gtg cgg 336
Asn Phe Glu Glu Ala Ala Arg Val Arg Asp Gln Ile Gln Ala Val Arg
100 105 110
gca gta att gaa aaa caa ttt gtc gcc aac gat cgc cat gac g 379
Ala Val Ile Glu Lys Gln Phe Val Ala Asn Asp Arg His Asp
115 120 125

<210> 98
<211> 126
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 98
Gly Glu Tyr Phe Gly Pro Tyr Pro Asn Ala Gly Ala Val Arg Glu Thr
1 5 10 15
Leu Ser Leu Leu Gln Lys Leu Phe Pro Ile Arg Gln Cys Glu Asn Ser
20 25 30

Val Tyr Asn Asn Arg Ser Arg Pro Cys Leu Gln Tyr Gln Ile Gly Arg
35 40 45

Cys Leu Ala Pro Cys Val Lys Gly Tyr Val Thr Asp Glu Ala Tyr Ala
50 55 60

Gln Gln Val Asn Phe Ala Arg Leu Phe Leu Gln Gly Lys Asp Gln Gln
65 70 75 80

Val Leu Asp His Leu Val Lys Gln Met Glu Gln Ala Ser Gln Gln Leu
85 90 95

Asn Phe Glu Glu Ala Ala Arg Val Arg Asp Gln Ile Gln Ala Val Arg
100 105 110

Ala Val Ile Glu Lys Gln Phe Val Ala Asn Asp Arg His Asp
115 120 125

<210> 99
<211> 625
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(624)

<400> 99
gca aaa acc tta gat ttt cag tcc gca ggg ccg gaa aaa ctc ccg aaa 48
Ala Lys Thr Leu Asp Phe Gln Ser Ala Gly Pro Glu Lys Leu Pro Lys
1 5 10 15
ttt caa ccg cac ttt ttg gcg caa agc caa caa tta atc gac att tgc 96
Phe Gln Pro His Phe Leu Ala Gln Ser Gln Gln Leu Ile Asp Ile Cys
20 25 30
cgc ogc ctg aca ccg gcg gat att gct tcg ctc atg tot atc agc gac 144
Arg Arg Leu Thr Pro Ala Asp Ile Ala Ser Leu Met Ser Ile Ser Asp
35 40 45
aaa ctt gcc ggg ttg aat gcc gca cgt ttc gcc gaa tgg cag ttg gaa 192
Lys Leu Ala Gly Leu Asn Ala Ala Arg Phe Ala Glu Trp Gln Leu Glu
50 55 60
cat aac gaa cac aat gcc aaa gcg gcg gtg tat gcc ttt aga ggc gat 240
His Asn Glu His Asn Ala Lys Ala Ala Val Tyr Ala Phe Arg Gly Asp
65 70 75 80
gtt tac acc ggc ttg gac gtg gat tcc tta agc aat gac gat atg ttg 288
Val Tyr Thr Gly Leu Asp Val Asp Ser Leu Ser Asn Asp Asp Met Leu
85 90 95
ttt gca caa cag cat ttg cgc att ttg tcc ggg tta tat ggg ctg tta 336
Phe Ala Gln Gln His Leu Arg Ile Leu Ser Gly Leu Tyr Gly Leu Leu

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100	105	110	
acg ccg ctg gat ttg att cag cct tat cgt ttg gaa atg ggc acc aaa			384
Thr Pro Leu Asp Leu Ile Gln Pro Tyr Arg Leu Glu Met Gly Thr Lys			
115	120	125	
tta gcc aac ggc aaa ggc gcc gat ttg tat gcc ttt tgg cat ggt ttg			432
Leu Ala Asn Gly Lys Gly Ala Asp Leu Tyr Ala Phe Trp His Gly Leu			
130	135	140	
gtg atg cag gcg tta caa cag gcg att gat gaa caa cag gac gat gtt			480
Val Met Gln Ala Leu Gln Gln Ala Ile Asp Glu Gln Gln Asp Asp Val			
145	150	155	160
ttg gtg aat ctg gcg tcc gat gaa tat tat aaa tcg gta caa ccg tcg			528
Leu Val Asn Leu Ala Ser Asp Glu Tyr Tyr Lys Ser Val Gln Pro Ser			
165	170	175	
aat tta acg gcg caa atc att aaa ccg gtg ttc ctg gat aat aaa aac			576
Asn Leu Thr Ala Gln Ile Ile Lys Pro Val Phe Leu Asp Asn Lys Asn			
180	185	190	
ggc aaa tat aaa att atc agt ttc tac gcg aaa aaa gcc cgc ggt tta a			625
Gly Lys Tyr Lys Ile Ile Ser Phe Tyr Ala Lys Lys Ala Arg Gly Leu			
195	200	205	

<210> 100
 <211> 208
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 100

Ala Lys Thr Leu Asp Phe Gln Ser Ala Gly Pro Glu Lys Leu Pro Lys
 1 5 10 15

Phe Gln Pro His Phe Leu Ala Gln Ser Gln Gln Leu Ile Asp Ile Cys
 20 25 30

Arg Arg Leu Thr Pro Ala Asp Ile Ala Ser Leu Met Ser Ile Ser Asp
 35 40 45

Lys Leu Ala Gly Leu Asn Ala Ala Arg Phe Ala Glu Trp Gln Leu Glu
 50 55 60

His Asn Glu His Asn Ala Lys Ala Ala Val Tyr Ala Phe Arg Gly Asp
 65 70 75 80

Val Tyr Thr Gly Leu Asp Val Asp Ser Leu Ser Asn Asp Asp Met Leu
 85 90 95

Phe Ala Gln Gln His Leu Arg Ile Leu Ser Gly Leu Tyr Gly Leu Leu
 100 105 110

10

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Thr Pro Leu Asp Leu Ile Gln Pro Tyr Arg Leu Glu Met Gly Thr Lys
115 120 125

Leu Ala Asn Gly Lys Gly Ala Asp Leu Tyr Ala Phe Trp His Gly Leu
130 135 140

Val Met Gln Ala Leu Gln Gln Ala Ile Asp Glu Gln Gln Asp Asp Val
145 150 155 160

Leu Val Asn Leu Ala Ser Asp Glu Tyr Tyr Lys Ser Val Gln Pro Ser
165 170 175

Asn Leu Thr Ala Gln Ile Ile Lys Pro Val Phe Leu Asp Asn Lys Asn
180 185 190

Gly Lys Tyr Lys Ile Ile Ser Phe Tyr Ala Lys Lys Ala Arg Gly Leu
195 200 205

<210> 101
<211> 500
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(498)

<400> 101
cac tgc ttt ata ccg cca tcg cta tgg ctt gct tac cgg cgt atg ccg 48
His Cys Phe Ile Pro Pro Ser Leu Trp Leu Ala Tyr Arg Arg Met Pro
1 5 10 15
aag aag ttt tta ccc ttg ggc aaa ttg agg tga ttg ccg ata gat caa 96
Lys Lys Phe Leu Pro Leu Gly Lys Leu Arg Leu Pro Ile Asp Gln
20 25 30
cgg att taa gca cca cac gca ttg aac agg ctg act tac aga aaa aca 144
Arg Ile Ala Pro His Ala Leu Asn Arg Leu Thr Tyr Arg Lys Thr
35 40 45
atc aaa cca atg tcg ccg agg tgg cga aaa cca cac cgg gcg tat ttt 192
Ile Lys Pro Met Ser Pro Arg Trp Arg Lys Pro His Arg Ala Tyr Phe
50 55 60
tgg atc gta gcg gcg cac gca atg aac ata att tgt tgg tac gcg gat 240
Trp Ile Val Ala Ala His Ala Met Asn Ile Ile Cys Trp Tyr Ala Asp
65 70 75
tta aag cca atc gcg tgc cag tgt tta ttg acg gca ttc cgg tgt atg 288
Leu Lys Pro Ile Ala Cys Gln Cys Leu Leu Thr Ala Phe Arg Cys Met
80 85 90
tgc cct atg acg gca ata tgg aca ttg gtc gct tca cca cct tcg att 336
Cys Pro Met Thr Ala Ile Trp Thr Leu Val Ala Ser Pro Pro Ser Ile

10

20

30

10

<400> 102

20

<400> 103

30

<400> 104

Ala Ala His Ala Met Asn Ile Ile Cys Trp Tyr Ala Asp Leu Lys Pro

35 40 45
 Ile Ala Cys Gln Cys Leu Leu Thr Ala Phe Arg Cys Met Cys Pro Met
 50 55 60
 Thr Ala Ile Trp Thr Leu Val Ala Ser Pro Pro Ser Ile Tyr Pro Ala
 65 70 75 80
 Leu Ile Phe Pro Arg Ala Gln Val Pro Cys Phe Met Ala Pro Thr Arg
 85 90 95
 Trp Ala Val Arg
 100

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<210> 105
 <211> 30
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 105

Ile Ser Leu Arg Lys Asn Arg Pro Asn Arg Leu Lys Ala Leu Ser Ala
 1 5 10 15

Thr Asp Leu Leu Thr Val Glu Ala Ala Ala Arg Ala Pro Ile
 20 25 30

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<210> 106
 <211> 303
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(303)

<400> 106
 gca ttc ttc tcc tta ttt tcc att atc atg agc ggc aga tta aaa gaa 48
 Ala Phe Phe Ser Leu Phe Ser Ile Ile Met Ser Gly Arg Leu Lys Glu
 1 5 10 15
 ttg ggc gaa cac tta aac gaa acc ggc tct ttc aaa gtg ggc atg att 96
 Leu Gly Glu His Leu Asn Glu Thr Gly Ser Phe Lys Val Gly Met Ile
 20 25 30
 tgg aaa gct ttt atc gtc atc acc acc ggt gta ctg gct ttc atg cta 144
 Trp Lys Ala Phe Ile Val Ile Thr Thr Gly Val Leu Ala Phe Met Leu
 35 40 45
 tac aaa gaa gca ggc aaa gtg ctc acc aaa ggc tac gaa ggc tat ccg 192
 Tyr Lys Glu Ala Gly Lys Val Leu Thr Lys Gly Tyr Glu Gly Tyr Pro
 50 55 60
 gac cgg ttc gtc aac acc ttc ggc tgg ggc atg gca atc gct ttg gtg 240

30

Asp Arg Phe Val Asn Thr Phe Gly Trp Gly Met Ala Ile Ala Leu Val
65 70 75 80

atc atc gca ttc ctg ctt tcc cgc ctg ccg tgg aaa cac tta acg caa 288
Ile Ile Ala Phe Leu Leu Ser Arg Leu Pro Trp Lys His Leu Thr Gln
85 90 95

aca caa gga gaa aaa 303
Thr Gln Gly Glu Lys
100

<210> 107
<211> 101
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 107

Ala Phe Phe Ser Leu Phe Ser Ile Ile Met Ser Gly Arg Leu Lys Glu
1 5 10 15

Leu Gly Glu His Leu Asn Glu Thr Gly Ser Phe Lys Val Gly Met Ile
20 25 30

Trp Lys Ala Phe Ile Val Ile Thr Thr Gly Val Leu Ala Phe Met Leu
35 40 45

Tyr Lys Glu Ala Gly Lys Val Leu Thr Lys Gly Tyr Glu Gly Tyr Pro
50 55 60

Asp Arg Phe Val Asn Thr Phe Gly Trp Gly Met Ala Ile Ala Leu Val
65 70 75 80

Ile Ile Ala Phe Leu Leu Ser Arg Leu Pro Trp Lys His Leu Thr Gln
85 90 95

Thr Gln Gly Glu Lys
100

<210> 108
<211> 465
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(465)

<400> 108
gtg ttt ata acc gct tgc aac aat ata aac ttc ccg aga tcg gtc tcg 48
Val Phe Ile Thr Ala Cys Asn Asn Ile Asn Phe Pro Arg Ser Val Ser
1 5 10 15

10

20

30

gga ggc ttc agg ttt acg aac ttt gac tac act aaa cag aga acg gat 96
 Gly Gly Phe Arg Phe Thr Asn Phe Asp Tyr Thr Lys Gln Arg Thr Asp
 20 25 30
 ctc ttt taa gta ttc atc aaa acc ttc ccc ctg aaa aac ttt tac tac 144
 Leu Phe Val Phe Ile Lys Thr Phe Pro Leu Lys Asn Phe Tyr Tyr
 35 40 45
 aaa act tcc ttt att agc gag aat ctg ctt gca cat atc aag cgc aag 192
 Lys Thr Ser Phe Ile Ser Glu Asn Leu Leu Ala His Ile Lys Arg Lys
 50 55 60
 ttc tac caa ata cat cgc acg cgg aat atc cac tga tgg cat ccc act 240
 Phe Tyr Gln Ile His Arg Thr Arg Asn Ile His Trp His Pro Thr
 65 70 75
 gaa att cgg tgc cat atc tga cat cac cac atc tac ttt gcc ttc acc 288
 Glu Ile Arg Cys His Ile His His His Ile Tyr Phe Ala Phe Thr
 80 85 90
 gac cgg ctg caa taa aat gtt taa cac att ttc atc acg gaa atc gcc 336
 Asp Pro Leu Gln Asn Val His Ile Phe Ile Thr Glu Ile Ala
 95 100 105
 ttg tag aaa atc cac gcc tac aat agg atc cat ttc cag aag atc aca 384
 Leu Lys Ile His Ala Tyr Asn Arg Ile His Phe Gln Lys Ile Thr
 110 115 120
 ggc aat aat cgg tcc att gcg ccc aat ttg gct tac cac ata ctg cga 432
 Gly Asn Asn Pro Ser Ile Ala Pro Asn Leu Ala Tyr His Ile Leu Arg
 125 130 135
 cca tcc gcc cgg cgc tgc acc taa atc aac cac 465
 Pro Ser Ala Arg Arg Cys Thr Ile Asn His
 140 145

10

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<210> 109
 <211> 34
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 109

Val Phe Ile Thr Ala Cys Asn Asn Ile Asn Phe Pro Arg Ser Val Ser
 1 5 10 15

Gly Gly Phe Arg Phe Thr Asn Phe Asp Tyr Thr Lys Gln Arg Thr Asp
 20 25 30

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Leu Phe

<210> 110
 <211> 40
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 110

Val Phe Ile Lys Thr Phe Pro Leu Lys Asn Phe Tyr Tyr Lys Thr Ser
 1 5 10 15

Phe Ile Ser Glu Asn Leu Leu Ala His Ile Lys Arg Lys Phe Tyr Gln
 20 25 30

Ile His Arg Thr Arg Asn Ile His
 35 40

<210> 111

<211> 10

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 111

Trp His Pro Thr Glu Ile Arg Cys His Ile
 1 5 10

<210> 112

<211> 13

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 112

His His His Ile Tyr Phe Ala Phe Thr Asp Pro Leu Gln
 1 5 10

<210> 113

<211> 9

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 113

His Ile Phe Ile Thr Glu Ile Ala Leu
 1 5

<210> 114

<211> 37

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 114

Lys Ile His Ala Tyr Asn Arg Ile His Phe Gln Lys Ile Thr Gly Asn
 1 5 10 15

Asn Pro Ser Ile Ala Pro Asn Leu Ala Tyr His Ile Leu Arg Pro Ser
 20 25 30

10

20

30

Ala Arg Arg Cys Thr
35

<210> 115
<211> 630
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(630)

<400> 115		
gaa ctg ggc tgg gga ggt tgg tgg ttc tgg gat ccg gtg gaa aat gcg	48	10
Glu Leu Gly Trp Gly Gly Trp Trp Phe Trp Asp Pro Val Glu Asn Ala		
1 5 10 15		
tcg ctc atg ccg tgg ttg ctc ggc ttg gca ttg ttg cac agt tta atc	96	
Ser Leu Met Pro Trp Leu Leu Gly Leu Ala Leu Leu His Ser Leu Ile		
20 25 30		
gtc agc gaa aaa cgc gga att ttt aat tac tgg acg acc tta ttt tcc	144	
Val Ser Glu Lys Arg Gly Ile Phe Asn Tyr Trp Thr Thr Leu Phe Ser		
35 40 45		
ttg ttg gca ttt gcc ttc agc gta tta ggc acg ttt atc gtg cgc tcc	192	
Leu Leu Ala Phe Ala Phe Ser Val Leu Gly Thr Phe Ile Val Arg Ser		
50 55 60		
ggc gcg ctt acc tcc gta cac gct ttc gct gtg gac agc caa cgc ggc	240	20
Gly Ala Leu Thr Ser Val His Ala Phe Ala Val Asp Ser Gln Arg Gly		
65 70 75 80		
tcg gca tta tta ctg att ttc ttc ctg ctc acc gtg ggt tct ctc ggt	288	
Ser Ala Leu Leu Leu Ile Phe Phe Leu Leu Thr Val Gly Ser Leu Gly		
85 90 95		
tta ttc gcg ttc aaa gcc aat ttg cag caa cgc cgc gtc aaa tta acg	336	
Leu Phe Ala Phe Lys Ala Asn Leu Gln Gln Arg Arg Val Lys Leu Thr		
100 105 110		
ctg ctt tcc aaa gaa agt gcg gtg ctt ttt ttg aat gtt tta ttg agt	384	
Leu Leu Ser Lys Glu Ser Ala Val Leu Phe Leu Asn Val Leu Leu Ser		
115 120 125		
atc gcc acc gtt agc acc ttt ctc ggc acc ttt tat ccc atg ctg ttc	432	30
Ile Ala Thr Val Ser Thr Phe Leu Gly Thr Phe Tyr Pro Met Leu Phe		
130 135 140		
caa gcc atg aat tgg ggt tcc att tcc gtc ggt gcg cct tat ttc aac	480	
Gln Ala Met Asn Trp Gly Ser Ile Ser Val Gly Ala Pro Tyr Phe Asn		
145 150 155 160		
agt att ttc ttg ccg ctg ctt acg ctg att tta atc gcc atg gtg ttt	528	
Ser Ile Phe Leu Pro Leu Leu Thr Leu Ile Leu Ile Ala Met Val Phe		
165 170 175		
tcc ctc ggc ttg cac tgg gcg aag gcg gac aaa ggc att ttg ttt aaa	576	
Ser Leu Gly Leu His Trp Ala Lys Ala Asp Lys Gly Ile Leu Phe Lys		

180 185 190
 ogc ggc ggc ttg tta ctg ccg tct ttg ttg atc gct tat ttt atg att 624
 Arg Ala Ala Leu Leu Leu Pro Ser Leu Leu Ile Ala Tyr Phe Met Ile
 195 200 205

cgt cag 630
 Arg Gln
 210

<210> 116
 <211> 210
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

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<400> 116

Glu Leu Gly Trp Gly Gly Trp Trp Phe Trp Asp Pro Val Glu Asn Ala
 1 5 10 15

Ser Leu Met Pro Trp Leu Leu Gly Leu Ala Leu Leu His Ser Leu Ile
 20 25 30

Val Ser Glu Lys Arg Gly Ile Phe Asn Tyr Trp Thr Thr Leu Phe Ser
 35 40 45

Leu Leu Ala Phe Ala Phe Ser Val Leu Gly Thr Phe Ile Val Arg Ser
 50 55 60

20

Gly Ala Leu Thr Ser Val His Ala Phe Ala Val Asp Ser Gln Arg Gly
 65 70 75 80

Ser Ala Leu Leu Leu Ile Phe Phe Leu Leu Thr Val Gly Ser Leu Gly
 85 90 95

Leu Phe Ala Phe Lys Ala Asn Leu Gln Gln Arg Arg Val Lys Leu Thr
 100 105 110

Leu Leu Ser Lys Glu Ser Ala Val Leu Phe Leu Asn Val Leu Leu Ser
 115 120 125

30

Ile Ala Thr Val Ser Thr Phe Leu Gly Thr Phe Tyr Pro Met Leu Phe
 130 135 140

Gln Ala Met Asn Trp Gly Ser Ile Ser Val Gly Ala Pro Tyr Phe Asn
 145 150 155 160

Ser Ile Phe Leu Pro Leu Leu Thr Leu Ile Leu Ile Ala Met Val Phe
 165 170 175

Ser Leu Gly Leu His Trp Ala Lys Ala Asp Lys Gly Ile Leu Phe Lys
180 185 190

Arg Ala Ala Leu Leu Leu Pro Ser Leu Leu Ile Ala Tyr Phe Met Ile
195 200 205

Arg Gln
210

<210> 117

<211> 876

<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> (1)..(876)

<400> 117

act cac cct gtg cat att tog atg caa tat atg gca gat gaa gtt aaa 48
Thr His Pro Val His Ile Ser Met Gln Tyr Met Ala Asp Glu Val Lys
1 5 10 15

aaa tta aca aat ggt gaa gtg gtg atc cga att tac oca aat agc cag 96
Lys Leu Thr Asn Gly Glu Val Val Ile Arg Ile Tyr Pro Asn Ser Gln
20 25 30

ctt ggt agc cag cgt gaa tca atg gaa tta ttg caa tcc ggg tca cta 144
Leu Gly Ser Gln Arg Glu Ser Met Glu Leu Leu Gln Ser Gly Ser Leu
35 40 45

gat atg gca aaa tca aac gca agt gaa tta gaa gca ttt gag cca tct 192
Asp Met Ala Lys Ser Asn Ala Ser Glu Leu Glu Ala Phe Glu Pro Ser
50 55 60

tat ggt gca tac aat att ccg tat ctt ttc cat aat gtt gat cat tat 240
Tyr Gly Ala Tyr Asn Ile Pro Tyr Leu Phe His Asn Val Asp His Tyr
65 70 75 80

tat cgt gct cta ctt gat cct gaa gtt ggg caa aaa att ctt gat tca 288
Tyr Arg Ala Leu Leu Asp Pro Glu Val Gly Gln Lys Ile Leu Asp Ser
85 90 95

tca aag ggc aaa ggt ttc att ggg ttg act tat tat gat ggt ggt gcg 336
Ser Lys Gly Lys Gly Phe Ile Gly Leu Thr Tyr Tyr Asp Gly Gly Ala
100 105 110

cgt agt ttc tat gcg ggt aag gca att aaa tog cct gcg gac ctc aaa 384
Arg Ser Phe Tyr Ala Gly Lys Ala Ile Lys Ser Pro Ala Asp Leu Lys
115 120 125

ggt atg aaa att cgc gtt caa cca agc cca acc gca gta gaa atg atc 432
Gly Met Lys Ile Arg Val Gln Pro Ser Pro Thr Ala Val Glu Met Ile
130 135 140

aaa tta atg ggt gct tct cca aca cct tta gct tat ggt gaa ctc tat 480
Lys Leu Met Gly Ala Ser Pro Thr Pro Leu Ala Tyr Gly Glu Leu Tyr

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145	150	155	160		
acc gca ctc caa caa aaa gtg gtt gat ggc gcg gaa aat aac caa aca				528	
Thr Ala Leu Gln Gln Lys Val Val Asp Gly Ala Glu Asn Asn Gln Thr					
	165	170	175		
gca tta acc tta tct cgt cat ggt gaa gtg gct aaa ttc ttt agt gaa				576	
Ala Leu Thr Leu Ser Arg His Gly Glu Val Ala Lys Phe Phe Ser Glu					
	180	185	190		
gat gaa cat act atg att cct gat gtg ctc gta att ggt caa aaa tct				624	
Asp Glu His Thr Met Ile Pro Asp Val Leu Val Ile Gly Gln Lys Ser					
	195	200	205		
tgg gat aaa tta act cca gaa caa caa aat gca ctt aaa aaa gcc gct				672	10
Trp Asp Lys Leu Thr Pro Glu Gln Gln Asn Ala Leu Lys Lys Ala Ala					
	210	215	220		
gat gat tca atg atg tat cac aaa gat tta tgg caa aaa atg att gct				720	
Asp Asp Ser Met Met Tyr His Lys Asp Leu Trp Gln Lys Met Ile Ala					
	225	230	235	240	
gaa acc act caa gaa gct aaa gat aaa ttg ggt gta gaa ttt gtg aaa				768	
Glu Thr Thr Gln Glu Ala Lys Asp Lys Leu Gly Val Glu Phe Val Lys					
	245	250	255		
gta gat aaa caa cct ttc att gat gca aca aaa agc atg cat gat gcg				816	
Val Asp Lys Gln Pro Phe Ile Asp Ala Thr Lys Ser Met His Asp Ala					
	260	265	270		
gca aaa gcc aat cct ttg ctt aaa gaa tac att gaa cgt att gat agt				864	20
Ala Lys Ala Asn Pro Leu Leu Lys Glu Tyr Ile Glu Arg Ile Asp Ser					
	275	280	285		
ttg gca acc aag				876	
Leu Ala Thr Lys					
	290				
<210> 118					
<211> 292					
<212> PRT					
<213> Actinobacillus actinomycetemcomitans					
<400> 118					
Thr His Pro Val His Ile Ser Met Gln Tyr Met Ala Asp Glu Val Lys					
1	5	10	15		30
Lys Leu Thr Asn Gly Glu Val Val Ile Arg Ile Tyr Pro Asn Ser Gln					
	20	25	30		
Leu Gly Ser Gln Arg Glu Ser Met Glu Leu Leu Gln Ser Gly Ser Leu					
	35	40	45		
Asp Met Ala Lys Ser Asn Ala Ser Glu Leu Glu Ala Phe Glu Pro Ser					
	50	55	60		

Tyr Gly Ala Tyr Asn Ile Pro Tyr Leu Phe His Asn Val Asp His Tyr
 65 70 75 80
 Tyr Arg Ala Leu Leu Asp Pro Glu Val Gly Gln Lys Ile Leu Asp Ser
 85 90 95
 Ser Lys Gly Lys Gly Phe Ile Gly Leu Thr Tyr Tyr Asp Gly Gly Ala
 100 105 110
 Arg Ser Phe Tyr Ala Gly Lys Ala Ile Lys Ser Pro Ala Asp Leu Lys
 115 120 125
 Gly Met Lys Ile Arg Val Gln Pro Ser Pro Thr Ala Val Glu Met Ile
 130 135 140
 Lys Leu Met Gly Ala Ser Pro Thr Pro Leu Ala Tyr Gly Glu Leu Tyr
 145 150 155 160
 Thr Ala Leu Gln Gln Lys Val Val Asp Gly Ala Glu Asn Asn Gln Thr
 165 170 175
 Ala Leu Thr Leu Ser Arg His Gly Glu Val Ala Lys Phe Phe Ser Glu
 180 185 190
 Asp Glu His Thr Met Ile Pro Asp Val Leu Val Ile Gly Gln Lys Ser
 195 200 205
 Trp Asp Lys Leu Thr Pro Glu Gln Gln Asn Ala Leu Lys Lys Ala Ala
 210 215 220
 Asp Asp Ser Met Met Tyr His Lys Asp Leu Trp Gln Lys Met Ile Ala
 225 230 235 240
 Glu Thr Thr Gln Glu Ala Lys Asp Lys Leu Gly Val Glu Phe Val Lys
 245 250 255
 Val Asp Lys Gln Pro Phe Ile Asp Ala Thr Lys Ser Met His Asp Ala
 260 265 270
 Ala Lys Ala Asn Pro Leu Leu Lys Glu Tyr Ile Glu Arg Ile Asp Ser
 275 280 285
 Leu Ala Thr Lys
 290

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<210> 119
 <211> 303
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(303)

<400> 119
 atg agt gtt tta agt tat gcc caa aaa atc ggg caa gcc tta atg gta 48
 Met Ser Val Leu Ser Tyr Ala Gln Lys Ile Gly Gln Ala Leu Met Val
 1 5 10 15
 ccc gtt gcc gtt ttg ccg gca gcc gcc gta tta atg ggg atc ggc tat 96
 Pro Val Ala Val Leu Pro Ala Ala Val Leu Met Gly Ile Gly Tyr
 20 25 30
 tgg ctt gac ccg gac ggc tgg ggc gca aac agc caa ctt gcc gcc tta 144
 Trp Leu Asp Pro Asp Gly Trp Gly Ala Asn Ser Gln Leu Ala Ala Leu
 35 40 45
 tta atc aag tcc ggc gcg gca atc atc gat aac atg ggc tta tta ttc 192
 Leu Ile Lys Ser Gly Ala Ala Ile Ile Asp Asn Met Gly Leu Leu Phe
 50 55 60
 gcc gtg ggc gta gca ttc ggg ttg tcc aaa gac aag cac ggt tct gct 240
 Ala Val Gly Val Ala Phe Gly Leu Ser Lys Asp Lys His Gly Ser Ala
 65 70 75 80
 gcg ctt tcc ggt tta gtg ggc tat tat gtg gtc act acc cta ctc gcc 288
 Ala Leu Ser Gly Leu Val Gly Tyr Tyr Val Val Thr Thr Leu Leu Ala
 85 90 95
 cct ggc ggc gta gcg 303
 Pro Gly Gly Val Ala
 100

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<210> 120
 <211> 101
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 120
 Met Ser Val Leu Ser Tyr Ala Gln Lys Ile Gly Gln Ala Leu Met Val
 1 5 10 15
 Pro Val Ala Val Leu Pro Ala Ala Ala Val Leu Met Gly Ile Gly Tyr
 20 25 30
 Trp Leu Asp Pro Asp Gly Trp Gly Ala Asn Ser Gln Leu Ala Ala Leu
 35 40 45
 Leu Ile Lys Ser Gly Ala Ala Ile Ile Asp Asn Met Gly Leu Leu Phe
 50 55 60

30

Ala Val Gly Val Ala Phe Gly Leu Ser Lys Asp Lys His Gly Ser Ala
65 70 75 80

Ala Leu Ser Gly Leu Val Gly Tyr Tyr Val Val Thr Thr Leu Leu Ala
85 90 95

Pro Gly Gly Val Ala
100

<210> 121

<211> 590

<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> {1}..{588}

<400> 121

gaa tat aaa aat ctt gct gtt gct tat atc cgt atg tct acg gag cat 48
Glu Tyr Lys Asn Leu Ala Val Ala Tyr Ile Arg Met Ser Thr Glu His
1 5 10 15

cag gaa ttt tca ccg gat ata caa cgt cgc ttc att caa aaa tat gct 96
Gln Glu Phe Ser Pro Asp Ile Gln Arg Arg Phe Ile Gln Lys Tyr Ala
20 25 30

aag gaa caa ggg ctt ata ctc act agg gaa tac cta gat gag gga agg 144
Lys Glu Gln Gly Leu Ile Leu Thr Arg Glu Tyr Leu Asp Glu Gly Arg
35 40 45

agt gga tta agc gca gaa aaa cgt cct cag ttt tta tca ctc att aat 192
Ser Gly Leu Ser Ala Glu Lys Arg Pro Gln Phe Leu Ser Leu Ile Asn
50 55 60

ttt gta caa tcc ggt aat gct gat ttt tca cat att ctt gtt tat gac 240
Phe Val Gln Ser Gly Asn Ala Asp Phe Ser His Ile Leu Val Tyr Asp
65 70 75 80

att agc cga tgg ggg cgc ttt cta aat att gat gaa tct gca cat tat 288
Ile Ser Arg Trp Gly Arg Phe Leu Asn Ile Asp Glu Ser Ala His Tyr
85 90 95

gaa caa att tgt tca aaa atg ggg att aaa gtg cat tac tgt gca gaa 336
Glu Gln Ile Cys Ser Lys Met Gly Ile Lys Val His Tyr Cys Ala Glu
100 105 110

cct ttt aag gga aac gac att ggt tct caa att ttt aaa gcg gta aaa 384
Pro Phe Lys Gly Asn Asp Ile Gly Ser Gln Ile Phe Lys Ala Val Lys
115 120 125

cgt tgg tct gcc gga gaa tac tgt cgt gag cta ggt gaa aaa gtt ttt 432
Arg Trp Ser Ala Gly Glu Tyr Cys Arg Glu Leu Gly Glu Lys Val Phe
130 135 140

aat ggg cag aag aat ttg att gag cgc gga ttt cgt caa ggt gga cca 480
Asn Gly Gln Lys Asn Leu Ile Glu Arg Gly Phe Arg Gln Gly Gly Pro

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145 150 155 160
gct gga ttt ggg tta aga cgc cta tta tta agt gct gat ggt tcg cca 528
Ala Gly Phe Gly Leu Arg Arg Leu Leu Leu Ser Ala Asp Gly Ser Pro
 165 170 175
aaa ttt gaa cta aaa acg ggt gac agg aag agt ttg cag tcg gat cgt 576
Lys Phe Glu Leu Lys Thr Gly Asp Arg Lys Ser Leu Gln Ser Asp Arg
 180 185 190
gtc att ctt att gc 590
Val Ile Leu Ile
 195

<210> 122
<211> 196
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 122

Glu Tyr Lys Asn Leu Ala Val Ala Tyr Ile Arg Met Ser Thr Glu His
1 5 10 15

Gln Glu Phe Ser Pro Asp Ile Gln Arg Arg Phe Ile Gln Lys Tyr Ala
 20 25 30

Lys Glu Gln Gly Leu Ile Leu Thr Arg Glu Tyr Leu Asp Glu Gly Arg
 35 40 45

Ser Gly Leu Ser Ala Glu Lys Arg Pro Gln Phe Leu Ser Leu Ile Asn
50 55 60

Phe Val Gln Ser Gly Asn Ala Asp Phe Ser His Ile Leu Val Tyr Asp
65 70 75 80

Ile Ser Arg Trp Gly Arg Phe Leu Asn Ile Asp Glu Ser Ala His Tyr
 85 90 95

Glu Gln Ile Cys Ser Lys Met Gly Ile Lys Val His Tyr Cys Ala Glu
 100 105 110

Pro Phe Lys Gly Asn Asp Ile Gly Ser Gln Ile Phe Lys Ala Val Lys
 115 120 125

Arg Trp Ser Ala Gly Glu Tyr Cys Arg Glu Leu Gly Glu Lys Val Phe
130 135 140

Asn Gly Gln Lys Asn Leu Ile Glu Arg Gly Phe Arg Gln Gly Gly Pro
145 150 155 160

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Ala Gly Phe Gly Leu Arg Arg Leu Leu Leu Ser Ala Asp Gly Ser Pro
 165 170 175

Lys Phe Glu Leu Lys Thr Gly Asp Arg Lys Ser Leu Gln Ser Asp Arg
 180 185 190

Val Ile Leu Ile
 195

<210> 123
 <211> 531
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(531)

<400> 123
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 Phe Leu Thr Lys Asp Lys Ile Lys Gln Ala Ile Gln Ala Gln Gln Gln
 1 5 10 15
 gaa ctg tta cta caa gtg atc ccg cag gat tac ttc aat aat gat ctg 96
 Glu Leu Leu Leu Gln Val Ile Pro Gln Asp Tyr Phe Asn Asn Asp Leu
 20 25 30
 acg cag gct tgt tat gca ccg caa gcg ggg aca tta caa gtc gtg gag 144
 Thr Gln Ala Cys Tyr Ala Pro Gln Ala Gly Thr Leu Gln Val Val Glu
 35 40 45
 ata agc aaa ata tgc acg gca aag aaa gac ggc gtg act act gcc tat 192
 Ile Ser Lys Ile Cys Thr Ala Lys Lys Asp Gly Val Thr Thr Ala Tyr
 50 55 60
 gcc ttt gaa agc acg gcg cat gat ggc tat tcc ggc gat att cat att 240
 Ala Phe Glu Ser Thr Ala His Asp Gly Tyr Ser Gly Asp Ile His Ile
 65 70 75 80
 ttg gtg ggc atg aaa cct gat ggc gaa gtg ctt ggc gtg cgc att acg 288
 Leu Val Gly Met Lys Pro Asp Gly Glu Val Leu Gly Val Arg Ile Thr
 85 90 95
 gaa cac cac gaa acc ccg gga tta ggc gat aaa att gaa acc cgc att 336
 Glu His His Glu Thr Pro Gly Leu Gly Asp Lys Ile Glu Thr Arg Ile
 100 105 110
 tcc aac tgg gtt tta agt ttt gat cat cag gtt atc agc aac gaa aat 384
 Ser Asn Trp Val Leu Ser Phe Asp His Gln Val Ile Ser Asn Glu Asn
 115 120 125
 gcc gca gaa tgg gcg gtg aaa aaa gac ggc ggt aaa ttc gat caa ttc 432
 Ala Ala Glu Trp Ala Val Lys Lys Asp Gly Gly Lys Phe Asp Gln Phe
 130 135 140
 gcc ggt gcc acc atc acg ccc cgc gct gtg gtt aac caa gtg aaa cgg 480
 Ala Gly Ala Thr Ile Thr Pro Arg Ala Val Val Asn Gln Val Lys Arg

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145	150	155	160	
gcg gca ttg gct atg ctg gat aat ctg ccg aaa gag aga gaa agt gat				528
Ala Ala Leu Ala Met Leu Asp Asn Leu Pro Lys Glu Arg Glu Ser Asp				
	165	170	175	
gga				531
Gly				

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<210> 124
<211> 177
<212> PRT
<213> Actinobacillus actinomycetemcomitans
<400> 124
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Phe Leu Thr Lys Asp Lys Ile Lys Gln Ala Ile Gln Ala Gln Gln Gln
1 5 10 15

Glu Leu Leu Leu Gln Val Ile Pro Gln Asp Tyr Phe Asn Asn Asp Leu
20 25 30

Thr Gln Ala Cys Tyr Ala Pro Gln Ala Gly Thr Leu Gln Val Val Glu
35 40 45

Ile Ser Lys Ile Cys Thr Ala Lys Lys Asp Gly Val Thr Thr Ala Tyr
50 55 60

Ala Phe Glu Ser Thr Ala His Asp Gly Tyr Ser Gly Asp Ile His Ile
65 70 75 80

Leu Val Gly Met Lys Pro Asp Gly Glu Val Leu Gly Val Arg Ile Thr
85 90 95

Glu His His Glu Thr Pro Gly Leu Gly Asp Lys Ile Glu Thr Arg Ile
100 105 110

Ser Asn Trp Val Leu Ser Phe Asp His Gln Val Ile Ser Asn Glu Asn
115 120 125

Ala Ala Glu Trp Ala Val Lys Lys Asp Gly Gly Lys Phe Asp Gln Phe
130 135 140

Ala Gly Ala Thr Ile Thr Pro Arg Ala Val Val Asn Gln Val Lys Arg
145 150 155 160

Ala Ala Leu Ala Met Leu Asp Asn Leu Pro Lys Glu Arg Glu Ser Asp
165 170 175

Gly

<210> 125
 <211> 783
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(783)

<400> 125		
atg gat aaa tta gac gaa aca caa gaa ctg caa caa acc gaa gcc aaa	48	10
Met Asp Lys Leu Asp Glu Thr Gln Glu Leu Gln Gln Thr Glu Ala Lys		
1 5 10 15		
agt gcg gtt gac aaa aaa caa cat ttt ttg aac gtt ggt tct gcc aac	96	
Ser Ala Val Asp Lys Lys Gln His Phe Leu Asn Val Gly Ser Ala Asn		
20 25 30		
ggc ccc gaa ggg gtg aat aag cga aca agt gag ctt atg aat aat att	144	
Gly Pro Glu Gly Val Asn Lys Arg Thr Ser Glu Leu Met Asn Asn Ile		
35 40 45		
tca aat gaa aaa agc att tgg aaa acg att ttc att cag ggc atc tgg	192	
Ser Asn Glu Lys Ser Ile Trp Lys Thr Ile Phe Ile Gln Gly Ile Trp		
50 55 60		
acc aac aat tcc acc gtg gtg caa ctg ctt ggg ttg tgt ccg ctg ctg	240	20
Thr Asn Asn Ser Thr Val Val Gln Leu Leu Gly Leu Cys Pro Leu Leu		
65 70 75 80		
gcg gtg tcc aac tcc gtg acc aac gcc ctc ggg ctg ggt tta gcc acc	288	
Ala Val Ser Asn Ser Val Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr		
85 90 95		
atg ctt gtg ctg acg tgt acg aac acg gta gtt tct ctt ttc cgt aag	336	
Met Leu Val Leu Thr Cys Thr Asn Thr Val Val Ser Leu Phe Arg Lys		
100 105 110		
cac atc ccc aat gaa atc cgc att ccg att tat gtg atg atc atc gca	384	
His Ile Pro Asn Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala		
115 120 125		
acc acg gta acc gct gtg caa tta ttg atg aat gcc tat acc tac gcg	432	30
Thr Thr Val Thr Ala Val Gln Leu Leu Met Asn Ala Tyr Thr Tyr Ala		
130 135 140		
ctt tat caa tct ctc ggg att ttt att ccg ctc atc gtc acc aac tgt	480	
Leu Tyr Gln Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys		
145 150 155 160		
att gtg atc ggt cgc gcc gaa gcc ttt gct tcc aag aac agc att tcc	528	
Ile Val Ile Gly Arg Ala Glu Ala Phe Ala Ser Lys Asn Ser Ile Ser		
165 170 175		
cat tcc gcc ttt gac ggt ttt tcc atg gga tta ggg atg tta ttc agt	576	
His Ser Ala Phe Asp Gly Phe Ser Met Gly Leu Gly Met Leu Phe Ser		

180	185	190		
tta gta ggc ctc ggc ggc atc cgc gaa atc atc ggc aac ggt act tta			624	
Leu Val Ala Leu Gly Gly Ile Arg Glu Ile Ile Gly Asn Gly Thr Leu				
195	200	205		
ttt gac ggc atc gaa aat ttg ctg ggc gat tgg gct aaa ttc atg cgg			672	
Phe Asp Gly Ile Glu Asn Leu Leu Gly Asp Trp Ala Lys Phe Met Arg				
210	215	220		
att gaa ttt ttc cac aat gac agt aat ctg tta ctt gcg att ttg cct			720	
Ile Glu Phe Phe His Asn Asp Ser Asn Leu Leu Leu Ala Ile Leu Pro				
225	230	235	240	
ccc ggc gca ttt att ggt tta gct ttg ttg tta gcc tta aaa aat gta			768	
Pro Gly Ala Phe Ile Gly Leu Ala Leu Leu Ala Leu Lys Asn Val				10
245	250	255		
ata gat aca aaa aag			783	
Ile Asp Thr Lys Lys				
260				
<210> 126				
<211> 261				
<212> PRT				
<213> Actinobacillus actinomycetemcomitans				
<400> 126				
Met Asp Lys Leu Asp Glu Thr Gln Glu Leu Gln Gln Thr Glu Ala Lys				20
1	5	10	15	
Ser Ala Val Asp Lys Lys Gln His Phe Leu Asn Val Gly Ser Ala Asn				
20	25	30		
Gly Pro Glu Gly Val Asn Lys Arg Thr Ser Glu Leu Met Asn Asn Ile				
35	40	45		
Ser Asn Glu Lys Ser Ile Trp Lys Thr Ile Phe Ile Gln Gly Ile Trp				
50	55	60		
Thr Asn Asn Ser Thr Val Val Gln Leu Leu Gly Leu Cys Pro Leu Leu				30
65	70	75	80	
Ala Val Ser Asn Ser Val Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr				
85	90	95		
Met Leu Val Leu Thr Cys Thr Asn Thr Val Val Ser Leu Phe Arg Lys				
100	105	110		
His Ile Pro Asn Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala				
115	120	125		

Thr Thr Val Thr Ala Val Gln Leu Leu Met Asn Ala Tyr Thr Tyr Ala
130 135 140

Leu Tyr Gln Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys
145 150 155 160

Ile Val Ile Gly Arg Ala Glu Ala Phe Ala Ser Lys Asn Ser Ile Ser
165 170 175

His Ser Ala Phe Asp Gly Phe Ser Met Gly Leu Gly Met Leu Phe Ser
180 185 190

Leu Val Ala Leu Gly Gly Ile Arg Glu Ile Ile Gly Asn Gly Thr Leu
195 200 205

Phe Asp Gly Ile Glu Asn Leu Leu Gly Asp Trp Ala Lys Phe Met Arg
210 215 220

Ile Glu Phe Phe His Asn Asp Ser Asn Leu Leu Leu Ala Ile Leu Pro
225 230 235 240

Pro Gly Ala Phe Ile Gly Leu Ala Leu Leu Leu Ala Leu Lys Asn Val
245 250 255

Ile Asp Thr Lys Lys
260

<210> 127
<211> 627
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(627)

<400> 127
atg aat ttt act aaa acg cta tat att ttt aaa tat act ggc gaa ctt 48
Met Asn Phe Thr Lys Thr Leu Tyr Ile Phe Lys Tyr Thr Gly Glu Leu 30
1 5 10 15
ttc ggc att ttt att tat aat gaa gac gct atg ttt tta aat ata cat 96
Phe Ala Ile Phe Ile Tyr Asn Glu Asp Ala Met Phe Leu Asn Ile His 30
20 25 30
cgt tat att ttt ctc aca ttc tgt tgg ggt aac atc atg aaa ttt gaa 144
Arg Tyr Ile Phe Leu Thr Phe Cys Trp Gly Asn Ile Met Lys Phe Glu 45
35 40 45
gtc att tac aaa ttc ctg ttg ttg tgt gtg ctg att atc agt ttg ttg 192
Val Ile Tyr Lys Phe Leu Leu Leu Cys Val Leu Ile Ile Ser Leu Leu

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50	55	60	
tgt gtt gtg ata agc ggc gcc gga tta ttc tac ggt tgg caa ttg agc			240
Cys Val Val Ile Ser Gly Ala Gly Leu Phe Tyr Gly Trp Gln Leu Ser			
65	70	75	80
atg ctg ttc aat att cat gtg agc ttt gcc gtt ttg ctg gtc gcc gcg			288
Met Leu Phe Asn Ile His Val Ser Phe Ala Val Leu Leu Val Ala Ala			
	85	90	95
ttg tta ctg cat att ctg aac cgc aaa aat aaa ttg gcg aaa atc aat			336
Leu Leu Leu His Ile Leu Asn Arg Lys Asn Lys Leu Ala Lys Ile Asn			
	100	105	110
acc caa ttt gcc gat ttg gtc tta cac aat aaa tac cgc agt tat tgc			384
Thr Gln Phe Ala Asp Leu Val Leu His Asn Lys Tyr Pro Ser Tyr Cys			
	115	120	125
aat tta gac cgc ttg atc atg acg ttc gag cat ttt tcc gtt gtg caa			432
Asn Leu Asp Arg Leu Ile Met Thr Phe Glu His Phe Ser Val Val Gln			
	130	135	140
att gcc gaa cag tta aac ctg gat ttg gat gcg ctg cta aaa gaa ctc			480
Ile Ala Glu Gln Leu Asn Leu Asp Leu Asp Ala Leu Leu Lys Glu Leu			
	145	150	155
gcc gaa gga aaa ata aac gtc aaa aat tcc cac agc act tta cgg gag			528
Ala Glu Gly Lys Ile Asn Val Lys Asn Ser His Ser Thr Leu Arg Glu			
	165	170	175
aat ttt ccc cat aat gat gaa aag att ttt gct gcg atc acc atc gtg			576
Asn Phe Pro His Asn Asp Glu Lys Ile Phe Ala Ala Ile Thr Ile Val			
	180	185	190
ctg caa ctt cgt tta att aat cct atc cct gct ttt aac tta aaa gga			624
Leu Gln Leu Arg Leu Ile Asn Pro Ile Pro Ala Phe Asn Leu Lys Gly			
	195	200	205
cat			627
His			

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20

<210> 128
 <211> 209
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 128

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Met Asn Phe Thr Lys Thr Leu Tyr Ile Phe Lys Tyr Thr Gly Glu Leu
1 5 10 15

Phe Ala Ile Phe Ile Tyr Asn Glu Asp Ala Met Phe Leu Asn Ile His
20 25 30

Arg Tyr Ile Phe Leu Thr Phe Cys Trp Gly Asn Ile Met Lys Phe Glu
35 40 45

Val Ile Tyr Lys Phe Leu Leu Leu Cys Val Leu Ile Ile Ser Leu Leu
50 55 60

Cys Val Val Ile Ser Gly Ala Gly Leu Phe Tyr Gly Trp Gln Leu Ser
65 70 75 80

Met Leu Phe Asn Ile His Val Ser Phe Ala Val Leu Leu Val Ala Ala
85 90 95

Leu Leu Leu His Ile Leu Asn Arg Lys Asn Lys Leu Ala Lys Ile Asn
100 105 110

Thr Gln Phe Ala Asp Leu Val Leu His Asn Lys Tyr Pro Ser Tyr Cys
115 120 125

Asn Leu Asp Arg Leu Ile Met Thr Phe Glu His Phe Ser Val Val Gln
130 135 140

Ile Ala Glu Gln Leu Asn Leu Asp Leu Asp Ala Leu Leu Lys Glu Leu
145 150 155 160

Ala Glu Gly Lys Ile Asn Val Lys Asn Ser His Ser Thr Leu Arg Glu
165 170 175

Asn Phe Pro His Asn Asp Glu Lys Ile Phe Ala Ala Ile Thr Ile Val
180 185 190

Leu Gln Leu Arg Leu Ile Asn Pro Ile Pro Ala Phe Asn Leu Lys Gly
195 200 205

His

<210> 129
<211> 663
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(663)

<400> 129
gtg caa tct tac gag cag caa agt aat aac ggc gtg ccg att caa ttc 48
Val Gln Ser Tyr Glu Gln Gln Ser Asn Asn Gly Val Pro Ile Gln Phe
1 5 10 15
cag cag tta gac caa tca caa acc gtt gaa ccg acc gtg ttg gat aat 96
Gln Gln Leu Asp Gln Ser Gln Thr Val Glu Pro Thr Val Leu Asp Asn

10

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	20	25	30	
ctg acc ccg caa acc gat aac act gtc gcg caa caa cct gct gcg gaa				144
Leu Thr Pro Gln Thr Asp Asn Thr Val Ala Gln Gln Pro Ala Ala Glu				
	35	40	45	
acc aat acg caa aat gtc aat gcc gcc ata gaa ccg caa gcg gtg				192
Thr Asn Thr Gln Asn Val Asn Ala Gly Ala Ile Glu Pro Gln Ala Val				
	50	55	60	
gaa caa ggg gca acc acc tcc gtt gct gag caa acg aca act gcg gcg				240
Glu Gln Gly Ala Thr Thr Ser Val Ala Glu Gln Thr Thr Thr Ala Ala				
	65	70	75	80
gta gaa aat aaa ccg gca gaa gtc aaa ccg gaa gag gtc gaa acc gtt				288
Val Glu Asn Lys Pro Ala Glu Val Lys Pro Glu Glu Val Glu Thr Val				
	85	90	95	
aaa ccg agt gag cct gca aaa gcg caa gaa gcc gtc aaa ccg cgt caa				336
Lys Pro Ser Glu Pro Ala Lys Ala Gln Glu Ala Val Lys Pro Arg Gln				
	100	105	110	
cat cag gaa agc gtg aaa aaa gag ccg gtg aaa acc gat aaa gtg aaa				384
His Gln Glu Ser Val Lys Lys Glu Pro Val Lys Thr Asp Lys Val Lys				
	115	120	125	
cag gct gaa aaa gcg act gct aaa aat caa ccg act aaa tcg gca aaa				432
Gln Ala Glu Lys Ala Thr Ala Lys Asn Gln Pro Thr Lys Ser Ala Lys				
	130	135	140	
acc gaa aaa gaa gta ccg gat att tta gaa gcc aaa aca acg act atc				480
Thr Glu Lys Glu Val Arg Asp Ile Leu Glu Gly Lys Thr Thr Thr Ile				
	145	150	155	160
acc aaa gca gca gcc ggt agc aaa acc tta acc att ccg caa gcc gtg				528
Thr Lys Ala Ala Ala Gly Ser Lys Thr Leu Thr Ile Pro Gln Gly Val				
	165	170	175	
acc tta atg cag gtg ttc cgt gac aac cat cta cct gtc ggt gat gtg				576
Thr Leu Met Gln Val Phe Arg Asp Asn His Leu Pro Val Gly Asp Val				
	180	185	190	
aat gcc atg acc aaa gcc aaa gcc gta gcc aag gtg tta agc agc ttc				624
Asn Ala Met Thr Lys Ala Lys Gly Val Gly Lys Val Leu Ser Ser Phe				
	195	200	205	
aag ccg ggt gat aag gta cag gtt tcc ctg aat gca caa				663
Lys Pro Gly Asp Lys Val Gln Val Ser Leu Asn Ala Gln				
	210	215	220	

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<210> 130
 <211> 221
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 130

Val Gln Ser Tyr Glu Gln Gln Ser Asn Asn Gly Val Pro Ile Gln Phe
1 5 10 15

Gln Gln Leu Asp Gln Ser Gln Thr Val Glu Pro Thr Val Leu Asp Asn
 20 25 30
 Leu Thr Pro Gln Thr Asp Asn Thr Val Ala Gln Gln Pro Ala Ala Glu
 35 40 45
 Thr Asn Thr Gln Asn Val Asn Ala Gly Ala Ile Glu Pro Gln Ala Val
 50 55 60
 Glu Gln Gly Ala Thr Thr Ser Val Ala Glu Gln Thr Thr Thr Ala Ala
 65 70 75 80
 Val Glu Asn Lys Pro Ala Glu Val Lys Pro Glu Glu Val Glu Thr Val
 85 90 95
 Lys Pro Ser Glu Pro Ala Lys Ala Gln Glu Ala Val Lys Pro Arg Gln
 100 105 110
 His Gln Glu Ser Val Lys Lys Glu Pro Val Lys Thr Asp Lys Val Lys
 115 120 125
 Gln Ala Glu Lys Ala Thr Ala Lys Asn Gln Pro Thr Lys Ser Ala Lys
 130 135 140
 Thr Glu Lys Glu Val Arg Asp Ile Leu Glu Gly Lys Thr Thr Thr Ile
 145 150 155 160
 Thr Lys Ala Ala Ala Gly Ser Lys Thr Leu Thr Ile Pro Gln Gly Val
 165 170 175
 Thr Leu Met Gln Val Phe Arg Asp Asn His Leu Pro Val Gly Asp Val
 180 185 190
 Asn Ala Met Thr Lys Ala Lys Gly Val Gly Lys Val Leu Ser Ser Phe
 195 200 205
 Lys Pro Gly Asp Lys Val Gln Val Ser Leu Asn Ala Gln
 210 215 220

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<210> 131
 <211> 478
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans
 <220>
 <221> CDS
 <222> (1)..(477)

<400> 131

atg tta aaa aaa atc tta cat tcc gca ctc atc ggt ttg gtt acg gca 48
 Met Leu Lys Lys Ile Leu His Ser Ala Leu Ile Gly Leu Val Thr Ala
 1 5 10 15

ggt gtg att ttg ttt gtg cta ccg aaa atc acc ggg aaa tcc gtg tta 96
 Gly Val Ile Leu Phe Val Leu Pro Lys Ile Thr Gly Lys Ser Val Leu
 20 25 30

ccg gag caa gaa atc gcc tct tat aaa gat gca gtg cgt att gct tcg 144
 Pro Glu Gln Glu Ile Ala Ser Tyr Lys Asp Ala Val Arg Ile Ala Ser
 35 40 45

ccg gcg gtt gtg aac gtt tat aat cag gcg ttt act tct tcg tcc gcg 192
 Pro Ala Val Val Asn Val Tyr Asn Gln Ala Phe Thr Ser Ser Ser Ala
 50 55 60

10

caa ttg cag gtg aat aac ctc ggt tcg ggc gtg atc atg tca aaa gac 240
 Gln Leu Gln Val Asn Asn Leu Gly Ser Gly Val Ile Met Ser Lys Asp
 65 70 75 80

ggt tat att ctg acg aac aaa cac gtt att caa aat gcc gat caa att 288
 Gly Tyr Ile Leu Thr Asn Lys His Val Ile Gln Asn Ala Asp Gln Ile
 85 90 95

gta gta gcg ttg caa aac ggg cat att ttt gat gcg gcg ctc att ggt 336
 Val Val Ala Leu Gln Asn Gly His Ile Phe Asp Ala Ala Leu Ile Gly
 100 105 110

tcc gat tct tta acg gat ttg gca gta tta aaa att aaa gcg gat aat 384
 Ser Asp Ser Leu Thr Asp Leu Ala Val Leu Lys Ile Lys Ala Asp Asn
 115 120 125

20

tta tcc acg att ccg caa aat ctc agc cgt ccg gtg cat gtg gga gat 432
 Leu Ser Thr Ile Pro Gln Asn Leu Ser Arg Pro Val His Val Gly Asp
 130 135 140

gtg gcg ctg gca atc ggc aat ccg tat aac ctg ggg caa agc gtg t 478
 Val Ala Leu Ala Ile Gly Asn Pro Tyr Asn Leu Gly Gln Ser Val
 145 150 155

<210> 132

<211> 159

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 132

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Met Leu Lys Lys Ile Leu His Ser Ala Leu Ile Gly Leu Val Thr Ala
 1 5 10 15

Gly Val Ile Leu Phe Val Leu Pro Lys Ile Thr Gly Lys Ser Val Leu
 20 25 30

Pro Glu Gln Glu Ile Ala Ser Tyr Lys Asp Ala Val Arg Ile Ala Ser
 35 40 45

Pro Ala Val Val Asn Val Tyr Asn Gln Ala Phe Thr Ser Ser Ser Ala
50 55 60

Gln Leu Gln Val Asn Asn Leu Gly Ser Gly Val Ile Met Ser Lys Asp
65 70 75 80

Gly Tyr Ile Leu Thr Asn Lys His Val Ile Gln Asn Ala Asp Gln Ile
85 90 95

Val Val Ala Leu Gln Asn Gly His Ile Phe Asp Ala Ala Leu Ile Gly
100 105 110

Ser Asp Ser Leu Thr Asp Leu Ala Val Leu Lys Ile Lys Ala Asp Asn
115 120 125

Leu Ser Thr Ile Pro Gln Asn Leu Ser Arg Pro Val His Val Gly Asp
130 135 140

Val Ala Leu Ala Ile Gly Asn Pro Tyr Asn Leu Gly Gln Ser Val
145 150 155

<210> 133
<211> 537
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(537)

<400> 133
gcc ggc tgg cag ata aaa aat aac aaa cct ttt gac ggt aaa gac tgg 48
Ala Gly Trp Gln Ile Lys Asn Asn Lys Pro Phe Asp Gly Lys Asp Trp
1 5 10 15
acc cgt tgg gtc gat gcg aga gaa tcc gga gcc att gcc ggt gca gta 96
Thr Arg Trp Val Asp Ala Arg Glu Ser Gly Ala Ile Ala Gly Ala Val
20 25 30
gaa ttt aac aat tat gtc aat tct cat aaa ggc aaa atg ttc tat gtg 144
Glu Phe Asn Asn Tyr Val Asn Ser His Lys Gly Lys Met Phe Tyr Val
35 40 45
tca aat cgc aaa gac agt aat gaa aaa gca ggt acc att gat gac atg 192
Ser Asn Arg Lys Asp Ser Asn Glu Lys Ala Gly Thr Ile Asp Asp Met
50 55 60
aaa cgt tta ggc ttt acc ggt gtt gat gaa tca tcc ctt tat ctg aaa 240
Lys Arg Leu Gly Phe Thr Gly Val Asp Glu Ser Ser Leu Tyr Leu Lys
65 70 75 80
aaa gat aaa tcc gcc aaa tct gcc cgt ttt gca gaa att gaa agt caa 288
Lys Asp Lys Ser Ala Lys Ser Ala Arg Phe Ala Glu Ile Glu Ser Gln

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      85              90              95
ggc tat gac atc gtg ctt tat gta ggc gac aac ctg gat gat ttc ggt    336
Gly Tyr Asp Ile Val Leu Tyr Val Gly Asp Asn Leu Asp Asp Phe Gly
      100              105              110

gat gca aca cac ggt aaa tta aat gcg gat cgt cga gac ttt gtt gct    384
Asp Ala Thr His Gly Lys Leu Asn Ala Asp Arg Arg Asp Phe Val Ala
      115              120              125

aaa aac cag gcg aaa ttc ggt aaa act tat atc gtt tta cct aat ccg    432
Lys Asn Gln Ala Lys Phe Gly Lys Thr Tyr Ile Val Leu Pro Asn Pro
      130              135              140

aat tac ggt ggt tgg gaa ggc ggt tta gcc aaa gac tac ttt aaa ggt    480
Asn Tyr Gly Gly Trp Glu Gly Gly Leu Ala Lys Asp Tyr Phe Lys Gly
      145              150              155              160

gat tcc caa agc aaa gtt gat gcc cgc tta aat gta att aag gca tgg    528
Asp Ser Gln Ser Lys Val Asp Ala Arg Leu Asn Val Ile Lys Ala Trp
      165              170              175

agt gga aaa    537
Ser Gly Lys

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<210> 134
<211> 179
<212> PRT
<213> Actinobacillus actinomycetemcomitans
<400> 134

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Ala Gly Trp Gln Ile Lys Asn Asn Lys Pro Phe Asp Gly Lys Asp Trp
1          5          10          15

Thr Arg Trp Val Asp Ala Arg Glu Ser Gly Ala Ile Ala Gly Ala Val
      20          25          30

Glu Phe Asn Asn Tyr Val Asn Ser His Lys Gly Lys Met Phe Tyr Val
      35          40          45

Ser Asn Arg Lys Asp Ser Asn Glu Lys Ala Gly Thr Ile Asp Asp Met
      50          55          60

Lys Arg Leu Gly Phe Thr Gly Val Asp Glu Ser Ser Leu Tyr Leu Lys
65          70          75          80

Lys Asp Lys Ser Ala Lys Ser Ala Arg Phe Ala Glu Ile Glu Ser Gln
      85          90          95

Gly Tyr Asp Ile Val Leu Tyr Val Gly Asp Asn Leu Asp Asp Phe Gly
      100          105          110

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Asp Ala Thr His Gly Lys Leu Asn Ala Asp Arg Arg Asp Phe Val Ala
115 120 125

Lys Asn Gln Ala Lys Phe Gly Lys Thr Tyr Ile Val Leu Pro Asn Pro
130 135 140

Asn Tyr Gly Gly Trp Glu Gly Gly Leu Ala Lys Asp Tyr Phe Lys Gly
145 150 155 160

Asp Ser Gln Ser Lys Val Asp Ala Arg Leu Asn Val Ile Lys Ala Trp
165 170 175

Ser Gly Lys

<210> 135
<211> 765
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(765)

<400> 135
atg tgg ata ttt tac aac acc cgg aca ttc gtg ccg aat tac cgg ctt 48
Met Trp Ile Phe Tyr Asn Thr Arg Thr Phe Val Pro Asn Tyr Arg Leu
1 5 10 15
atg cca act ggc cga cat tcc cgc aat tat ggg tgg aag gcg agc tca 96
Met Pro Thr Gly Arg His Ser Arg Asn Tyr Gly Trp Lys Ala Ser Ser
20 25 30
tcg gtg gtt gcg aca tcg tgt tgg aaa tgt acc aac aag gtg agc tta 144
Ser Val Val Ala Thr Ser Cys Trp Lys Cys Thr Asn Lys Val Ser Leu
35 40 45
aaa cct tgt tac aag agg ttg ccg caa gac atc cgc aag cgt aaa aac 192
Lys Pro Cys Tyr Lys Arg Leu Pro Gln Asp Ile Arg Lys Arg Lys Asn
50 55 60
gcg ttt caa aat gac cgt act ttg gtt tcc gga gtg ccg ttt ttt gct 240
Ala Phe Gln Asn Asp Arg Thr Leu Val Ser Gly Val Arg Phe Phe Ala
65 70 75 80
gct tgg cgc agg gaa aaa cag gcg gtt tgt gct ata att ctc cgc aaa 288
Ala Trp Arg Arg Glu Lys Gln Ala Val Cys Ala Ile Ile Leu Arg Lys
85 90 95
ttt tta ccg cac ttt agg atc aat atg tcg ttt caa ttc aac gcg atc 336
Phe Leu Pro His Phe Arg Ile Asn Met Ser Phe Gln Phe Asn Ala Ile
100 105 110
gcc tta ctt ttg gtg att tta att tta tta ggt gta ctc agc cac aac 384
Ala Leu Leu Leu Val Ile Leu Ile Leu Leu Gly Val Leu Ser His Asn

10

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30

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      115              120              125
agt tcc atc acc att tcc gct gcc gta ttg ctc atc atg caa caa acc      432
Ser Ser Ile Thr Ile Ser Ala Ala Val Leu Leu Ile Met Gln Gln Thr
      130              135              140

ttg ctc gca aaa tat att cct tac ttg gaa aaa tac gcc ttg agc atc      480
Leu Leu Ala Lys Tyr Ile Pro Tyr Leu Glu Lys Tyr Gly Leu Ser Ile
      145              150              155              160

ggt atc gta att tta acc atc gcc gta cta agc ccg ttg gtt tcc gcc      528
Gly Ile Val Ile Leu Thr Ile Gly Val Leu Ser Pro Leu Val Ser Gly
      165              170              175

aga att caa ctg cct gcc ttg tcg gca ttt ttt agc tgg cga atg ttt      576
Arg Ile Gln Leu Pro Gly Leu Ser Ala Phe Phe Ser Trp Arg Met Phe
      180              185              190

ggt gcc att gcc gtc gcc gta tta gtg gcg tgg ctt gcc gcc aaa gcc      624
Val Ala Ile Gly Val Gly Val Leu Val Ala Trp Leu Ala Gly Lys Gly
      195              200              205

ggt ccg ctc atg ggg gaa gag cct gtt ctg gta acc gcc ttg gtt atc      672
Val Pro Leu Met Gly Glu Glu Pro Val Leu Val Thr Gly Leu Val Ile
      210              215              220

ggc acc att atc gcc gtt tct ttt ctc ggt ggt att ccc gtt ggt ccc      720
Gly Thr Ile Ile Gly Val Ser Phe Leu Gly Gly Ile Pro Val Gly Pro
      225              230              235              240

ctt att gog gca ggg att ttg gca tta tta ata gga aaa ttt taa      765
Leu Ile Ala Ala Gly Ile Leu Ala Leu Leu Ile Gly Lys Phe
      245              250

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<210> 136
<211> 254
<212> PRT
<213> Actinobacillus actinomycetemcomitans

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<400> 136

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Met Trp Ile Phe Tyr Asn Thr Arg Thr Phe Val Pro Asn Tyr Arg Leu
1              5              10              15

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Met Pro Thr Gly Arg His Ser Arg Asn Tyr Gly Trp Lys Ala Ser Ser
20              25              30

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Ser Val Val Ala Thr Ser Cys Trp Lys Cys Thr Asn Lys Val Ser Leu
35              40              45

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Lys Pro Cys Tyr Lys Arg Leu Pro Gln Asp Ile Arg Lys Arg Lys Asn
50              55              60

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Ala Phe Gln Asn Asp Arg Thr Leu Val Ser Gly Val Arg Phe Phe Ala
65              70              75              80

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Ala Trp Arg Arg Glu Lys Gln Ala Val Cys Ala Ile Ile Leu Arg Lys
85 90 95

Phe Leu Pro His Phe Arg Ile Asn Met Ser Phe Gln Phe Asn Ala Ile
100 105 110

Ala Leu Leu Leu Val Ile Leu Ile Leu Leu Gly Val Leu Ser His Asn
115 120 125

Ser Ser Ile Thr Ile Ser Ala Ala Val Leu Leu Ile Met Gln Gln Thr
130 135 140

Leu Leu Ala Lys Tyr Ile Pro Tyr Leu Glu Lys Tyr Gly Leu Ser Ile
145 150 155 160

Gly Ile Val Ile Leu Thr Ile Gly Val Leu Ser Pro Leu Val Ser Gly
165 170 175

Arg Ile Gln Leu Pro Gly Leu Ser Ala Phe Phe Ser Trp Arg Met Phe
180 185 190

Val Ala Ile Gly Val Gly Val Leu Val Ala Trp Leu Ala Gly Lys Gly
195 200 205

Val Pro Leu Met Gly Glu Glu Pro Val Leu Val Thr Gly Leu Val Ile
210 215 220

Gly Thr Ile Ile Gly Val Ser Phe Leu Gly Gly Ile Pro Val Gly Pro
225 230 235 240

Leu Ile Ala Ala Gly Ile Leu Ala Leu Leu Ile Gly Lys Phe
245 250

<210> 137
<211> 387
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(387)

<400> 137
atg aaa aac aaa tgg tta ttg att gcc gcc gtg agc ggt ttt tta tgt 48
Met Lys Asn Lys Trp Leu Leu Ile Ala Ala Val Ser Gly Phe Leu Cys
1 5 10 15
gtg act atc ggt gcg ttt gcg gcg cac ggt tta agc caa gtg ttg gac 96
Val Thr Ile Gly Ala Phe Ala Ala His Gly Leu Ser Gln Val Leu Asp

10

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      20      25      30
gcg aaa gcc tta gcg tgg att gac acc ggc gtg aaa tat caa atg ttc      144
Ala Lys Ala Leu Ala Trp Ile Asp Thr Gly Val Lys Tyr Gln Met Phe
      35      40      45

cac acc ctc gcc atc atg gga atc ggc atc gca caa tta tgt cgc gaa      192
His Thr Leu Ala Ile Met Gly Ile Gly Ile Ala Gln Leu Cys Arg Glu
      50      55      60

cca ttt gcc gcc aac aaa agc gcc aat gtt gcc gcc ggc gcg tgg tca      240
Pro Phe Ala Ala Asn Lys Ser Ala Asn Val Ala Ala Gly Ala Trp Ser
      65      70      75      80

ttc gga atc ctt ctc ttt agc ggc agt tta tac gcc ctc gca ctt ggc      288
Phe Gly Ile Leu Leu Phe Ser Gly Ser Leu Tyr Ala Leu Ala Leu Gly
      85      90      95

tca ggt aaa ttt atg gtt tgg ctc acg ccc atc ggc ggc acg cta ttt      336
Ser Gly Lys Phe Met Val Trp Leu Thr Pro Ile Gly Gly Thr Leu Phe
      100      105      110

tta atc ggc tgg ctt ggt tta gct tac ggc gct ttc aaa agt aaa tca      384
Leu Ile Gly Trp Leu Gly Leu Ala Tyr Gly Ala Phe Lys Ser Lys Ser
      115      120      125

gaa      387
Glu

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<210> 138
<211> 129
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 138

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Met Lys Asn Lys Trp Leu Leu Ile Ala Ala Val Ser Gly Phe Leu Cys
1      5      10      15

Val Thr Ile Gly Ala Phe Ala Ala His Gly Leu Ser Gln Val Leu Asp
      20      25      30

Ala Lys Ala Leu Ala Trp Ile Asp Thr Gly Val Lys Tyr Gln Met Phe
      35      40      45

His Thr Leu Ala Ile Met Gly Ile Gly Ile Ala Gln Leu Cys Arg Glu
      50      55      60

Pro Phe Ala Ala Asn Lys Ser Ala Asn Val Ala Ala Gly Ala Trp Ser
      65      70      75      80

Phe Gly Ile Leu Leu Phe Ser Gly Ser Leu Tyr Ala Leu Ala Leu Gly
      85      90      95

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30

Ser Gly Lys Phe Met Val Trp Leu Thr Pro Ile Gly Gly Thr Leu Phe
 100 105 110

Leu Ile Gly Trp Leu Gly Leu Ala Tyr Gly Ala Phe Lys Ser Lys Ser
 115 120 125

Glu

<210> 139
 <211> 684
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

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<220>
 <221> CDS
 <222> (1)..(684)

<400> 139
 atc aat ttg gca cat aat tat cag caa aaa tgg cag gcg gac atc ggt 48
 Ile Asn Leu Ala His Asn Tyr Gln Gln Lys Trp Gln Ala Asp Ile Gly
 1 5 10 15

cgg cac gcc gtg cag tat ttt gct tac gat aac ccg cgg gcg gat ttt 96
 Arg His Ala Val Gln Tyr Phe Ala Tyr Asp Asn Pro Arg Ala Asp Phe
 20 25 30

tac gcc gaa caa att cat ttc tcc gaa caa gcc gcc tat ttc tta ctc 144
 Tyr Ala Glu Gln Ile His Phe Ser Glu Gln Gly Ala Tyr Phe Leu Leu
 35 40 45 20

cac acg ccg caa gcc cgc gtg caa atc aat tca ccg tat ttg ggt gag 192
 His Thr Pro Gln Gly Arg Val Gln Ile Asn Ser Pro Tyr Leu Gly Glu
 50 55 60

cat aat atc tct aat gcg ttg gcg gca act gcc ttg gcg atg aac gtg 240
 His Asn Ile Ser Asn Ala Leu Ala Ala Thr Ala Leu Ala Met Asn Val
 65 70 75 80

ggt gcc acc acg gcg cag gtg aaa aaa ggg ttg gaa acg ccc tct ttg 288
 Gly Ala Thr Thr Ala Gln Val Lys Lys Gly Leu Glu Thr Pro Ser Leu
 85 90 95

gtg aaa ggg cgt ttg ttc ccg att cag cct tgt gaa aat ctg tta ttg 336
 Val Lys Gly Arg Leu Phe Pro Ile Gln Pro Cys Glu Asn Leu Leu Leu
 100 105 110 30

ctg gac gat act tac aac gcc aat gtg gga tct atg aaa tcg gcg att 384
 Leu Asp Asp Thr Tyr Asn Ala Asn Val Gly Ser Met Lys Ser Ala Ile
 115 120 125

tcc gtg tta caa aaa tat cct gct ttt cgc gtc ttt gtt gtt ggt gat 432
 Ser Val Leu Gln Lys Tyr Pro Ala Phe Arg Val Phe Val Val Gly Asp
 130 135 140

atg gcc gaa tta gcc gat aat gcg caa ctt tgc cat caa gag gtg ggg 480
 Met Gly Glu Leu Gly Asp Asn Ala Gln Leu Cys His Gln Glu Val Gly

145	150	155	160		
gag ttc gct cat gcc gcc aag tta gac tta gtg ctt tct ttc ggg tgt				528	
Glu Phe Ala His Ala Ala Lys Leu Asp Leu Val Leu Ser Phe Gly Cys	165	170	175		
tcg agt ggc gtt ata agt gcg gtt aat tcg gga cgc cat ttt acc gat				576	
Ser Ser Gly Val Ile Ser Ala Val Asn Ser Gly Arg His Phe Thr Asp	180	185	190		
aaa acg gaa ctt gta act tat tta aca ccg att att caa caa caa tta				624	
Lys Thr Glu Leu Val Thr Tyr Leu Thr Pro Ile Ile Gln Gln Gln Leu	195	200	205		
gca caa caa aaa gtc gtt gtt ttg gtg aaa gga tca cgc agc atg aaa				672	10
Ala Gln Gln Lys Val Val Val Leu Val Lys Gly Ser Arg Ser Met Lys	210	215	220		
atg gaa gaa gtg				684	
Met Glu Glu Val					
225					
<210>	140				
<211>	228				
<212>	PRT				
<213>	Actinobacillus actinomycetemcomitans				
<400>	140				
Ile Asn Leu Ala His Asn Tyr Gln Gln Lys Trp Gln Ala Asp Ile Gly					20
1	5	10	15		
Arg His Ala Val Gln Tyr Phe Ala Tyr Asp Asn Pro Arg Ala Asp Phe					
	20	25	30		
Tyr Ala Glu Gln Ile His Phe Ser Glu Gln Gly Ala Tyr Phe Leu Leu					
	35	40	45		
His Thr Pro Gln Gly Arg Val Gln Ile Asn Ser Pro Tyr Leu Gly Glu					
	50	55	60		
His Asn Ile Ser Asn Ala Leu Ala Ala Thr Ala Leu Ala Met Asn Val					30
65	70	75	80		
Gly Ala Thr Thr Ala Gln Val Lys Lys Gly Leu Glu Thr Pro Ser Leu					
	85	90	95		
Val Lys Gly Arg Leu Phe Pro Ile Gln Pro Cys Glu Asn Leu Leu Leu					
	100	105	110		
Leu Asp Asp Thr Tyr Asn Ala Asn Val Gly Ser Met Lys Ser Ala Ile					
	115	120	125		

Ser Val Leu Gln Lys Tyr Pro Ala Phe Arg Val Phe Val Val Gly Asp
 130 135 140

Met Gly Glu Leu Gly Asp Asn Ala Gln Leu Cys His Gln Glu Val Gly
 145 150 155 160

Glu Phe Ala His Ala Ala Lys Leu Asp Leu Val Leu Ser Phe Gly Cys
 165 170 175

Ser Ser Gly Val Ile Ser Ala Val Asn Ser Gly Arg His Phe Thr Asp
 180 185 190

Lys Thr Glu Leu Val Thr Tyr Leu Thr Pro Ile Ile Gln Gln Gln Leu
 195 200 205

Ala Gln Gln Lys Val Val Val Leu Val Lys Gly Ser Arg Ser Met Lys
 210 215 220

Met Glu Glu Val
 225

<210> 141
 <211> 267
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(267)

<400> 141
 gat ggc ggt aag gcg ggt tcg agg tat gca ggt att atc tat aaa tct 48
 Asp Gly Gly Lys Ala Gly Ser Arg Tyr Ala Gly Ile Ile Tyr Lys Ser
 1 5 10 15
 gtg aag cca tat ttt cgt ggt gat agt cgt ttt ttt ggt aag gtc tgt 96
 Val Lys Pro Tyr Phe Arg Gly Asp Ser Arg Phe Phe Gly Lys Val Cys
 20 25 30
 gat att aga att gag ctt tct agt gat ggc act att tta tct tac caa 144
 Asp Ile Arg Ile Glu Leu Ser Ser Asp Gly Thr Ile Leu Ser Tyr Gln
 35 40 45
 aag gtc tcc ggg cca aat gat tta tgt ggg gcg gct tta aat gct att 192
 Lys Val Ser Gly Pro Asn Asp Leu Cys Gly Ala Ala Leu Asn Ala Ile
 50 55 60
 ggt caa acc aga aaa atg aac gaa ccg cct acg ccg gaa gaa tat gaa 240
 Gly Gln Thr Arg Lys Met Asn Glu Pro Pro Thr Pro Glu Glu Tyr Glu
 65 70 75 80
 ata ttt aaa agg tcc att gta acc ttt 267
 Ile Phe Lys Arg Ser Ile Val Thr Phe

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85

<210> 142
 <211> 89
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 142

Asp Gly Gly Lys Ala Gly Ser Arg Tyr Ala Gly Ile Ile Tyr Lys Ser
 1 5 10 15

Val Lys Pro Tyr Phe Arg Gly Asp Ser Arg Phe Phe Gly Lys Val Cys
 20 25 30

10

Asp Ile Arg Ile Glu Leu Ser Ser Asp Gly Thr Ile Leu Ser Tyr Gln
 35 40 45

Lys Val Ser Gly Pro Asn Asp Leu Cys Gly Ala Ala Leu Asn Ala Ile
 50 55 60

Gly Gln Thr Arg Lys Met Asn Glu Pro Pro Thr Pro Glu Glu Tyr Glu
 65 70 75 80

Ile Phe Lys Arg Ser Ile Val Thr Phe
 85

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<210> 143
 <211> 683
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(681)

<400> 143

ggt gcc tta tat ttt gta ttc agt ctg atg ggc gtg ttc gcc agt ttg 48
 Gly Ala Leu Tyr Phe Val Phe Ser Leu Met Gly Val Phe Ala Ser Leu
 1 5 10 15

tta tcc acc gcg cgc ggc ggc tgg att ggt atc cct ttt gtt ctc ctg 96
 Leu Ser Thr Ala Arg Gly Gly Trp Ile Gly Ile Pro Phe Val Leu Leu
 20 25 30

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tta atc ctc ttt gct tat cgt cgt tat tta tgg aaa aaa ttc gtc gcc 144
 Leu Ile Leu Phe Ala Tyr Arg Arg Tyr Leu Ser Lys Lys Phe Val Ala
 35 40 45

ggc ttt ttt att gtg ctt gcc ctg att gta aca acc gtt gcg atg ttg 192
 Gly Phe Phe Ile Val Leu Ala Leu Ile Val Thr Thr Val Ala Met Leu
 50 55 60

cca aat acc aaa att aaa gaa cgc att gcc gcc gca gaa tac gac atc 240

Pro Asn Thr Lys Ile Lys Glu Arg Ile Ala Ala Ala Glu Tyr Asp Ile
65 70 75 80
atc gcc tat ttt caa caa aat aac ggt tct acc tcc gtc ggc gcc cgt 288
Ile Ala Tyr Phe Gln Gln Asn Asn Gly Ser Thr Ser Val Gly Ala Arg
85 90 95
ttt gat atg tgg aaa agc gtg atg tta atg acg cag gaa aaa ccg att 336
Phe Asp Met Trp Lys Ser Val Met Leu Met Thr Gln Glu Lys Pro Ile
100 105 110
ttc ggt tgg ggc gta caa ggg gtc agc gaa aaa cgc aaa ctg caa tat 384
Phe Gly Trp Gly Val Gln Gly Val Ser Glu Lys Arg Lys Leu Gln Tyr
115 120 125
gag caa ggt ttg ata agc caa tat gcc gcc gcc ttt aac cac gcg cac 432
Glu Gln Gly Leu Ile Ser Gln Tyr Ala Ala Ala Phe Asn His Ala His
130 135 140
aac caa tat ttt gat gat tta tcc aaa cgc ggc gca tta ggt tta ctc 480
Asn Gln Tyr Phe Asp Asp Leu Ser Lys Arg Gly Ala Leu Gly Leu Leu
145 150 155 160
gcc tta ctc ggc gta ttt tta gtg ccg ttg cgt ttc ttt ata cgg cat 528
Ala Leu Leu Gly Val Phe Leu Val Pro Leu Arg Phe Phe Ile Arg His
165 170 175
ctc aaa agc gtc gat tta gaa ctg aaa ctc gtt tcg ttg tta ggt gcg 576
Leu Lys Ser Val Asp Leu Glu Leu Lys Leu Val Ser Leu Leu Gly Ala
180 185 190
gtt cat att gtc tcc gtg atg ttc tac tgt ttc agc caa ggc ttt ttc 624
Val His Ile Val Ser Val Met Phe Tyr Cys Phe Ser Gln Gly Phe Phe
195 200 205
agc cat aac tcg ggc aat att ttc tat ttt ttc ccg gtg att gtg ttt 672
Ser His Asn Ser Gly Asn Ile Phe Tyr Phe Phe Pro Val Ile Val Phe
210 215 220
tac gcc ttg gt 683
Tyr Ala Leu
225

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<210> 144
<211> 227
<212> PRT
<213> Actinobacillus actinomycetemcomitans

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<400> 144

Gly Ala Leu Tyr Phe Val Phe Ser Leu Met Gly Val Phe Ala Ser Leu
1 5 10 15

Leu Ser Thr Ala Arg Gly Gly Trp Ile Gly Ile Pro Phe Val Leu Leu
20 25 30

Leu Ile Leu Phe Ala Tyr Arg Arg Tyr Leu Ser Lys Lys Phe Val Ala
35 40 45

Gly Phe Phe Ile Val Leu Ala Leu Ile Val Thr Thr Val Ala Met Leu
50 55 60

Pro Asn Thr Lys Ile Lys Glu Arg Ile Ala Ala Ala Glu Tyr Asp Ile
65 70 75 80

Ile Ala Tyr Phe Gln Gln Asn Asn Gly Ser Thr Ser Val Gly Ala Arg
85 90 95

Phe Asp Met Trp Lys Ser Val Met Leu Met Thr Gln Glu Lys Pro Ile
100 105 110

10

Phe Gly Trp Gly Val Gln Gly Val Ser Glu Lys Arg Lys Leu Gln Tyr
115 120 125

Glu Gln Gly Leu Ile Ser Gln Tyr Ala Ala Ala Phe Asn His Ala His
130 135 140

Asn Gln Tyr Phe Asp Asp Leu Ser Lys Arg Gly Ala Leu Gly Leu Leu
145 150 155 160

Ala Leu Leu Gly Val Phe Leu Val Pro Leu Arg Phe Phe Ile Arg His
165 170 175

20

Leu Lys Ser Val Asp Leu Glu Leu Lys Leu Val Ser Leu Leu Gly Ala
180 185 190

Val His Ile Val Ser Val Met Phe Tyr Cys Phe Ser Gln Gly Phe Phe
195 200 205

Ser His Asn Ser Gly Asn Ile Phe Tyr Phe Phe Pro Val Ile Val Phe
210 215 220

Tyr Ala Leu
225

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<210> 145
<211> 408
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(408)

<400> 145
gcc gat tat gcc atc gac tat ggt aac gat ttc gta ggt atc att gaa 48

Ala Asp Tyr Gly Ile Asp Tyr Gly Asn Asp Phe Val Gly Ile Ile Glu
 1 5 10 15
 gga aaa ttg aag tta aac aaa tca acg tta cat gat aat aac gcc tcc 96
 Gly Lys Leu Lys Leu Asn Lys Ser Thr Leu His Asp Asn Asn Ala Ser
 20 25 30
 ggc tac cgt ggc aaa ctg aac gaa aag gca cgt ttg ggc gta agt tac 144
 Gly Tyr Arg Gly Lys Leu Asn Glu Lys Ala Arg Leu Gly Val Ser Tyr
 35 40 45
 tta caa ggc tat cgc gta aca cca agc att ctt cct tat gcc aaa gtt 192
 Leu Gln Gly Tyr Arg Val Thr Pro Ser Ile Leu Pro Tyr Ala Lys Val
 50 55 60
 ggg gtg caa act gct aaa ttt gaa agt gag gtt cgt aca cgc aac tac 240
 Gly Val Gln Thr Ala Lys Phe Glu Ser Glu Val Arg Thr Arg Asn Tyr
 65 70 75 80
 tca gct acg cat agt gat acc aaa aac ggt ata ggt ttt ggt gcg ggt 288
 Ser Ala Thr His Ser Asp Thr Lys Asn Gly Ile Gly Phe Gly Ala Gly
 85 90 95
 gtt aag gtc aat ctg gta ccg gac ttt gag cta agc ttg gaa tat tta 336
 Val Lys Val Asn Leu Val Pro Asp Phe Glu Leu Ser Leu Glu Tyr Leu
 100 105 110
 agg act cat aac aaa ttt gat ggt caa aag tta aga ggt aat gta tat 384
 Arg Thr His Asn Lys Phe Asp Gly Gln Lys Leu Arg Gly Asn Val Tyr
 115 120 125
 agc acc aac gct aca tat cgt ttc 408
 Ser Thr Asn Ala Thr Tyr Arg Phe
 130 135

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<210> 146
 <211> 136
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 146

Ala Asp Tyr Gly Ile Asp Tyr Gly Asn Asp Phe Val Gly Ile Ile Glu
 1 5 10 15
 Gly Lys Leu Lys Leu Asn Lys Ser Thr Leu His Asp Asn Asn Ala Ser
 20 25 30
 Gly Tyr Arg Gly Lys Leu Asn Glu Lys Ala Arg Leu Gly Val Ser Tyr
 35 40 45
 Leu Gln Gly Tyr Arg Val Thr Pro Ser Ile Leu Pro Tyr Ala Lys Val
 50 55 60
 Gly Val Gln Thr Ala Lys Phe Glu Ser Glu Val Arg Thr Arg Asn Tyr
 65 70 75 80

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Ser Ala Thr His Ser Asp Thr Lys Asn Gly Ile Gly Phe Gly Ala Gly
85 90 95

Val Lys Val Asn Leu Val Pro Asp Phe Glu Leu Ser Leu Glu Tyr Leu
100 105 110

Arg Thr His Asn Lys Phe Asp Gly Gln Lys Leu Arg Gly Asn Val Tyr
115 120 125

Ser Thr Asn Ala Thr Tyr Arg Phe
130 135

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<210> 147
<211> 426
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(426)

<400> 147
atg aaa aaa att ctt acc gca ctt ttt tgc agt tgt ctc att tcc cct 48
Met Lys Lys Ile Leu Thr Ala Leu Phe Cys Ser Cys Leu Ile Ser Pro
1 5 10 15
ctc aca aac gct gaa acc ttg tct gat ggt tta cca cca cag gca gct 96
Leu Thr Asn Ala Glu Thr Leu Ser Asp Gly Leu Pro Pro Gln Ala Ala
20 25 30
ggt gat tat gtg ttc ttg gac ccg cat caa aac aat acg gat ata caa 144
Gly Asp Tyr Val Phe Leu Asp Pro His Gln Asn Asn Thr Asp Ile Gln
35 40 45
ttt cgt tta aaa ctt aaa ggc aaa caa tgg ctg gca gac ggt tcc caa 192
Phe Arg Leu Lys Leu Lys Gly Lys Gln Trp Leu Ala Asp Gly Ser Gln
50 55 60
aat gcc ggc aaa agc tgg tgc cct gtg tgc gaa gtc agt ggc gaa tgc 240
Asn Ala Gly Lys Ser Trp Ser Pro Val Cys Glu Val Ser Gly Glu Cys
65 70 75 80
aaa ctg gag aca tcc tcc aaa gcg gaa atc gaa cgc ttc ttt gag caa 288
Lys Leu Glu Thr Ser Ser Lys Ala Glu Ile Glu Arg Phe Phe Glu Gln
85 90 95
tat ccg caa gta cta aac cga aca gat gtc agc tgc att cac aat atg 336
Tyr Pro Gln Val Leu Asn Arg Thr Asp Val Ser Cys Ile His Asn Met
100 105 110
gcg ttc gct ttc tgc ggg tta act tta gat aaa aaa acc gat tat gtg 384
Ala Phe Ala Phe Cys Gly Leu Thr Leu Asp Lys Lys Thr Asp Tyr Val
115 120 125
atg gtc gca tta gtg acc aat ccg cca caa gtc aca tgc tat 426

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Met Val Ala Leu Val Thr Asn Pro Pro Gln Val Thr Ser Tyr
 130 135 140

<210> 148
 <211> 142
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 148

Met Lys Lys Ile Leu Thr Ala Leu Phe Cys Ser Cys Leu Ile Ser Pro
 1 5 10 15

Leu Thr Asn Ala Glu Thr Leu Ser Asp Gly Leu Pro Pro Gln Ala Ala
 20 25 30

Gly Asp Tyr Val Phe Leu Asp Pro His Gln Asn Asn Thr Asp Ile Gln
 35 40 45

Phe Arg Leu Lys Leu Lys Gly Lys Gln Trp Leu Ala Asp Gly Ser Gln
 50 55 60

Asn Ala Gly Lys Ser Trp Ser Pro Val Cys Glu Val Ser Gly Glu Cys
 65 70 75 80

Lys Leu Glu Thr Ser Ser Lys Ala Glu Ile Glu Arg Phe Phe Glu Gln
 85 90 95

Tyr Pro Gln Val Leu Asn Arg Thr Asp Val Ser Cys Ile His Asn Met
 100 105 110

Ala Phe Ala Phe Cys Gly Leu Thr Leu Asp Lys Lys Thr Asp Tyr Val
 115 120 125

Met Val Ala Leu Val Thr Asn Pro Pro Gln Val Thr Ser Tyr
 130 135 140

<210> 149
 <211> 679
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(678)

<400> 149

cgc cga att att ggc aca acg aca aca gga tat tca cta atg cgc gca
 Arg Arg Ile Ile Gly Thr Thr Thr Thr Gly Tyr Ser Leu Met Arg Ala
 1 5 10 15

48

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tta ttg cct ttt ctt cgt tta ttt aaa ttc gcc aaa ctg ccg tta att 96
 Leu Leu Pro Phe Leu Arg Leu Phe Lys Phe Ala Lys Leu Pro Leu Ile
 20 25 30
 tta ggc ggc ttg ctg atg att tta ggg ctg gcg tcc agt atc ggg ttg 144
 Leu Gly Gly Leu Leu Met Ile Leu Gly Leu Ala Ser Ser Ile Gly Leu
 35 40 45
 ctc acc ctt tcc ggc tgg ttt ctt gcc gcc acc gcc atc gcc ggt ttc 192
 Leu Thr Leu Ser Gly Trp Phe Leu Ala Ala Thr Ala Ile Ala Gly Phe
 50 55 60
 ggc tgc cta ttt aac ttt ttc tac cca tcc gcc agc gta cgc ggt ttg 240
 Gly Ser Leu Phe Asn Phe Phe Tyr Pro Ser Ala Ser Val Arg Gly Leu
 65 70 75 80
 gca atc ggg cgt acc gtg gcg cgc tac ctt gaa aaa gtg gtc acc cat 288
 Ala Ile Gly Arg Thr Val Ala Arg Tyr Leu Glu Lys Val Val Thr His
 85 90 95
 gac gcc acc ttc cgc gta ttg gca aaa ctg cgt gtg cag gtg ttt gac 336
 Asp Ala Thr Phe Arg Val Leu Ala Lys Leu Arg Val Gln Val Phe Asp
 100 105 110
 aaa atc att ccg tta agc cct gcg ctg ctc aac cgt tat cgt aac agc 384
 Lys Ile Ile Pro Leu Ser Pro Ala Leu Leu Asn Arg Tyr Arg Asn Ser
 115 120 125
 gat tta tta aac cgc ttg gtt gcc gat gtg gac acc ctc gac agc cta 432
 Asp Leu Leu Asn Arg Leu Val Ala Asp Val Asp Thr Leu Asp Ser Leu
 130 135 140
 tat ctt cgc ctc att gcg ccc ttt atc agc gcc ata gtg gtg att gcg 480
 Tyr Leu Arg Leu Ile Ala Pro Phe Ile Ser Ala Ile Val Val Ile Ala
 145 150 155 160
 ttc att acc ttt ggc ttg agt ttt att aat gcc ccg ctc gcg ctg ttt 528
 Phe Ile Thr Phe Gly Leu Ser Phe Ile Asn Ala Pro Leu Ala Leu Phe
 165 170 175
 atc ggt ttc aca tta ctg gcg ctc ttg ctg gtt atc ccg acg att ttt 576
 Ile Gly Phe Thr Leu Leu Ala Leu Leu Val Ile Pro Thr Ile Phe
 180 185 190
 tac cat ttg ggt aac aaa ttc ggc gcc aaa ctt acc caa tcc cgc gcc 624
 Tyr His Leu Gly Asn Lys Phe Gly Ala Lys Leu Thr Gln Ser Arg Ala
 195 200 205
 ctt tac cgc acg caa ttt atc gaa ttt att cag gcg caa gcg gaa tta 672
 Leu Tyr Arg Thr Gln Phe Ile Glu Phe Ile Gln Ala Gln Ala Glu Leu
 210 215 220
 ttg ctg t 679
 Leu Leu
 225

<210> 150

<211> 226

<212> PRT

<213> Actinobacillus actinomycetemcomitans

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<400> 150

Arg Arg Ile Ile Gly Thr Thr Thr Thr Gly Tyr Ser Leu Met Arg Ala
 1 5 10 15

Leu Leu Pro Phe Leu Arg Leu Phe Lys Phe Ala Lys Leu Pro Leu Ile
 20 25 30

Leu Gly Gly Leu Leu Met Ile Leu Gly Leu Ala Ser Ser Ile Gly Leu
 35 40 45

Leu Thr Leu Ser Gly Trp Phe Leu Ala Ala Thr Ala Ile Ala Gly Phe
 50 55 60

Gly Ser Leu Phe Asn Phe Phe Tyr Pro Ser Ala Ser Val Arg Gly Leu
 65 70 75 80

Ala Ile Gly Arg Thr Val Ala Arg Tyr Leu Glu Lys Val Val Thr His
 85 90 95

Asp Ala Thr Phe Arg Val Leu Ala Lys Leu Arg Val Gln Val Phe Asp
 100 105 110

Lys Ile Ile Pro Leu Ser Pro Ala Leu Leu Asn Arg Tyr Arg Asn Ser
 115 120 125

Asp Leu Leu Asn Arg Leu Val Ala Asp Val Asp Thr Leu Asp Ser Leu
 130 135 140

Tyr Leu Arg Leu Ile Ala Pro Phe Ile Ser Ala Ile Val Val Ile Ala
 145 150 155 160

Phe Ile Thr Phe Gly Leu Ser Phe Ile Asn Ala Pro Leu Ala Leu Phe
 165 170 175

Ile Gly Phe Thr Leu Leu Ala Leu Leu Val Ile Pro Thr Ile Phe
 180 185 190

Tyr His Leu Gly Asn Lys Phe Gly Ala Lys Leu Thr Gln Ser Arg Ala
 195 200 205

Leu Tyr Arg Thr Gln Phe Ile Glu Phe Ile Gln Ala Gln Ala Glu Leu
 210 215 220

Leu Leu
 225

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<210> 151
 <211> 323
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(321)

<400> 151
 cct tcc aaa ttg acg tta gct ctt gct att gca agt ggc tta agt gta 48
 Pro Ser Lys Leu Thr Leu Ala Leu Ala Ile Ala Ser Gly Leu Ser Val
 1 5 10 15
 aca aat tta agc tat gcc act aac gat act att caa gcg ggc aac ggc 96
 Thr Asn Leu Ser Tyr Ala Thr Asn Asp Thr Ile Gln Ala Gly Asn Gly
 20 25 30
 att gcc gtg gta caa acc caa tcg ggt gaa atc caa ggt tat att cat 144
 Ile Ala Val Val Gln Thr Gln Ser Gly Glu Ile Gln Gly Tyr Ile His
 35 40 45
 aac gat att ttg acc tat aaa ggc att ccg tat gcc aca gca gaa cgt 192
 Asn Asp Ile Leu Thr Tyr Lys Gly Ile Pro Tyr Ala Thr Ala Glu Arg
 50 55 60
 ttt atg cca cca aaa ccg gtg gag aat tgg caa ggg aca aaa atg gcg 240
 Phe Met Pro Pro Lys Pro Val Glu Asn Trp Gln Gly Thr Lys Met Ala
 65 70 75 80
 ttg act tat ggc gat gtc tgc ccg caa gtg ccg atg ggc ggt cgt agt 288
 Leu Thr Tyr Gly Asp Val Cys Pro Gln Val Pro Met Gly Gly Arg Ser
 85 90 95
 ttc ttc ttt acc gga cct gaa atg acg gaa agt ga 323
 Phe Phe Phe Thr Gly Pro Glu Met Thr Glu Ser
 100 105

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<210> 152
 <211> 107
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 152

Pro Ser Lys Leu Thr Leu Ala Leu Ala Ile Ala Ser Gly Leu Ser Val
 1 5 10 15
 Thr Asn Leu Ser Tyr Ala Thr Asn Asp Thr Ile Gln Ala Gly Asn Gly
 20 25 30
 Ile Ala Val Val Gln Thr Gln Ser Gly Glu Ile Gln Gly Tyr Ile His
 35 40 45
 Asn Asp Ile Leu Thr Tyr Lys Gly Ile Pro Tyr Ala Thr Ala Glu Arg

30

50 55 60

Phe Met Pro Pro Lys Pro Val Glu Asn Trp Gln Gly Thr Lys Met Ala
 65 70 75 80

Leu Thr Tyr Gly Asp Val Cys Pro Gln Val Pro Met Gly Gly Arg Ser
 85 90 95

Phe Phe Phe Thr Gly Pro Glu Met Thr Glu Ser
 100 105

<210> 153
 <211> 177
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(177)

<400> 153
 ggc ggc ggt gcc tgg gtt cag gcg gat ttg aag atg ttc caa atg cac 48
 Gly Gly Gly Ala Trp Val Gln Ala Asp Leu Lys Met Phe Gln Met His
 1 5 10 15

agg atg tcg ttt ggt tca tcg gtg gcc gcg caa aat acc ttg aac gtg 96
 Arg Met Ser Phe Gly Ser Ser Val Ala Ala Gln Asn Thr Leu Asn Val
 20 25 30

gtt gat att tac gcc gtg tca ctc aaa acc atc caa tgt cag ctg aaa 144
 Val Asp Ile Tyr Ala Val Ser Leu Lys Thr Ile Gln Cys Gln Leu Lys
 35 40 45

gcc att gtg aca gat ttt gat att tcg cac ctt 177
 Ala Ile Val Thr Asp Phe Asp Ile Ser His Leu
 50 55

<210> 154
 <211> 59
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 154
 Gly Gly Gly Ala Trp Val Gln Ala Asp Leu Lys Met Phe Gln Met His
 1 5 10 15

Arg Met Ser Phe Gly Ser Ser Val Ala Ala Gln Asn Thr Leu Asn Val
 20 25 30

Val Asp Ile Tyr Ala Val Ser Leu Lys Thr Ile Gln Cys Gln Leu Lys
 35 40 45

10

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Ala Ile Val Thr Asp Phe Asp Ile Ser His Leu
50 55

<210> 155
<211> 469
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(468)

<400> 155
atg gag aaa aaa caa acc tca cgg gta caa aaa ctg gaa ttt ttg ctc 48 10
Met Glu Lys Lys Gln Thr Ser Arg Val Gln Lys Leu Glu Phe Leu Leu
1 5 10 15
aaa caa aca gat aaa atc cat ctg cgc gac gcg gca caa atg ctt gat 96
Lys Gln Thr Asp Lys Ile His Leu Arg Asp Ala Ala Gln Met Leu Asp
20 25 30
gtg tcg gaa atg act tta cgt cgg gat tta agt tcc gac agc ggc aat 144
Val Ser Glu Met Thr Leu Arg Arg Asp Leu Ser Ser Asp Ser Gly Asn
35 40 45
gtg gtg tta ttg ggc ggc tat atc gtg atg aac cca caa aaa agc ggc 192
Val Val Leu Leu Gly Gly Tyr Ile Val Met Asn Pro Gln Lys Ser Gly
50 55 60
aat cat tat cag att ttt gac caa caa acg cgc cac att acg gaa aaa 240 20
Asn His Tyr Gln Ile Phe Asp Gln Gln Thr Arg His Ile Thr Glu Lys
65 70 75 80
atg tgg ctc ggt aaa ctc gcc gcc aat ctc gtc aag gac gga gat acc 288
Met Trp Leu Gly Lys Leu Ala Ala Asn Leu Val Lys Asp Gly Asp Thr
85 90 95
gtg ttc ttc gat tgc ggt agc acc att ccg ttt atc att tcg caa atc 336
Val Phe Phe Asp Cys Gly Ser Thr Ile Pro Phe Ile Ile Ser Gln Ile
100 105 110
gat ccg cag ata aaa ttc acc gca ctt ttt tgc tcc atc aat agt ttt 384
Asp Pro Gln Ile Lys Phe Thr Ala Leu Phe Cys Ser Ile Asn Ser Phe
115 120 125
atg gcg ttg cag gac aaa ccg cac tgc gaa gtg att ctg tgc ggc gga 432 30
Met Ala Leu Gln Asp Lys Pro His Cys Glu Val Ile Leu Cys Gly Gly
130 135 140
cat tat tcg cgc cac aat tct ttc ctg act tcc gtg c 469
His Tyr Ser Arg His Asn Ser Phe Leu Thr Ser Val
145 150 155

<210> 156
<211> 156
<212> PRT
<213> Actinobacillus actinomycetemcomitans

<400> 156

Met Glu Lys Lys Gln Thr Ser Arg Val Gln Lys Leu Glu Phe Leu Leu
1 5 10 15

Lys Gln Thr Asp Lys Ile His Leu Arg Asp Ala Ala Gln Met Leu Asp
20 25 30

Val Ser Glu Met Thr Leu Arg Arg Asp Leu Ser Ser Asp Ser Gly Asn
35 40 45

Val Val Leu Leu Gly Gly Tyr Ile Val Met Asn Pro Gln Lys Ser Gly
50 55 60

Asn His Tyr Gln Ile Phe Asp Gln Gln Thr Arg His Ile Thr Glu Lys
65 70 75 80

Met Trp Leu Gly Lys Leu Ala Ala Asn Leu Val Lys Asp Gly Asp Thr
85 90 95

Val Phe Phe Asp Cys Gly Ser Thr Ile Pro Phe Ile Ile Ser Gln Ile
100 105 110

Asp Pro Gln Ile Lys Phe Thr Ala Leu Phe Cys Ser Ile Asn Ser Phe
115 120 125

Met Ala Leu Gln Asp Lys Pro His Cys Glu Val Ile Leu Cys Gly Gly
130 135 140

His Tyr Ser Arg His Asn Ser Phe Leu Thr Ser Val
145 150 155

<210> 157

<211> 340

<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> (1)..(339)

<400> 157

atg aca tat cca ggt gga aaa ggt aaa tgt ttc caa aaa atc att aat 48
Met Thr Tyr Pro Gly Gly Lys Gly Lys Cys Phe Gln Lys Ile Ile Asn
1 5 10 15

tta atg cct ccg cat gac gta tat att gaa act cat ctt ggt agt ggt 96
Leu Met Pro Pro His Asp Val Tyr Ile Glu Thr His Leu Gly Ser Gly
20 25 30

gca gta cta cga aat aaa aaa cca gca cta aaa aat att gga ata gat 144
Ala Val Leu Arg Asn Lys Lys Pro Ala Leu Lys Asn Ile Gly Ile Asp

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35	40	45	
cta gat ttt gat gtt att caa tca tgg att ggt tat tct cct gaa aat			192
Leu Asp Phe Asp Val Ile Gln Ser Trp Ile Gly Tyr Ser Pro Glu Asn			
50	55	60	
cat aag ttt ttt aat aat gat gca ttg gcg ttt cta act aag tac ctg			240
His Lys Phe Phe Asn Asn Asp Ala Leu Ala Phe Leu Thr Lys Tyr Leu			
65	70	75	80
ttt act ggg aaa gag tta gta tat tgt gat cct cca tat gtt ctt tca			288
Phe Thr Gly Lys Glu Leu Val Tyr Cys Asp Pro Pro Tyr Val Leu Ser			
	85	90	95
act aga aga aga caa aaa ata tat aaa tat gaa tac act gat gag cag			336
Thr Arg Arg Arg Gln Lys Ile Tyr Lys Tyr Glu Tyr Thr Asp Glu Gln			
	100	105	110
cat g			340
His			

<210> 158
 <211> 113
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 158

Met Thr Tyr Pro Gly Gly Lys Gly Lys Cys Phe Gln Lys Ile Ile Asn			
1	5	10	15
Leu Met Pro Pro His Asp Val Tyr Ile Glu Thr His Leu Gly Ser Gly			
	20	25	30
Ala Val Leu Arg Asn Lys Lys Pro Ala Leu Lys Asn Ile Gly Ile Asp			
	35	40	45
Leu Asp Phe Asp Val Ile Gln Ser Trp Ile Gly Tyr Ser Pro Glu Asn			
	50	55	60
His Lys Phe Phe Asn Asn Asp Ala Leu Ala Phe Leu Thr Lys Tyr Leu			
	65	70	75
			80
Phe Thr Gly Lys Glu Leu Val Tyr Cys Asp Pro Pro Tyr Val Leu Ser			
	85	90	95
Thr Arg Arg Arg Gln Lys Ile Tyr Lys Tyr Glu Tyr Thr Asp Glu Gln			
	100	105	110
His			

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<210> 159
 <211> 771
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(771)

<400> 159
 atc gac gct ttt ttc tct cgc caa aac aat caa ttt cac ttg gaa caa 48
 Ile Asp Ala Phe Ser Arg Gln Asn Asn Gln Phe His Leu Glu Gln
 1 5 10 15
 caa agc cat tgc gtt aac caa att atc gag caa tgg cgt tat aac ggg 96
 Gln Ser His Cys Val Asn Gln Ile Ile Glu Gln Trp Arg Tyr Asn Gly
 20 25 30
 caa att atc ggg cgt gaa att ccg caa ttt gtc gcc gaa cag aaa aac 144
 Gln Ile Ile Gly Arg Glu Ile Pro Gln Phe Val Ala Glu Gln Lys Asn
 35 40 45
 caa caa ggc ttg gca gtg cgt gtc acc tgc ccc gag caa acc tct ctt 192
 Gln Gln Gly Leu Ala Val Arg Val Thr Cys Pro Glu Gln Thr Ser Leu
 50 55 60
 tta gcg gaa ttt aac aat caa ccg gtg aac gat gcc ctt caa acg gca 240
 Leu Ala Glu Phe Asn Asn Gln Pro Val Asn Asp Ala Leu Gln Thr Ala
 65 70 75 80
 gaa aag tgc ggt gta tct ttt gag agt ttt cat att gtg gcg gaa gat 288
 Glu Lys Cys Gly Val Ser Phe Glu Ser Phe His Ile Val Ala Glu Asp
 85 90 95
 ctc aat tct gaa atc acc gcc acg gaa aca ccc gct tgg caa ctg ctc 336
 Leu Asn Ser Glu Ile Thr Ala Thr Glu Thr Pro Ala Trp Gln Leu Leu
 100 105 110
 tac acc acc tat ttg cag tct tgt tct ccc ctg caa agc ggt gaa tcc 384
 Tyr Thr Thr Tyr Leu Gln Ser Cys Ser Pro Leu Gln Ser Gly Glu Ser
 115 120 125
 ctg caa ccg att ccg ctg tat aaa caa ctg aaa aac ata ccg cac tta 432
 Leu Gln Pro Ile Pro Leu Tyr Lys Gln Leu Lys Asn Ile Pro His Leu
 130 135 140
 gca atg gat ttg gtt aaa tgg cag gaa aat tgg cag gcg tgc gat caa 480
 Ala Met Asp Leu Val Lys Trp Gln Glu Asn Trp Gln Ala Cys Asp Gln
 145 150 155 160
 ttg caa atg aac ggt tcc gtg ttg gaa caa cag gct ttg gtg caa att 528
 Leu Gln Met Asn Gly Ser Val Leu Glu Gln Gln Ala Leu Val Gln Ile
 165 170 175
 tca gac acc caa agc acg ctg ttt aag cat ggt tac cat cta acg cag 576
 Ser Asp Thr Gln Ser Thr Leu Phe Lys His Gly Tyr His Leu Thr Gln
 180 185 190
 gaa att gag cga cac agc ggc att cct act tac tat tat tta tac cgc 624
 Glu Ile Glu Arg His Ser Gly Ile Pro Thr Tyr Tyr Tyr Leu Tyr Arg

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195	200	205	
atc ggt gga aaa agc tgt gaa gcg gag ctg caa tca cgc tgt ccg tta			672
Ile Gly Gly Lys Ser Cys Glu Ala Glu Leu Gln Ser Arg Cys Pro Leu			
210	215	220	
tgt aaa aga aaa tgg acg tta agc cac cgc ctt ttt gac ttc tta tat			720
Cys Lys Arg Lys Trp Thr Leu Ser His Pro Leu Phe Asp Phe Leu Tyr			
225	230	235	240
ttt aaa tgt gat cat tgt cgc ctc gtt tca aac ctc tca tgg cat tgg			768
Phe Lys Cys Asp His Cys Arg Leu Val Ser Asn Leu Ser Trp His Trp			
	245	250	255
caa			771
Gln			

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<210> 160
 <211> 257
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 160

Ile Asp Ala Phe Phe Ser Arg Gln Asn Asn Gln Phe His Leu Glu Gln
1 5 10 15

Gln Ser His Cys Val Asn Gln Ile Ile Glu Gln Trp Arg Tyr Asn Gly
20 25 30

20

Gln Ile Ile Gly Arg Glu Ile Pro Gln Phe Val Ala Glu Gln Lys Asn
35 40 45

Gln Gln Gly Leu Ala Val Arg Val Thr Cys Pro Glu Gln Thr Ser Leu
50 55 60

Leu Ala Glu Phe Asn Asn Gln Pro Val Asn Asp Ala Leu Gln Thr Ala
65 70 75 80

Glu Lys Cys Gly Val Ser Phe Glu Ser Phe His Ile Val Ala Glu Asp
85 90 95

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Leu Asn Ser Glu Ile Thr Ala Thr Glu Thr Pro Ala Trp Gln Leu Leu
100 105 110

Tyr Thr Thr Tyr Leu Gln Ser Cys Ser Pro Leu Gln Ser Gly Glu Ser
115 120 125

Leu Gln Pro Ile Pro Leu Tyr Lys Gln Leu Lys Asn Ile Pro His Leu
130 135 140

Ala Met Asp Leu Val Lys Trp Gln Glu Asn Trp Gln Ala Cys Asp Gln
145 150 155 160

Leu Gln Met Asn Gly Ser Val Leu Glu Gln Gln Ala Leu Val Gln Ile
165 170 175

Ser Asp Thr Gln Ser Thr Leu Phe Lys His Gly Tyr His Leu Thr Gln
180 185 190

Glu Ile Glu Arg His Ser Gly Ile Pro Thr Tyr Tyr Tyr Leu Tyr Arg
195 200 205

Ile Gly Gly Lys Ser Cys Glu Ala Glu Leu Gln Ser Arg Cys Pro Leu
210 215 220

Cys Lys Arg Lys Trp Thr Leu Ser His Pro Leu Phe Asp Phe Leu Tyr
225 230 235 240

Phe Lys Cys Asp His Cys Arg Leu Val Ser Asn Leu Ser Trp His Trp
245 250 255

Gln

<210> 161
<211> 330
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(330)

<400> 161
gag gcg gat aaa ttt aaa gtg gat att ccg tct atg gca aga ctg aga 48
Glu Ala Asp Lys Phe Lys Val Asp Ile Pro Ser Met Ala Arg Leu Arg
1 5 10 15
atc agc ccg aat atc gac atc agt gcg aca ccg aag ctg ttg gaa ctt 96
Ile Ser Pro Asn Ile Asp Ile Ser Ala Thr Pro Lys Leu Leu Glu Leu
20 25 30
tcc ggc aat att gat att ccc tgg gcg cgc att gcc att gaa aac ctg 144
Ser Gly Asn Ile Asp Ile Pro Trp Ala Arg Ile Ala Ile Glu Asn Leu
35 40 45
ccg gac agt gca gtg gcg gtc agc tcc gat gaa gtg att tta aat ggc 192
Pro Asp Ser Ala Val Ala Val Ser Ser Asp Glu Val Ile Leu Asn Gly
50 55 60
aat aag aag agt act ctg ccg aaa aca ttg ccg agc gaa acc caa agc 240
Asn Lys Lys Ser Thr Leu Pro Lys Thr Leu Pro Ser Glu Thr Gln Ser

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65          70          75          80
ggc atg gca att cgt tct gat tta aga atc aat atc ggc gat gat gtc 288
Gly Met Ala Ile Arg Ser Asp Leu Arg Ile Asn Ile Gly Asp Asp Val
          85          90          95

agt tta aat gcc tat ggc ttg aaa acc cat ctc cac ggg ttg 330
Ser Leu Asn Ala Tyr Gly Leu Lys Thr His Leu His Gly Leu
          100          105          110

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<210> 162
<211> 110
<212> PRT
<213> Actinobacillus actinomycetemcomitans

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<400> 162

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Glu Ala Asp Lys Phe Lys Val Asp Ile Pro Ser Met Ala Arg Leu Arg
1          5          10          15

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Ile Ser Pro Asn Ile Asp Ile Ser Ala Thr Pro Lys Leu Leu Glu Leu
          20          25          30

```

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Ser Gly Asn Ile Asp Ile Pro Trp Ala Arg Ile Ala Ile Glu Asn Leu
          35          40          45

```

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Pro Asp Ser Ala Val Ala Val Ser Ser Asp Glu Val Ile Leu Asn Gly
          50          55          60

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20

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Asn Lys Lys Ser Thr Leu Pro Lys Thr Leu Pro Ser Glu Thr Gln Ser
65          70          75          80

```

```

Gly Met Ala Ile Arg Ser Asp Leu Arg Ile Asn Ile Gly Asp Asp Val
          85          90          95

```

```

Ser Leu Asn Ala Tyr Gly Leu Lys Thr His Leu His Gly Leu
          100          105          110

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<210> 163
<211> 625
<212> DNA
<213> Actinobacillus actinomycetemcomitans

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<220>
<221> CDS
<222> (1)..(624)

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<400> 163
gat aag aca gaa acg atg caa caa aat gaa gaa aaa atc acg ccg tca 48
Asp Lys Thr Glu Thr Met Gln Gln Asn Glu Glu Lys Ile Thr Pro Ser
1          5          10          15

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gag caa aaa ccg atc gtg cat gaa acc gtt gtg gtg aag aaa acc ggt 96

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Glu Gln Lys Pro Ile Val His Glu Thr Val Val Val Lys Lys Thr Gly
 20 25 30
 tcc gcg tta ggt ttg ctg gca ctt tta att gcg ttg ggt tta ggc ggc 144
 Ser Ala Leu Gly Leu Leu Ala Leu Leu Ile Ala Leu Gly Leu Gly Gly
 35 40 45
 gcg ggc tat tat ttc ggt cag cta cag gtt gac gaa ata cag caa aaa 192
 Ala Gly Tyr Tyr Phe Gly Gln Leu Gln Val Asp Glu Ile Gln Gln Lys
 50 55 60
 ctg acc gca ctt gaa aac caa ttg caa caa aaa ggc act tcc gcc gat 240
 Leu Thr Ala Leu Glu Asn Gln Leu Gln Gln Lys Gly Thr Ser Ala Asp
 65 70 75 80
 gtt gcc ggc atg ccg gat ttt agt gca gag aaa aat cag ctg gcg aaa 288
 Val Ala Gly Met Pro Asp Phe Ser Ala Glu Lys Asn Gln Leu Ala Lys
 85 90 95
 tta acg gaa ttt tcc caa gtg gca agt gat caa atc agc gcc ttg aat 336
 Leu Thr Glu Phe Ser Gln Val Ala Ser Asp Gln Ile Ser Ala Leu Asn
 100 105 110
 cag aat ttg tcc gcc aaa gaa caa agc ctg tcg gca ttg caa caa cag 384
 Gln Asn Leu Ser Ala Lys Glu Gln Ser Leu Ser Ala Leu Gln Gln Gln
 115 120 125
 gtg caa cgt ttg tcc aat caa gcc aaa gcg gag cag ccg aat gac tgg 432
 Val Gln Arg Leu Ser Asn Gln Ala Lys Ala Glu Gln Pro Asn Asp Trp
 130 135 140
 tta ctg acc gaa gcg gat ttt ctg tta aat aac gct ttg cgc aaa ctg 480
 Leu Leu Thr Glu Ala Asp Phe Leu Leu Asn Asn Ala Leu Arg Lys Leu
 145 150 155 160
 gtg ttg gat aac gac gtg gat acc agt gtg tcc ttg ttg aaa gtt gcc 528
 Val Leu Asp Asn Asp Val Asp Thr Ser Val Ser Leu Leu Lys Val Ala
 165 170 175
 gat gaa acc ctt tcc aaa gtc gcc atg cca caa gtg gcg cag gtg cgt 576
 Asp Glu Thr Leu Ser Lys Val Ala Met Pro Gln Val Ala Gln Val Arg
 180 185 190
 agc gcc att aac gcc gat tta aaa cag ttg ttg tcc ctg aac aat gtg g 625
 Ser Ala Ile Asn Ala Asp Leu Lys Gln Leu Leu Ser Leu Asn Asn Val
 195 200 205

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<210> 164
 <211> 208
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

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<400> 164

Asp Lys Thr Glu Thr Met Gln Gln Asn Glu Glu Lys Ile Thr Pro Ser
 1 5 10 15

Glu Gln Lys Pro Ile Val His Glu Thr Val Val Val Lys Lys Thr Gly
 20 25 30

Ser Ala Leu Gly Leu Leu Ala Leu Leu Ile Ala Leu Gly Leu Gly Gly
35 40 45

Ala Gly Tyr Tyr Phe Gly Gln Leu Gln Val Asp Glu Ile Gln Gln Lys
50 55 60

Leu Thr Ala Leu Glu Asn Gln Leu Gln Gln Lys Gly Thr Ser Ala Asp
65 70 75 80

Val Ala Gly Met Pro Asp Phe Ser Ala Glu Lys Asn Gln Leu Ala Lys
85 90 95

10

Leu Thr Glu Phe Ser Gln Val Ala Ser Asp Gln Ile Ser Ala Leu Asn
100 105 110

Gln Asn Leu Ser Ala Lys Glu Gln Ser Leu Ser Ala Leu Gln Gln Gln
115 120 125

Val Gln Arg Leu Ser Asn Gln Ala Lys Ala Glu Gln Pro Asn Asp Trp
130 135 140

Leu Leu Thr Glu Ala Asp Phe Leu Leu Asn Asn Ala Leu Arg Lys Leu
145 150 155 160

20

Val Leu Asp Asn Asp Val Asp Thr Ser Val Ser Leu Leu Lys Val Ala
165 170 175

Asp Glu Thr Leu Ser Lys Val Ala Met Pro Gln Val Ala Gln Val Arg
180 185 190

Ser Ala Ile Asn Ala Asp Leu Lys Gln Leu Leu Ser Leu Asn Asn Val
195 200 205

<210> 165

<211> 684

<212> DNA

<213> Actinobacillus actinomycetemcomitans

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<220>

<221> CDS

<222> (1)..(684)

<400> 165

atg acg att tta gtt ctg ggt atc aat cac aaa act gct tcc gtg gca 48
Met Thr Ile Leu Val Leu Gly Ile Asn His Lys Thr Ala Ser Val Ala
1 5 10 15

ttg cgg gaa aag gtg gcg ttt tcc gac gaa aag cgc act ttt gct ttg 96

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Leu Arg Glu Lys Val Ala Phe Ser Asp Glu Lys Arg Thr Phe Ala Leu
      20      25      30
cgt cac att caa caa acg cag ttg gcg gaa agt gcg gtg att tta tcc 144
Arg His Ile Gln Gln Thr Gln Leu Ala Glu Ser Ala Val Ile Leu Ser
      35      40      45
acc tgt aat cgc acg gaa gtt tat ctg cac aat aaa agc gtt ccg ccg 192
Thr Cys Asn Arg Thr Glu Val Tyr Leu His Asn Lys Ser Val Pro Pro
      50      55      60
caa gag acg caa acc tgg atc aca ctg gcg gtg cag tgg ttt gcc ggc 240
Gln Glu Thr Gln Thr Trp Ile Thr Leu Ala Val Gln Trp Phe Ala Gly
      65      70      75      80
att cat caa cta gcg ttg gcg gag ctg cag cac tgt gtt tat act cac 288
Ile His Gln Leu Ala Leu Ala Glu Leu Gln His Cys Val Tyr Thr His
      85      90      95
gaa aat ctt cag gcg gcg aat cat tta atg gaa gtg gcg tgc ggt ttg 336
Glu Asn Leu Gln Ala Ala Asn His Leu Met Glu Val Ala Cys Gly Leu
      100      105      110
gat tcg ctg att tta ggc gaa ccg cag att ttg ggg cag gtg aag caa 384
Asp Ser Leu Ile Leu Gly Glu Pro Gln Ile Leu Gly Gln Val Lys Gln
      115      120      125
gcc tac cac atg agc gag cag cat tat caa cag gaa ggg caa acc att 432
Ala Tyr His Met Ser Glu Gln His Tyr Gln Gln Glu Gly Gln Thr Ile
      130      135      140
tcc ggc gaa cta tcc cgt tta ttc caa aaa acc ttt gct acc gct aaa 480
Ser Gly Glu Leu Ser Arg Leu Phe Gln Lys Thr Phe Ala Thr Ala Lys
      145      150      155      160
cgg gtg cgc acc gaa acc aac atc ggc gag agt gcg gtg tcc gtt gcc 528
Arg Val Arg Thr Glu Thr Asn Ile Gly Glu Ser Ala Val Ser Val Ala
      165      170      175
tat gcc gcc tgt agc cta gca cgt cag att ttt gaa tcc ctg cgt gac 576
Tyr Ala Ala Cys Ser Leu Ala Arg Gln Ile Phe Glu Ser Leu Arg Asp
      180      185      190
ttg acg att tta tta gtg ggc gca ggt gaa acc att gaa ctg gtg aac 624
Leu Thr Ile Leu Leu Val Gly Ala Gly Glu Thr Ile Glu Leu Val Asn
      195      200      205
cgc cat ttg tta cgt cac ggc gtg aaa aac tta ttt atc gcc aac cgt 672
Arg His Leu Leu Arg His Gly Val Lys Asn Leu Phe Ile Ala Asn Arg
      210      215      220
aca ttg gcg cgc 684
Thr Leu Ala Arg
225

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<210> 166

<211> 228

<212> PRT

<213> Actinobacillus actinomycetemcomitans

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<400> 166

Met Thr Ile Leu Val Leu Gly Ile Asn His Lys Thr Ala Ser Val Ala
1 5 10 15

Leu Arg Glu Lys Val Ala Phe Ser Asp Glu Lys Arg Thr Phe Ala Leu
20 25 30

Arg His Ile Gln Gln Thr Gln Leu Ala Glu Ser Ala Val Ile Leu Ser
35 40 45

Thr Cys Asn Arg Thr Glu Val Tyr Leu His Asn Lys Ser Val Pro Pro
50 55 60

10

Gln Glu Thr Gln Thr Trp Ile Thr Leu Ala Val Gln Trp Phe Ala Gly
65 70 75 80

Ile His Gln Leu Ala Leu Ala Glu Leu Gln His Cys Val Tyr Thr His
85 90 95

Glu Asn Leu Gln Ala Ala Asn His Leu Met Glu Val Ala Cys Gly Leu
100 105 110

Asp Ser Leu Ile Leu Gly Glu Pro Gln Ile Leu Gly Gln Val Lys Gln
115 120 125

20

Ala Tyr His Met Ser Glu Gln His Tyr Gln Gln Glu Gly Gln Thr Ile
130 135 140

Ser Gly Glu Leu Ser Arg Leu Phe Gln Lys Thr Phe Ala Thr Ala Lys
145 150 155 160

Arg Val Arg Thr Glu Thr Asn Ile Gly Glu Ser Ala Val Ser Val Ala
165 170 175

Tyr Ala Ala Cys Ser Leu Ala Arg Gln Ile Phe Glu Ser Leu Arg Asp
180 185 190

30

Leu Thr Ile Leu Leu Val Gly Ala Gly Glu Thr Ile Glu Leu Val Asn
195 200 205

Arg His Leu Leu Arg His Gly Val Lys Asn Leu Phe Ile Ala Asn Arg
210 215 220

Thr Leu Ala Arg
225

<210> 167
 <211> 138
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(138)

<400> 167
 atg cgc cgt tgg aag ctg aaa atc ttc cgc aaa atg aac cgc act ttg 48
 Met Arg Arg Trp Lys Leu Lys Ile Phe Arg Lys Met Asn Arg Thr Leu
 1 5 10 15
 cgc gtt cgc ctt tgg ttc cca atg cac cga ttc gtg ccg gac ctt aat 96
 Arg Val Arg Leu Ser Phe Pro Met His Arg Phe Val Pro Asp Leu Asn
 20 25 30
 tta ttt aac ttc gat ctt tgt ata ttc cgt cgt tta att cgt 138
 Leu Phe Asn Phe Asp Leu Cys Ile Phe Arg Arg Leu Ile Arg
 35 40 45

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<210> 168
 <211> 46
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 168

Met Arg Arg Trp Lys Leu Lys Ile Phe Arg Lys Met Asn Arg Thr Leu
 1 5 10 15
 Arg Val Arg Leu Ser Phe Pro Met His Arg Phe Val Pro Asp Leu Asn
 20 25 30
 Leu Phe Asn Phe Asp Leu Cys Ile Phe Arg Arg Leu Ile Arg
 35 40 45

20

<210> 169
 <211> 1950
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(1950)

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<400> 169
 atg gct gat gta tta acc cgt ttc aac agt ggc aag ctt tgg gaa ttc 48
 Met Ala Asp Val Leu Thr Arg Phe Asn Ser Gly Lys Leu Trp Glu Phe
 1 5 10 15
 gat ggc ggc att cat ccg ccc gac atg aaa tcc caa tcc aac cgc gcg 96
 Asp Gly Gly Ile His Pro Pro Asp Met Lys Ser Gln Ser Asn Arg Ala
 20 25 30

cct att cgt acc ttg cgg ttg ccc gat aat ttc tac gtt ctt ctg aaa Pro Ile Arg Thr Leu Pro Leu Pro Asp Asn Phe Tyr Val Leu Leu Lys 35 40 45	144
caa cac gcc ggc aca gcg ggc aat tta ttg gta aaa tgc ggc gat cat Gln His Ala Gly Thr Ala Gly Asn Leu Leu Val Lys Cys Gly Asp His 50 55 60	192
gtt ttg aaa ggt caa cgg ctc acc cag ggg gac ggt ttg cgt tgc ctg Val Leu Lys Gly Gln Pro Leu Thr Gln Gly Asp Gly Leu Arg Ser Leu 65 70 75 80	240
cgg gtt cat gcg cct act tca ggc acg gtc att gat gtg atg cct tat Pro Val His Ala Pro Thr Ser Gly Thr Val Ile Asp Val Met Pro Tyr 85 90 95	288
gtc acc gcc cat cct tcc ggt cta cgg gaa acc tgt gtg cat att aaa Val Thr Ala His Pro Ser Gly Leu Pro Glu Thr Cys Val His Ile Lys 100 105 110	336
gcg gat gga tta gat caa tgg cgc gag caa acc cgg ttg gag gat ttc Ala Asp Gly Leu Asp Gln Trp Arg Glu Gln Thr Pro Leu Glu Asp Phe 115 120 125	384
ctt agc caa acg cgg gaa cag tta atc gaa aaa att tat cag gcg ggc Leu Ser Gln Thr Pro Glu Gln Leu Ile Glu Lys Ile Tyr Gln Ala Gly 130 135 140	432
att gcc ggt ctg ggt ggc gcg gta ttc cgg acc gcg gca aaa att cat Ile Ala Gly Leu Gly Gly Ala Val Phe Pro Thr Ala Ala Lys Ile His 145 150 155 160	480
tcc gcc gag aaa cag gtg aaa tta ctg att att aac ggc gcg gaa tgt Ser Ala Glu Lys Gln Val Lys Leu Leu Ile Ile Asn Gly Ala Glu Cys 165 170 175	528
gaa cct tac att acc tgc gac gat cgc tta atg cat gat tat gct gat Glu Pro Tyr Ile Thr Cys Asp Asp Arg Leu Met His Asp Tyr Ala Asp 180 185 190	576
gaa att atc gaa ggc gtg cgt att ttg cgc tac att tta cgc cct gag Glu Ile Ile Glu Gly Val Arg Ile Leu Arg Tyr Ile Leu Arg Pro Gln 195 200 205	624
aaa gtg gtg atc gcc gtt gaa gat aat aaa cca aaa gcg gtg aaa tcc Lys Val Val Ile Ala Val Glu Asp Asn Lys Pro Lys Ala Val Lys Ser 210 215 220	672
ttg gaa cgc gcc tta cac ggc gcc aac gat att gaa atc cga gtg att Leu Glu Arg Ala Leu His Gly Ala Asn Asp Ile Glu Ile Arg Val Ile 225 230 235 240	720
cgg acc aaa tac cct tcc ggc gcg gca aaa cag tta att caa gtg ctg Pro Thr Lys Tyr Pro Ser Gly Ala Ala Lys Gln Leu Ile Gln Val Leu 245 250 255	768
acc ggc atg gag gta cct agc ggt caa cgc tcc tcc ggt atc ggc gtg Thr Gly Met Glu Val Pro Ser Gly Gln Arg Ser Ser Gly Ile Gly Val 260 265 270	816
ctg atg caa aac atc ggc acc gct ttt gct att aaa cgc gca gtg atg	864

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Leu Met Gln Asn Ile Gly Thr Ala Phe Ala Ile Lys Arg Ala Val Met	
275 280 285	
gat gat gaa cgc ctg att gag cgc gtc gtc acc ctc acc ggt gat aaa	912
Asp Asp Glu Pro Leu Ile Glu Arg Val Val Thr Leu Thr Gly Asp Lys	
290 295 300	
atc gcc gat aaa ggc aac tat tgg gcg cgt ttt gga acg ccg att tat	960
Ile Ala Asp Lys Gly Asn Tyr Trp Ala Arg Phe Gly Thr Pro Ile Tyr	
305 310 315 320	
cac ttg ttg cgc gaa acg ggc tat caa tac gac gat cgt ttc ccg gtc	1008
His Leu Leu Arg Gly Thr Tyr Gln Tyr Asp Asp Arg Phe Pro Val	
325 330 335	
ttc atg ggc ggt ccg atg atg ggc ttt att ctg ccc gat tta aat gcg	1056
Phe Met Gly Gly Pro Met Met Gly Phe Ile Leu Pro Asp Leu Asn Ala	
340 345 350	
ccg atg acc aaa gtg acc aac tgc ctg ttg gcg ccg gat cat ttt gaa	1104
Pro Met Thr Lys Val Thr Asn Cys Leu Leu Ala Pro Asp His Phe Glu	
355 360 365	
tac gcc ccg ccg gaa gaa gaa aaa aat tgt att cgc tgt tct gcc tgt	1152
Tyr Ala Pro Pro Glu Glu Glu Lys Asn Cys Ile Arg Cys Ser Ala Cys	
370 375 380	
tcc gat gcc tgc ccg gtg aaa ctc atg ccg cag caa ttg tat tgg ttt	1200
Ser Asp Ala Cys Pro Val Lys Leu Met Pro Gln Gln Leu Tyr Trp Phe	
385 390 395 400	
gca cgc agc gaa gat cac gaa aaa tcg gaa gaa tat tcc ctc aaa gat	1248
Ala Arg Ser Glu Asp His Glu Lys Ser Glu Glu Tyr Ser Leu Lys Asp	
405 410 415	
tgt att gaa tgc ggc gtg tgc gct tat gtt tgc cca agt cac att ccg	1296
Cys Ile Glu Cys Gly Val Cys Ala Tyr Val Cys Pro Ser His Ile Pro	
420 425 430	
tta att caa tat ttc cgc ccg gaa aaa gct aaa atc tgg gaa atc aaa	1344
Leu Ile Gln Tyr Phe Arg Arg Glu Lys Ala Lys Ile Trp Glu Ile Lys	
435 440 445	
cac aaa gcc aaa ttg gcg gaa gaa gct aaa ata cgt ttt gaa caa cgc	1392
His Lys Ala Lys Leu Ala Glu Glu Ala Lys Ile Arg Phe Glu Gln Arg	
450 455 460	
caa gcc cgt ttg gaa cgg gaa gaa cag gaa cgc aaa gat cgc tca caa	1440
Gln Ala Arg Leu Glu Arg Glu Glu Gln Glu Arg Lys Asp Arg Ser Gln	
465 470 475 480	
cgt gct gca gcc gcc cgt cgt gaa gaa ttg gcg caa caa aaa ggc gtg	1488
Arg Ala Ala Ala Arg Arg Glu Glu Leu Ala Gln Gln Lys Gly Val	
485 490 495	
gat ccg gtg gct gcc gcc tta gcg cgc tta aaa gcg aaa aaa gcc gaa	1536
Asp Pro Val Ala Ala Ala Leu Ala Arg Leu Lys Ala Lys Lys Ala Glu	
500 505 510	
acg acg gaa gct acg cag gca gaa cag aaa acc att gtt gac gaa aaa	1584
Thr Thr Glu Ala Thr Gln Ala Glu Gln Lys Thr Ile Val Asp Glu Lys	

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515	520	525	
ggt cat atc ctg cct gac aac agc gac atc atg gca caa cgc aaa gcc			1632
Gly His Ile Leu Pro Asp Asn Ser Asp Ile Met Ala Gln Arg Lys Ala			
530	535	540	
cgt cgt tta gcc cgt cag gcg gaa gcg gca cac tcg ccg tcg cag aaa			1680
Arg Arg Leu Ala Arg Gln Ala Glu Ala Ala His Ser Pro Ser Gln Lys			
545	550	555	560
aca gaa aaa acg cta gaa aaa acg cta gaa aaa acc acc gca ctt gag			1728
Thr Glu Lys Thr Leu Glu Lys Thr Leu Glu Lys Thr Thr Ala Leu Glu			
	565	570	575
gat aaa aaa tct acc gtt gcc gcc gcc att gcc cgt gcg aaa gcc aag			1776
Asp Lys Lys Ser Thr Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys			
	580	585	590
aaa gcg gcg cag caa acg gaa gcc gtc gaa gca aac gaa cct gaa acg			1824
Lys Ala Ala Gln Gln Thr Glu Ala Val Glu Ala Asn Glu Pro Glu Thr			
	595	600	605
gca aaa agt gcg gtc aat att tcc ggt gaa aat ggc gca gag aac gat			1872
Ala Lys Ser Ala Val Asn Ile Ser Gly Glu Asn Gly Ala Glu Asn Asp			
	610	615	620
ccg cgc aaa gcc gct gtt gcc gcc gct att gcc cgt gcg aaa gcg aag			1920
Pro Arg Lys Ala Ala Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys			
	625	630	635
aaa gcc caa cgt gaa aac acg caa caa gat			1950
Lys Ala Gln Arg Glu Asn Thr Gln Gln Asp			
	645	650	

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<210> 170
 <211> 650
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 170

Met Ala Asp Val Leu Thr Arg Phe Asn Ser Gly Lys Leu Trp Glu Phe
1 5 10 15

Asp Gly Gly Ile His Pro Pro Asp Met Lys Ser Gln Ser Asn Arg Ala
20 25 30

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Pro Ile Arg Thr Leu Pro Leu Pro Asp Asn Phe Tyr Val Leu Leu Lys
35 40 45

Gln His Ala Gly Thr Ala Gly Asn Leu Leu Val Lys Cys Gly Asp His
50 55 60

Val Leu Lys Gly Gln Pro Leu Thr Gln Gly Asp Gly Leu Arg Ser Leu
65 70 75 80

Pro Val His Ala Pro Thr Ser Gly Thr Val Ile Asp Val Met Pro Tyr
 85 90 95
 Val Thr Ala His Pro Ser Gly Leu Pro Glu Thr Cys Val His Ile Lys
 100 105 110
 Ala Asp Gly Leu Asp Gln Trp Arg Glu Gln Thr Pro Leu Glu Asp Phe
 115 120 125
 Leu Ser Gln Thr Pro Glu Gln Leu Ile Glu Lys Ile Tyr Gln Ala Gly
 130 135 140
 Ile Ala Gly Leu Gly Gly Ala Val Phe Pro Thr Ala Ala Lys Ile His
 145 150 155 160
 Ser Ala Glu Lys Gln Val Lys Leu Leu Ile Ile Asn Gly Ala Glu Cys
 165 170 175
 Glu Pro Tyr Ile Thr Cys Asp Asp Arg Leu Met His Asp Tyr Ala Asp
 180 185 190
 Glu Ile Ile Glu Gly Val Arg Ile Leu Arg Tyr Ile Leu Arg Pro Glu
 195 200 205
 Lys Val Val Ile Ala Val Glu Asp Asn Lys Pro Lys Ala Val Lys Ser
 210 215 220
 Leu Glu Arg Ala Leu His Gly Ala Asn Asp Ile Glu Ile Arg Val Ile
 225 230 235 240
 Pro Thr Lys Tyr Pro Ser Gly Ala Ala Lys Gln Leu Ile Gln Val Leu
 245 250 255
 Thr Gly Met Glu Val Pro Ser Gly Gln Arg Ser Ser Gly Ile Gly Val
 260 265 270
 Leu Met Gln Asn Ile Gly Thr Ala Phe Ala Ile Lys Arg Ala Val Met
 275 280 285
 Asp Asp Glu Pro Leu Ile Glu Arg Val Val Thr Leu Thr Gly Asp Lys
 290 295 300
 Ile Ala Asp Lys Gly Asn Tyr Trp Ala Arg Phe Gly Thr Pro Ile Tyr
 305 310 315 320

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His Leu Leu Arg Glu Thr Gly Tyr Gln Tyr Asp Asp Arg Phe Pro Val
 325 330 335
 Phe Met Gly Gly Pro Met Met Gly Phe Ile Leu Pro Asp Leu Asn Ala
 340 345 350
 Pro Met Thr Lys Val Thr Asn Cys Leu Leu Ala Pro Asp His Phe Glu
 355 360 365
 Tyr Ala Pro Pro Glu Glu Glu Lys Asn Cys Ile Arg Cys Ser Ala Cys
 370 375 380
 Ser Asp Ala Cys Pro Val Lys Leu Met Pro Gln Gln Leu Tyr Trp Phe
 385 390 395 400
 Ala Arg Ser Glu Asp His Glu Lys Ser Glu Glu Tyr Ser Leu Lys Asp
 405 410 415
 Cys Ile Glu Cys Gly Val Cys Ala Tyr Val Cys Pro Ser His Ile Pro
 420 425 430
 Leu Ile Gln Tyr Phe Arg Arg Glu Lys Ala Lys Ile Trp Glu Ile Lys
 435 440 445
 His Lys Ala Lys Leu Ala Glu Glu Ala Lys Ile Arg Phe Glu Gln Arg
 450 455 460
 Gln Ala Arg Leu Glu Arg Glu Glu Gln Glu Arg Lys Asp Arg Ser Gln
 465 470 475 480
 Arg Ala Ala Ala Ala Arg Arg Glu Glu Leu Ala Gln Gln Lys Gly Val
 485 490 495
 Asp Pro Val Ala Ala Ala Leu Ala Arg Leu Lys Ala Lys Lys Ala Glu
 500 505 510
 Thr Thr Glu Ala Thr Gln Ala Glu Gln Lys Thr Ile Val Asp Glu Lys
 515 520 525
 Gly His Ile Leu Pro Asp Asn Ser Asp Ile Met Ala Gln Arg Lys Ala
 530 535 540
 Arg Arg Leu Ala Arg Gln Ala Glu Ala Ala His Ser Pro Ser Gln Lys
 545 550 555 560
 Thr Glu Lys Thr Leu Glu Lys Thr Leu Glu Lys Thr Thr Ala Leu Glu

10

20

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565 570 575
 Asp Lys Lys Ser Thr Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys
 580 585 590
 Lys Ala Ala Gln Gln Thr Glu Ala Val Glu Ala Asn Glu Pro Glu Thr
 595 600 605
 Ala Lys Ser Ala Val Asn Ile Ser Gly Glu Asn Gly Ala Glu Asn Asp
 610 615 620
 Pro Arg Lys Ala Ala Val Ala Ala Ala Ile Ala Arg Ala Lys Ala Lys
 625 630 635 640
 Lys Ala Gln Arg Glu Asn Thr Gln Gln Asp
 645 650

 <210> 171
 <211> 525
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

 <220>
 <221> CDS
 <222> (1)..(525)

 <400> 171
 atg aag ttt aaa acg cta ctt ggc gcg ctc tta ttg agc gtg ttt tcc 48
 Met Lys Phe Lys Thr Leu Leu Gly Ala Leu Leu Ser Val Phe Ser
 1 5 10 15
 act tcc gtt tgg gct gat cgc gtg att acc gat caa ctt gat cga caa 96
 Thr Ser Val Trp Ala Asp Arg Val Ile Thr Asp Gln Leu Asp Arg Gln
 20 25 30
 gtg acc atc ccc gac cat att cat cgc gct gtg ata tta cag cac cag 144
 Val Thr Ile Pro Asp His Ile His Arg Ala Val Ile Leu Gln His Gln
 35 40 45
 acc tta aat ctc gcg gtg caa ctg gat gcc acc aaa caa att gcg ggc 192
 Thr Leu Asn Leu Ala Val Gln Leu Asp Ala Thr Lys Gln Ile Ala Gly
 50 55 60
 gtg ctt tcc aac tgg caa aaa cag ctg ggc aaa gac ttc gtg cgc ctt 240
 Val Leu Ser Asn Trp Gln Lys Gln Leu Gly Lys Asp Phe Val Arg Leu
 65 70 75 80
 gcg ccg gaa ttg gca aat tta ccg atg ccc ggt gat ttg aat acg gtc 288
 Ala Pro Glu Leu Ala Asn Leu Pro Met Pro Gly Asp Leu Asn Thr Val
 85 90 95
 aat att gaa agc cta atg gaa atc aaa ccg gat gtt gtt ttc gtg acc 336
 Asn Ile Glu Ser Leu Met Glu Ile Lys Pro Asp Val Val Phe Val Thr
 100 105 110

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aat tac gcg ccg aaa gaa atg att gaa aaa atc agc caa atg aac gtg 384
 Asn Tyr Ala Pro Lys Glu Met Ile Glu Lys Ile Ser Gln Met Asn Val
 115 120 125
 ccg gtg att gcc att tog tta cgc agc ggc gat aaa acc gaa caa agc 432
 Pro Val Ile Ala Ile Ser Leu Arg Ser Gly Asp Lys Thr Glu Gln Ser
 130 135 140
 aaa ctc aac ccg acc ctt gcc gat gaa aac aat gcc tac aac gaa ggg 480
 Lys Leu Asn Pro Thr Leu Ala Asp Glu Asn Asn Ala Tyr Asn Glu Gly
 145 150 155 160
 tta aaa cgc ggg att gaa att att gcc gat gtt ttt gat aaa aaa 525
 Leu Lys Arg Gly Ile Glu Ile Ile Ala Asp Val Phe Asp Lys Lys
 165 170 175

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<210> 172
 <211> 175
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 172

Met Lys Phe Lys Thr Leu Leu Gly Ala Leu Leu Leu Ser Val Phe Ser
 1 5 10 15

Thr Ser Val Trp Ala Asp Arg Val Ile Thr Asp Gln Leu Asp Arg Gln
 20 25 30

20

Val Thr Ile Pro Asp His Ile His Arg Ala Val Ile Leu Gln His Gln
 35 40 45

Thr Leu Asn Leu Ala Val Gln Leu Asp Ala Thr Lys Gln Ile Ala Gly
 50 55 60

Val Leu Ser Asn Trp Gln Lys Gln Leu Gly Lys Asp Phe Val Arg Leu
 65 70 75 80

Ala Pro Glu Leu Ala Asn Leu Pro Met Pro Gly Asp Leu Asn Thr Val
 85 90 95

Asn Ile Glu Ser Leu Met Glu Ile Lys Pro Asp Val Val Phe Val Thr
 100 105 110

30

Asn Tyr Ala Pro Lys Glu Met Ile Glu Lys Ile Ser Gln Met Asn Val
 115 120 125

Pro Val Ile Ala Ile Ser Leu Arg Ser Gly Asp Lys Thr Glu Gln Ser
 130 135 140

Lys Leu Asn Pro Thr Leu Ala Asp Glu Asn Asn Ala Tyr Asn Glu Gly

<400> 174

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Met Ala Glu Leu Val Tyr Lys Pro Leu Glu Gln Pro Val Glu Ala Pro
1 5 10 15

Asn Pro Asn Leu Lys Ile Glu Ala Val Asn Glu Gln Phe Ala Ala Lys
20 25 30

Tyr Pro Lys Gln Phe Ala Ser Trp Lys Ala Thr Glu Lys Gly Asp Lys
35 40 45

Ile Ile Tyr Ala Asp Glu Glu Asn Pro Arg Leu Ile Ile Leu Trp Gly
50 55 60

Gly Tyr Ala Phe Ala Lys Glu Tyr Asn Ala Pro Arg Gly His Ile Tyr
65 70 75 80

Ala Ile Lys Asp Leu Arg Asn Ile Leu Arg Thr Gly Ala Pro Lys Thr
85 90 95

Ala Asn Asp Gly Pro Gln Pro Met Ala Cys Trp Thr Cys Lys Gly Pro
100 105 110

Asp Val Pro Arg Leu Ile Ala Glu Trp Gly Glu Glu Gly Tyr Phe Asn
115 120 125

Gly Lys
130

<210> 175
<211> 540
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(540)

<400> 175
aaa gcc atg ccg gca tta gac tta aat aaa gac ggc aaa atc caa tat 48
Lys Ala Met Pro Ala Leu Asp Leu Asn Lys Asp Gly Lys Ile Gln Tyr
1 5 10 15
gtg tta tta aaa ggc gaa ccg ggc cac cct gat gcg gaa gca cgt acc 96
Val Leu Leu Lys Gly Glu Pro Gly His Pro Asp Ala Glu Ala Arg Thr
20 25 30
aag tat gtg att gag caa cta aac gcg caa ggc att cca acg gaa caa 144
Lys Tyr Val Ile Glu Gln Leu Asn Ala Gln Gly Ile Pro Thr Glu Gln
35 40 45
ctc ttt atc gac acc ggg atg tgg gat gcg gca ctg gca aaa gac aaa 192
Leu Phe Ile Asp Thr Gly Met Trp Asp Ala Ala Leu Ala Lys Asp Lys
50 55 60

10

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atg gat gcg tgg tta tcc agc tct aaa gcc aat gac att gaa gtc att 240
 Met Asp Ala Trp Leu Ser Ser Ser Lys Ala Asn Asp Ile Glu Val Ile
 65 70 75 80
 att tcc aac aac gac ggc atg gcg atg ggc gca ttg gaa gca acc aaa 288
 Ile Ser Asn Asn Asp Gly Met Ala Met Gly Ala Leu Glu Ala Thr Lys
 85 90 95
 gca cac ggc aaa aaa tta ccg att ttc ggg gta gat gcg ttg cct gaa 336
 Ala His Gly Lys Lys Leu Pro Ile Phe Gly Val Asp Ala Leu Pro Glu
 100 105 110
 gta tta caa ctc atc aag aaa ggc gac att gca ggt acc gta ttg aat 384
 Val Leu Gln Leu Ile Lys Lys Gly Asp Ile Ala Gly Thr Val Leu Asn
 115 120 125
 gac ggc gcg act caa ggt aaa gcg att gtg gat tta tcc aac aac ctg 432
 Asp Gly Ala Thr Gln Gly Lys Ala Ile Val Asp Leu Ser Asn Asn Leu
 130 135 140
 gca aac ggc aaa ccg gct acc gaa ggc acc aaa tgg gag ctt aaa gat 480
 Ala Asn Gly Lys Pro Ala Thr Glu Gly Thr Lys Trp Glu Leu Lys Asp
 145 150 155 160
 cgc gtt gtg cgc att cct tat gtt ggc gta gat aaa gac aac ttg tct 528
 Arg Val Val Arg Ile Pro Tyr Val Gly Val Asp Lys Asp Asn Leu Ser
 165 170 175
 caa ttc tta aaa 540
 Gln Phe Leu Lys
 180

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<210> 176
 <211> 180
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 176

Lys Ala Met Pro Ala Leu Asp Leu Asn Lys Asp Gly Lys Ile Gln Tyr
 1 5 10 15
 Val Leu Leu Lys Gly Glu Pro Gly His Pro Asp Ala Glu Ala Arg Thr
 20 25 30
 Lys Tyr Val Ile Glu Gln Leu Asn Ala Gln Gly Ile Pro Thr Glu Gln
 35 40 45
 Leu Phe Ile Asp Thr Gly Met Trp Asp Ala Ala Leu Ala Lys Asp Lys
 50 55 60
 Met Asp Ala Trp Leu Ser Ser Ser Lys Ala Asn Asp Ile Glu Val Ile
 65 70 75 80

30

Ile Ser Asn Asn Asp Gly Met Ala Met Gly Ala Leu Glu Ala Thr Lys
 85 90 95

Ala His Gly Lys Lys Leu Pro Ile Phe Gly Val Asp Ala Leu Pro Glu
 100 105 110

Val Leu Gln Leu Ile Lys Lys Gly Asp Ile Ala Gly Thr Val Leu Asn
 115 120 125

Asp Gly Ala Thr Gln Gly Lys Ala Ile Val Asp Leu Ser Asn Asn Leu
 130 135 140

Ala Asn Gly Lys Pro Ala Thr Glu Gly Thr Lys Trp Glu Leu Lys Asp
 145 150 155 160

Arg Val Val Arg Ile Pro Tyr Val Gly Val Asp Lys Asp Asn Leu Ser
 165 170 175

Gln Phe Leu Lys
 180

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<210> 177
 <211> 1071
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

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<220>
 <221> CDS
 <222> (1)..(1071)

<400> 177
 atg gca gga aat acc atc gga caa tta ttt cgc gtc acc acc ttc ggc 48
 Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly
 1 5 10 15

gag tcc cac ggc att gcc ttg ggt tgc att gtg gac ggc gta ccg ccg 96
 Glu Ser His Gly Ile Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro
 20 25 30

aac atg gca tta tcg gaa gcg gat att caa ccg gat ttg gat cgt cgt 144
 Asn Met Ala Leu Ser Glu Ala Asp Ile Gln Pro Asp Leu Asp Arg Arg
 35 40 45

aaa ccc ggc acc tcg cgc tat acc aca ccg cgc cgc gaa gac gat gaa 192
 Lys Pro Gly Thr Ser Arg Tyr Thr Thr Pro Arg Arg Glu Asp Asp Glu
 50 55 60

gtg cag att tta tcc ggt gtc ttt gaa gga aaa acc acc ggc acc agt 240
 Val Gln Ile Leu Ser Gly Val Phe Glu Gly Lys Thr Thr Gly Thr Ser
 65 70 75 80

att ggc ata atc att aag aac ggc gat caa cgc tcg cag gac tat ggc 288
 Ile Gly Ile Ile Ile Lys Asn Gly Asp Gln Arg Ser Gln Asp Tyr Gly
 85 90 95

30

gaa att aaa gat cgc ttc cgt ccg gga cat gca gat ttt act tat caa 336
 Glu Ile Lys Asp Arg Phe Arg Pro Gly His Ala Asp Phe Thr Tyr Gln
 100 105 110
 caa aaa tac ggc att cgt gat tat cgc ggc ggc ggt cgt tct tcc gcc 384
 Gln Lys Tyr Gly Ile Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala
 115 120 125
 cgc gaa act gcc atg cgc gtg gcg gcg ggt gcc atc gcg aaa aaa tat 432
 Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr
 130 135 140
 tta cgc gaa caa ttc ggc att gaa gtg cgt ggt ttc tta agc caa atc 480
 Leu Arg Glu Gln Phe Gly Ile Glu Val Arg Gly Phe Leu Ser Gln Ile
 145 150 155 160
 ggc gat gtc aaa att gcg ccg caa tcc gtg gaa cat att gat tgg gca 528
 Gly Asp Val Lys Ile Ala Pro Gln Ser Val Glu His Ile Asp Trp Ala
 165 170 175
 gaa gta aat agc aat ctg ttt ttc tgc ccc gat aaa agt gcg gtg gaa 576
 Glu Val Asn Ser Asn Leu Phe Phe Cys Pro Asp Lys Ser Ala Val Glu
 180 185 190
 aaa ttc gat gaa tta att cgt gat ctg aaa aaa caa ggg gat tct atc 624
 Lys Phe Asp Glu Leu Ile Arg Asp Leu Lys Lys Gln Gly Asp Ser Ile
 195 200 205
 ggt gct aaa ttg acc gtg gtg gcg gaa aac gtc ccc gtc ggg ttg gcc 672
 Gly Ala Lys Leu Thr Val Val Ala Glu Asn Val Pro Val Gly Leu Gly
 210 215 220
 gaa ccg gtg ttt gat cgt ttg gat gcg gat tta gcc cac gca tta atg 720
 Glu Pro Val Phe Asp Arg Leu Asp Ala Asp Leu Ala His Ala Leu Met
 225 230 235 240
 agc att aat gcg gta aaa ggc gtg gaa att ggt gac ggt ttc gct gtg 768
 Ser Ile Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Ala Val
 245 250 255
 gta gaa caa aaa ggt agc caa cat cgt gac gaa atg atc ccg caa gga 816
 Val Glu Gln Lys Gly Ser Gln His Arg Asp Glu Met Ile Pro Gln Gly
 260 265 270
 ttt ctt tcc aac tat gcc ggc ggg att ttg ggc ggc atc agt tca gga 864
 Phe Leu Ser Asn Tyr Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly
 275 280 285
 caa ccg att atc gcc acg att gcc ctc aaa ccc act tcc agc att acc 912
 Gln Pro Ile Ile Ala Thr Ile Ala Leu Lys Pro Thr Ser Ser Ile Thr
 290 295 300
 att ccg ggg cgc tcg gtg aat ctc gac aat gaa tot gtc gaa gtt gtt 960
 Ile Pro Gly Arg Ser Val Asn Leu Asp Asn Glu Ser Val Glu Val Val
 305 310 315 320
 act aaa ggt cgc cac gat cct tgt gtc ggc atc cgc gcc gtg ccg att 1008
 Thr Lys Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile
 325 330 335

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gcg gaa gct atg acg gcg att gta ttg ttg gat cat ttg ttg cgt ttt 1056
 Ala Glu Ala Met Thr Ala Ile Val Leu Leu Asp His Leu Leu Arg Phe
 340 345 350

aaa gcg caa tgc cga 1071
 Lys Ala Gln Cys Arg
 355

<210> 178
 <211> 357
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 178

Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly
 1 5 10 15

Glu Ser His Gly Ile Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro
 20 25 30

Asn Met Ala Leu Ser Glu Ala Asp Ile Gln Pro Asp Leu Asp Arg Arg
 35 40 45

Lys Pro Gly Thr Ser Arg Tyr Thr Thr Pro Arg Arg Glu Asp Asp Glu
 50 55 60

Val Gln Ile Leu Ser Gly Val Phe Glu Gly Lys Thr Thr Gly Thr Ser
 65 70 75 80

Ile Gly Ile Ile Ile Lys Asn Gly Asp Gln Arg Ser Gln Asp Tyr Gly
 85 90 95

Glu Ile Lys Asp Arg Phe Arg Pro Gly His Ala Asp Phe Thr Tyr Gln
 100 105 110

Gln Lys Tyr Gly Ile Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala
 115 120 125

Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr
 130 135 140

Leu Arg Glu Gln Phe Gly Ile Glu Val Arg Gly Phe Leu Ser Gln Ile
 145 150 155 160

Gly Asp Val Lys Ile Ala Pro Gln Ser Val Glu His Ile Asp Trp Ala
 165 170 175

Glu Val Asn Ser Asn Leu Phe Phe Cys Pro Asp Lys Ser Ala Val Glu

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180 185 190
 Lys Phe Asp Glu Leu Ile Arg Asp Leu Lys Lys Gln Gly Asp Ser Ile
 195 200 205
 Gly Ala Lys Leu Thr Val Val Ala Glu Asn Val Pro Val Gly Leu Gly
 210 215 220
 Glu Pro Val Phe Asp Arg Leu Asp Ala Asp Leu Ala His Ala Leu Met
 225 230 235 240
 Ser Ile Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Ala Val
 245 250 255
 Val Glu Gln Lys Gly Ser Gln His Arg Asp Glu Met Ile Pro Gln Gly
 260 265 270
 Phe Leu Ser Asn Tyr Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly
 275 280 285
 Gln Pro Ile Ile Ala Thr Ile Ala Leu Lys Pro Thr Ser Ser Ile Thr
 290 295 300
 Ile Pro Gly Arg Ser Val Asn Leu Asp Asn Glu Ser Val Glu Val Val
 305 310 315 320
 Thr Lys Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile
 325 330 335
 Ala Glu Ala Met Thr Ala Ile Val Leu Leu Asp His Leu Leu Arg Phe
 340 345 350
 Lys Ala Gln Cys Arg
 355
 <210> 179
 <211> 633
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans
 <220>
 <221> CDS
 <222> (1)..(633)
 <400> 179
 gac ctc ttg gtg gat tcc tac gtg aaa tgg cgt atc aat gat tta ggt
 Asp Leu Leu Val Asp Ser Tyr Val Lys Trp Arg Ile Asn Asp Leu Gly
 1 5 10 15

10

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48

cgt ttc ttc acc acg acc ggt ggt ggc gat tat gca caa gca gcc aac 96
 Arg Phe Phe Thr Thr Thr Gly Gly Asp Tyr Ala Gln Ala Ala Asn
 20 25 30
 tta tta cgt cgt aaa gtc aat gac cgt ttg cgt tcc gaa atc ggt tcc 144
 Leu Leu Arg Arg Lys Val Asn Asp Arg Leu Arg Ser Glu Ile Gly Ser
 35 40 45
 cgc acc att aaa gac atc gtt tcc ggt aca cga ggc gaa ctc atg gta 192
 Arg Thr Ile Lys Asp Ile Val Ser Gly Thr Arg Gly Glu Leu Met Val
 50 55 60
 ggc acg aaa aaa gcg ctc aac agt ggg caa gac agc acc gcc gaa ctg 240
 Gly Thr Lys Lys Ala Leu Asn Ser Gly Gln Asp Ser Thr Ala Glu Leu
 65 70 75 80
 ggg att gaa gtg ctc gac gta cgg att aaa caa att aac ttg ccg gat 288
 Gly Ile Glu Val Leu Asp Val Arg Ile Lys Gln Ile Asn Leu Pro Asp
 85 90 95
 gaa gtg tct tcc tcc att tac cag cgt atg cgc gcc gaa cgg gat gcg 336
 Glu Val Ser Ser Ser Ile Tyr Gln Arg Met Arg Ala Glu Arg Asp Ala
 100 105 110
 gta gcc cgt gaa cac cgc tct caa ggt aaa gaa aaa gcg gca ttt att 384
 Val Ala Arg Glu His Arg Ser Gln Gly Lys Glu Lys Ala Ala Phe Ile
 115 120 125
 cag gcg gat gta gat cgt aaa gtc acc tta att atc gcc aat gcg gaa 432
 Gln Ala Asp Val Asp Arg Lys Val Thr Leu Ile Ile Ala Asn Ala Glu
 130 135 140
 aaa acc gca cag gaa tta cgc ggt gac ggc gac gcg acc gca gcc aaa 480
 Lys Thr Ala Gln Glu Leu Arg Gly Asp Gly Asp Ala Thr Ala Ala Lys
 145 150 155 160
 atc ttt gcc gat gcc ttt ggt aaa gag cct gaa ttt tac agc ttc att 528
 Ile Phe Ala Asp Ala Phe Gly Lys Glu Pro Glu Phe Tyr Ser Phe Ile
 165 170 175
 cgt agc ctg aaa gcc tat gaa agc agc ttc gcc gac tcg gac aat ttg 576
 Arg Ser Leu Lys Ala Tyr Glu Ser Ser Phe Ala Asp Ser Asp Asn Leu
 180 185 190
 ttg att tta aaa ccg gac agt gac ttc ttc cgt ttt atg caa tca cca 624
 Leu Ile Leu Lys Pro Asp Ser Asp Phe Phe Arg Phe Met Gln Ser Pro
 195 200 205
 agt aaa taa 633
 Ser Lys
 210

<210> 180
 <211> 210
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 180

Asp Leu Leu Val Asp Ser Tyr Val Lys Trp Arg Ile Asn Asp Leu Gly

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1	5	10	15
Arg Phe Phe Thr Thr Thr Gly Gly Gly Asp Tyr Ala Gln Ala Ala Asn	20	25	30
Leu Leu Arg Arg Lys Val Asn Asp Arg Leu Arg Ser Glu Ile Gly Ser	35	40	45
Arg Thr Ile Lys Asp Ile Val Ser Gly Thr Arg Gly Glu Leu Met Val	50	55	60
Gly Thr Lys Lys Ala Leu Asn Ser Gly Gln Asp Ser Thr Ala Glu Leu	65	70	75
Gly Ile Glu Val Leu Asp Val Arg Ile Lys Gln Ile Asn Leu Pro Asp	85	90	95
Glu Val Ser Ser Ser Ile Tyr Gln Arg Met Arg Ala Glu Arg Asp Ala	100	105	110
Val Ala Arg Glu His Arg Ser Gln Gly Lys Glu Lys Ala Ala Phe Ile	115	120	125
Gln Ala Asp Val Asp Arg Lys Val Thr Leu Ile Ile Ala Asn Ala Glu	130	135	140
Lys Thr Ala Gln Glu Leu Arg Gly Asp Gly Asp Ala Thr Ala Ala Lys	145	150	155
Ile Phe Ala Asp Ala Phe Gly Lys Glu Pro Glu Phe Tyr Ser Phe Ile	165	170	175
Arg Ser Leu Lys Ala Tyr Glu Ser Ser Phe Ala Asp Ser Asp Asn Leu	180	185	190
Leu Ile Leu Lys Pro Asp Ser Asp Phe Phe Arg Phe Met Gln Ser Pro	195	200	205
Ser Lys	210		

<210> 181
 <211> 582
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans
 <220>

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<221> CDS

<222> (1)..(582)

<400> 181

atg atc gac aac atc aac gaa ctt cgc acc ttt atc acc gcg gcg caa 48
 Met Ile Asp Asn Ile Asn Glu Leu Arg Thr Phe Ile Thr Ala Ala Gln
 1 5 10 15

gaa ggc agt ttc acc aaa gcc gcc gca aaa tta aac gtt tcc acc tcc 96
 Glu Gly Ser Phe Thr Lys Ala Ala Lys Leu Asn Val Ser Thr Ser
 20 25 30

gca tta agc cat tcc att cgc aag ctg gaa gaa cag ctc aac atc aaa 144
 Ala Leu Ser His Ser Ile Arg Lys Leu Glu Glu Gln Leu Asn Ile Lys
 35 40 45

ctg ttc aac cgc acc aca cgc agc att gcc acc acg gag gcg ggc gag 192
 Leu Phe Asn Arg Thr Thr Arg Ser Ile Ala Thr Thr Glu Ala Gly Glu
 50 55 60

cag ttg ttt caa aat ctc ttg ccg ttg ttt gaa agt att gaa gat aat 240
 Gln Leu Phe Gln Asn Leu Leu Pro Leu Phe Glu Ser Ile Glu Asp Asn
 65 70 75 80

ctc aac gca tta agc acc ttt cgc aac acg ttg aaa ggg aaa tta tgc 288
 Leu Asn Ala Leu Ser Thr Phe Arg Asn Thr Leu Lys Gly Lys Leu Cys
 85 90 95

att aac ggt aac gat cat gtt ttt tta tcc att ttg tgg gat aaa ttg 336
 Ile Asn Gly Asn Asp His Val Phe Leu Ser Ile Leu Trp Asp Lys Leu
 100 105 110

atg gcg ttc gcg gaa caa tac ccc gaa atg gaa ttg gaa ttg acc agt 384
 Met Ala Phe Ala Glu Gln Tyr Pro Glu Met Glu Leu Glu Leu Thr Ser
 115 120 125

gac acc aaa ttt gtg gat atc gtg gcg ggg cgg ttt gat gcg ggt att 432
 Asp Thr Lys Phe Val Asp Ile Val Ala Gly Arg Phe Asp Ala Gly Ile
 130 135 140

cgc tta gga tcg gac gtg gca caa gat atg atc gcc gtg aga tta agc 480
 Arg Leu Gly Ser Asp Val Ala Gln Asp Met Ile Ala Val Arg Leu Ser
 145 150 155 160

gac aaa atg caa atg gcg gtg gtc gcc acg cca gag tat ttc gcc aaa 528
 Asp Lys Met Gln Met Ala Val Val Gly Thr Pro Glu Tyr Phe Ala Lys
 165 170 175

aaa gcc aca ccg aag aaa gta gaa gac ttg ggc gaa cac gag tgc ttg 576
 Lys Ala Thr Pro Lys Lys Val Glu Asp Leu Gly Glu His Glu Cys Leu
 180 185 190

ctg gtg 582
 Leu Val

<210> 182

<211> 194

<212> PRT

<213> Actinobacillus actinomycetemcomitans

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<400> 182

Met Ile Asp Asn Ile Asn Glu Leu Arg Thr Phe Ile Thr Ala Ala Gln
 1 5 10 15

Glu Gly Ser Phe Thr Lys Ala Ala Lys Leu Asn Val Ser Thr Ser
 20 25 30

Ala Leu Ser His Ser Ile Arg Lys Leu Glu Glu Gln Leu Asn Ile Lys
 35 40 45

Leu Phe Asn Arg Thr Thr Arg Ser Ile Ala Thr Thr Glu Ala Gly Glu
 50 55 60

Gln Leu Phe Gln Asn Leu Leu Pro Leu Phe Glu Ser Ile Glu Asp Asn
 65 70 75 80

Leu Asn Ala Leu Ser Thr Phe Arg Asn Thr Leu Lys Gly Lys Leu Cys
 85 90 95

Ile Asn Gly Asn Asp His Val Phe Leu Ser Ile Leu Trp Asp Lys Leu
 100 105 110

Met Ala Phe Ala Glu Gln Tyr Pro Glu Met Glu Leu Glu Leu Thr Ser
 115 120 125

Asp Thr Lys Phe Val Asp Ile Val Ala Gly Arg Phe Asp Ala Gly Ile
 130 135 140

Arg Leu Gly Ser Asp Val Ala Gln Asp Met Ile Ala Val Arg Leu Ser
 145 150 155 160

Asp Lys Met Gln Met Ala Val Val Gly Thr Pro Glu Tyr Phe Ala Lys
 165 170 175

Lys Ala Thr Pro Lys Lys Val Glu Asp Leu Gly Glu His Glu Cys Leu
 180 185 190

Leu Val

<210> 183

<211> 662

<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

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<221> CDS

<222> (1)..(660)

<400> 183

taa	tct	ogg	caa	tgt	tog	cca	cct	tgc	ttt	ttt	tgc	ctg	cat	tat	ttc	48
Ser	Arg	Gln	Cys	Thr	Asn	Arg	Pro	Pro	Cys	Phe	Phe	Cys	Leu	His	Tyr	Phe
1				5					10						15	

gcc	gtt	atc	aaa	aca	aac	cgc	gca	ccc	cga	acc	caa	aag	tgc	ggt	gga	96
Ala	Val	Ile	Lys	Thr	Asn	Arg	Ala	Pro	Arg	Thr	Gln	Lys	Cys	Gly	Gly	
			20				25							30		

ttt	tgg	atg	cgt	ttt	tta	cgc	atg	ggc	gtg	gtt	tca	atc	ctg	tta	ggg	144
Phe	Trp	Met	Arg	Phe	Leu	Arg	Met	Gly	Val	Val	Ser	Ile	Leu	Leu	Gly	
		35					40						45			

ggg	att	ttt	atc	gtc	ggc	ggt	ttg	tat	cgt	tcc	gaa	tgg	cgt	gat	gat	192
Gly	Ile	Phe	Ile	Val	Gly	Gly	Leu	Tyr	Arg	Ser	Glu	Trp	Arg	Asp	Asp	
		50					55					60				

att	cgt	caa	tgg	gtt	tct	atg	cgc	cag	gtg	atg	tta	gac	gag	gcg	aag	240
Ile	Arg	Gln	Trp	Val	Ser	Met	Pro	Gln	Val	Met	Leu	Asp	Glu	Ala	Lys	
		65				70					75					

caa	atc	gct	gac	ttg	acc	ggc	gtg	gat	ttg	ggc	aac	cgt	tat	ttc	ctg	288
Gln	Ile	Ala	Asp	Leu	Thr	Gly	Val	Asp	Leu	Gly	Asn	Arg	Tyr	Phe	Leu	
80				85					90					95		

gtg	ctt	gcc	gac	aac	gac	gat	gcc	tta	ctg	gaa	aaa	gaa	cgg	gcg	ctg	336
Val	Leu	Ala	Asp	Asn	Asp	Asp	Ala	Leu	Leu	Glu	Lys	Glu	Arg	Ala	Leu	
			100					105						110		

aca	aca	aaa	ctg	gat	gaa	cag	cac	atc	cct	tat	cgc	gcc	ctt	tcc	caa	384
Thr	Thr	Lys	Leu	Asp	Glu	Gln	His	Ile	Pro	Tyr	Arg	Ala	Leu	Ser	Gln	
		115					120						125			

tgg	atg	atg	tgc	gaa	gcg	caa	cag	cgc	caa	ttt	ata	gtg	gaa	ttg	cag	432
Trp	Met	Met	Ser	Glu	Ala	Gln	Gln	Arg	Gln	Phe	Ile	Val	Glu	Leu	Gln	
		130					135					140				

gca	aaa	ctc	aaa	cgc	cag	gat	tat	gcc	gta	ttg	gat	gag	att	ggc	gtg	480
Ala	Lys	Leu	Lys	Pro	Gln	Asp	Tyr	Ala	Val	Leu	Asp	Glu	Ile	Gly	Val	
	145				150						155					

cgc	tgc	gaa	aga	tta	caa	cag	gca	ctg	cgc	gaa	ttg	aac	acg	cag	cgc	528
Pro	Ser	Glu	Arg	Leu	Gln	Gln	Ala	Leu	Arg	Glu	Leu	Asn	Thr	Gln	Pro	
160				165					170					175		

cgc	tta	tcc	ttg	cag	cag	gcg	ttg	caa	tct	acc	gtc	ggg	caa	gca	tgg	576
Pro	Leu	Ser	Leu	Gln	Gln	Ala	Leu	Gln	Ser	Thr	Val	Gly	Gln	Ala	Trp	
			180					185						190		

ctg	cgc	ctc	tat	tta	ggc	aaa	tta	gcg	gaa	aat	cag	gtg	gct	ggc	atc	624
Leu	Pro	Leu	Tyr	Leu	Gly	Lys	Leu	Ala	Glu	Asn	Gln	Val	Ala	Gly	Ile	
			195				200						205			

gtg	cag	gta	agc	gga	cac	agt	gcc	gtt	tcc	ctt	gcg	ca				662
Val	Gln	Val	Ser	Gly	His	Ser	Ala	Val	Ser	Leu	Ala					
		210					215									

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<210> 184
 <211> 219
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 184

Ser Arg Gln Cys Ser Pro Pro Cys Phe Phe Cys Leu His Tyr Phe Ala
 1 5 10 15

Val Ile Lys Thr Asn Arg Ala Pro Arg Thr Gln Lys Cys Gly Gly Phe
 20 25 30

Trp Met Arg Phe Leu Arg Met Gly Val Val Ser Ile Leu Leu Gly Gly
 35 40 45

Ile Phe Ile Val Gly Gly Leu Tyr Arg Ser Glu Trp Arg Asp Asp Ile
 50 55 60

Arg Gln Trp Val Ser Met Pro Gln Val Met Leu Asp Glu Ala Lys Gln
 65 70 75 80

Ile Ala Asp Leu Thr Gly Val Asp Leu Gly Asn Arg Tyr Phe Leu Val
 85 90 95

Leu Ala Asp Asn Asp Asp Ala Leu Leu Glu Lys Glu Arg Ala Leu Thr
 100 105 110

Thr Lys Leu Asp Glu Gln His Ile Pro Tyr Arg Ala Leu Ser Gln Trp
 115 120 125

Met Met Ser Glu Ala Gln Gln Arg Gln Phe Ile Val Glu Leu Gln Ala
 130 135 140

Lys Leu Lys Pro Gln Asp Tyr Ala Val Leu Asp Glu Ile Gly Val Pro
 145 150 155 160

Ser Glu Arg Leu Gln Gln Ala Leu Arg Glu Leu Asn Thr Gln Pro Pro
 165 170 175

Leu Ser Leu Gln Gln Ala Leu Gln Ser Thr Val Gly Gln Ala Trp Leu
 180 185 190

Pro Leu Tyr Leu Gly Lys Leu Ala Glu Asn Gln Val Ala Gly Ile Val
 195 200 205

Gln Val Ser Gly His Ser Ala Val Ser Leu Ala
 210 215

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<210> 185
 <211> 247
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(246)

<400> 185
 ggg gtg ttt atg tcc gcg cat aat ttc ccg aaa tcc cgt gaa acc cgt 48
 Gly Val Phe Met Ser Ala His Asn Phe Pro Lys Ser Arg Glu Thr Arg
 1 5 10 15
 gca cct aaa gtg gcg gaa ttg gcg tta tat cgt gag cgg ctg ccg gaa 96
 Ala Pro Lys Val Ala Glu Leu Ala Leu Tyr Arg Glu Arg Leu Pro Glu
 20 25 30
 aaa tta agc tat ctg gct gac gca cca caa acg gat ccg gaa ggc agt 144
 Lys Leu Ser Tyr Leu Ala Asp Ala Pro Gln Thr Asp Pro Glu Gly Ser
 35 40 45
 gaa gcc atc att cgc ttt agt cgt aaa gaa aaa cgt caa tat gtc acc 192
 Glu Ala Ile Ile Arg Phe Ser Arg Lys Glu Lys Arg Gln Tyr Val Thr
 50 55 60
 tcc gaa aag aat ggc aag gcg aca aaa tgg ata gtg gat ttt gtt gat 240
 Ser Glu Lys Asn Gly Lys Ala Thr Lys Trp Ile Val Asp Phe Val Asp
 65 70 75 80
 ggg aag t 247
 Gly Lys

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<210> 186
 <211> 82
 <212> FRT
 <213> Actinobacillus actinomycetemcomitans

<400> 186

Gly Val Phe Met Ser Ala His Asn Phe Pro Lys Ser Arg Glu Thr Arg
 1 5 10 15
 Ala Pro Lys Val Ala Glu Leu Ala Leu Tyr Arg Glu Arg Leu Pro Glu
 20 25 30
 Lys Leu Ser Tyr Leu Ala Asp Ala Pro Gln Thr Asp Pro Glu Gly Ser
 35 40 45
 Glu Ala Ile Ile Arg Phe Ser Arg Lys Glu Lys Arg Gln Tyr Val Thr
 50 55 60
 Ser Glu Lys Asn Gly Lys Ala Thr Lys Trp Ile Val Asp Phe Val Asp

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65 70 75 80

Gly Lys

<210> 187
 <211> 357
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(357)

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<400> 187
 tgc gtc cac tcc ggt cct ctc gta cta gga gca gcc cca acc aat tct 48
 Cys Val His Ser Gly Pro Leu Val Leu Gly Ala Ala Pro Thr Asn Ser
 1 5 10 15
 cct acg ccc acg gca gat agg gac cga act gtc tca cga cgt tct aaa 96
 Pro Thr Pro Thr Ala Asp Arg Asp Arg Thr Val Ser Arg Arg Ser Lys
 20 25 30
 ccc agc tcg cgt acc act tta aat ggc gaa cag cca tac cct tgg gac 144
 Pro Ser Ser Arg Thr Thr Leu Asn Gly Glu Gln Pro Tyr Pro Trp Asp
 35 40 45
 cta ctt cag ccc cag gat gtg atg agc cga cat cga ggt gcc aaa cac 192
 Leu Leu Gln Pro Gln Asp Val Met Ser Arg His Arg Gly Ala Lys His
 50 55 60
 cgc cgt cga tat gaa ctc ttg ggc ggt atc agc ctg tta tcc ccg gag 240
 Arg Arg Arg Tyr Glu Leu Leu Gly Gly Ile Ser Leu Leu Ser Pro Glu
 65 70 75 80
 tac ctt tta tcc gtt gag cga tgg ccc ttc cat gca gaa cca ccg gat 288
 Tyr Leu Leu Ser Val Glu Arg Trp Pro Phe His Ala Glu Pro Pro Asp
 85 90 95
 cac tat gac cta ctt tcg tac ctg ccc gac ctg tcc gtc tcg cag tta 336
 His Tyr Asp Leu Leu Ser Tyr Leu Pro Asp Leu Ser Val Ser Gln Leu
 100 105 110
 agc ttg ctt ata cca ttg cac 357
 Ser Leu Leu Ile Pro Leu His
 115

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<210> 188
 <211> 119
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 188
 Cys Val His Ser Gly Pro Leu Val Leu Gly Ala Ala Pro Thr Asn Ser
 1 5 10 15

Pro Thr Pro Thr Ala Asp Arg Asp Arg Thr Val Ser Arg Arg Ser Lys
20 25 30

Pro Ser Ser Arg Thr Thr Leu Asn Gly Glu Gln Pro Tyr Pro Trp Asp
35 40 45

Leu Leu Gln Pro Gln Asp Val Met Ser Arg His Arg Gly Ala Lys His
50 55 60

Arg Arg Arg Tyr Glu Leu Leu Gly Gly Ile Ser Leu Leu Ser Pro Glu
65 70 75 80

Tyr Leu Leu Ser Val Glu Arg Trp Pro Phe His Ala Glu Pro Pro Asp
85 90 95

His Tyr Asp Leu Leu Ser Tyr Leu Pro Asp Leu Ser Val Ser Gln Leu
100 105 110

Ser Leu Leu Ile Pro Leu His
115

<210> 189
<211> 222
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(222)

<400> 189
gaa acc gtg tgc tat gaa atc atg cgc gaa atc att cgc gta cac cat 48
Glu Thr Val Cys Tyr Glu Ile Met Arg Glu Ile Ile Arg Val His His
1 5 10 15
gta ttt gcc agc gaa caa ttc gtg gtt tat gcc tct cac gcc gtc gcc 96
Val Phe Ala Ser Glu Gln Phe Val Val Tyr Ala Ser His Ala Val Ala
20 25 30
gat tat ctg att aac gaa gaa tcc cac ggc tta ctg gct gaa ctg gaa 144
Asp Tyr Leu Ile Asn Glu Glu Ser His Gly Leu Leu Ala Glu Leu Glu
35 40 45
gtg ttc atc ggc aaa caa atc caa gta aaa act gaa gtg ttt tat act 192
Val Phe Ile Gly Lys Gln Ile Gln Val Lys Thr Glu Val Phe Tyr Thr
50 55 60
cag gaa cag ttt gat gtg gtg gtg atg tag 222
Gln Glu Gln Phe Asp Val Val Val Met
65 70

<210> 190
<211> 73

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<212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 190
 Glu Thr Val Cys Tyr Glu Ile Met Arg Glu Ile Ile Arg Val His His
 1 5 10 15
 Val Phe Ala Ser Glu Gln Phe Val Val Tyr Ala Ser His Ala Val Ala
 20 25 30
 Asp Tyr Leu Ile Asn Glu Glu Ser His Gly Leu Leu Ala Glu Leu Glu
 35 40 45
 Val Phe Ile Gly Lys Gln Ile Gln Val Lys Thr Glu Val Phe Tyr Thr
 50 55 60
 Gln Glu Gln Phe Asp Val Val Val Met
 65 70

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<210> 191
 <211> 1670
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(1668)

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<400> 191
 atc gaa cgt tat caa cgt tat aac aac acc tca tac aat ott gag ccg 48
 Ile Glu Arg Tyr Gln Arg Tyr Asn Asn Thr Ser Tyr Asn Leu Glu Pro
 1 5 10 15
 gac atc aaa tac agt ccg ggc ggg ttg cgc gat ttg cat ttg ttg tat 96
 Asp Ile Lys Tyr Ser Pro Gly Gly Leu Arg Asp Leu His Leu Leu Tyr
 20 25 30
 tgg atc gcg ttg cgc cat aac ggg gct aaa aat tta cag gaa att tta 144
 Trp Ile Ala Leu Arg His Asn Gly Ala Lys Asn Leu Gln Glu Ile Leu
 35 40 45
 cag gcg ggg ttt att cat ccg gca gaa cac gcc ttg tta cta aaa agc 192
 Gln Ala Gly Phe Ile His Pro Ala Glu His Ala Leu Leu Lys Ser
 50 55 60
 cag caa ttt ctg ttt aaa gtg cgg tac gct ttg cac tta att tta aag 240
 Gln Gln Phe Leu Phe Lys Val Arg Tyr Ala Leu His Leu Ile Leu Lys
 65 70 75 80
 cgt tat gac aac cgc ctg ttg ttt gat cgc caa ctg aaa gtc agc gaa 288
 Arg Tyr Asp Asn Arg Leu Leu Phe Asp Arg Gln Leu Lys Val Ser Glu
 85 90 95
 ttg ttg ggt ttc cag ggg gaa ggc aat caa ggc gtg gaa gcc atg atg 336
 Leu Leu Gly Phe Gln Gly Glu Gly Asn Gln Gly Val Glu Ala Met Met

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100	105	110	
aag cgc ttt ttt cag gcg ttg cat tcc att tcg tta cta agc gaa ttg Lys Arg Phe Phe Gln Ala Leu His Ser Ile Ser Leu Leu Ser Glu Leu 115 120 125			384
ttg gta aaa cat tat cag gaa cat ttt tta acc cgt cat gca gtg gtg Leu Val Lys His Tyr Gln Glu His Phe Leu Thr Arg His Ala Val Val 130 135 140			432
agc gag caa ata ctc gat gac aat ttc agc ctg atc aat caa tcc att Ser Glu Gln Ile Leu Asp Asp Asn Phe Ser Leu Ile Asn Gln Ser Ile 145 150 155 160			480
tgc tta cgt aat cat caa tgc ttt gag cag cag ccg gaa agc att ctt Cys Leu Arg Asn His Gln Cys Phe Glu Gln Gln Pro Glu Ser Ile Leu 165 170 175			528
gac ctt ttt tat cat tta acc caa tat ccg cag gcg gaa att cat tcc Asp Leu Phe Tyr His Leu Thr Gln Tyr Pro Gln Ala Glu Ile His Ser 180 185 190			576
ttt gtc ttg cgc gag ctt tat ttg gcg ctg gag caa ccg cag ggc tat Phe Val Leu Arg Glu Leu Tyr Leu Ala Leu Glu Gln Arg Gln Gly Tyr 195 200 205			624
ttg tgt gat ttg cca gcg gcg ccg gaa aaa ttc gtg cgc ctg ttt aat Leu Cys Asp Leu Pro Ala Ala Arg Glu Lys Phe Val Arg Leu Phe Asn 210 215 220			672
cag ccg aat gcg att aaa cgt gct ttt ttc cct atg cac caa tac ggc Gln Pro Asn Ala Ile Lys Arg Ala Phe Phe Pro Met His Gln Tyr Gly 225 230 235 240			720
gtg ctt acc gcc tat tta ccg caa tgg ggc aac gtc gtc ggt tta atg Val Leu Thr Ala Tyr Leu Pro Gln Trp Gly Asn Val Val Gly Leu Met 245 250 255			768
cag ttt gat tta ttt cat tgt tac acc gtg gac gag cat att ctg cgc Gln Phe Asp Leu Phe His Cys Tyr Thr Val Asp Glu His Ile Leu Arg 260 265 270			816
gtg atg tta aaa ctg gaa agt ttt tta gag ggc gct tcg gca caa agc Val Met Leu Lys Leu Glu Ser Phe Leu Glu Gly Ala Ser Ala Gln Ser 275 280 285			864
cat ccc att tgc cat caa ata ttc agc cga att tcc gac cgc act ttg His Pro Ile Cys His Gln Ile Phe Ser Arg Ile Ser Asp Arg Thr Leu 290 295 300			912
ttg tat att gcc gct tta ttt cac gac atc gcc aaa ggg cgc ggc ggt Leu Tyr Ile Ala Ala Leu Phe His Asp Ile Ala Lys Gly Arg Gly Gly 305 310 315 320			960
tct cat gaa tta ttg ggt gcg gtg gat gtg cgc gaa ttt gcc gtt cgg Ser His Glu Leu Leu Gly Ala Val Asp Val Arg Glu Phe Ala Val Arg 325 330 335			1008
cac ggt ttt gat caa ccg gaa acg gaa acc atg gtg tgg ctg gtg gag His Gly Phe Asp Gln Arg Glu Thr Glu Thr Met Val Trp Leu Val Glu 340 345 350			1056

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cag cat ttg ctt atg tcg gtc acg gca caa cgg cgg gat att cat gat 1104
 Gln His Leu Leu Met Ser Val Thr Ala Gln Arg Arg Asp Ile His Asp
 355 360 365
 ccg gaa att gta ctg aat ttc gcc gaa ctg gtg cgt aat cag gtg cgt 1152
 Pro Glu Ile Val Leu Asn Phe Ala Glu Leu Val Arg Asn Gln Val Arg
 370 375 380
 ttg gat tat tta acc tgc ctg acc gtc gcc gat att gtg gcg acc aat 1200
 Leu Asp Tyr Leu Thr Cys Leu Thr Val Ala Asp Ile Val Ala Thr Asn
 385 390 395 400
 gaa act ttg tgg aat agc tgg aag cgt tct ttg ctg gcg act ttg tac 1248
 Glu Thr Leu Trp Asn Ser Trp Lys Arg Ser Leu Leu Ala Thr Leu Tyr
 405 410 415
 gat tac gcc acc caa caa ttc gcc caa ggg ctg gaa agt atc ttg gat 1296
 Asp Tyr Ala Thr Gln Gln Phe Ala Gln Gly Leu Glu Ser Ile Leu Asp
 420 425 430
 aat caa gcg aaa gcg aaa gga cac cgc cga tta gca ctg cag gaa ata 1344
 Asn Gln Ala Lys Ala Lys Gly His Arg Arg Leu Ala Leu Gln Glu Ile
 435 440 445
 cgt gaa aaa acc acc gca ctt tcc gac aaa cac atc gaa aaa ttg tgg 1392
 Arg Glu Lys Thr Thr Ala Leu Ser Asp Lys His Ile Glu Lys Leu Trp
 450 455 460
 cag cgt ttt ccg ata gat tat ttc ttg cgc aat tcg cca caa caa att 1440
 Gln Arg Phe Pro Ile Asp Tyr Phe Leu Arg Asn Ser Pro Gln Gln Ile
 465 470 475 480
 ggt tgg cat acc cgt ttg ctt gcc gaa ttt gaa ggg gaa ttg ttg gtg 1488
 Gly Trp His Thr Arg Leu Ala Glu Phe Glu Gly Glu Leu Leu Val
 485 490 495
 aaa gtc agt aac cgg ttt tct gcc ggc ggc acg gaa att ttc att tat 1536
 Lys Val Ser Asn Arg Phe Ser Ala Gly Gly Thr Glu Ile Phe Ile Tyr
 500 505 510
 acc aaa gac cga ccg aac ctg ttt cac aaa gtg gta agt act atc ggc 1584
 Thr Lys Asp Arg Pro Asn Leu Phe His Lys Val Val Ser Thr Ile Gly
 515 520 525
 gcg aaa aaa ctc agt atc cat gat gcg caa att atc acc gcc aaa gac 1632
 Ala Lys Lys Leu Ser Ile His Asp Ala Gln Ile Ile Thr Ala Lys Asp
 530 535 540
 ggc tat gtg ttg gac agt ttt att gtg acg gaa tta ga 1670
 Gly Tyr Val Leu Asp Ser Phe Ile Val Thr Glu Leu
 545 550 555

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<210> 192
 <211> 556
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 192

Ile Glu Arg Tyr Gln Arg Tyr Asn Asn Thr Ser Tyr Asn Leu Glu Pro
 1 5 10 15
 Asp Ile Lys Tyr Ser Pro Gly Gly Leu Arg Asp Leu His Leu Leu Tyr
 20 25 30
 Trp Ile Ala Leu Arg His Asn Gly Ala Lys Asn Leu Gln Glu Ile Leu
 35 40 45
 Gln Ala Gly Phe Ile His Pro Ala Glu His Ala Leu Leu Leu Lys Ser
 50 55 60
 Gln Gln Phe Leu Phe Lys Val Arg Tyr Ala Leu His Leu Ile Leu Lys
 65 70 75 80
 Arg Tyr Asp Asn Arg Leu Leu Phe Asp Arg Gln Leu Lys Val Ser Glu
 85 90 95
 Leu Leu Gly Phe Gln Gly Glu Gly Asn Gln Gly Val Glu Ala Met Met
 100 105 110
 Lys Arg Phe Phe Gln Ala Leu His Ser Ile Ser Leu Leu Ser Glu Leu
 115 120 125
 Leu Val Lys His Tyr Gln Glu His Phe Leu Thr Arg His Ala Val Val
 130 135 140
 Ser Glu Gln Ile Leu Asp Asp Asn Phe Ser Leu Ile Asn Gln Ser Ile
 145 150 155 160
 Cys Leu Arg Asn His Gln Cys Phe Glu Gln Gln Pro Glu Ser Ile Leu
 165 170 175
 Asp Leu Phe Tyr His Leu Thr Gln Tyr Pro Gln Ala Glu Ile His Ser
 180 185 190
 Phe Val Leu Arg Glu Leu Tyr Leu Ala Leu Glu Gln Arg Gln Gly Tyr
 195 200 205
 Leu Cys Asp Leu Pro Ala Ala Arg Glu Lys Phe Val Arg Leu Phe Asn
 210 215 220
 Gln Pro Asn Ala Ile Lys Arg Ala Phe Phe Pro Met His Gln Tyr Gly
 225 230 235 240
 Val Leu Thr Ala Tyr Leu Pro Gln Trp Gly Asn Val Val Gly Leu Met

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Lys Val Ser Asn Arg Phe Ser Ala Gly Gly Thr Glu Ile Phe Ile Tyr
500 505 510

Thr Lys Asp Arg Pro Asn Leu Phe His Lys Val Val Ser Thr Ile Gly
515 520 525

Ala Lys Lys Leu Ser Ile His Asp Ala Gln Ile Ile Thr Ala Lys Asp
530 535 540

Gly Tyr Val Leu Asp Ser Phe Ile Val Thr Glu Leu
545 550 555

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<210> 193
<211> 567
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(567)

<400> 193
gtc aac cat tcg ctt tat tcc gta ttg aga ccg att aat ggc gaa agc 48
Val Asn His Ser Leu Tyr Ser Val Leu Arg Pro Ile Asn Gly Glu Ser
1 5 10 15
acc ctt att aaa ggt caa gcg aag tgg gtg att tca aga ggt tcg cgt 96
Thr Leu Ile Lys Gly Gln Ala Lys Trp Val Ile Ser Arg Gly Ser Arg
20 25 30
aat cgc act ttt cgt gtc ggt caa tct tat tgt cct tgt tgt tta ggg 144
Asn Arg Thr Phe Arg Val Gly Gln Ser Tyr Cys Pro Cys Cys Leu Gly
35 40 45
gaa aca cct tat ttg cgt aat gaa tgg cgt ttt gcg tgg cat ttt ggt 192
Glu Thr Pro Tyr Leu Arg Asn Glu Trp Arg Phe Ala Trp His Phe Gly
50 55 60
tgt tcg aaa cat caa gtt tta ctt gaa tct aaa tgc cct tgt tgt ggc 240
Cys Ser Lys His Gln Val Leu Leu Glu Ser Lys Cys Pro Cys Cys Gly
65 70 75 80
gaa ctg tat caa cct cat ttg ctt tcc gca gaa aaa cga cac tta aat 288
Glu Leu Tyr Gln Pro His Leu Leu Ser Ala Glu Lys Arg His Leu Asn
85 90 95
tac tgt cat caa tgt ggt gag aaa tta cag gtt gtt aca aca ccg ctt 336
Tyr Cys His Gln Cys Gly Glu Lys Leu Gln Val Val Thr Thr Pro Leu
100 105 110
aat gaa gta gaa att gca aca atg gaa aca ctt aat aac gta ttt atg 384
Asn Glu Val Glu Ile Ala Thr Met Glu Thr Leu Asn Asn Val Phe Met
115 120 125
act aac tca ggt gaa tgt ttc agg aaa cgt gtg aat gca caa gtg tac 432

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Thr Asn Ser Gly Glu Cys Phe Arg Lys Arg Val Asn Ala Gln Val Tyr
 130 135 140
 ttt gct ata ttg cgt tac ttc atc aat ctt att cgg cgt gct acg gtc 480
 Phe Ala Ile Leu Arg Tyr Phe Ile Asn Leu Ile Arg Arg Ala Thr Val
 145 150 155 160
 gta aaa tct act cac gct ttt gca aaa ttt gtg gaa gaa tgt ggt att 528
 Val Lys Ser Thr His Ala Phe Ala Lys Phe Val Glu Glu Cys Gly Ile
 165 170 175
 tct caa gcg gaa ata tgc caa acc aaa acc gcc ctt gca 567
 Ser Gln Ala Glu Ile Cys Gln Thr Lys Thr Ala Leu Ala
 180 185

<210> 194
 <211> 189
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 194

Val Asn His Ser Leu Tyr Ser Val Leu Arg Pro Ile Asn Gly Glu Ser
 1 5 10 15

Thr Leu Ile Lys Gly Gln Ala Lys Trp Val Ile Ser Arg Gly Ser Arg
 20 25 30

Asn Arg Thr Phe Arg Val Gly Gln Ser Tyr Cys Pro Cys Cys Leu Gly
 35 40 45

Glu Thr Pro Tyr Leu Arg Asn Glu Trp Arg Phe Ala Trp His Phe Gly
 50 55 60

Cys Ser Lys His Gln Val Leu Leu Glu Ser Lys Cys Pro Cys Cys Gly
 65 70 75 80

Glu Leu Tyr Gln Pro His Leu Leu Ser Ala Glu Lys Arg His Leu Asn
 85 90 95

Tyr Cys His Gln Cys Gly Glu Lys Leu Gln Val Val Thr Thr Pro Leu
 100 105 110

Asn Glu Val Glu Ile Ala Thr Met Glu Thr Leu Asn Asn Val Phe Met
 115 120 125

Thr Asn Ser Gly Glu Cys Phe Arg Lys Arg Val Asn Ala Gln Val Tyr
 130 135 140

Phe Ala Ile Leu Arg Tyr Phe Ile Asn Leu Ile Arg Arg Ala Thr Val
 145 150 155 160

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Val Lys Ser Thr His Ala Phe Ala Lys Phe Val Glu Glu Cys Gly Ile
 165 170 175

Ser Gln Ala Glu Ile Cys Gln Thr Lys Thr Ala Leu Ala
 180 185

<210> 195
 <211> 492
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(492)

<400> 195
 acc ttg gat gtg ctt cgt tcc gaa act ttc gtt tcc gaa tta aaa ggc 48
 Thr Leu Asp Val Leu Arg Ser Glu Thr Phe Val Ser Glu Leu Lys Gly
 1 5 10 15
 tta aat gct tat cgc acc acc gtg cct gtc atc ggc gga cac tcc ggt 96
 Leu Asn Ala Tyr Arg Thr Thr Val Pro Val Ile Gly Gly His Ser Gly
 20 25 30
 gtg act att ctt ccg tta tta tct caa gtg caa tac gtt gaa tgg aaa 144
 Val Thr Ile Leu Pro Leu Leu Ser Gln Val Gln Tyr Val Glu Trp Lys
 35 40 45
 gag gac gaa att gaa ccg tta acc aaa cgc att caa aat gcc ggc acc 192
 Glu Asp Glu Ile Glu Pro Leu Thr Lys Arg Ile Gln Asn Ala Gly Thr
 50 55 60
 gaa gta gta aac gcg aaa gcc ggc ggc ggt tcc gca acc tta tcc atg 240
 Glu Val Val Asn Ala Lys Ala Gly Gly Gly Ser Ala Thr Leu Ser Met
 65 70 75 80
 gcg cag gcg gca gcc cgt ttt gct aat gct gta gtc cgc ggt tta caa 288
 Ala Gln Ala Ala Ala Arg Phe Ala Asn Ala Val Val Arg Gly Leu Gln
 85 90 95
 ggt gaa acc gtc gta gaa tgc agc tat gtg gaa ggc gac ggc aaa tac 336
 Gly Glu Thr Val Val Glu Cys Ser Tyr Val Glu Gly Asp Gly Lys Tyr
 100 105 110
 gcc cgc ttc ttc gca caa ccg gtt cgc ttc ggc aag gaa ggt gtg gaa 384
 Ala Arg Phe Phe Ala Gln Pro Val Arg Phe Gly Lys Glu Gly Val Glu
 115 120 125
 gaa atc cta cca atc ggt aaa ctc agc gcc ttg gaa caa cag gct tta 432
 Glu Ile Leu Pro Ile Gly Lys Leu Ser Ala Leu Glu Gln Gln Ala Leu
 130 135 140
 gaa acc atg tta ccg aca ttg cgt gca gat att gaa tta ggt gag aag 480
 Glu Thr Met Leu Pro Thr Leu Arg Ala Asp Ile Glu Leu Gly Glu Lys
 145 150 155 160
 ttt att aat cca 492

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Phe Ile Asn Pro

<210> 196
 <211> 164
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 196

Thr Leu Asp Val Leu Arg Ser Glu Thr Phe Val Ser Glu Leu Lys Gly
 1 5 10 15

Leu Asn Ala Tyr Arg Thr Thr Val Pro Val Ile Gly Gly His Ser Gly
 20 25 30

Val Thr Ile Leu Pro Leu Leu Ser Gln Val Gln Tyr Val Glu Trp Lys
 35 40 45

Glu Asp Glu Ile Glu Pro Leu Thr Lys Arg Ile Gln Asn Ala Gly Thr
 50 55 60

Glu Val Val Asn Ala Lys Ala Gly Gly Gly Ser Ala Thr Leu Ser Met
 65 70 75 80

Ala Gln Ala Ala Ala Arg Phe Ala Asn Ala Val Val Arg Gly Leu Gln
 85 90 95

Gly Glu Thr Val Val Glu Cys Ser Tyr Val Glu Gly Asp Gly Lys Tyr
 100 105 110

Ala Arg Phe Phe Ala Gln Pro Val Arg Phe Gly Lys Glu Gly Val Glu
 115 120 125

Glu Ile Leu Pro Ile Gly Lys Leu Ser Ala Leu Glu Gln Gln Ala Leu
 130 135 140

Glu Thr Met Leu Pro Thr Leu Arg Ala Asp Ile Glu Leu Gly Glu Lys
 145 150 155 160

Phe Ile Asn Pro

<210> 197
 <211> 667
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>

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<221> CDS

<222> (1)..(666)

<400> 197

gca tta agc ctg caa agt ttc aac ctt gaa gtg ccg gtt gat gat aaa 48
 Ala Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val Asp Asp Lys
 1 5 10 15

gaa cgt atc gaa aac atc aaa cgt tac acc ggt gaa aaa tta gat acg 96
 Glu Arg Ile Glu Asn Ile Lys Arg Tyr Thr Gly Glu Lys Leu Asp Thr
 20 25 30

gcg ttt gtc aac gga tta gtg gaa gcc tcg agc cgt tta cgt cgc tta 144
 Ala Phe Val Asn Gly Leu Val Glu Ala Ser Ser Arg Leu Arg Arg Leu
 35 40 45

tcc ccg ccg gca ttc cgt ttc caa tta acc gaa tta gcc cgc gcc gcc 192
 Ser Pro Pro Ala Phe Arg Phe Gln Leu Thr Glu Leu Ala Arg Ala Ala
 50 55 60

caa aaa cgc atc gtc tta ccg gaa gcc gac gaa ccg cgc acc att aaa 240
 Gln Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg Thr Ile Lys
 65 70 75 80

gcg gcg att tta tgt gcc gaa cgc ggt atc gca gaa tgt gtg ctg tta 288
 Ala Ala Ile Leu Cys Ala Glu Arg Gly Ile Ala Glu Cys Val Leu Leu
 85 90 95

gcc aaa ccg gaa gac gta caa cgc gtg gcg gaa tcc caa gcc gtt aag 336
 Ala Lys Pro Glu Asp Val Gln Arg Val Ala Glu Ser Gln Gly Val Lys
 100 105 110

ttg gta aac gcc att acc gtt atc gac ccg gcg agc gtg cgt gaa aac 384
 Leu Val Asn Gly Ile Thr Val Ile Asp Pro Ala Ser Val Arg Glu Asn
 115 120 125

tat gtg gca cgt ttg gtt gag cta cgc aaa gcc aaa gcc atg acc gaa 432
 Tyr Val Ala Arg Leu Val Glu Leu Arg Lys Ala Lys Gly Met Thr Glu
 130 135 140

acc atg gcg cgt gaa caa ttg gaa gac aat gtt gtg ctc ggt acc atg 480
 Thr Met Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu Gly Thr Met
 145 150 155 160

atg ttg gaa gcc aac caa gta gac ggt ttg gta tcc gcc gcc gta cac 528
 Met Leu Glu Ala Asn Gln Val Asp Gly Leu Val Ser Gly Ala Val His
 165 170 175

acc acc gcc aac acc att cgc ccg cca atg caa atc atc aaa acc gca 576
 Thr Thr Ala Asn Thr Ile Arg Pro Pro Met Gln Ile Ile Lys Thr Ala
 180 185 190

ccg gcc agc tcc att att tct tcc atc ttc ttc atg ttg cta ccg gat 624
 Pro Gly Ser Ser Ile Ile Ser Ser Ile Phe Phe Met Leu Leu Pro Asp
 195 200 205

caa gta ttg gtc tat gcc gat tgc gca gtg aac ccg gat ccg a 667
 Gln Val Leu Val Tyr Gly Asp Cys Ala Val Asn Pro Asp Pro
 210 215 220

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<210> 198
 <211> 222
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 198

Ala Leu Ser Leu Gln Ser Phe Asn Leu Glu Val Pro Val Asp Asp Lys
 1 5 10 15

Glu Arg Ile Glu Asn Ile Lys Arg Tyr Thr Gly Glu Lys Leu Asp Thr
 20 25 30

Ala Phe Val Asn Gly Leu Val Glu Ala Ser Ser Arg Leu Arg Arg Leu
 35 40 45

Ser Pro Pro Ala Phe Arg Phe Gln Leu Thr Glu Leu Ala Arg Ala Ala
 50 55 60

Gln Lys Arg Ile Val Leu Pro Glu Gly Asp Glu Pro Arg Thr Ile Lys
 65 70 75 80

Ala Ala Ile Leu Cys Ala Glu Arg Gly Ile Ala Glu Cys Val Leu Leu
 85 90 95

Ala Lys Pro Glu Asp Val Gln Arg Val Ala Glu Ser Gln Gly Val Lys
 100 105 110

Leu Val Asn Gly Ile Thr Val Ile Asp Pro Ala Ser Val Arg Glu Asn
 115 120 125

Tyr Val Ala Arg Leu Val Glu Leu Arg Lys Ala Lys Gly Met Thr Glu
 130 135 140

Thr Met Ala Arg Glu Gln Leu Glu Asp Asn Val Val Leu Gly Thr Met
 145 150 155 160

Met Leu Glu Ala Asn Gln Val Asp Gly Leu Val Ser Gly Ala Val His
 165 170 175

Thr Thr Ala Asn Thr Ile Arg Pro Pro Met Gln Ile Ile Lys Thr Ala
 180 185 190

Pro Gly Ser Ser Ile Ile Ser Ser Ile Phe Phe Met Leu Leu Pro Asp
 195 200 205

Gln Val Leu Val Tyr Gly Asp Cys Ala Val Asn Pro Asp Pro
 210 215 220

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<210> 199
 <211> 267
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(267)

<400> 199
 ggt ata cgc cct gag cat tta att ccg tct gat gag gca gaa gtt acg 48
 Gly Ile Arg Pro Glu His Leu Ile Pro Ser Asp Glu Ala Glu Val Thr
 1 5 10 15
 ttg cgc agc aat gtg cag gtg gtg gaa ttg ctt ggt aac gaa acg caa 96
 Leu Arg Ser Asn Val Gln Val Val Glu Leu Leu Gly Asn Glu Thr Gln
 20 25 30
 att cac ctt gaa atc cct gaa att aaa caa ccg acc tta att tat cgc 144
 Ile His Leu Glu Ile Pro Glu Ile Lys Gln Pro Thr Leu Ile Tyr Arg
 35 40 45
 caa aat gat gtg gtg ttg gtg aag gag ggg gaa acg atg gac atc ggc 192
 Gln Asn Asp Val Val Leu Val Lys Glu Gly Glu Thr Met Asp Ile Gly
 50 55 60
 atc att ccg gaa cgt tgc cat ctg ttt aaa gaa gac ggc acc gcc tgc 240
 Ile Ile Pro Glu Arg Cys His Leu Phe Lys Glu Asp Gly Thr Ala Cys
 65 70 75 80
 caa cgt ttg tat aaa gaa aaa ggc gtt 267
 Gln Arg Leu Tyr Lys Glu Lys Gly Val
 85

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<210> 200
 <211> 89
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 200

Gly Ile Arg Pro Glu His Leu Ile Pro Ser Asp Glu Ala Glu Val Thr
 1 5 10 15
 Leu Arg Ser Asn Val Gln Val Val Glu Leu Leu Gly Asn Glu Thr Gln
 20 25 30
 Ile His Leu Glu Ile Pro Glu Ile Lys Gln Pro Thr Leu Ile Tyr Arg
 35 40 45
 Gln Asn Asp Val Val Leu Val Lys Glu Gly Glu Thr Met Asp Ile Gly
 50 55 60
 Ile Ile Pro Glu Arg Cys His Leu Phe Lys Glu Asp Gly Thr Ala Cys

30

Val Phe Phe Ala Ile Pro Leu Ala Thr Leu Val Lys Ala Val Val Asn
50 55 60

30

Ala Trp Pro Ser Asn Glu Ala Val Glu
65 70

<210> 203
<211> 631
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(630)

<400> 203

cct ttc gcc atc gaa agt gac gag aaa ttt gcc tcc gcc tgc att cgt Pro Phe Ala Ile Glu Ser Asp Glu Lys Phe Ala Ser Ala Cys Ile Arg 1 5 10 15	48	10
tgc ggt cag tgc gtg caa gcc tgc cct tat gat atg ttg cat ttg gca Cys Gly Gln Cys Val Gln Ala Cys Pro Tyr Asp Met Leu His Leu Ala 20 25 30	96	
tgc ttg cta tca cca atg gaa gcg ggg acg ccg tat ttt atc gcg cgc Ser Leu Leu Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg 35 40 45	144	
gat aaa cct tgc gaa atg tgt ccg gat att cct tgc gcc cat gcg tgt Asp Lys Pro Cys Glu Met Cys Pro Asp Ile Pro Cys Ala His Ala Cys 50 55 60	192	
ccg agc ggt gcg tta gat cgt gag gcg cag gat att aat caa tcc cgt Pro Ser Gly Ala Leu Asp Arg Glu Ala Gln Asp Ile Asn Gln Ser Arg 65 70 75 80	240	20
atg ggg ctg gcg gtg ttg ctg gat cat gaa acc tgc ttg aac tgg caa Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln 85 90 95	288	
ggc ttg cgt tgc gat gtg tgt tat ccg gtt tgt ccg ttg att gat aaa Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asp Lys 100 105 110	336	
gcc att acg ctg gaa agc cat cgt aat gag ccg acc ggc aag cac gcg Ala Ile Thr Leu Glu Ser His Arg Asn Glu Arg Thr Gly Lys His Ala 115 120 125	384	
gtg ttt att ccg acg gtg cat tcc gat ggc tgt acc ggc tgt ggc aaa Val Phe Ile Pro Thr Val His Ser Asp Gly Cys Thr Gly Cys Gly Lys 130 135 140	432	30
tgc gaa caa gcg tgt gtc ttg gaa gaa gcg gca atc aaa gta tta ccg Cys Glu Gln Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro 145 150 155 160	480	
atg cat ttg gcg aaa ggc atg tta ggc aaa cat tat cgt ttg ggt tgg Met His Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp 165 170 175	528	
gaa gaa aag gcg aaa gcc gga cat tcc ttg gcg ccg aaa gat ttg att Glu Glu Lys Ala Lys Ala Gly His Ser Leu Ala Pro Lys Asp Leu Ile 180 185 190	576	

tgc atg ccg acc cgt atg ccg gaa gcc aca atg ccg gta atg ggc gca 624
 Ser Met Pro Thr Arg Met Pro Glu Ala Thr Met Pro Val Met Gly Ala
 195 200 205

gaa gac a 631
 Glu Asp
 210

<210> 204
 <211> 210
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 204

Pro Phe Ala Ile Glu Ser Asp Glu Lys Phe Ala Ser Ala Cys Ile Arg
 1 5 10 15

Cys Gly Gln Cys Val Gln Ala Cys Pro Tyr Asp Met Leu His Leu Ala
 20 25 30

Ser Leu Leu Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg
 35 40 45

Asp Lys Pro Cys Glu Met Cys Pro Asp Ile Pro Cys Ala His Ala Cys
 50 55 60

Pro Ser Gly Ala Leu Asp Arg Glu Ala Gln Asp Ile Asn Gln Ser Arg
 65 70 75 80

Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln
 85 90 95

Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asp Lys
 100 105 110

Ala Ile Thr Leu Glu Ser His Arg Asn Glu Arg Thr Gly Lys His Ala
 115 120 125

Val Phe Ile Pro Thr Val His Ser Asp Gly Cys Thr Gly Cys Gly Lys
 130 135 140

Cys Glu Gln Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
 145 150 155 160

Met His Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
 165 170 175

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Glu Glu Lys Ala Lys Ala Gly His Ser Leu Ala Pro Lys Asp Leu Ile
 180 185 190

Ser Met Pro Thr Arg Met Pro Glu Ala Thr Met Pro Val Met Gly Ala
 195 200 205

Gln Asp
 210

<210> 205
 <211> 354
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

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<220>
 <221> CDS
 <222> (1)..(354)

<400> 205
 tgc ctg gaa cgg gtg aaa cgg ttg gag aag caa ggg gtg att atg ggg 48
 Cys Leu Glu Arg Val Lys Arg Leu Glu Lys Gln Gly Val Ile Met Gly
 1 5 10 15
 tat cgt gct ttg ctg aat ccc gca tta ttg gat tcg ccg ttg ttg gtg 96
 Tyr Arg Ala Leu Leu Asn Pro Ala Leu Leu Asp Ser Pro Leu Leu Val
 20 25 30
 atc gtg gaa att acg ctg gta cgt ggc aag ccc gat gtg ttt gaa gaa 144
 Ile Val Glu Ile Thr Leu Val Arg Gly Lys Pro Asp Val Phe Glu Glu
 35 40 45
 ttt aac gcg gcg gtg cag cag tta gat gaa att cag gaa tgc cat ttg 192
 Phe Asn Ala Ala Val Gln Gln Leu Asp Glu Ile Gln Glu Cys His Leu
 50 55 60
 gtt tcc ggt gat ttc gat tat tta ttg aaa aca cgg gtg gcg gat atg 240
 Val Ser Gly Asp Phe Asp Tyr Leu Leu Lys Thr Arg Val Ala Asp Met
 65 70 75 80
 gcg gcg tat cgt aaa ttg ctg ggg acc acc ttg ctg cgc ctg ccc ggg 288
 Ala Ala Tyr Arg Lys Leu Leu Gly Thr Thr Leu Leu Arg Leu Pro Gly
 85 90 95
 gtg aac gac acg cgc act tat gtg gtg atg gaa gaa gtg aaa caa acg 336
 Val Asn Asp Thr Arg Thr Tyr Val Met Glu Glu Val Lys Gln Thr
 100 105 110
 aat ttt tta cag tta aaa 354
 Asn Phe Leu Gln Leu Lys
 115

20

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<210> 206
 <211> 118
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 206

Cys Leu Glu Arg Val Lys Arg Leu Glu Lys Gln Gly Val Ile Met Gly
1 5 10 15

Tyr Arg Ala Leu Leu Asn Pro Ala Leu Leu Asp Ser Pro Leu Leu Val
20 25 30

Ile Val Glu Ile Thr Leu Val Arg Gly Lys Pro Asp Val Phe Glu Glu
35 40 45

Phe Asn Ala Ala Val Gln Gln Leu Asp Glu Ile Gln Glu Cys His Leu
50 55 60

Val Ser Gly Asp Phe Asp Tyr Leu Leu Lys Thr Arg Val Ala Asp Met
65 70 75 80

Ala Ala Tyr Arg Lys Leu Leu Gly Thr Thr Leu Leu Arg Leu Pro Gly
85 90 95

Val Asn Asp Thr Arg Thr Tyr Val Val Met Glu Glu Val Lys Gln Thr
100 105 110

Asn Phe Leu Gln Leu Lys
115

<210> 207
<211> 613
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(612)

<400> 207
atg agt tta aaa ata tta tta aat cag ccg caa tac gat ccg att cgt 48
Met Ser Leu Lys Ile Leu Leu Asn Gln Pro Gln Tyr Asp Pro Ile Arg
1 5 10 15
gac aaa aaa gcc gag cgc aac tta ttt gcc cgt cgc got ttg gtg tca 96
Asp Lys Lys Ala Glu Arg Asn Leu Phe Ala Arg Arg Ala Leu Val Ser
20 25 30
ttt atc gcc gtg ttg gtg ttg tcg gtg gtg tta att tta aac ttg tat 144
Phe Ile Gly Val Leu Val Leu Ser Val Val Leu Ile Leu Asn Leu Tyr
35 40 45
gat ttg cag gtg gtc aat tat gac ggt tat caa acc cgt tcc aac gcc 192
Asp Leu Gln Val Val Asn Tyr Asp Gly Tyr Gln Thr Arg Ser Asn Gly
50 55 60
aat cgt att aag ttg ttg ccg ctg ccg ccg act cgc ggy ttg att tat 240
Asn Arg Ile Lys Leu Leu Pro Leu Pro Pro Thr Arg Gly Leu Ile Tyr

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65	70	75	80		
gat cgc aac ggc aaa ctg ctg gcg gaa aat ctg acc ttt ttc ggg ctt				288	
Asp Arg Asn Gly Lys Leu Leu Ala Glu Asn Leu Thr Phe Phe Gly Leu					
	85	90	95		
tat atc gtg cct gaa aag gtg gaa aat tta gac cgc act ttt gag gag				336	
Tyr Ile Val Pro Glu Lys Val Glu Asn Leu Asp Arg Thr Phe Glu Glu					
	100	105	110		
ctg agg gtg ttg gta ggc tta act gat gaa gat att gcg aat ttt aac				384	
Leu Arg Val Leu Val Gly Leu Thr Asp Glu Asp Ile Ala Asn Phe Asn					
	115	120	125		
aag gaa cgg cgt cgc tcc tcc cgt tat atg ccg att atg ctg aaa cga				432	
Lys Glu Arg Arg Arg Ser Ser Arg Tyr Met Pro Ile Met Leu Lys Arg					10
	130	135	140		
aat cta acg gaa gag caa att gcc cgt ttt gcg gtg aat caa tac aat				480	
Asn Leu Thr Glu Glu Gln Ile Ala Arg Phe Ala Val Asn Gln Tyr Asn					
	145	150	155	160	
ttc cag agt ttg gat gtg aaa ccc tac ttt aag cgc cat tat tta tac				528	
Phe Gln Ser Leu Asp Val Lys Pro Tyr Phe Lys Arg His Tyr Leu Tyr					
	165	170	175		
ggc gaa ccg ctg acc cat gtt ttg ggc tat gtg tca aaa att aac gat				576	
Gly Glu Pro Leu Thr His Val Leu Glu Tyr Val Ser Lys Ile Asn Asp					
	180	185	190		
cgt gat gta gaa cgc ttg aaa aaa gag gaa aag tac g				613	
Arg Asp Val Glu Arg Leu Lys Lys Glu Glu Lys Tyr					20
	195	200			
<210> 208					
<211> 204					
<212> PRT					
<213> Actinobacillus actinomycetemcomitans					
<400> 208					
Met Ser Leu Lys Ile Leu Leu Asn Gln Pro Gln Tyr Asp Pro Ile Arg					
1	5	10	15		
Asp Lys Lys Ala Glu Arg Asn Leu Phe Ala Arg Arg Ala Leu Val Ser					
	20	25	30		30
Phe Ile Gly Val Leu Val Leu Ser Val Val Leu Ile Leu Asn Leu Tyr					
	35	40	45		
Asp Leu Gln Val Val Asn Tyr Asp Gly Tyr Gln Thr Arg Ser Asn Gly					
	50	55	60		
Asn Arg Ile Lys Leu Leu Pro Leu Pro Pro Thr Arg Gly Leu Ile Tyr					
65	70	75	80		

Asp Arg Asn Gly Lys Leu Leu Ala Glu Asn Leu Thr Phe Phe Gly Leu
85 90 95

Tyr Ile Val Pro Glu Lys Val Glu Asn Leu Asp Arg Thr Phe Glu Glu
100 105 110

Leu Arg Val Leu Val Gly Leu Thr Asp Glu Asp Ile Ala Asn Phe Asn
115 120 125

Lys Glu Arg Arg Arg Ser Ser Arg Tyr Met Pro Ile Met Leu Lys Arg
130 135 140

Asn Leu Thr Glu Glu Gln Ile Ala Arg Phe Ala Val Asn Gln Tyr Asn
145 150 155 160

Phe Gln Ser Leu Asp Val Lys Pro Tyr Phe Lys Arg His Tyr Leu Tyr
165 170 175

Gly Glu Pro Leu Thr His Val Leu Gly Tyr Val Ser Lys Ile Asn Asp
180 185 190

Arg Asp Val Glu Arg Leu Lys Lys Glu Glu Lys Tyr
195 200

<210> 209
<211> 631
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(630)

<400> 209
cgc tta gca caa cat tca tcg gaa aaa ctg acc gca ctt tcc cat gca 48
Arg Leu Ala Gln His Ser Ser Glu Lys Leu Thr Ala Leu Ser His Ala
1 5 10 15
acc acg cat tct gac gcc caa agt gcg gta gaa aat cag agt gaa tct 96
Thr Thr His Ser Asp Ala Gln Ser Ala Val Glu Asn Gln Ser Glu Ser
20 25 30
gat agc gac gaa act gat gcg gat gtg ttg tta ggc gag gat tat cgt 144
Asp Ser Asp Glu Thr Asp Ala Asp Val Leu Leu Gly Glu Asp Tyr Arg
35 40 45
tgg gag tgg agc aac ccc gag ctt gcc aat att gag caa ggc cct aag 192
Trp Glu Trp Ser Asn Pro Glu Leu Ala Asn Ile Glu Gln Gly Pro Lys
50 55 60
ccc tcc gaa atc aaa gcc gcc att ttg cag gac atc act cct gaa tta 240
Pro Ser Glu Ile Lys Ala Ala Ile Leu Gln Asp Ile Thr Pro Glu Leu

10

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65	70	75	80	
cag caa aaa atc gtc aat tta act caa acg caa gat cgc tgg gcg cag				288
Gln Gln Lys Ile Val Asn Leu Thr Gln Thr Gln Asp Arg Trp Ala Gln	85	90	95	
ctg att gag caa agc ggt gta gaa aat ctc acc aaa gag ttc gcc tta				336
Leu Ile Glu Phe Ile Ser Gly Val Glu Asn Leu Thr Lys Glu Phe Ala Leu	100	105	110	
aat acc ttc att tgg cag gaa aat gac gcg gag ttt aaa ctt ggt gtg				384
Asn Thr Phe Ile Trp Gln Glu Asn Asp Ala Glu Phe Lys Leu Gly Val	115	120	125	
ogt tcc agc cac ggg cat tta aat cag gat aag cat cgg aag ctg tta				432
Arg Ser Ser His Gly His Leu Asn Gln Asp Lys His Arg Lys Leu Leu	130	135	140	
caa cag gca ctt tca gtg gtg tta cag aaa gaa att gca ctg acc gtg				480
Gln Gln Ala Leu Ser Val Val Leu Gln Lys Glu Ile Ala Leu Thr Val	145	150	155	160
gaa att aac gac gac gaa caa tat ctg acg ccg acg gat tat cgc cgt				528
Glu Ile Asn Asp Asp Glu Gln Tyr Leu Thr Pro Thr Asp Tyr Arg Arg	165	170	175	
aaa acc tat gct caa ttg cgt gag cag gcg aaa cag gat ttg ttg caa				576
Lys Thr Tyr Ala Gln Leu Arg Glu Gln Ala Lys Gln Asp Leu Leu Gln	180	185	190	
gat gaa aag ttg caa cta ttg gag cgt gaa ttt gat tgt cag gtt gat				624
Asp Glu Lys Leu Gln Leu Leu Glu Arg Glu Phe Asp Cys Gln Val Asp	195	200	205	
gtg aaa a				631
Val Lys				
210				

<210> 210
 <211> 210
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 210

Arg Leu Ala Gln His Ser Ser Glu Lys Leu Thr Ala Leu Ser His Ala	1	5	10	15
Thr Thr His Ser Asp Ala Gln Ser Ala Val Glu Asn Gln Ser Glu Ser	20	25	30	
Asp Ser Asp Glu Thr Asp Ala Asp Val Leu Leu Gly Glu Asp Tyr Arg	35	40	45	
Trp Glu Trp Ser Asn Pro Glu Leu Ala Asn Ile Glu Gln Gly Pro Lys	50	55	60	

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Pro Ser Glu Ile Lys Ala Ala Ile Leu Gln Asp Ile Thr Pro Glu Leu
65 70 75 80

Gln Gln Lys Ile Val Asn Leu Thr Gln Thr Gln Asp Arg Trp Ala Gln
85 90 95

Leu Ile Glu Gln Ser Gly Val Glu Asn Leu Thr Lys Glu Phe Ala Leu
100 105 110

Asn Thr Phe Ile Trp Gln Glu Asn Asp Ala Glu Phe Lys Leu Gly Val
115 120 125

Arg Ser Ser His Gly His Leu Asn Gln Asp Lys His Arg Lys Leu Leu
130 135 140

Gln Gln Ala Leu Ser Val Val Leu Gln Lys Glu Ile Ala Leu Thr Val
145 150 155 160

Glu Ile Asn Asp Asp Glu Gln Tyr Leu Thr Pro Thr Asp Tyr Arg Arg
165 170 175

Lys Thr Tyr Ala Gln Leu Arg Glu Gln Ala Lys Gln Asp Leu Leu Gln
180 185 190

Asp Glu Lys Leu Gln Leu Leu Glu Arg Glu Phe Asp Cys Gln Val Asp
195 200 205

Val Lys
210

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<210> 211
<211> 1155
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(1155)

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<400> 211
ccc gaa cat ata aaa gac aag gta tcg aga ggt ttc att atg gca agt 48
Pro Glu His Ile Lys Asp Lys Val Ser Arg Gly Phe Ile Met Ala Ser
1 5 10 15

gta aca ttg cgc aat gtg ggc aaa tct tac gga aac gta cat att tcc 96
Val Thr Leu Arg Asn Val Gly Lys Ser Tyr Gly Asn Val His Ile Ser
20 25 30

aaa gat att aat ttg gat att gaa gaa ggc gaa ttt gtc gtc ttt gtc 144
Lys Asp Ile Asn Leu Asp Ile Glu Glu Gly Glu Phe Val Val Phe Val

35	40	45	
gga ccg tcc ggt tgc ggt aaa tcc aca tta ttg cga atg att gcc gga Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu Arg Met Ile Ala Gly 50 55 60			192
ctt gag gat att acc acc ggt gaa ctt tac atc ggt gaa aaa cgg atg Leu Glu Asp Ile Thr Thr Gly Glu Leu Tyr Ile Gly Glu Lys Arg Met 65 70 75 80			240
aac gat gtg ccg ccg gca aag cgc ggt atc ggt atg gtg ttc caa tct Asn Asp Val Pro Pro Ala Lys Arg Gly Ile Gly Met Val Phe Gln Ser 85 90 95			288
tac gcc ctg tac ccg cac ttg gat gtg gca gaa aat atg tct ttc ggg Tyr Ala Leu Ala Gly Val His Leu Asp Val Ala Glu Asn Met Ser Phe Gly 100 105 110			336
ctg aaa tta gcc ggt gta aat aaa acg gaa cgg gat cag cgc gtt aat Leu Lys Leu Ala Gly Val Asn Lys Thr Glu Arg Asp Gln Arg Val Asn 115 120 125			384
cag gtt gcc gaa att tta cag ctt gcc cat ttg ctt gaa cgt aaa ccg Gln Val Ala Glu Ile Leu Cag Leu Ala His Leu Leu Glu Arg Lys Pro 130 135 140			432
aaa gcc ttg tgg ggc ggt cag cgt caa cgt gtg gcg att ggg cga acc Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Ile Gly Arg Thr 145 150 155 160			480
ctt gtt tcc cag cca gaa gta ttc ttg ctg gac gaa ccg ctt tcc aac Leu Val Ser Gln Pro Glu Val Phe Leu Leu Asp Glu Pro Leu Ser Asn 165 170 175			528
tta gat gcc gcc ttg cgc gta caa atg cgg gtg gaa atc tcc aaa tta Leu Asp Ala Ala Leu Arg Val Gln Met Arg Val Glu Ile Ser Lys Leu 180 185 190			576
cac aaa aaa ctc aac cgc acc atg att tat gtt acc cat gac caa gtg His Lys Lys Leu Asn Arg Thr Met Ile Tyr Val Thr His Asp Gln Val 195 200 205			624
gaa gcc atg acc ctg gcg gac aaa atc gtg gtg ttg aat gcg ggc ggt Glu Ala Met Thr Leu Ala Asp Lys Ile Val Val Leu Asn Ala Gly Gly 210 215 220			672
att gcg cag gtg ggg aaa ccg ctg gaa ctt tac cat tat ccg caa aat Ile Ala Gln Val Gly Lys Pro Leu Glu Leu Tyr His Tyr Pro Gln Asn 225 230 235 240			720
cgt ttc gtg gcc ggt ttt atc ggt tca ccg aaa atg aat ttc ctg ccg Arg Phe Val Ala Gly Phe Ile Gly Ser Pro Lys Met Asn Phe Leu Pro 245 250 255			768
gtg aaa gtg act gct gtg gaa aaa gag cgg gtg caa atc gaa ttg ccc Val Lys Val Thr Ala Val Glu Lys Glu Arg Val Gln Ile Glu Leu Pro 260 265 270			816
gac gcc aac cat cat aac ttc tgg atc ccg gtt tcc ggt aat ggc gtg Asp Ala Asn His His Asn Phe Trp Ile Pro Val Ser Gly Asn Gly Val 275 280 285			864

10

20

30

aaa gtg ggt gaa aac ctt tca tta ggt ata cgc cct gag cat tta att 912
 Lys Val Gly Glu Asn Leu Ser Leu Gly Ile Arg Pro Glu His Leu Ile
 290 295 300
 ccg tct gat gag gca gaa gtt acg ttg cgc agc aat gtg cag gtg gtg 960
 Pro Ser Asp Glu Ala Glu Val Thr Leu Arg Ser Asn Val Gln Val Val
 305 310 315 320
 gaa ttg ctt ggt aac gaa acg caa att cac ctt gaa atc cct gaa att 1008
 Glu Leu Leu Gly Asn Glu Thr Gln Ile His Leu Glu Ile Pro Glu Ile
 325 330 335
 aaa caa ccg acc tta att tat cgc caa aat gat gtg gtg ttg gtg aag 1056
 Lys Gln Pro Thr Leu Ile Tyr Arg Gln Asn Asp Val Val Leu Val Lys
 340 345 350
 gag ggg gaa acg atg gac atc ggc atc att ccg gaa cgt tgc cat ctg 1104
 Glu Gly Glu Thr Met Asp Ile Gly Ile Ile Pro Glu Arg Cys His Leu
 355 360 365
 ttt aaa gaa gac ggc acc gcc tgc caa cgt ttg tat aaa gaa aaa ggc 1152
 Phe Lys Glu Asp Gly Thr Ala Cys Gln Arg Leu Tyr Lys Glu Lys Gly
 370 375 380
 gtt 1155
 Val
 385

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<210> 212
 <211> 385
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans
 <400> 212

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Pro Glu His Ile Lys Asp Lys Val Ser Arg Gly Phe Ile Met Ala Ser
 1 5 10 15
 Val Thr Leu Arg Asn Val Gly Lys Ser Tyr Gly Asn Val His Ile Ser
 20 25 30
 Lys Asp Ile Asn Leu Asp Ile Glu Glu Gly Glu Phe Val Val Phe Val
 35 40 45
 Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu Arg Met Ile Ala Gly
 50 55 60
 Leu Glu Asp Ile Thr Thr Gly Glu Leu Tyr Ile Gly Glu Lys Arg Met
 65 70 75 80
 Asn Asp Val Pro Pro Ala Lys Arg Gly Ile Gly Met Val Phe Gln Ser
 85 90 95

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Tyr Ala Leu Tyr Pro His Leu Asp Val Ala Glu Asn Met Ser Phe Gly
 100 105 110
 Leu Lys Leu Ala Gly Val Asn Lys Thr Glu Arg Asp Gln Arg Val Asn
 115 120 125
 Gln Val Ala Glu Ile Leu Gln Leu Ala His Leu Leu Glu Arg Lys Pro
 130 135 140
 Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Ile Gly Arg Thr
 145 150 155 160
 Leu Val Ser Gln Pro Glu Val Phe Leu Leu Asp Glu Pro Leu Ser Asn
 165 170 175
 Leu Asp Ala Ala Leu Arg Val Gln Met Arg Val Glu Ile Ser Lys Leu
 180 185 190
 His Lys Lys Leu Asn Arg Thr Met Ile Tyr Val Thr His Asp Gln Val
 195 200 205
 Glu Ala Met Thr Leu Ala Asp Lys Ile Val Val Leu Asn Ala Gly Gly
 210 215 220
 Ile Ala Gln Val Gly Lys Pro Leu Glu Leu Tyr His Tyr Pro Gln Asn
 225 230 235 240
 Arg Phe Val Ala Gly Phe Ile Gly Ser Pro Lys Met Asn Phe Leu Pro
 245 250 255
 Val Lys Val Thr Ala Val Glu Lys Glu Arg Val Gln Ile Glu Leu Pro
 260 265 270
 Asp Ala Asn His His Asn Phe Trp Ile Pro Val Ser Gly Asn Gly Val
 275 280 285
 Lys Val Gly Glu Asn Leu Ser Leu Gly Ile Arg Pro Glu His Leu Ile
 290 295 300
 Pro Ser Asp Glu Ala Glu Val Thr Leu Arg Ser Asn Val Gln Val Val
 305 310 315 320
 Glu Leu Leu Gly Asn Gln Thr Gln Ile His Leu Glu Ile Pro Glu Ile
 325 330 335
 Lys Gln Pro Thr Leu Ile Tyr Arg Gln Asn Asp Val Val Leu Val Lys

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340          345          350
Glu Gly Glu Thr Met Asp Ile Gly Ile Ile Pro Glu Arg Cys His Leu
355          360          365

Phe Lys Glu Asp Gly Thr Ala Cys Gln Arg Leu Tyr Lys Glu Lys Gly
370          375          380

Val
385

<210> 213
<211> 447
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(447)

<400> 213
atg cca aaa aat gcg caa ttc tac ctg ctt tcc gat gcc tct ccc gca      48
Met Pro Lys Asn Ala Gln Phe Tyr Leu Leu Ser Asp Ala Ser Pro Ala
1          5          10          15

cag acg aat ttg tct gcg gtg gaa agc ctt gcc tgc aat ttg gcg gcg      96
Gln Thr Asn Leu Ser Ala Val Glu Ser Leu Ala Cys Asn Leu Ala Ala
20          25          30

tcc gcc tgg cgt ttg gga aaa cgg gtt ctg ttg gcg tgt gaa aat gaa      144
Ser Ala Trp Arg Leu Gly Lys Arg Val Leu Leu Ala Cys Glu Asn Glu
35          40          45

gcg cag gcg ctc aat att gat gaa gcc ctt tgg caa cgg gaa ccg gac      192
Ala Gln Ala Leu Asn Ile Asp Glu Ala Leu Trp Gln Arg Glu Pro Asp
50          55          60

gaa ttc gtc ccg cac aac ctt tcc gcc gaa gcc acc acg tat gcc acg      240
Glu Phe Val Pro His Asn Leu Ser Gly Glu Ala Thr Thr Tyr Ala Thr
65          70          75          80

ccc atc gaa atc agc tgg acg gcc aaa cgc aac gca caa agc cgc gat      288
Pro Ile Glu Ile Ser Trp Thr Gly Lys Arg Asn Ala Gln Ser Arg Asp
85          90          95

ttg ctg att aat tta caa ccg cag ctg ccg gaa ttc atc aac agc ttt      336
Leu Leu Ile Asn Leu Gln Pro Gln Leu Pro Glu Phe Ile Asn Ser Phe
100          105          110

aac caa att atc gat ttc gta ccc gcc gaa gaa caa caa aaa got tta      384
Asn Gln Ile Ile Asp Phe Val Pro Ala Glu Glu Gln Gln Lys Ala Leu
115          120          125

gcg cgg gaa cgt tat aaa caa ttg agg cag ttg gcc tgg gaa ttg agt      432
Ala Arg Glu Arg Tyr Lys Gln Leu Arg Gln Leu Gly Trp Glu Leu Ser
130          135          140

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acg gag cag gcg ggg
 Thr Glu Gln Ala Gly
 145

447

<210> 214
 <211> 149
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 214

Met Pro Lys Asn Ala Gln Phe Tyr Leu Leu Ser Asp Ala Ser Pro Ala
 1 5 10 15

Gln Thr Asn Leu Ser Ala Val Glu Ser Leu Ala Cys Asn Leu Ala Ala
 20 25 30

Ser Ala Trp Arg Leu Gly Lys Arg Val Leu Leu Ala Cys Glu Asn Glu
 35 40 45

Ala Gln Ala Leu Asn Ile Asp Glu Ala Leu Trp Gln Arg Glu Pro Asp
 50 55 60

Glu Phe Val Pro His Asn Leu Ser Gly Glu Ala Thr Thr Tyr Ala Thr
 65 70 75 80

Pro Ile Glu Ile Ser Trp Thr Gly Lys Arg Asn Ala Gln Ser Arg Asp
 85 90 95

Leu Leu Ile Asn Leu Gln Pro Gln Leu Pro Glu Phe Ile Asn Ser Phe
 100 105 110

Asn Gln Ile Ile Asp Phe Val Pro Ala Glu Glu Gln Gln Lys Ala Leu
 115 120 125

Ala Arg Glu Arg Tyr Lys Gln Leu Arg Gln Leu Gly Trp Glu Leu Ser
 130 135 140

Thr Glu Gln Ala Gly
 145

<210> 215
 <211> 774
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(774)

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<400> 215
aaa gac aac aaa atc tgg cac ttc acc tta cga aaa gaa gca ata tgg      48
Lys Asp Asn Lys Ile Trp His Phe Thr Leu Arg Lys Glu Ala Ile Trp
1          5          10          15

tct aac ggc gaa cgg gtg act gcg cag caa ttt gtt gca agc tgg caa      96
Ser Asn Gly Glu Pro Val Thr Ala Gln Gln Phe Val Ala Ser Trp Gln
          20          25          30

cgg ctg gcg caa tcg gat tct cct tta aag cac tat tta cgc tac ctt      144
Arg Leu Ala Gln Ser Asp Ser Pro Leu Lys His Tyr Leu Arg Tyr Leu
          35          40          45

aac tta gtc aac gcg gag aaa gtg tta cag caa act ctg ctg cca gag      192
Asn Leu Val Asn Ala Glu Lys Val Leu Gln Gln Thr Leu Leu Pro Glu
          50          55          60

cag ttg gga att gtc gcg gaa aat gac cgc act tta cgc tta act tta      240
Gln Leu Gly Ile Val Ala Glu Asn Asp Arg Thr Leu Arg Leu Thr Leu
        65          70          75          80

gat aaa gcg acc cct tac ttg ccg caa atg ctg gcg cat atc agc ctg      288
Asp Lys Ala Thr Pro Tyr Leu Pro Gln Met Leu Ala His Ile Ser Leu
          85          90          95

ttg cca caa tat ttg tcg cca cat gaa ggc att gtg acc aac ggg gcg      336
Leu Pro Gln Tyr Leu Ser Pro His Glu Gly Ile Val Thr Asn Gly Ala
          100          105          110

tat caa gtg atg ggg cag caa ggc aat ctc atc cat ttg gaa aag aac      384
Tyr Gln Val Met Gly Gln Gln Asn Leu Ile His Leu Glu Lys Asn
          115          120          125

ccg caa tat tgg gcg aaa gaa aaa gtg gcg ttt aaa aat gtg gat tat      432
Pro Gln Tyr Trp Ala Lys Glu Lys Val Ala Phe Lys Asn Val Asp Tyr
          130          135          140

cag aaa atc gca ctg caa cag gac gtc agc gcc tta gat gtg gtg tgg      480
Gln Lys Ile Ala Leu Gln Gln Asp Val Ser Ala Leu Asp Val Val Trp
          145          150          155          160

cag ccg cag caa caa acg gat caa acg caa tac ttc ccg caa ctt tgc      528
Gln Pro Gln Gln Gln Thr Asp Gln Thr Gln Tyr Phe Pro Gln Leu Cys
          165          170          175

acc tat ttt tac acc ttt aat ttt aac atg cca caa ctg gcg caa agc      576
Thr Tyr Phe Tyr Thr Phe Asn Phe Asn Met Pro Gln Leu Ala Gln Ser
          180          185          190

ccg gtg cgt aag gca ttg gca atg atg aca tct gcc cgc agt tta ttg      624
Pro Val Arg Lys Ala Leu Ala Met Met Thr Ser Ala Arg Ser Leu Leu
          195          200          205

ccg gaa agt aaa aac agg att cct tta acg gat aat ttt tta cca att      672
Pro Glu Ser Lys Asn Arg Ile Pro Leu Thr Asp Asn Phe Leu Pro Ile
          210          215          220

tcc atg caa acc atc gat agc cgg tgg gag caa acg ccg gtt gaa caa      720
Ser Met Gln Thr Ile Asp Ser Arg Trp Glu Gln Thr Pro Val Glu Gln
          225          230          235          240

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tta tta agc caa gcg cga att gga gag aag gca ccg ctc aaa ctg acc 768
 Leu Leu Ser Gln Ala Arg Ile Gly Glu Lys Ala Pro Leu Lys Leu Thr 255
 245 250
 cta agt 774
 Leu Ser

<210> 216
 <211> 258
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 216

Lys Asp Asn Lys Ile Trp His Phe Thr Leu Arg Lys Glu Ala Ile Trp
 1 5 10 15

Ser Asn Gly Glu Pro Val Thr Ala Gln Gln Phe Val Ala Ser Trp Gln
 20 25 30

Arg Leu Ala Gln Ser Asp Ser Pro Leu Lys His Tyr Leu Arg Tyr Leu
 35 40 45

Asn Leu Val Asn Ala Glu Lys Val Leu Gln Gln Thr Leu Leu Pro Glu
 50 55 60

Gln Leu Gly Ile Val Ala Glu Asn Asp Arg Thr Leu Arg Leu Thr Leu
 65 70 75 80

Asp Lys Ala Thr Pro Tyr Leu Pro Gln Met Leu Ala His Ile Ser Leu
 85 90 95

Leu Pro Gln Tyr Leu Ser Pro His Glu Gly Ile Val Thr Asn Gly Ala
 100 105 110

Tyr Gln Val Met Gly Gln Gln Gly Asn Leu Ile His Leu Glu Lys Asn
 115 120 125

Pro Gln Tyr Trp Ala Lys Glu Lys Val Ala Phe Lys Asn Val Asp Tyr
 130 135 140

Gln Lys Ile Ala Leu Gln Gln Asp Val Ser Ala Leu Asp Val Val Trp
 145 150 155 160

Gln Pro Gln Gln Gln Thr Asp Gln Thr Gln Tyr Phe Pro Gln Leu Cys
 165 170 175

Thr Tyr Phe Tyr Thr Phe Asn Phe Asn Met Pro Gln Leu Ala Gln Ser

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180 185 190
 Pro Val Arg Lys Ala Leu Ala Met Met Thr Ser Ala Arg Ser Leu Leu
 195 200 205
 Pro Glu Ser Lys Asn Arg Ile Pro Leu Thr Asp Asn Phe Leu Pro Ile
 210 215 220
 Ser Met Gln Thr Ile Asp Ser Arg Trp Glu Gln Thr Pro Val Glu Gln
 225 230 235 240
 Leu Leu Ser Gln Ala Arg Ile Gly Glu Lys Ala Pro Leu Lys Leu Thr
 245 250 255

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Leu Ser

<210> 217
 <211> 363
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(363)

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<400> 217
 atc cgt att caa ccg gac gaa ggc att tct atg cgt ttt ggc ttg aaa 48
 Ile Arg Ile Gln Pro Asp Glu Gly Ile Ser Met Arg Phe Gly Leu Lys
 1 5 10 15
 aaa ccg ggc gcc ggc ttt gaa gcc aaa gaa gtg tcg atg gat ttc cgc 96
 Lys Pro Gly Ala Gly Phe Glu Ala Lys Glu Val Ser Met Asp Phe Arg
 20 25 30
 tat gcc gat ctt gcg ggt gcc acc gtc atg acc gct tat gag cgt tta 144
 Tyr Ala Asp Leu Ala Gly Ala Thr Val Met Thr Ala Tyr Glu Arg Leu
 35 40 45
 ttg ctt gat gcc atg aaa ggc gac gcg acc cta ttt gcg cgt acc gat 192
 Leu Leu Asp Ala Met Lys Gly Asp Ala Thr Leu Phe Ala Arg Thr Asp
 50 55 60
 gcc gta cac gcc gcc tgg aaa ttc gtt caa ccg att ttg aac tat aaa 240
 Ala Val His Ala Ala Trp Lys Phe Val Gln Pro Ile Leu Asn Tyr Lys
 65 70 75 80
 gcc caa ggc gcc aga ctt tat gat tac gag gcc gcc acc tgg gga ccg 288
 Ala Gln Gly Gly Arg Leu Tyr Asp Tyr Glu Ala Gly Thr Trp Gly Pro
 85 90 95
 acg gca gcc gat aaa ctc atc gcc aaa agc ggt cgt gta tgg cgc cgc 336
 Thr Ala Ala Asp Lys Leu Ile Ala Lys Ser Gly Arg Val Trp Arg Arg
 100 105 110

30

cca agc ggg ttg atg aag aaa aaa gtg
 Pro Ser Gly Leu Met Lys Lys Lys Val
 115 120

363

<210> 218
 <211> 121
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 218

Ile Arg Ile Gln Pro Asp Glu Gly Ile Ser Met Arg Phe Gly Leu Lys
 1 5 10 15

Lys Pro Gly Ala Gly Phe Glu Ala Lys Glu Val Ser Met Asp Phe Arg
 20 25 30

Tyr Ala Asp Leu Ala Gly Ala Thr Val Met Thr Ala Tyr Glu Arg Leu
 35 40 45

Leu Leu Asp Ala Met Lys Gly Asp Ala Thr Leu Phe Ala Arg Thr Asp
 50 55 60

Ala Val His Ala Ala Trp Lys Phe Val Gln Pro Ile Leu Asn Tyr Lys
 65 70 75 80

Ala Gln Gly Gly Arg Leu Tyr Asp Tyr Glu Ala Gly Thr Trp Gly Pro
 85 90 95

Thr Ala Ala Asp Lys Leu Ile Ala Lys Ser Gly Arg Val Trp Arg Arg
 100 105 110

Pro Ser Gly Leu Met Lys Lys Lys Val
 115 120

<210> 219
 <211> 159
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(159)

<400> 219

atg gca aca ggc aaa agc att att tta atg gga gtt tcc agt aca gga
 Met Ala Thr Gly Lys Ser Ile Ile Leu Met Gly Val Ser Ser Thr Gly
 1 5 10 15

48

aaa aca tca gtg ggg acg gaa gta gca cgt cgt ttg gag ata aaa ctg
 Lys Thr Ser Val Gly Thr Glu Val Ala Arg Arg Leu Glu Ile Lys Leu
 20 25 30

96

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20

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att gat ggc gat gat ctg cac ccg cgc gcc aat atc ata aaa atg ggc 144
 Ile Asp Gly Asp Asp Leu His Pro Arg Ala Asn Ile Ile Lys Met Gly
 35 40 45

 gaa gga cat ccg ctc 159
 Glu Gly His Pro Leu
 50

 <210> 220
 <211> 53
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

 <400> 220 10

 Met Ala Thr Gly Lys Ser Ile Ile Leu Met Gly Val Ser Ser Thr Gly
 1 5 10 15

 Lys Thr Ser Val Gly Thr Glu Val Ala Arg Arg Leu Glu Ile Lys Leu
 20 25 30

 Ile Asp Gly Asp Asp Leu His Pro Arg Ala Asn Ile Ile Lys Met Gly
 35 40 45

 Glu Gly His Pro Leu
 50 20

 <210> 221
 <211> 289
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

 <220>
 <221> CDS
 <222> (1)..(288)

 <400> 221
 aac att gct tat gcg gcg aaa gac aaa tac agt cgt gaa gaa atc atc 48
 Asn Ile Ala Tyr Ala Ala Lys Asp Lys Tyr Ser Arg Glu Glu Ile Ile
 1 5 10 15

 aaa gcg gca aaa gcg gcg cac gcc atg gaa ttt atc gag cat ttg gaa 96
 Lys Ala Ala Lys Ala Ala His Ala Met Glu Phe Ile Glu His Leu Glu 30
 20 25 30

 aac ggt ctg gat acg gtt atc ggc gaa aac ggc gcc agc tta tcc ggc 144
 Asn Gly Leu Asp Thr Val Ile Gly Glu Asn Gly Ala Ser Leu Ser Gly
 35 40 45

 ggt caa cgc cag cgt tta gcc atc gcc cgc gcc ttg ttg cgt aac tcg 192
 Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Arg Asn Ser
 50 55 60

 ccg gta ttg att tta gat gaa gcc acc tcg gca ttg gat acg gaa tcc 240
 Pro Val Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser

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65 70 75 80
 gaa cgc gca att caa gcg gca ttg gaa gaa atc caa aaa gat cgc acg g 289
 Glu Arg Ala Ile Gln Ala Ala Leu Glu Glu Ile Gln Lys Asp Arg Thr
 85 90 95

<210> 222
 <211> 96
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 222

Asn Ile Ala Tyr Ala Ala Lys Asp Lys Tyr Ser Arg Glu Glu Ile Ile
 1 5 10 15

10

Lys Ala Ala Lys Ala Ala His Ala Met Glu Phe Ile Glu His Leu Glu
 20 25 30

Asn Gly Leu Asp Thr Val Ile Gly Glu Asn Gly Ala Ser Leu Ser Gly
 35 40 45

Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Arg Asn Ser
 50 55 60

Pro Val Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
 65 70 75 80

20

Glu Arg Ala Ile Gln Ala Ala Leu Glu Glu Ile Gln Lys Asp Arg Thr
 85 90 95

<210> 223
 <211> 353
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(351)

<400> 223
 tcg aac atc aac cct gat gat cca agt gcg att atc gaa ggc aac gaa 48
 Ser Asn Ile Asn Pro Asp Asp Pro Ser Ala Ile Ile Glu Gly Asn Glu
 1 5 10 15

30

aaa gtg gtt cgc cct cgt tta acc gac gcg gaa ttc ttc tcc aaa acc 96
 Lys Val Val Arg Pro Arg Leu Thr Asp Ala Glu Phe Phe Ser Lys Thr
 20 25 30

gac tta aaa caa aaa tta gtg gat cgc tta ccg cgc ttg gaa act gtg 144
 Asp Leu Lys Gln Lys Leu Val Asp Arg Leu Pro Arg Leu Glu Thr Val
 35 40 45

ttg ttc caa caa caa ctt ggc aca ttg cgt gat aaa acc gac cgc atc 192

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Leu Phe Gln Gln Gln Leu Gly Thr Leu Arg Asp Lys Thr Asp Arg Ile
 50          55          60
gaa caa ctt gcg ggt gca atc gcc aaa caa atc ggt gcc gac gaa gcg      240
Glu Gln Leu Ala Gly Ala Ile Ala Lys Gln Ile Gly Ala Asp Glu Ala
65          70          75          80
aaa gca aaa cgt gcg ggc ttg ctg tca aaa tgc gat ttg atg acc aat      288
Lys Ala Lys Arg Ala Gly Leu Leu Ser Lys Cys Asp Leu Met Thr Asn
          85          90          95
atg gtg ttt gaa ttc acc gac acc caa ggc gta atg ggt atg cac tat      336
Met Val Phe Glu Phe Thr Asp Thr Gln Gly Val Met Gly Met His Tyr
          100          105          110
gcc cgt cac gac ggc ga      353
Ala Arg His Asp Gly
          115

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<210> 224
<211> 117
<212> PRT
<213> Actinobacillus actinomycetemcomitans
<400> 224

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Ser Asn Ile Asn Pro Asp Asp Pro Ser Ala Ile Ile Glu Gly Asn Glu
 1          5          10          15

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Lys Val Val Arg Pro Arg Leu Thr Asp Ala Glu Phe Phe Ser Lys Thr
          20          25          30

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Asp Leu Lys Gln Lys Leu Val Asp Arg Leu Pro Arg Leu Glu Thr Val
          35          40          45

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Leu Phe Gln Gln Gln Leu Gly Thr Leu Arg Asp Lys Thr Asp Arg Ile
 50          55          60

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Glu Gln Leu Ala Gly Ala Ile Ala Lys Gln Ile Gly Ala Asp Glu Ala
65          70          75          80

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Lys Ala Lys Arg Ala Gly Leu Leu Ser Lys Cys Asp Leu Met Thr Asn
          85          90          95

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Met Val Phe Glu Phe Thr Asp Thr Gln Gly Val Met Gly Met His Tyr
          100          105          110

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Ala Arg His Asp Gly
          115

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<210> 225
<211> 366

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<212> DNA

<213> Actinobacillus actinomycetemcomitans

<220>

<221> CDS

<222> (1)..(366)

<400> 225

cta ttg gaa aaa caa ggg tta att aaa tta aaa gat ccg acc aac ctg 48
 Leu Leu Glu Lys Gln Gly Leu Ile Lys Leu Lys Asp Pro Thr Asn Leu
 1 5 10 15

ttc tcc act tct ata gat atc att gaa aat ccg aaa aat tta caa atc 96
 Phe Ser Thr Ser Ile Asp Ile Ile Glu Asn Pro Lys Asn Leu Gln Ile
 20 25 30

aaa gaa gtg gat acc tcc gtt gcg gca cgt gcc tta gat gac gtt gat 144
 Lys Glu Val Asp Thr Ser Val Ala Ala Arg Ala Leu Asp Asp Val Asp
 35 40 45

ttg gcg gta gtg aat aac aac tac gcc ggt caa gta ggc tta aat gcg 192
 Leu Ala Val Val Asn Asn Asn Tyr Ala Gly Gln Val Gly Leu Asn Ala
 50 55 60

caa gat cac ggc gta ttt gtg gaa gat aaa gat tca ccg tat gta aat 240
 Gln Asp His Gly Val Phe Val Glu Asp Lys Asp Ser Pro Tyr Val Asn
 65 70 75 80

att atc gtg gca cgg acc gat aac aaa gac agc aaa gcc gta cag act 288
 Ile Ile Val Ala Arg Thr Asp Asn Lys Asp Ser Lys Ala Val Gln Thr
 85 90 95

ttc gtg aaa gcc tac caa acc ccg gaa gtg gaa caa gaa gcg aaa aaa 336
 Phe Val Lys Ala Tyr Gln Thr Pro Glu Val Glu Gln Glu Ala Lys Lys
 100 105 110

cac ttt aaa gac ggc gtg gta aaa ggc tgg 366
 His Phe Lys Asp Gly Val Val Lys Gly Trp
 115 120

<210> 226

<211> 122

<212> PRT

<213> Actinobacillus actinomycetemcomitans

<400> 226

Leu Leu Glu Lys Gln Gly Leu Ile Lys Leu Lys Asp Pro Thr Asn Leu 30
 1 5 10 15

Phe Ser Thr Ser Ile Asp Ile Ile Glu Asn Pro Lys Asn Leu Gln Ile
 20 25 30

Lys Glu Val Asp Thr Ser Val Ala Ala Arg Ala Leu Asp Asp Val Asp
 35 40 45

Leu Ala Val Val Asn Asn Asn Tyr Ala Gly Gln Val Gly Leu Asn Ala

50 55 60

Gln Asp His Gly Val Phe Val Glu Asp Lys Asp Ser Pro Tyr Val Asn
65 70 75 80

Ile Ile Val Ala Arg Thr Asp Asn Lys Asp Ser Lys Ala Val Gln Thr
85 90 95

Phe Val Lys Ala Tyr Gln Thr Pro Glu Val Glu Gln Glu Ala Lys Lys
100 105 110

His Phe Lys Asp Gly Val Val Lys Gly Trp
115 120

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<210> 227
<211> 465
<212> DNA
<213> Actinobacillus actinomycetemcomitans

<220>
<221> CDS
<222> (1)..(465)

<400> 227
atg act tgg caa aac gtg tcg atc atc gtt agt tat cct caa act gac 48
Met Thr Trp Gln Asn Val Ser Ile Ile Val Ser Tyr Pro Gln Thr Asp
1 5 10 15

ata aaa agg gga tct ttt atg aac ttg aaa aaa tta tta ggc gtc gca 96
Ile Lys Arg Gly Ser Phe Met Asn Leu Lys Lys Leu Leu Gly Val Ala
20 25 30

aca tta gcc tcc gta ttc gcc tta acg gct tgt aat gaa gag aaa aaa 144
Thr Leu Ala Ser Val Phe Ala Leu Thr Ala Cys Asn Glu Glu Lys Lys
35 40 45

ccg gaa gcc gca ccg gca gac aaa ccg gcg gca gaa gcc ccg gca aca 192
Pro Glu Ala Ala Pro Ala Asp Lys Pro Ala Ala Glu Ala Pro Ala Thr
50 55 60

atc aaa gtg ggc gtg atg gca gga ccg gaa cac caa gtg gct gaa atc 240
Ile Lys Val Gly Val Met Ala Gly Pro Glu His Gln Val Ala Glu Ile
65 70 75 80

gca gcg aaa gtg gca aaa gaa aaa tac aac tta gac gta gaa tac gtt 288
Ala Ala Lys Val Ala Lys Glu Lys Tyr Asn Leu Asp Val Glu Tyr Val
85 90 95

tta ttc aat gac tac gcc ttg cca aac act gca gtg tct aaa ggt gat 336
Leu Phe Asn Asp Tyr Ala Leu Pro Asn Thr Ala Val Ser Lys Gly Asp
100 105 110

tta gac gtt aac gca atg caa cat aaa ccg tat tta gac aaa gat tcc 384
Leu Asp Val Asn Ala Met Gln His Lys Pro Tyr Leu Asp Lys Asp Ser
115 120 125

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caa gcg aaa gga ttg aac aac tta gtg atc gtg ggt aat acc ttc gtt 432
 Gln Ala Lys Gly Leu Asn Asn Leu Val Ile Val Gly Asn Thr Phe Val
 130 135 140

tac ccg tta gcc ggc tat tca aaa aaa atc aaa 465
 Tyr Pro Leu Ala Gly Tyr Ser Lys Lys Ile Lys
 145 150 155

<210> 228
 <211> 155
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 228

Met Thr Trp Gln Asn Val Ser Ile Ile Val Ser Tyr Pro Gln Thr Asp
 1 5 10 15

Ile Lys Arg Gly Ser Phe Met Asn Leu Lys Lys Leu Leu Gly Val Ala
 20 25 30

Thr Leu Ala Ser Val Phe Ala Leu Thr Ala Cys Asn Glu Glu Lys Lys
 35 40 45

Pro Glu Ala Ala Pro Ala Asp Lys Pro Ala Ala Glu Ala Pro Ala Thr
 50 55 60

Ile Lys Val Gly Val Met Ala Gly Pro Glu His Gln Val Ala Glu Ile
 65 70 75 80

Ala Ala Lys Val Ala Lys Glu Lys Tyr Asn Leu Asp Val Glu Tyr Val
 85 90 95

Leu Phe Asn Asp Tyr Ala Leu Pro Asn Thr Ala Val Ser Lys Gly Asp
 100 105 110

Leu Asp Val Asn Ala Met Gln His Lys Pro Tyr Leu Asp Lys Asp Ser
 115 120 125

Gln Ala Lys Gly Leu Asn Asn Leu Val Ile Val Gly Asn Thr Phe Val
 130 135 140

Tyr Pro Leu Ala Gly Tyr Ser Lys Lys Ile Lys
 145 150 155

<210> 229
 <211> 1008
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

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<220>
<221> CDS
<222> (1)..(1008)

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 Gly Ile Ser Ala Arg Asn Met Ser Tyr Ala Gly Leu Lys Asp Arg Lys
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Lys Pro Leu Tyr Pro Leu His Leu Glu Ser Gly Asp Tyr Cys Val Asn	
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ggc gat gat gtg cta tat tcc gcc acg gtc gcg gca gca ttt gaa ggg	336
Gly Asp Asp Val Leu Tyr Ser Gly Thr Val Ala Ala Ala Phe Glu Gly	
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Arg His Leu Gly Leu Pro Ser Ile Ala Val Ser Leu Asp Gly Arg Gln	
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cat ttt gaa acg gcg gcg cgc gtg gta tgc gat ttg gtg ccg aaa tta	432
His Phe Glu Thr Ala Ala Arg Val Val Cys Asp Leu Val Pro Lys Leu	
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cac gcc caa tta tta ggc aaa cac gaa att ctg aat att aac gtg ccc	480
His Ala Gln Leu Leu Gly Lys His Glu Ile Leu Asn Ile Asn Val Pro	
145 150 155 160	
gat gtg cct tac gaa gaa ctg aaa ggc att aaa gtg tgc cat ttg ggc	528
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165 170 175	
tac cgt tot tcc gct tct gaa gtg att aaa cag caa agc ccg cgt ggc	576
Tyr Arg Ser Ser Ala Ser Glu Val Ile Lys Gln Gln Ser Pro Arg Gly	
180 185 190	
gaa gac atg tat tgg atc ggg ctc agc ggc ttg ccg gaa tat gaa agc	624
Glu Asp Met Tyr Trp Ile Gly Leu Ser Gly Leu Pro Glu Tyr Glu Ser	
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 180 185 190

Glu Asp Met Tyr Trp Ile Gly Leu Ser Gly Leu Pro Glu Tyr Glu Ser
 195 200 205

Glu Gly Thr Asp Phe His Ala Val Lys Asn Gly Tyr Val Ser Ile Thr
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gtg gca cat ccg gcg caa acg gcg ttt tat tat ttc gtg gca gac ggc 336
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Lys Asp Leu Glu Thr Pro Thr Pro Tyr Asn Thr Tyr Val Ile Asp Gly
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Leu Pro Pro Thr Pro Ile Ala Met Pro Ser Glu Glu Ala Leu Gln Ala
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Val Gln Gln Tyr Leu Arg Trp Tyr Arg Glu Gln Asn Gly Lys
 130 135 140

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【国際調査報告】

INTERNATIONAL SEARCH REPORT		International application No. PCT/US03/32645									
A. CLASSIFICATION OF SUBJECT MATTER IPC(7) : A61K 38/00; C07K 1/00, 14/00, 17/00 US CL : 530/330, 300, 350; 424/190.1 According to International Patent Classification (IPC) or to both national classification and IPC											
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) U.S. : 530/330, 300, 350; 424/190.1 Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) Please See Continuation Sheet											
C. DOCUMENTS CONSIDERED TO BE RELEVANT <table border="1"> <thead> <tr> <th>Category *</th> <th>Citation of document, with indication, where appropriate, of the relevant passages</th> <th>Relevant to claim No.</th> </tr> </thead> <tbody> <tr> <td>X</td> <td>WO 02/077183 A2 (ELITRA PHARM INC.) 03 October 2002 (03.10.02), see SEQ ID NO:67236 in particular residues 73-91 are identical to residues 236-254 of SEQ ID NO:2 of claim 1 herein.</td> <td>1, 17</td> </tr> <tr> <td>A</td> <td></td> <td>2</td> </tr> </tbody> </table>			Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.	X	WO 02/077183 A2 (ELITRA PHARM INC.) 03 October 2002 (03.10.02), see SEQ ID NO:67236 in particular residues 73-91 are identical to residues 236-254 of SEQ ID NO:2 of claim 1 herein.	1, 17	A		2
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.									
X	WO 02/077183 A2 (ELITRA PHARM INC.) 03 October 2002 (03.10.02), see SEQ ID NO:67236 in particular residues 73-91 are identical to residues 236-254 of SEQ ID NO:2 of claim 1 herein.	1, 17									
A		2									
☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.											
* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family											
Date of the actual completion of the international search 20 July 2004 (20.07.2004)		Date of mailing of the international search report 03 NOV 2004									
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703) 305-3230		Authorized officer Patricia A. Duffy Telephone No. 703-308-0196									

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US03/32645

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1, 2 and 17 (in part as drawn to SEQ ID NO:2)

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

PCT/US03/32645

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING

The inventions listed as Groups 1-1052 do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: in the instant case the technical features are defined as recited below.

Groups 1-116, claims 1, 2 and 17 (in part), drawn to polypeptides (the first appearing technical feature each represented by a unique sequence identifier).

Groups 117-233, claims 3-8 and 21-23 (in part), drawn to nucleic acids, vectors and host cells (the second appearing technical feature each represented by a unique sequence identifier)..

Groups 234-350, claims 9-12 (in part), drawn to antibodies (the third appearing technical feature each represented by and antibody binding a unique sequence identifier)..

Groups 351-467, claims 13 and 14 (in part), drawn to methods of treatment using the antibodies (the first method of use of the third technical feature).

Groups 468-584, claims 15 and 16 (in part), drawn to methods of detecting using the antibodies (the second method of use of the third technical feature).

Groups 585-701, claims 18-20 (in part), drawn to methods of using the polypeptides to elicit an immune response (the first method of use of the first appearing technical feature).

Groups 702-818, claims 24-26 (in part), drawn to methods of using the nucleic acids to elicit an immune response (the first method of use of the second technical feature).

Groups 819-935, claim 27 (in part), drawn to methods of detection of a microbe using the nucleic acid (the second method of use of the second technical feature).

Groups 936-1052, claim 28 (in part), drawn to methods of detection of antibodies using the polypeptides (the second method of use of the first technical feature).

Each of the polypeptides of Groups 1-116 fail to share a common technical feature that defines the polypeptides over the art. The polypeptides do not share a common core sequence / structure and therefore do not relate to a single general inventive concept within the meaning of PCT Rule 13.1. Further, the first appearing technical feature of the polypeptide comprising at least contiguous 5 amino acids of SEQ ID NO:2 of claim 1 is anticipated by the disclosure of the polypeptide sequence of SEQ ID NO:67236 of WO200277183, published 03 October 2002. SEQ ID NO:67236 of the prior art has 19 consecutive amino acids in common with the claimed polypeptide of SEQ ID NO:2 and meets the limitations of the claimed invention. Therefore, the groups of inventions (1, 117, 234, 351, 468, 585, 702, 819 and 936) as they relate to the polypeptide of SEQ ID NO:2, do not recite a technical feature that is "special" within the meaning of PCT Rule 13.2 because the claims do not recite a technical feature that provides for a novel contribution over the prior art. As such, the polypeptides, nucleic acids, antibodies and associated methods of use as drawn to the polypeptide of SEQ ID NO:2, do not share a single general inventive concept because the first appearing technical feature defined by claim 1 is not "special".

INTERNATIONAL SEARCH REPORT

PCT/US03/32645

Continuation of B. FIELDS SEARCHED Item 3:

BIOTECH SEQUENCE SEARCH: SEQ ID NO:2 and oligomers thereof. WEST, MEDLINE, EMBASE, WIPO, JAPIO: search terms: actinomycetemcomitans, Actinobacillus, antigens, vaccines, polypeptides, isolate, purify.

フロントページの続き

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C 1 2 N 1/21 (2006.01)	C 1 2 N 1/21	4 C 0 8 5
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(81)指定国 AP(GH,GM,KE,LS,MW,MZ,SD,SL,SZ,TZ,UG,ZM,ZW),EA(AM,AZ,BY,KG,KZ,MD,RU,TJ,TM),EP(AT, BE,BG,CH,CY,CZ,DE,DK,EE,ES,FI,FR,GB,GR,HU,IE,IT,LU,MC,NL,PT,RO,SE,SI,SK,TR),OA(BF,BJ,CF,CG,CI,CM,GA, GN,GQ,GW,ML,MR,NE,SN,TD,TG),AE,AG,AL,AM,AT,AU,AZ,BA,BB,BG,BR,BY,BZ,CA,CH,CN,CO,CR,CU,CZ,DE,DK,DM,DZ, EC,EE,ES,FI,GB,GD,GE,GH,GM,HR,HU,ID,IL,IN,IS,JP,KE,KG,KP,KR,KZ,LC,LK,LR,LS,LT,LU,LV,MA,MD,MG,MK,MN,M W,MX,MZ,NI,NO,NZ,OM,PG,PH,PL,PT,RO,RU,SC,SD,SE,SG,SK,SL,SY,TJ,TM,TN,TR,TT,TZ,UA,UG,US,UZ,VC,VN,YU,ZA ,ZM,ZW

(特許庁注：以下のものは登録商標)

U N I X

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1 5 5 エスダブリュ

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アメリカ合衆国 3 2 6 0 8 フロリダ州 ゲインズビル, トゥエンティーシックス プレイス
2 6 2 4 エスダブリュ

(72)発明者 プログルスク - フォックス, アン
アメリカ合衆国 3 2 6 5 6 フロリダ州 キーストーン ハイツイ, 6 3 9 2 シーアール 2 1
4

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专利名称(译)	鉴定Actinobacillus actinomycetemcomitans抗原用于诊断，治疗 and 监测牙周病		
公开(公告)号	JP2006519586A	公开(公告)日	2006-08-31
申请号	JP2004553443	申请日	2003-10-15
[标]申请(专利权)人(译)	佛罗里达州研究基金会股份有限公司雷开球德大学		
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其他公开文献	JP2006519586A5		
外部链接	Espacenet		

摘要(译)

设置引起的放线放线杆菌病，预防，改善和治疗为，抗体，多肽和多核苷酸的检测。

