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(54) COLON CANCER ANTIGEN PANEL

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(57) **ABSTRACT**

The invention provides methods for diagnosing cancer including colon cancer, based on the identification of certain colon cancer-associated polypeptides as antigens that elicit immune responses in colon cancer. The identified antigens can be utilized as markers for diagnosing colon cancer, and for following the course of treatment of colon cancer.

COLON CANCER ANTIGEN PANEL

FIELD OF THE INVENTION

[0001] The invention relates to use of novel colon cancer-associated nucleic acid molecules and the polypeptides they encode as markers for cancer, including colon cancer. The invention also relates to the use of a panel of colon cancer-associated nucleic acid molecules and the polypeptides they encode and their use as markers for colon cancer. In addition, the invention relates to the use of such nucleic acid molecules and the polypeptides they encode for diagnosing colon cancer, and monitoring the colon cancer's response to treatment.

BACKGROUND OF THE INVENTION

[0002] Colon cancer, which is also known as cancer of the large bowel and colorectal cancer, is second only to lung cancer as a cause of cancer death in the United States. Colorectal cancer is a common malignant condition that generally occurs in individuals 50 years of age or older; and the overall incidence rate of colon cancer has not changed substantially during the past 40 years. (Harrison's Principles of Internal Medicine, 14/e, McGraw-Hill Companies, New York, 1998). The treatment of colon cancer once diagnosis is made depends on the extent of the cancer's invasion of the colon tissue, lymph nodes, and metastasis to other organs such as the liver. The survival rate for patients diagnosed with early-stage cancer is about 90% survival after 5 years. The five-year survival rate drops if the cancer is not detected until the cancer has spread beyond the mucosal layer of the colon, and drops significantly further if, when detected, the cancer has spread beyond the colon to the lymph nodes and beyond. Thus, it is critical to diagnose colon cancer at the earliest possible stage to increase the likelihood of a positive prognosis and outcome.

[0003] The traditional method of colon cancer diagnosis is through the use of non-invasive or mildly invasive diagnostic tests, more invasive visual examination, and histologic examination of biopsy. Although these tests may detect colon cancers, each has drawbacks that limit its effectiveness as a diagnostic tool. One primary source of difficulty with most of the currently available methods for diagnosing colorectal cancer, is patient reluctance to submit to, or follow through with the procedures, due to the uncomfortable or perceived embarrassing nature of the tests.

[0004] Some of the less invasive diagnostic methods include fecal occult blood testing and digital rectal exam. A digital exam may detect tumors at the distal end of the colon/rectum, but is not effective at more proximal levels. The usefulness of tests for occult blood is hampered by the intermittent bleeding patterns of colon cancers, which can result in a high percentage of false negative results. For example, approximately 50 percent of patients with documented colorectal cancers have a negative fecal blood test. In addition, false-positive fecal occult blood tests may also present problems for accurate diagnosis of colon cancer, because a number of non-colon cancer conditions (e.g.: gingivitis, ulcer, or aspirin use) may yield positive test results, resulting in unnecessary invasive follow-up procedures. These limitations of the less-invasive tests for colon cancer may delay a patient's procurement of rapid diagnosis and appropriate colon cancer treatment.

[0005] Visual examination of the colon for abnormalities can be performed through endoscopic or radiographic techniques such as rigid proctosigmoidoscopy, flexible sigmoidoscopy, colonoscopy, and barium-contrast enema. These methods are expensive, and uncomfortable, and also carry with them a risk of complications.

[0006] Another method of colon cancer diagnosis is the detection of carcinoembryonic antigen (CEA) in a blood sample from a subject, which when present at high levels, may indicate the presence of advanced colon cancer. But CEA levels may also be abnormally high when no cancer is present. Thus, this test is not selective for colon cancer, which limits the test's value as an accurate and reliable diagnostic tool. In addition, elevated CEA levels are not detectable until late-stage colon cancer, when the cure rate is low, treatment options limited, and patient prognosis poor.

[0007] More effective techniques for colon cancer diagnosis, and evaluation of colon cancer treatments are needed. Although available diagnostic procedures for colon cancer may be partially successful, the methods for detecting colon cancer remain unsatisfactory. There is a critical need for diagnostic tests that can detect colon cancer at its early stages, when appropriate treatment may substantially increase the likelihood of positive outcome for the patient.

SUMMARY OF THE INVENTION

[0008] The invention provides methods for diagnosing colon cancer based on the identification of certain colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof, as antigens that elicit immune responses in colon cancer. The identified antigens can be utilized as markers for diagnosing colon cancer, for following the course of treatment of colon cancer, and for assessing colon cancer treatments.

[0009] According to one aspect of the invention, methods for diagnosing colon cancer in a subject are provided. The methods include obtaining a biological sample from a subject, contacting the sample with at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, and determining specific binding between the colon cancer-associated polypeptides and agents in the sample, wherein the presence of specific binding is diagnostic for colon cancer in the subject.

[0010] According to another aspect of the invention, methods of determining onset, progression, or regression, of colon cancer in a subject are provided. The methods include obtaining from a subject a first biological sample, contacting the first sample with at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected form the group consisting of SEQ ID NOs:1-15, determining specific binding between agents in the first sample and the at least two different colon cancer-associated polypeptides, obtaining from a subject a second biological sample, contacting the second biological sample with at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected form the group consisting of SEQ ID NOs:1-15, determining specific binding between agents in the second sample and the at least two different colon cancer-associated polypep-

tides, and comparing the determination of binding in the first sample to the determination of specific binding in the second sample as a determination of the onset, progression, or regression of the colon cancer.

[0011] According to yet another aspect of the invention, methods for selecting a course of treatment of a subject having or suspected of having colon cancer is provided. The methods include obtaining from the subject a biological sample, contacting the sample with at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, determining specific binding between agents in the sample that are differentially expressed in different types of cancer, and the colon cancer-associated polypeptides, and selecting a course of treatment appropriate to the cancer of the subject. In some embodiments, the treatment is administering antibodies that specifically bind to the colon cancer-associated polypeptides. In some embodiments, the antibodies are labeled with one or more cytotoxic agents.

[0012] In some embodiments of the foregoing methods, the biological sample is a blood sample. In some embodiments, the agents are antibodies or antigen-binding fragments thereof. In some embodiments of the foregoing methods, the biological sample is contacted with at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:15. In some embodiments of the foregoing methods, the biological sample is contacted with a colon cancer-associated polypeptide other than those encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

[0013] According to another aspect of the invention, methods for diagnosing colon cancer in a subject are provided. The methods include obtaining a biological sample from a subject, contacting the sample with antibodies or antigen-binding fragments thereof, that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, and determining specific binding between the antibodies or antigen-binding fragments thereof and colon cancer-associated polypeptides in the sample, wherein the presence of specific binding is diagnostic for colon cancer in the subject.

[0014] According to another aspect of the invention, methods for determining onset, progression, or regression, of colon cancer in a subject are provided. The methods include, obtaining from a subject a first biological sample, contacting the first sample with antibodies or antigen-binding fragments thereof, that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, determining specific binding between colon cancer-associated polypeptides in the first sample and the antibodies or antigen-binding fragments thereof, obtaining from a subject a second biological sample, contacting the second sample with antibodies or antigen-binding fragments thereof, that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, determining specific binding between colon cancer-associated polypeptides in the second sample and the antibodies or antigen-binding fragments thereof, and comparing the determination of specific binding in the first sample to the determination of specific binding in the second sample as a determination of the onset, progression, or regression of colon cancer.

[0015] According to another aspect of the invention methods for selecting a course of treatment of a subject having or suspected of having colon cancer are provided. The methods include obtaining from the subject a biological sample, contacting the sample with antibodies or antigen-binding fragments thereof that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, determining specific binding between colon cancer-associated polypeptides in the sample that are differentially expressed in different types of cancer, and the antibodies or antigen-binding fragments thereof, and selecting a course of treatment appropriate to the cancer of the subject. In some embodiments, the treatment is administering antibodies that specifically bind to the colon cancer-associated polypeptides. In some embodiments, the antibodies are labeled with one or more cytotoxic agents.

[0016] In some embodiments of the foregoing methods, the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus. In preferred embodiments of the foregoing methods, the tissue is colorectal tissue. In some embodiments of the foregoing methods, the antibodies are monoclonal or polyclonal antibodies, and in some embodiments, of the foregoing methods the antibodies are chimeric, human, or humanized antibodies. In some embodiments the antibodies are single chain antibodies, and in some embodiments of the foregoing methods, the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments. In some embodiments of the foregoing methods, the biological sample is contacted with antibodies or antigen-binding fragments thereof, that bind specifically to at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments of the foregoing methods, the biological sample is contacted with an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide other than those encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

[0017] According to yet another aspect of the invention, kits for the diagnosis of colon cancer in a subject are provided. The kits include at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs:1-15, one or more control antigens, and instructions for the use of the polypeptides in the diagnosis of colon cancer. In some embodiments, the colon cancer-associated polypeptides are bound to a substrate. In some embodiments, the one or more agents are antibodies or antigen-binding fragments thereof. In some embodiments, the kit includes at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated

polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the kit further includes a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

[0018] According to yet another aspect of the invention, kits for the diagnosis of colon cancer in a subject are provided. The kits include antibodies or antigen-binding fragments thereof that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, one or more control agents, and instructions for the use of the agents in the diagnosis of colon cancer. In some embodiments, the one or more agents are antibodies or antigen-binding fragments thereof. In some embodiments, the one or more agents are bound to a substrate. In some embodiments, the kit includes antibodies or antigen-binding fragments thereof, that bind specifically to least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the kit further includes an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

[0019] According to another aspect of the invention, protein microarrays are provided, which include at least two different colon cancer-associated polypeptides, wherein the colon cancer-associated polypeptides are encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs:1-15, fixed to a solid substrate. In some embodiments, the microarray comprises at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the microarrays further consist essentially of a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, microarray further consists essential of at least one control polypeptide molecule.

[0020] According to yet another aspect of the invention, protein microarrays are provided, which include antibodies or antigen-binding fragments thereof, that specifically bind at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs:1-15, fixed to a solid substrate. In some embodiments, the protein microarray consists essentially of antibodies or antigen-binding fragments thereof, that bind specifically to least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1-15. In some embodiments, the protein microarrays further consist essentially of an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the protein microarrays further consist essentially of at least one control polypeptide molecule. In some embodiments, the antibodies are monoclonal or polyclonal antibodies. In some embodiments, the antibodies are chimeric, human, or humanized antibodies. In some embodiments, the antibodies are single chain antibodies, and in some embodiments, the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

[0021] According to another aspect of the invention nucleic acid microarrays are provided. The nucleic acid microarrays include at least two nucleic acids selected from the group consisting of SEQ ID NOs:1-15, fixed to a solid substrate. In some embodiments, the microarray consists essentially of at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the microarray further consists essentially of a nucleic acid molecule other than those selected from the group consisting of SEQ ID NOs:1-15. In yet another embodiment, the microarrays further consist essentially of at least one control nucleic acid molecule.

[0022] According to another aspect of the invention, methods for diagnosing colon cancer in a subject are provided. The methods include obtaining from the subject a biological sample, and determining the expression of at least two colon cancer-associated nucleic acid molecules or expression products thereof in the sample, wherein the nucleic acid molecules comprise a nucleotide sequence selected from the group consisting of: SEQ ID NO: 1-15, wherein the expression is diagnosis of the colon cancer in the subject. In some embodiments, expression is determined for at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the method includes determining expression of a colon cancer-associated nucleic acid molecule other than those comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus. In preferred embodiments, the tissue is colorectal tissue. In some embodiments, the expression of colon cancer-associated nucleic acid molecules is determined by a method selected from the group consisting of nucleic acid hybridization and nucleic acid amplification. In preferred embodiments, the hybridization is performed using a nucleic acid microarray.

[0023] According to yet another aspect of the invention, methods for determining onset, progression, or regression, of colon cancer in a subject are provided. The methods include obtaining from a subject a first biological sample, determining a level of expression of at least two colon cancer-associated nucleic acid molecules or expression products thereof in the first sample, wherein the nucleic acid molecules are selected from the group consisting of: SEQ ID NOs: 1-15, obtaining from the subject a second biological sample, determining a level of expression of at least two colon cancer-associated nucleic acid molecules or expression products thereof in the second sample, wherein the nucleic acid molecules are selected from the group consist-

ing of: SEQ ID NOs: 1-15, and comparing the level of expression in the first sample to the level of expression in the second sample as a determination of the onset, progression, or regression of the colon cancer. In some embodiments, expression is determined for at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 nucleic acid molecules selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the method further includes determining expression for a colon cancer-associated nucleic acid molecule other than those comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15. In some embodiments, the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus. In preferred embodiments, the tissue is colorectal tissue. In some embodiments, the expression of colon cancer-associated nucleic acid molecules is determined by a method selected from the group consisting of nucleic acid hybridization and nucleic acid amplification. In preferred embodiments, the hybridization is performed using a nucleic acid microarray.

[0024] According to another aspect of the invention, methods for diagnosing cancer in a subject are provided. The methods include obtaining a biological sample from a subject, contacting the sample with a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, and determining specific binding between the colon cancer-associated polypeptide and agents in the sample, wherein the presence of specific binding is diagnostic for cancer in the subject.

[0025] According to another aspect of the invention, methods for determining onset, progression, or regression, of cancer in a subject are provided. The methods include obtaining from a subject a first biological sample, contacting the first sample with a colon cancer associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, determining specific binding between agents in the first sample and the colon cancer-associated, obtaining from a subject a second biological sample, contacting the second sample with a colon cancer associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, determining specific binding between agents in the second sample and the colon cancer-associated polypeptide, and comparing the determination of binding in the first sample to the determination of specific binding in the second sample as a determination of the onset, progression, or regression of cancer.

[0026] According to another aspect of the invention, methods for selecting a course of treatment of a subject having or suspected of having cancer are provided. The methods include obtaining from the subject a biological sample, contacting the sample with a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, determining specific binding between agents in the sample that are differentially expressed in different types of cancer, and the colon cancer-associated polypeptide, and selecting a course of treatment appropriate to the cancer of the subject. In some embodiments, the treatment is administering antibodies that specifically bind to the colon cancer-associated polypeptide. In some embodiments, the antibodies are labeled with one or more cytotoxic agents.

[0027] In some embodiments of the foregoing methods, the sample is blood. In some embodiments of the foregoing methods, the agents are antibodies or antigen-binding fragments thereof. In preferred embodiments of the foregoing methods, the cancer is colon cancer.

[0028] According to another aspect of the invention, methods for diagnosing cancer in a subject are provided. The methods include obtaining a biological sample from a subject, contacting the sample with an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, and determining specific binding between the antibody or antigen-binding fragment thereof and the colon cancer-associated polypeptide in the sample, wherein the presence of specific binding is diagnostic for cancer in the subject.

[0029] According to another aspect of the invention, methods for determining onset, progression, or regression, of cancer in a subject are provided. The methods include obtaining from a subject a first biological sample, contacting the first sample with antibodies or antigen-binding fragments thereof, that bind specifically to a colon cancer-associated polypeptides encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, determining specific binding between colon cancer-associated polypeptides in the first sample and the antibodies or antigen-fragments thereof, obtaining from a subject a second biological sample, contacting the second sample with antibodies or antigen-binding fragments thereof, that bind specifically to a colon cancer-associated polypeptides encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, determining specific binding between colon cancer-associated polypeptides in the second sample and the antibodies or antigen-binding fragments thereof, and comparing the determination of specific binding in the first sample to the determination of specific binding in the second sample as a determination of the onset, progression, or regression of cancer.

[0030] According to another aspect of the invention, methods for selecting a course of treatment of a subject having or suspected of having cancer are provided. The methods include obtaining from the subject a biological sample, contacting the sample with antibodies or antigen-binding fragments thereof that bind specifically to a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, determining specific binding between colon cancer-associated polypeptides in the sample that are differentially expressed in different types of cancer, and the antibodies or antigen-binding fragments thereof, and selecting a course of treatment appropriate to the cancer of the subject. In some embodiments, the treatment is administering antibodies that specifically bind to the colon cancer-associated polypeptide. In some embodiments, the antibodies are labeled with one or more cytotoxic agents.

[0031] In some embodiments of the foregoing methods, the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus. In some embodiments of the foregoing methods, the tissue is colorectal tissue. In preferred embodiments of the foregoing methods, the antibodies are monoclonal or polyclonal antibodies, chimeric, human, or humanized antibodies. In some embodiments of the foregoing methods, the antibodies are single chain antibodies or antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments. In preferred embodiments of the foregoing methods, the cancer is colon cancer.

[0032] According to another aspect of the invention, kits for the diagnosis of cancer in a subject are provided. The kits include a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs: 1, 2, 5, and 6; one or more control antigens; and instructions for the use of the polypeptide and control antigens in the diagnosis of cancer. In some embodiments, the colon cancer-associated polypeptide is bound to a substrate. In some embodiments, the one or more agents are antibodies or antigen-binding fragments thereof. In preferred embodiments, the cancer is colon cancer.

[0033] According to another aspect of the invention, kits for the diagnosis of cancer in a subject, are provided. The kits include antibodies or antigen-binding fragments thereof that bind specifically to a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6; one or more control agents; and instructions for the use of the antibodies, antigen-binding fragments, and agents in the diagnosis of cancer. In some embodiments, the one or more agents are antibodies or antigen-binding fragments thereof. In some embodiments, the one or more agents are bound to a substrate. In preferred embodiments, the cancer is colon cancer.

[0034] According to another aspect of the invention, protein microarrays are provided. The protein microarrays include a colon cancer-associated polypeptide, wherein the colon cancer-associated polypeptide is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs: 1, 2, 5, and 6, fixed to a solid substrate. In some embodiments, the protein microarray further includes at least one control polypeptide molecule.

[0035] According to yet another aspect of the invention, protein microarrays are provided. The protein microarrays include antibodies or antigen-binding fragments thereof, that specifically bind a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs:1, 2, 5, and 6, fixed to a solid substrate. In some embodiments, the protein microarrays further include at least one control polypeptide molecule. In some embodiments, the antibodies are monoclonal or polyclonal antibodies. In some embodiments, the antibodies are chimeric, human, or humanized antibodies and in some embodiments, the antibodies are single chain antibodies. In some embodiments, the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

[0036] According to another aspect of the invention, nucleic acid microarrays are provided. The nucleic acid microarrays include a nucleic acid selected from the group consisting of SEQ ID NOs: 1, 2, 5, and 6, fixed to a solid substrate. In some embodiments, the nucleic acid microarrays further include at least one control nucleic acid molecule.

[0037] According to yet another aspect of the invention, methods for diagnosing cancer in a subject are provided. The methods include obtaining from the subject a biological sample, and determining the expression of a colon cancer-associated nucleic acid molecule or expression product thereof in the sample, wherein the nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of: SEQ ID NO: 1, 2, 5, and 6, wherein the expression is diagnostic of cancer in the subject. In some embodiments, the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus. In preferred embodiments, the tissue is colorectal tissue. In some embodiments, the expression of colon cancer-associated nucleic acid molecules is determined by a method selected from the group consisting of nucleic acid hybridization and nucleic acid amplification. In preferred embodiments, the hybridization is performed using a nucleic acid microarray. In preferred embodiments, the cancer is colon cancer.

[0038] According to another aspect of the invention, methods for determining onset, progression, or regression, of cancer in a subject are provided. The methods include obtaining from a subject a first biological sample, determining a level of expression of a colon cancer-associated nucleic acid molecule or expression products thereof in the first sample, wherein the nucleic acid molecule is selected from the group consisting of: SEQ ID NOs: 1, 2, 5, and 6, obtaining from the subject a second biological sample, determining a level of expression of a colon cancer-associated nucleic acid molecule or expression product thereof in the second sample, wherein the nucleic acid molecule is selected from the group consisting of: SEQ ID NOs: 1, 2, 5, and 6, and comparing the level of expression in the first sample to the level of expression in the second sample as a determination of the onset, progression, or regression of the cancer. In some embodiments, the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus. In preferred embodiments, the tissue is colorectal tissue. In some embodiments, the expression of colon cancer-associated nucleic acid molecules is determined by a method selected from the group consisting of nucleic acid hybridization and nucleic acid amplification. In some embodiments, the hybridization is performed using a nucleic acid microarray. In preferred embodiments, the cancer is colon cancer.

DETAILED DESCRIPTION OF THE INVENTION

[0039] The invention described herein relates to the identification of polypeptides that elicit specific immune responses in subjects with cancer, particularly colon cancer, which is also known as large-bowel cancer and colorectal cancer. Colon cancer-associated polypeptides have been identified through SEREX screening of patients with cancer. The SEREX method (serological analysis of antigens by recombinant expression cloning), has been described by Sahin et al. (*Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995). The newly identified colon cancer-associated polypeptides and the encoding nucleic acid molecules

thereof may be used as markers for cancer, including colon cancer, and may be used in the diagnosis and treatment assessment of colon cancer in humans. In addition, sets of at least two colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof, may be used as markers in the diagnosis and treatment assessment of colon cancer in humans.

[0040] Polypeptides that elicit specific immune responses in colon cancer have now been identified and this identification allows use of these newly identified colon cancer-associated polypeptides or the encoding nucleic acids molecules thereof in cancer diagnostic assays and kits. In addition, sets of at least two of these new or previously identified polypeptides or the encoding nucleic acid molecules thereof, may be used in colon cancer diagnostic assays and kits. Such assays and kits are useful to detect colon cancer in human subjects, and for staging the progression, regression, or onset of colon cancer in subjects. The methods and kits described herein may also be used to evaluate treatments for colon cancer.

[0041] As used herein, "colon cancer-associated polypeptides" means polypeptides that elicit specific immune responses in animals having colon cancer and thus, include colon cancer-associated antigens and fragments of colon cancer-associated antigens, that are recognized by the immune system (e.g., by antibodies and/or T lymphocytes). The invention also relates to the use of the nucleic acid molecules that encode the colon cancer-associated polypeptides. In all embodiments, human colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof, are preferred. As used herein, the "encoding nucleic acid molecules thereof" means the nucleic acid molecules that code for the polypeptides.

[0042] As used herein, a subject is preferably a human, non-human primate, cow, horse, pig, sheep, goat, dog, cat, or rodent. In all embodiments, human subjects are preferred. In some embodiments, the subject is suspected of having cancer and in preferred embodiments the subject is suspected of having colon cancer. In some embodiments the subject has been diagnosed with cancer, and in preferred embodiments the subject has been diagnosed with colon cancer.

[0043] As used herein, "different types" of cancer may include different histological types, cell types, different stages of cancer, (e.g., primary tumor or metastatic growth).

[0044] Methods for identifying subjects suspected of having colon cancer may include fecal occult blood examination, digital examination, CEA testing, endoscopic or radiographic techniques, biopsy, subject's family medical history, subject's medical history, or imaging technologies, such as magnetic resonance imaging (MRI). Such methods for identifying subjects suspected of having colon cancer are well-known to those of skill in the medical arts. As used herein, a biological sample includes, but is not limited to: tissue, body fluid (e.g. blood), bodily exudate, mucus, and stool specimen. The tissue may be obtained from a subject or may be grown in culture (e.g. from a cell line).

[0045] As used herein, a colorectal tissue sample is tissue obtained (e.g., from a colorectal tissue biopsy) using methods well-known to those of ordinary skill in the related medical arts. The phrase "suspected of being cancerous" as used herein means a colon cancer tissue sample believed by one of ordinary skill in the medical arts to contain cancerous cells. Methods for obtaining the sample from the biopsy include gross apportioning of a mass, microdissection, laser-based microdissection, or other art-known cell-separation methods.

[0046] Because of the variability of the cell types in diseased-tissue biopsy material, and the variability in sensitivity of the diagnostic methods used, the sample size required for analysis may range from 1, 10, 50, 100, 200, 300, 500, 1000, 5000, 10,000, to 50,000 or more cells. The appropriate sample size may be determined based on the cellular composition and condition of the biopsy and the standard preparative steps for this determination and subsequent isolation of the nucleic acid for use in the invention are well known to one of ordinary skill in the art. An example of this, although not intended to be limiting, is that in some instances a sample from the biopsy may be sufficient for assessment of RNA expression without amplification, but in other instances the lack of suitable cells in a small biopsy region may require use of RNA conversion and/or amplification methods or other methods to enhance resolution of the nucleic acid molecules. Such methods, which allow use of limited biopsy materials, are well known to those of ordinary skill in the art and include, but are not limited to: direct RNA amplification, reverse transcription of RNA to cDNA, amplification of cDNA, or the generation of radiolabeled nucleic acids.

[0047] In some embodiments, the colon cancer-associated nucleic acid molecules from the group of nucleic acid sequences numbered 1 through 15 in Table 3 (SEQ ID Nos: 1-15) and the colon cancer-associated polypeptides encoded by SEQ ID NOs: 1-15, are the group of polypeptide sequences SEQ ID NOs: 16 through 30 in Table 3. In some embodiments, colon cancer-associated polypeptides may include polypeptides other than those encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

[0048] The invention involves in some embodiments, diagnosing or monitoring colon cancer in subjects by determining the presence of an immune response to at least two colon cancer-associated polypeptides. In some embodiments, cancer, such as colon cancer, in subjects may be diagnosed or monitored by determining the presence of an immune response to one of the novel colon cancer-associated polypeptides described herein. In preferred embodiments, this determination is performed by assaying a bodily fluid obtained from the subject, preferably blood, for the presence of antibodies against at least two colon cancer-associated polypeptides or the nucleic acid molecules that encode the cancer-associated polypeptides, or for the presence of antibodies against one of the novel colon cancer-associated polypeptides or the encoding nucleic acid molecules thereof as described herein. This determination may also be performed by assaying a tissue of the subject for the presence of at least two colon cancer-associated polypeptides and/or the encoding nucleic acid molecules thereof, or assaying a tissue of the subject for the presence of one of the novel colon cancer-associated polypeptides or the encoding nucleic acid molecules thereof as described herein.

[0049] Measurement of the immune response against one of the novel colon cancer-associated polypeptides described

herein, or at least two colon cancer-associated polypeptides in a subject over time by sequential determinations permits monitoring of the disease and/or the effects of a course of treatment. For example, a sample may be obtained from a subject, tested for an immune response to one of the novel colon cancer-associated polypeptides or may be tested for an immune response to at least two colon cancer-associated polypeptides and at a second, subsequent time, another sample may be obtained from the subject and similarly tested. The results of the first and second (subsequent) tests can be compared as a measure of the onset, regression or progression of colon cancer, or, if colon-cancer treatment was undertaken during the interval between obtaining the samples, the effectiveness of the treatment may be evaluated by comparing the results of the two tests.

[0050] The invention also involves in some embodiments diagnosing or monitoring colon cancer by determining the presence of at least two colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof, or by determining the presence of one of the novel colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof as described herein. In some important embodiments, this determination is performed by assaying a tissue sample from subject, preferably one believed to be cancerous, for the presence of at least two colon cancer-associated polypeptides or the encoding nucleic acid molecules thereof, or for the presence of one of the novel colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof as described herein.

[0051] In other important embodiments, the presence of at least two colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof, or the presence of one of the novel colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof as described herein, are measured in mucus or fecal/stool samples. Such samples may contain colon cancer-associated polypeptides, or the encoding nucleic acids thereof, for example in shed cells. Measurement of the presence of at least two colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof, or the presence of one of the novel colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof as described herein, in subject's samples over time by sequential determinations at temporal intervals permits monitoring of the disease and/or the effects of a course of treatment.

[0052] In all embodiments, treatment for colon cancer may include, but is not limited to: surgical intervention, chemotherapy, radiotherapy, and adjuvant systemic therapies. In a preferred embodiment, treatment may include administering antibodies that specifically bind to the colon cancer-associated antigen. Optionally, an antibody can be linked to one or more detectable markers, antitumor agents or immunomodulators. Antitumor agents can include cytotoxic agents and agents that act on tumor neovasculature. Detectable markers include, for example, radioactive or fluorescent markers. Cytotoxic agents include cytotoxic radionuclides, chemical toxins and protein toxins.

[0053] The cytotoxic radionuclide or radiotherapeutic isotope may be an alpha-emitting isotope such as ^{225}Ac, ^{211}At, ^{212}Bi, or ^{213}Bi. Alternatively, the cytotoxic radionuclide may be a beta-emitting isotope such as ^{186}Rh, ^{188}Rh, ^{90}Y, ^{131}I or ^{67}Cu. Further, the cytotoxic radionuclide may emit Auger and low energy electrons such as the isotopes ^{125}i, ^{123}I or ^{77}Br.

[0054] Suitable chemical toxins or chemotherapeutic agents include members of the enediyne family of molecules, such as chalicheamicin and esperamicin. Chemical toxins can also be taken from the group consisting of methotrexate, doxorubicin, melphalan, chlorambucil, ARA-C, vindesine, mitomycin C, cis-platinum, etoposide, bleomycin and 5-fluorouaracil. Other chemotherapeutic agents are known to those skilled in the art.

[0055] Agents that act on the tumor neovasculature can include tubulin-binding agents such as combrestatin A4 (Griggs et al., Lancet Oncol. 2:82, 2001) and angiostatin and endostatin (reviewed in Rosen, Oncologist 5:20, 2000, incorporated by reference herein). Immunomodulators may also be conjugated to colon cancer-associated antibodies.

[0056] The invention thus involves in one aspect, colon cancer-associated polypeptides, genes encoding those polypeptides, functional modifications and variants of the foregoing, useful fragments of the foregoing, as well as diagnostics relating thereto, and diagnostic uses thereof. In some embodiments, the colon cancer-associated polypeptide genes correspond to SEQ ID NOs: 1-15. Encoded polypeptides (e.g., proteins), peptides and antisera thereto are also preferred for diagnosis and correspond to SEQ ID NOs: 16-30. In some embodiments, encoded polypeptides (e.g. proteins), peptides, and antisera thereto are ones other than those corresponding to SEQ ID NOs:16-30.

[0057] Some of the amino acid sequences identified by SEREX as colon cancer-associated polypeptides, and the nucleotide sequences encoding them, are newly identified and some are sequences deposited in databases such as GenBank. The use of the newly identified sequences in diagnostic assays for cancer is novel, as is the use of sets of at least two or more of the sequences in colon cancer diagnostic assays and kits.

[0058] Homologs and alleles of the colon cancer-associated polypeptide nucleic acids of the invention can be identified by conventional techniques. Thus, an aspect of the invention is those nucleic acid sequences that code for colon cancer-associated antigens and antigenic fragments thereof. As used herein, a homolog to a colon cancer-associated polypeptide is a polypeptide from a human or other animal that has a high degree of structural similarity to the identified colon cancer-associated polypeptides.

[0059] Identification of human and other organism homologs of colon cancer-associated polypeptides will be familiar to those of skill in the art. In general, nucleic acid hybridization is a suitable method for identification of homologous sequences of another species (e.g., human, cow, sheep), which correspond to a known sequence. Standard nucleic acid hybridization procedures can be used to identify related nucleic acid sequences of selected percent identity. For example, one can construct a library of cDNAs reverse transcribed from the mRNA of a selected tissue (e.g., colon) and use the nucleic acids that encode colon cancer-associated polypeptide identified herein to screen the library for related nucleotide sequences. The screening preferably is performed using high-stringency conditions to identify those sequences that are closely related by sequence identity.

Nucleic acids so identified can be translated into polypeptides and the polypeptides can be tested for activity.

[0060] The term "high stringency" as used herein refers to parameters with which the art is familiar. Nucleic acid hybridization parameters may be found in references that compile such methods, e.g. *Molecular Cloning: A Laboratory Manual,* J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989, or *Current Protocols in Molecular Biology,* F. M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. More specifically, high-stringency conditions, as used herein, refers, for example, to hybridization at 65° C. in hybridization buffer (3.5×SSC, 0.02% Ficoll, 0.02% polyvinyl pyrrolidone, 0.02% Bovine Serum Albumin, 2.5 mM NaH_2PO_4(pH7), 0.5% SDS, 2 mM EDTA). SSC is 0.15M sodium chloride/0.015M sodium citrate, pH7; SDS is sodium dodecyl sulphate; and EDTA is ethylenediaminetetracetic acid. After hybridization, the membrane upon which the DNA is transferred is washed, for example, in 2×SSC at room temperature and then at 0.1-0.5×SSC/0.1×SDS at temperatures up to 68° C.

[0061] There are other conditions, reagents, and so forth that can be used, which result in a similar degree of stringency. The skilled artisan will be familiar with such conditions, and thus they are not given here. It will be understood, however, that the skilled artisan will be able to manipulate the conditions in a manner to permit the clear identification of homologs and alleles of colon cancer-associated polypeptide nucleic acids of the invention (e.g., by using lower stringency conditions). The skilled artisan also is familiar with the methodology for screening cells and libraries for expression of such molecules, which then are routinely isolated, followed by isolation of the pertinent nucleic acid molecule and sequencing.

[0062] In general homologs and alleles typically will share at least 75% nucleotide identity and/or at least 90% amino acid identity to the sequences of colon cancer-associated antigen, antigenic fragment thereof, and antigen precursor thereof nucleic acid and polypeptides, respectively, in some instances will share at least 90% nucleotide identity and/or at least 95% amino acid identity, and in other instances will share at least 95% nucleotide identity and/or at least 99% amino acid identity. The homology can be calculated using various, publicly available software tools developed by NCBI (Bethesda, Md.) that can be obtained through the internet. Exemplary tools include the BLAST system available from the website of the National Center for Biotechnology Information (NCBI) at the National Institutes of Health. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained using the MacVector sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

[0063] In screening for colon cancer-associated polypeptide genes, a Southern blot may be performed using the foregoing conditions, together with a delectably labeled probe (e.g. radioactive or chemiluminescent probes). After washing the membrane to which the DNA is finally transferred, the membrane can be placed against X-ray film or a phosphorimager to detect the radioactive or chemiluminescent signal. In screening for the expression of colon cancer-associated polypeptide nucleic acids, Northern blot hybridizations using the foregoing conditions can be performed on samples taken from colon cancer patients or subjects suspected of having a condition characterized by abnormal cell proliferation or neoplasia of the colorectal tissues. Amplification protocols such as polymerase chain reaction using primers that hybridize to the sequences presented also can be used for detection of the colon cancer-associated polypeptide genes or expression thereof.

[0064] Identification of related sequences can also be achieved using polymerase chain reaction (PCR) and other amplification techniques suitable for cloning related nucleic acid sequences. Preferably, PCR primers are selected to amplify portions of a nucleic acid sequence believed to be conserved (e.g., a catalytic domain, a DNA-binding domain, etc.). Again, nucleic acids are preferably amplified from a tissue-specific library (e.g., colon). One also can use expression cloning utilizing the antisera described herein to identify nucleic acids that encode related antigenic proteins in humans or other species using the SEREX procedure to screen the appropriate expression libraries. (See: Sahin et al. *Proc. Natl. Acad. Sci. USA* 92:11810-11813, 1995).

[0065] The invention also includes degenerate nucleic acids that include alternative codons to those present in the native materials. For example, serine residues are encoded by the codons TCA, AGT, TCC, TCG, TCT and AGC. Each of the six codons is equivalent for the purposes of encoding a serine residue. Thus, it will be apparent to one of ordinary skill in the art that any of the serine-encoding nucleotide triplets may be employed to direct the protein synthesis apparatus, in vitro or in vivo, to incorporate a serine residue into an elongating colon cancer-associated polypeptide. Similarly, nucleotide sequence triplets which encode other amino acid residues include, but are not limited to: CCA, CCC, CCG, and CCT (proline codons); CGA, CGC, CGG, CGT, AGA, and AGG (arginine codons); ACA, ACC, ACG, and ACT (threonine codons); AAC and AAT (asparagine codons); and ATA, ATC, and ATT (isoleucine codons). Other amino acid residues may be encoded similarly by multiple nucleotide sequences. Thus, the invention embraces degenerate nucleic acids that differ from the biologically isolated nucleic acids in codon sequence due to the degeneracy of the genetic code.

[0066] The invention also provides modified nucleic acid molecules, which include additions, substitutions and deletions of one or more nucleotides. In preferred embodiments, these modified nucleic acid molecules and/or the polypeptides they encode retain at least one activity or function of the unmodified nucleic acid molecule and/or the polypeptides, such as antigenicity, receptor binding, etc. In certain embodiments, the modified nucleic acid molecules encode modified polypeptides, preferably polypeptides having conservative amino acid substitutions as are described elsewhere herein. The modified nucleic acid molecules are structurally related to the unmodified nucleic acid molecules and in preferred embodiments are sufficiently structurally related to the unmodified nucleic acid molecules so that the modified and unmodified nucleic acid molecules hybridize under stringent conditions known to one of skill in the art.

[0067] For example, modified nucleic acid molecules that encode polypeptides having single amino acid changes can be prepared. Each of these nucleic acid molecules can have

one, two or three nucleotide substitutions exclusive of nucleotide changes corresponding to the degeneracy of the genetic code as described herein. Likewise, modified nucleic acid molecules that encode polypeptides having two amino acid changes can be prepared which have, e.g., 2-6 nucleotide changes. Numerous modified nucleic acid molecules like these will be readily envisioned by one of skill in the art, including for example, substitutions of nucleotides in codons encoding amino acids 2 and 3, 2 and 4, 2 and 5, 2 and 6, and so on. In the foregoing example, each combination of two amino acids is included in the set of modified nucleic acid molecules, as well as all nucleotide substitutions which code for the amino acid substitutions. Additional nucleic acid molecules that encode polypeptides having additional substitutions (i.e., 3 or more), additions or deletions (e.g., by introduction of a stop codon or a splice site(s)) also can be prepared and are embraced by the invention as readily envisioned by one of ordinary skill in the art. Any of the foregoing nucleic acids or polypeptides can be tested by routine experimentation for retention of structural relation or activity to the nucleic acids and/or polypeptides disclosed herein.

[0068] The invention also provides nucleic acid molecules that encode antigenic fragments of colon cancer-associated proteins.

[0069] Fragments, can be used as probes in Southern and Northern blot assays to identify such nucleic acids, or can be used in amplification assays such as those employing PCR. As known to those skilled in the art, large probes such as 200, 250, 300 or more nucleotides are preferred for certain uses such as Southern and Northern blots, while smaller fragments will be preferred for uses such as PCR. Fragments also can be used to produce fusion proteins for generating antibodies or determining binding of the polypeptide fragments, or for generating immunoassay components. Likewise, fragments can be employed to produce nonfused fragments of the colon cancer-associated polypeptides, useful, for example, in the preparation of antibodies, and in immunoassays. Preferred fragments are antigenic fragments, which are recognized by agents that specifically bind to colon cancer-associated polypeptides. As used herein, colon cancer-associated antibodies, are antibodies that specifically bind to colon cancer-associated polypeptides.

[0070] The invention also permits the construction of colon cancer-associated polypeptide gene "knock-outs" or "knock-ins" in cells and in animals, providing materials for studying certain aspects of colon cancer and immune system responses to colon cancer by regulating the expression of colon cancer-associated polypeptides. For example, a knock-in mouse may be constructed and examined for clinical parallels between the model and a colon cancer-infected mouse with upregulated expression of a colon cancer-associated polypeptide, which may be useful to trigger an immune reaction to the polypeptide. Such a cellular or animal model may also be useful for assessing treatment strategies for colon cancer.

[0071] Alternative types of animal models for colon cancer may be developed based on the invention. Stimulating an immune response to a colon cancer-associated polypeptide in an animal may provide a model in which to test treatments, and assess the etiology of colon cancers.

[0072] The invention also provides isolated polypeptides (including whole proteins and partial proteins) encoded by the foregoing colon cancer-associated nucleic acids. Such polypeptides are useful, for example, alone or as fusion proteins to generate antibodies, and as components of an immunoassay or diagnostic assay. Colon cancer-associated polypeptides can be isolated from biological samples including tissue or cell homogenates, and can also be expressed recombinantly in a variety of prokaryotic and eukaryotic expression systems by constructing an expression vector appropriate to the expression system, introducing the expression vector into the expression system, and isolating the recombinantly expressed protein. Short polypeptides, such as colon cancer-associated antigen fragments including antigenic peptides also can be synthesized chemically using well-established methods of peptide synthesis.

[0073] Fragments of a polypeptide preferably are those fragments that retain a distinct functional capability of the polypeptide. Functional capabilities that can be retained in a fragment of a polypeptide include interaction with antibodies (e.g. antigenic fragments), interaction with other polypeptides or fragments thereof, selective binding of nucleic acids or proteins, and enzymatic activity. One important activity is the ability to provoke in a subject an immune response. As will be recognized by those skilled in the art, the size of the fragment will depend upon factors such as whether the epitope recognized by an antibody is a linear epitope or a conformational epitope. Thus, some antigenic fragments of colon cancer-associated polypeptides will consist of longer segments while others will consist of shorter segments, (e.g. 5, 6, 7, 8, 9, 10, 11 or 12 or more amino acids long, including each integer up to the full length of the colon cancer-associated polypeptide). Those skilled in the art are well versed in methods for selecting antitgenic fragments of proteins.

[0074] The skilled artisan will also realize that conservative amino acid substitutions may be made in colon cancer-associated polypeptides to provide functionally equivalent variants, or homologs of the foregoing polypeptides, i.e, the variants retain the functional capabilities of the colon cancer-associated antigen polypeptides. As used herein, a "conservative amino acid substitution" refers to an amino acid substitution that does not alter the relative charge or size characteristics of the protein in which the amino acid substitution is made. Variants can be prepared according to methods for altering polypeptide sequence known to one of ordinary skill in the art such as are found in references that compile such methods, e.g. *Molecular Cloning: A Laboratory Manual,* J. Sambrook, et al., eds., Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989, or *Current Protocols in Molecular Biology,* F. M. Ausubel, et al., eds., John Wiley & Sons, Inc., New York. Exemplary functionally equivalent variants or homologs of the colon cancer-associated polypeptides include conservative amino acid substitutions of in the amino acid sequences of proteins disclosed herein. Conservative substitutions of amino acids include substitutions made amongst amino acids within the following groups: (a) M, I, L, V; (b) F, Y, W; (c) K, R, H; (d) A, G; (e) S, T; (f) Q, N; and (g) E, D.

[0075] For example, upon determining that a peptide is a colon cancer-associated polypeptide, one can make conservative amino acid substitutions to the amino acid sequence of the peptide, and still have the polypeptide retain its specific antibody-binding characteristics.

[0076] Conservative amino-acid substitutions in the amino acid sequence of colon cancer-associated polypeptides to produce functionally equivalent variants of colon cancer-associated polypeptides typically are made by alteration of a nucleic acid encoding a colon cancer-associated polypeptide. Such substitutions can be made by a variety of methods known to one of ordinary skill in the art. For example, amino acid substitutions may be made by PCR-directed mutation, site-directed mutagenesis according to the method of Kunkel (Kunkel, *Proc. Nat. Acad. Sci. U.S.A.* 82: 488-492, 1985), or by chemical synthesis of a gene encoding a colon cancer-associated polypeptide. Where amino acid substitutions are made to a small unique fragment of a colon cancer-associated polypeptide, such as an antigenic epitope recognized by autologous or allogeneic sera or cytolytic T lymphocytes, the substitutions can be made by directly synthesizing the peptide. The activity of functionally equivalent fragments of colon cancer-associated polypeptides can be tested by cloning the gene encoding the altered colon cancer-associated polypeptide into a bacterial or mammalian expression vector, introducing the vector into an appropriate host cell, expressing the altered polypeptide, and testing for a functional capability of the colon cancer-associated polypeptides as disclosed herein. Peptides that are chemically synthesized can be tested directly for function, e.g., for binding to antisera recognizing associated antigens.

[0077] The invention as described herein has a number of uses, some of which are described elsewhere herein. First, the invention permits isolation of the colon cancer-associated protein molecules. A variety of methodologies well-known to the skilled practitioner can be utilized to obtain isolated colon cancer-associated polypeptide molecules. The polypeptide may be purified from cells that naturally produce the polypeptide, by chromatographic means or immunological recognition. Alternatively, an expression vector may be introduced into cells to cause production of the polypeptide. In another method, mRNA transcripts may be microinjected or otherwise introduced into cells to cause production of the encoded polypeptide. Translation of mRNA in cell-free extracts such as the reticulocyte lysate system also may be used to produce polypeptide. Those skilled in the art also can readily follow known methods for isolating colon cancer-associated polypeptides. These include, but are not limited to, immunochromatography, HPLC, size-exclusion chromatography, ion-exchange chromatography, and immune-affinity chromatography.

[0078] The isolation and identification of colon cancer-associated polypeptides also permits the artisan to diagnose a disorder characterized by expression of colon cancer-associated polypeptides, and characterized preferably by an immune response against the colon cancer-associated polypeptides.

[0079] The methods related to colon cancer-associated polypeptide immune responses involve determining the immune response (antibody or cellular) against one or more colon cancer-associated polypeptides. The immune response can be assayed by any of the various immunoassay methodologies known to one of ordinary skill in the art. For example, the antigenic colon cancer-associated polypeptides can be used as a target to capture antibodies from a blood sample drawn from a patient in an ELISA assay.

[0080] The methods related to colon cancer-associated polypeptide expression involve determining expression of one or more colon cancer-associated nucleic acids, and/or encoded colon cancer-associated polypeptides and/or peptides derived therefrom and comparing the expression with that in a colon cancer-free subject. Such determinations can be carried out via any standard nucleic acid determination assay, including the polymerase chain reaction, or assaying with labeled hybridization probes. Such hybridization methods include, but are not limited to microarray techniques.

[0081] The invention also makes it possible to isolate proteins that specifically bind to colon cancer-associated antigens as disclosed herein, including antibodies and cellular binding partners of the colon cancer-associated polypeptides. Additional uses are described further herein.

[0082] The invention also involves agents such as polypeptides that bind to colon cancer-associated polypeptides. Such binding agents can be used, for example, in screening assays to detect the presence or absence of colon cancer-associated polypeptides and complexes of colon cancer-associated polypeptides and their binding partners and in purification protocols to isolate colon cancer-associated polypeptides and complexes of colon cancer-associated polypeptides and their binding partners. Such agents also may be used to inhibit the native activity of the colon cancer-associated polypeptides, for example, by binding to such polypeptides.

[0083] The invention, therefore, embraces peptide binding agents which, for example, can be antibodies or fragments of antibodies having the ability to selectively bind to colon cancer-associated polypeptides. Antibodies include polyclonal and monoclonal antibodies, prepared according to conventional methodology.

[0084] Significantly, as is well-known in the art, only a small portion of an antibody molecule, the paratope, is involved in the binding of the antibody to its epitope (see, in general, Clark, W. R. (1986) *The Experimental Foundations of Modern Immunology* Wiley & Sons, Inc., New York; Roitt, I. (1991) *Essential Immunology,* 7th Ed., Blackwell Scientific Publications, Oxford). The pFc' and Fc regions, for example, are effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically cleaved, or which has been produced without the pFc' region, designated an $F(ab')_2$ fragment, retains both of the antigen binding sites of an intact antibody. Similarly, an antibody from which the Fc region has been enzymatically cleaved, or which has been produced without the Fc region, designated an Fab fragment, retains one of the antigen binding sites of an intact antibody molecule. Proceeding further, Fab fragments consist of a covalently bound antibody light chain and a portion of the antibody heavy chain denoted Fd. The Fd fragments are the major determinant of antibody specificity (a single Fd fragment may be associated with up to ten different light chains without altering antibody specificity) and Fd fragments retain epitope-binding ability in isolation.

[0085] Within the antigen-binding portion of an antibody, as is well-known in the art, there are complementarity determining regions (CDRs), which directly interact with the epitope of the antigen, and framework regions (FRs), which maintain the tertiary structure of the paratope (see, in general, Clark, 1986; Roitt, 1991). In both the heavy chain Fd fragment and the light chain of IgG immunoglobulins, there are four framework regions (FR1 through FR4) sepa-

rated respectively by three complementarity determining regions (CDR1 through CDR3). The CDRs, and in particular the CDR3 regions, and more particularly the heavy chain CDR3, are largely responsible for antibody specificity.

[0086] It is now well-established in the art that the non-CDR regions of a mammalian antibody may be replaced with similar regions of conspecific or heterospecific antibodies while retaining the epitopic specificity of the original antibody. This is most clearly manifested in the development and use of "humanized" antibodies in which non-human CDRs are covalently joined to human FR and/or Fc/pFc' regions to produce a functional antibody. See, e.g., U.S. Pat. Nos. 4,816,567, 5,225,539, 5,585,089, 5,693,762 and 5,859,205.

[0087] Fully human monoclonal antibodies also can be prepared by immunizing mice transgenic for large portions of human immunoglobulin heavy and light chain loci. Following immunization of these mice (e.g., XenoMouse (Abgenix), HuMAb mice (Medarex/GenPharm)), monoclonal antibodies can be prepared according to standard hybridoma technology. These monoclonal antibodies will have human immunoglobulin amino acid sequences and therefore will not provoke human anti-mouse antibody (HAMA) responses when administered to humans.

[0088] Thus, as will be apparent to one of ordinary skill in the art, the present invention also provides for $F(ab')_2$, Fab, Fv and Fd fragments; chimeric antibodies in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric $F(ab')_2$ fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; chimeric Fab fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain CDR3 regions have been replaced by homologous human or non-human sequences; and chimeric Fd fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced by homologous human or non-human sequences. The present invention also includes so-called single chain antibodies.

[0089] Thus, the invention involves polypeptides of numerous size and type that bind specifically to colon cancer-associated polypeptides, and complexes of both colon cancer-associated polypeptides and their binding partners. These polypeptides may be derived also from sources other than antibody technology. For example, such polypeptide binding agents can be provided by degenerate peptide libraries which can be readily prepared in solution, in immobilized form or as phage display libraries. Combinatorial libraries also can be synthesized of peptides containing one or more amino acids. Libraries further can be synthesized of peptoids and non-peptide synthetic moieties.

[0090] Phage display can be particularly effective in identifying binding peptides useful according to the invention. Briefly, one prepares a phage library (using e.g. m13, fd, or lambda phage), displaying inserts from 4 to about 80 amino acid residues using conventional procedures. The inserts may represent, for example, a completely degenerate or biased array. One then can select phage-bearing inserts which bind to the colon cancer-associated polypeptide. This process can be repeated through several cycles of reselection of phage that bind to the colon cancer-associated polypeptide. Repeated rounds lead to enrichment of phage bearing particular sequences. DNA sequence analysis can be conducted to identify the sequences of the expressed polypeptides. The minimal linear portion of the sequence that binds to the colon cancer-associated polypeptide can be determined. One can repeat the procedure using a biased library containing inserts containing part or all of the minimal linear portion plus one or more additional degenerate residues upstream or downstream thereof. Yeast two-hybrid screening methods also may be used to identify polypeptides that bind to the colon cancer-associated polypeptides.

[0091] Thus, the colon cancer-associated polypeptides of the invention, including fragments thereof, can be used to screen peptide libraries, including phage display libraries, to identify and select peptide binding partners of the colon cancer-associated polypeptides of the invention. Such molecules can be used, as described, for screening assays, for purification protocols, for interfering directly with the functioning of colon cancer-associated polypeptides and for other purposes that will be apparent to those of ordinary skill in the art. For example, isolated colon cancer-associated polypeptides can be attached to a substrate (e.g., chromatographic media, such as polystyrene beads, or a filter), and then a solution suspected of containing the binding partner may be applied to the substrate. If a binding partner that can interact with colon cancer-associated polypeptides is present in the solution, then it will bind to the substrate-bound colon cancer-associated polypeptide. The binding partner then may be isolated.

[0092] As detailed herein, the foregoing antibodies and other binding molecules may be used for example, to identify tissues expressing protein or to purify protein. Antibodies also may be coupled to specific diagnostic labeling agents for imaging of cells and tissues that express colon cancer-associated polypeptides or to therapeutically useful agents according to standard coupling procedures. Diagnostic agents include, but are not limited to, barium sulfate, iocetamic acid, iopanoic acid, ipodate calcium, diatrizoate sodium, diatrizoate meglumine, metrizamide, tyropanoate sodium and radiodiagnostics including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technitium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance such as fluorine and gadolinium.

[0093] The invention also includes methods to monitor the onset, progression, or regression of colon cancer in a subject by, for example, obtaining samples at sequential times from a subject and assaying such samples for the presence and/or absence of an antigenic response that is a marker of the condition. A subject may be suspected of having colon cancer or may be believed not to have colon cancer and in the latter case, the sample may serve as a normal baseline level for comparison with subsequent samples.

[0094] Onset of a condition is the initiation of the changes associated with the condition in a subject. Such changes may be evidenced by physiological symptoms, or may be clinically asymptomatic. For example, the onset of colon cancer may be followed by a period during which there may be colon cancer-associated physiological changes in the subject, even though clinical symptoms may not be evident at that time. The progression of a condition follows onset and is the advancement of the physiological elements of the

condition, which may or may not be marked by an increase in clinical symptoms. In contrast, the regression of a condition is a decrease in physiological characteristics of the condition, perhaps with a parallel reduction in symptoms, and may result from a treatment or may be a natural reversal in the condition.

[0095] A marker for colon cancer may be the specific binding of a colon cancer-associated polypeptide with an antibody. Onset of a colon cancer condition may be indicated by the appearance of such a marker(s) in a subject's samples where there was no such marker(s) determined previously. For example, if marker(s) for colon cancer are determined not to be present in a first sample from a subject, and colon cancer marker(s) are determined to be present in a second or subsequent sample from the subject, it may indicate the onset of cancer.

[0096] Progression and regression of a colon cancer condition may be generally indicated by the increase or decrease, respectively, of marker(s) in a subject's samples over time. For example, if marker(s) for colon cancer are determined to be present in a first sample from a subject and additional marker(s) or more of the initial marker(s) for colon cancer are determined to be present in a second or subsequent sample from the subject, it may indicate the progression of cancer. Regression of cancer may be indicated by finding that marker(s) determined to be present in a sample from a subject are not determined to be found, or found at lower amounts in a second or subsequent sample from the subject.

[0097] The progression and regression of a colon cancer condition may also be indicated based on characteristics of the colon cancer-associated polypeptides determined in the subject. For example, some colon cancer-associated polypeptides may be abnormally expressed at specific stages of colon cancer (e.g. early-stage colon cancer-associated polypeptides; mid-stage colon cancer-associated polypeptides; and late-stage colon cancer-associated polypeptides). Another example, although not intended to be limiting, is that colon cancer-associated polypeptides may be differentially expressed in primary tumors versus metastases, thereby allowing the stage and/or diagnostic level of the disease to be established, based on the identification of selected colon cancer-associated polypeptides in a subject sample.

[0098] Another method of staging colon cancer may be based on variation in a subject's immune response to colon cancer-associated polypeptides, which may or may not be abnormally expressed in the subject. Variability in the immune response to the polypeptides may be used to indicate the stage of colon cancer in a subject, for example, some colon cancer-associated polypeptides may trigger an immune response at different stages of the colon cancer than that triggered by other colon cancer-associated polypeptides.

[0099] Different types of colon cancer, such as familial adenomatous polyposis (FAP) or hereditary nonpolyposis colon cancer (HNPCC), also known as Lynch syndrome, may express different colon cancer-associated polypeptides and the encoding nucleic acid molecules thereof, or may have different spatial or temporal expression patterns. Such variations may allow cancer-specific diagnosis and subsequent treatment tailored to the patient's specific condition. These colon cancer-specific diagnoses may also be based on the variations in immune responses to the different colon cancer-associated polypeptides.

[0100] The invention includes kits for assaying the presence of colon cancer-associated polypeptides and/or antibodies that specifically bind to colon cancer-associated polypeptides. An example of such a kit may include the above-mentioned polypeptides bound to a substrate, for example a dipstick, which is dipped into a blood or body fluid sample of a subject. The surface of the substrate may then be processed using procedures well known to those of skill in the art, to assess whether specific binding occurred between the polypeptides and agents (e.g. antibodies) in the subject's sample. For example, procedures may include, but are not limited to, contact with a secondary antibody, or other method that indicates the presence of specific binding.

[0101] Another example of a kit may include an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide. The antibody or antigen-binding fragment thereof, may be applied to a tissue sample from a patient with colon cancer and the sample then processed to assess whether specific binding occurs between the antibody and a polypeptide or other component of the sample. In addition, the antibody or antigen-binding fragment thereof, may be applied to a stool sample from a subject, either suspected of having colon cancer, diagnosed with colon cancer, or believed to be free of colon cancer. As will be understood by one of skill in the art, such binding assays may also be performed with a sample or object contacted with an antibody and/or colon cancer-associated polypeptide that is in solution, for example in a 96-well plate or applied directly to an object surface.

[0102] The foregoing kits can include instructions or other printed material on how to use the various components of the kits for diagnostic purposes.

[0103] The invention further includes nucleic acid or protein microarrays with colon cancer-associated peptides or nucleic acids encoding such polypeptides. In this aspect of the invention, standard techniques of microarray technology are utilized to assess expression of the colon cancer-associated polypeptides and/or identify biological constituents that bind such polypeptides. The constituents of biological samples include antibodies, lymphocytes (particularly T lymphocytes), and the like. Protein microarray technology, which is also known by other names including: protein chip technology and solid-phase protein array technology, is well known to those of ordinary skill in the art and is based on, but not limited to, obtaining an array of identified peptides or proteins on a fixed substrate, binding target molecules or biological constituents to the peptides, and evaluating such binding. See, e.g., G. MacBeath and S. L. Schreiber, "Printing Proteins as Microarrays for High-Throughput Function Determination,"*Science* 289(5485):1760-1763, 2000. Nucleic acid arrays, particularly arrays that bind colon cancer-associated peptides, also can be used for diagnostic applications, such as for identifying subjects that have a condition characterized by colon cancer-associated polypeptide expression.

[0104] Microarray substrates include but are not limited to glass, silica, aluminosilicates, borosilicates, metal oxides such as alumina and nickel oxide, various clays, nitrocellulose, or nylon. The microarray substrates may be coated with a compound to enhance synthesis of a probe (peptide or

nucleic acid) on the substrate. Coupling agents or groups on the substrate can be used to covalently link the first nucleotide or amino acid to the substrate. A variety of coupling agents or groups are known to those of skill in the art. Peptide or nucleic acid probes thus can be synthesized directly on the substrate in a predetermined grid. Alternatively, peptide or nucleic acid probes can be spotted on the substrate, and in such cases the substrate may be coated with a compound to enhance binding of the probe to the substrate. In these embodiments, presynthesized probes are applied to the substrate in a precise, predetermined volume and grid pattern, preferably utilizing a computer-controlled robot to apply probe to the substrate in a contact-printing manner or in a non-contact manner such as ink jet or piezo-electric delivery. Probes may be covalently linked to the substrate.

[0105] Targets are peptides or proteins and may be natural or synthetic. The tissue may be obtained from a subject or may be grown in culture (e.g. from a cell line).

[0106] In some embodiments of the invention, one or more control peptide or protein molecules are attached to the substrate. Preferably, control peptide or protein molecules allow determination of factors such as peptide or protein quality and binding characteristics, reagent quality and effectiveness, hybridization success, and analysis thresholds and success.

[0107] Nucleic acid microarray technology, which is also known by other names including: DNA chip technology, gene chip technology, and solid-phase nucleic acid array technology, is well known to those of ordinary skill in the art and is based on, but not limited to, obtaining an array of identified nucleic acid probes on a fixed substrate, labeling target molecules with reporter molecules (e.g., radioactive, chemiluminescent, or fluorescent tags such as fluorescein, Cye3-dUTP, or Cye5-dUTP), hybridizing target nucleic acids to the probes, and evaluating target-probe hybridization. A probe with a nucleic acid sequence that perfectly matches the target sequence will, in general, result in detection of a stronger reporter-molecule signal than will probes with less perfect matches. Many components and techniques utilized in nucleic acid microarray technology are presented in *The Chipping Forecast,* Nature Genetics, Vol.21, January 1999, the entire contents of which is incorporated by reference herein.

[0108] According to the present invention, nucleic acid microarray substrates may include but are not limited to glass, silica, aluminosilicates, borosilicates, metal oxides such as alumina and nickel oxide, various clays, nitrocellulose, or nylon. In all embodiments, a glass substrate is preferred. According to the invention, probes are selected from the group of nucleic acids including, but not limited to: DNA, genomic DNA, cDNA, and oligonucleotides; and may be natural or synthetic. Oligonucleotide probes preferably are 20 to 25-mer oligonucleotides and DNA/cDNA probes preferably are 500 to 5000 bases in length, although other lengths may be used. Appropriate probe length may be determined by one of ordinary skill in the art by following art-known procedures. In one embodiment, preferred probes are sets of more than two of the colon cancer-associated polypeptide nucleic acid molecules set forth herein, or one of the novel colon cancer-associated polypeptide nucleic acid molecules as described herein. Probes may be purified to remove contaminants using standard methods known to those of ordinary skill in the art such as gel filtration or precipitation.

[0109] In one embodiment, the microarray substrate may be coated with a compound to enhance synthesis of the probe on the substrate. Such compounds include, but are not limited to, oligoethylene glycols. In another embodiment, coupling agents or groups on the substrate can be used to covalently link the first nucleotide or olignucleotide to the substrate. These agents or groups may include, for example, amino, hydroxy, bromo, and carboxy groups. These reactive groups are preferably attached to the substrate through a hydrocarbyl radical such as an alkylene or phenylene divalent radical, one valence position occupied by the chain bonding and the remaining attached to the reactive groups. These hydrocarbyl groups may contain up to about ten carbon atoms, preferably up to about six carbon atoms. Alkylene radicals are usually preferred containing two to four carbon atoms in the principal chain. These and additional details of the process are disclosed, for example, in U.S. Pat. No. 4,458,066, which is incorporated by reference in its entirety.

[0110] In one embodiment, probes are synthesized directly on the substrate in a predetermined grid pattern using methods such as light-directed chemical synthesis, photochemical deprotection, or delivery of nucleotide precursors to the substrate and subsequent probe production.

[0111] In another embodiment, the substrate may be coated with a compound to enhance binding of the probe to the substrate. Such compounds include, but are not limited to: polylysine, amino silanes, amino-reactive silanes (Chipping Forecast, 1999) or chromium. In this embodiment, presynthesized probes are applied to the substrate in a precise, predetermined volume and grid pattern, utilizing a computer-controlled robot to apply probe to the substrate in a contact-printing manner or in a non-contact manner such as ink jet or piezo-electric delivery. Probes may be covalently linked to the substrate with methods that include, but are not limited to, UV-irradiation. In another embodiment probes are linked to the substrate with heat.

[0112] Targets for microarrays are nucleic acids selected from the group, including but not limited to: DNA, genomic DNA, cDNA, RNA, mRNA and may be natural or synthetic. In all embodiments, nucleic acid target molecules from human tissue are preferred. The tissue may be obtained from a subject or may be grown in culture (e.g. from a cell line).

[0113] In embodiments of the invention one or more control nucleic acid molecules are attached to the substrate. Preferably, control nucleic acid molecules allow determination of factors such as nucleic acid quality and binding characteristics, reagent quality and effectiveness, hybridization success, and analysis thresholds and success. Control nucleic acids may include but are not limited to expression products of genes such as housekeeping genes or fragments thereof.

[0114] In some embodiments, one or more control nucleic acid molecules are attached to the substrate. Preferably, control nucleic acid molecules allow determination of factors such as binding characteristics, reagent quality and effectiveness, hybridization success, and analysis thresholds and success.

EXAMPLES

Example 1

[0115] Method

[0116] Serum samples from patients with colon cancer were screened using a modification of the plaque assay, termed a spot assay. In this method, 80×120 mm nitrocellulose membranes were precoated with a film of NZY/0.7% Agarose/2.5 mM IPTG and placed on a reservoir layer of NZY/0.7% Agarose in a 86×128 mm Omni Tray (Nalge Nunc International Corp., Naperville, Ill.). Approximately 1.0×10^5 pfu of monoclonal phage encoding individual serologically defined colon cancer antigens, in a volume of 20 μl, were mixed with 20 μl of exponentially growing *E. coli* XL-1 Blue MRF and spotted (0.7-μl aliquots) on the precoated nitrocellulose membranes. Membranes were incubated for 15 hours at 37° C. A total of 75 different serologically defined colon cancer antigens were spotted in duplicate per nitrocellulose membrane. The agarose film was then removed from the membrane and the filters were processed for reactivity with individual serum samples (1:200 dilution), as described in Scanlan, et al., Int. J. Cancer 76:652-658 (1998) and Scanlan, et al., Int. J. Cancer 83:456-64, (1999).

[0117] Results

[0118] The results (see Table 1) indicate that 37/75 sera (49%) reacted with at least 1 antigen, 17/75 sera (23%) reacted with 2 or more antigens, 6/75 sera (8%) reacted with 3 or more antigens, and 2/75 sera (3%) reacted with 4 or more antigens. The reactivity of individual antigens is shown in Table 2.

TABLE 1

Colon Cancer Serology
Reactivity of 75 sera from colon cancer patients versus 15 antigens comprising, none of which react with normal sera (0/75, assayed by spot blot as described).

Sera Number	Reactive NY-antigens
COF1	Negative
COF2	Negative
COF3	Negative
COF4	Negative
COF5	Negative
COF6	CO61 + + +
COF7	CO26 + + + +, ESO-1 + + + +, CO61 + + + +
COF8	Negative
COF9	REN32 + + +
COF10	p53 + + +, CO58 + +
COF11	TNKL +, ESO-1 + + + +
COF12	CO94 + +
COF13	Negative
COF14	Negative
COF15	SSX-2 + +
COF16	CO45 + +, CO42 + +
COF17	Negative
COF18	Negative
COF19	Negative
COF20	Negative
COF21	CO58 +
COF22	TNKL + +, CO45 + +, CO42 + +
COF23	CO41 + +
CO24	Negative
CO25	Negative
CO26	TNKL + + +
CO27	CO45 + + + +

TABLE 1-continued

Colon Cancer Serology
Reactivity of 75 sera from colon cancer patients versus 15 antigens comprising, none of which react with normal sera (0/75, assayed by spot blot as described).

Sera Number	Reactive NY-antigens
CO28	CO9 + + + +, ESO-1 + + + +, CO58 + + + +, CO61 + +
CO29	MAGE-3 +, ESO-1 +
CO30	p53 + + +
CO31	Negative
CO32	Negative
CO33	MAGE 3 + + +
CO34	Negative
CO35	Negative
CO36	CO41 + + +
CO37	Negative
CO38	Negative
CO39	Negative
CO40	CO42 +, CO95 +
CO41	Negative
CO42	p53 + + + +
CO43	p53 + + + +, CO94 + + + +
CO44	Negative
CO45	p53 + + +
CO46	Negative
CO47	CO61 +
CO48	p53 + + + +, MAGE 3 + +
CO49	Negative
CO50	Negative
CO51	CO9 +
COF52	Negative
CO53	TNKL +, p53 + + + +
CO54	Negative
CO55	ESO-1 + + + +
CO56	Negative
CO57	Negative
CO58	Negative
CO59	Negative
CO60	SSX-1 +, MAGE-3 +, CO42 +, CO61 + + + +
CO61	TNKL + +
**CO62	**same sera as CO28
**CO63	**same sera as CO29
CO64	TNKL +
CO65	Negative
**CO66	**same sera as CO30
CO67	p53 + +
CO68	MAGE-3 +, CO42 +
CO69	Negative
CO70	Negative
CO71	REN32 +, MAGE-3 +
CO72	Negative
CO73	REN32 + +, p53 +
CO74	Negative
CO75	p53 + + +
CO76	Negative
CO77	CO94 + + + +, CO95 + + +, p53 + +
CO78	CO42 + +, CO94 + + + +, CO95 + +

[0119]

TABLE 2

Reactivity of individual antigens (includes autologous where applicable)

CO13 (p53)	13/76
CO-26 (MNK 1):	2/76
ESO-1:	5/75
REN-32 (Lamin C):	3/75
TNKL (BC-203):	6/75
SSX-2:	2/75
CO-45 (Tudor like):	4/76
CO-41 (MBD2):	3/76

TABLE 2-continued

Reactivity of individual antigens (includes autologous where applicable)	
MAGE-3	6/75
CO-9 (HDAC 5)	3/76
CO-42 (TRIP4):	7/76
CO-61 (HIP1R):	5/75
CO-58 (KNSL6):	3/75
CO-94 (seb4D):	4/75
CO-95 (KIAA1416)	4/75

[0120]

TABLE 3

	Sequence Identification Numbers	
Sequence Name	Nucleotide SEQ ID NO	Protein SEQ ID NO.
CO-95 (KIAA1416)	1	16
CO-94 (seb4D)	2	17
CO-9 (HDAC 5)	3	18
CO-61 (HIP1R)	4	19
CO-58 (KNSL6)	5	20
CO-45	6	21
CO-42 (TRIP4)	7	22
CO-41 (MBD2)	8	23
CO-13 (P53)	9	24

TABLE 3-continued

	Sequence Identification Numbers	
Sequence Name	Nucleotide SEQ ID NO	Protein SEQ ID NO.
Ren-32 (Lamin C)	10	25
TNKL (BC-203)	11	26
CO-26 (MNK 1)	12	27
SSX-2	13	28
MAGE-3	14	29
ESO-1	15	30

[0121] Other aspects of the invention will be clear to the skilled artisan and need not be repeated here. Each reference cited herein is incorporated by reference in its entirety.

[0122] The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, it being recognized that various modifications are possible within the scope of the invention.

SEQUENCE LISTING

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cagggccaga acaagttcct ttcagagatt gaggatgagc tttttaatcc agattatgtg 360

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<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 3

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gagcggcccc cctgggacgc ctccctccta caaactgcct ttgcctgggc cctacgacag 180

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<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 4

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atcaagccgg tggtggtgat ccccgaggag gccccggaag atgaggagcc ggagaatctc 420

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<213> ORGANISM: Homo sapien

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<213> ORGANISM: Homo sapien
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<221> NAME/KEY: Unsure
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agcctttcca tgttgcctct cagggtttaa catttcagaa ggattatgtt ctcaagaggg 1140

aaatgactat ttctatgaaa taataacaga agatgtgttg gaaataacaa tactagaaat 1200

cagaagggat gtttgtgata tccctttagc aattgttgac ttgaaaagca aaggtaaaag 1260

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ccctaaaact gataacattt gtgaagggtt tgaaaacccc tgcaaagata aaattgatac 1560

tgaggaactg gaaggtgaat tagagtgcca tctggttgac aaagcagagt ttgatgataa 1620

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cctgagaatg tctggaatgn nanacccaaa ttggataaga gtccacctga gaaaaggggt 2460

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<212> TYPE: DNA
<213> ORGANISM: Homo sapien
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<222> LOCATION: (151)..(151)
<223> OTHER INFORMATION: n = a, g, c, or t/u
<220> FEATURE:
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<222> LOCATION: (209)..(209)
<223> OTHER INFORMATION: n = a, g, c, or t/u
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ttgtcaattg anagtgctga agagatacga naatatgtta ctgatctcct ccaggggaaa 180

tgaaggcaaa aaaggtcaat tcatacaana acttataacc naatggcaaa agaatgatca 240

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gaaatcaggc gaccatctaa agcggggtat gaagaaaggg agaaacagac aggaagttcc 360

tgcatttact gaacctgaca cgactgcaga ggttaaaaca cttttgattg gccaaggcac 420

aagagaacag caactccgta aagaagaaga caaagtttgt cnatttatac acaagagagg 480

gacaggacag gcttgcagtc ctgctccctg gtcgtcaccc ttgtgattgc ctgggccaga 540

ancacaagct catcaataac tgtctgatct gtgggcgcat tgtctgtgaa caagaaggct 600

caggcccttg cttattctgt ggcantctgg tgtgtactct tnaggaacaa gatattttnc 660

agngtnactc anacnaaagc cagaanctgc tananaaact catgtcagga gtggacaatt 720

ctgnaaatgt ggacatctct accaaggacc ttcttcctca tcaagaattg cgaattangt 780

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ggttgtccaa acttgagcgg gaaaccttgc agaagcgaga ggaggagctg agagaacttc 960

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ccaatggaac cttgaaccag ccactgacca aattggatag atcttctgaa gagcctttgg 1140

gagttntggt aaatcccaac atgtaccagt cccctcccca gtgggttgac cacacaggtg 1200

cagcctcaca gaagaaggct ttccgttctt caggatttgg actagagttc aactcatttc 1260

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gatcctggta cacccccac agaggacgac tttggatagc agccacagct aaaaaaccct 1440

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aatttcctaa tgactatccg tcaggttgtc ttctgggctg tgtggaccta attgactgct 1560

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agaataaagc tgtctgaccc aggagaaaag gaactataca gcatagtgga gttttgtgta 1800

ctaaaattgc tatctactgg tcctttggaa ttgaagtagt agaaacctaa aggcttggcg 1860

tcaggcttga atatntcaga acttaaactc ttaccaaaat ctgtatattt ttcttaagga 1920

gtgggattcc tactttatgt aatggggtcg aaatctttga acacattatt tataaaaacc 1980

tgtttaaaaa ttctaaa 1997

<210> SEQ ID NO 8
<211> LENGTH: 1087
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 8

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ttcaaacaac cggtaaccaa agtcacaaat catcctagta ataaagtgaa atcagaccca 180

caacgaatga atgaacagcc acgtcagctt ttctgggaga agaggctaca aggacttagt 240

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agctctgcgc caatcacagg gcaagtctcc gctgctgtgg aaaagaaccc tgctgtttgg 420

cttaacacat ctcaacccct ctgcaaagct tttattgtca cagatgaaga catcaggaaa 480

caggaagagc gagtacagca agtacgcaag aaattggaag aagcactgat ggcagacatc 540

ttgtcgcgag ctgctgatac agaagagatg gatattgaaa tggacagtgg agatgaagcc 600

taagaatatg atcaggtaac tttcgaccga ctttccccaa gagaaaattc ctagaaattg 660

aacaaaaatg tttccactgg cttttgcctg taagaaaaaa aatgtacccg agcacataga 720

gctttttaat agcactaacc aatgcctttt tagatgtatt tttgatgtat atatctatta 780

ttcaaaaaat catgtttatt ttgagtccta ggacttaaaa ttagtctttt gtaatatcaa 840

gcaggaccct aagatgaagc tgagcttttg atgccaggtg caatttactg gaaatgtagc 900

acttacgtaa aacatttgtt tcccccacag ttttaataag aacagatcag gaattctaaa 960

taaatttccc agttaaagat tattgtgact tcactgtata taaacatatt tttatacttt 1020

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attcaca 1087

<210> SEQ ID NO 9
<211> LENGTH: 1760
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 9

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cggggacact ttgcgttcgg gctgggagcg tgctttccac gacggtgaca cgcttccctg 180

gattggcagc cagactgcct tccgggtcac tgccatggag gagccgcagt cagatcctag 240

cgtcgagccc cctctgagtc aggaaacatt ttcagaccta tggaaactac ttcctgaaaa 300

caacgttctg tccccttgc cgtcccaagc aatggatgat ttgatgctgt ccccggacga 360

tattgaacaa tggttcactg aagacccagg tccagatgaa gctcccagaa tgccagaggc 420

tgctcccccc gtggcccctg caccagcagc tcctacaccg gcggcccctg caccagcccc 480

ctcctggccc ctgtcatctt ctgtcccttc ccagaaaacc taccagggca gctacggttt 540

ccgtctgggc ttcttgcatt ctgggacagc caagtctgtg acttgcacgt actcccctgc 600

cctcaacaag atgttttgcc aactggccaa gacctgccct gtgcagctgt gggttgattc 660

cacacccccg cccggcaccc gcgtccgcgc catggccatc tacaagcagt cacagcacat 720

gacggaggtt gtgaggcgct gccccccacca tgagcgctgc tcagatagcg atggtctggc 780

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taccaccatc cactacaact acatgtgtaa cagttcctgc atgggcggca tgaaccggag 960

gcccatcctc accatcatca cactggaaga ctccagtggt aatctactgg gacggaacag 1020

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ccgcaagaaa ggggagcctc accacgagct gcccccaggg agcactaagc gagcactgcc 1140

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gaagtccaaa aagggtcagt ctacctcccg ccataaaaaa ctcatgttca agacagaagg 1380

gcctgactca gactgacatt ctccacttct tgttccccac tgacagcctc ccacccccat 1440

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cgtcagaagc acccaggact tccatttgct ttgtcccggg gctccactga acaagttggc 1560

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<210> SEQ ID NO 10
<211> LENGTH: 1953
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 10

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ccaacctgcc ggccatggag accccgtccc agcggcgcgc cacccgcagc ggggcgcagg 180

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ccaaggagcg cgcccgcctg cagctggagc tgagcaaagt gcgtgaggag tttaaggagc 480

tgaaagcgcg caataccaag aaggagggtg acctgatagc tgctcaggct cggctgaagg 540

acctggaggc tctgctgaac tccaaggagg ccgcactgag cactgctctc agtgagaagc 600

gcacgctgga gggcgagctg catgatctgc ggggccaggt ggccaagctt gaggcagccc 660

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gtgagaccaa gcgccgtcat gagacccgac tggtggagat tgacaatggg aagcagcgtg 840

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acaagtccaa tgaggaccag tccatgggca attggcagat caagcgccag aatggagatg 1560

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<210> SEQ ID NO 11
<211> LENGTH: 6018
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 11

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gagcgcgtct tctccggggg gcctcgccct cctgctcgcg gggccggggc tcctgctccg 180

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cggcgggggа gcggcctgcg cgagcgccgc ggccgaggcc gtggagccgg ccgcccgaga 300

gctgttcgag gcgtgccgca acggggacgt ggaacgagtc aagaggctgg tgacgcctga 360

gaaggtgaac agccgcgaca cggcgggcag gaaatccacc ccgctgcact tcgccgcagg 420

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gaacagggtt gaagtatgtt ctcttctctt aagttatggt gcagacccaa cactgctcaa 1140

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atatgaattt aaaggccact cgttgctgca agctgcacga gaagctgatg ttactcgaat 1260

caaaaaacat ctctctctgg aaatggtgaa tttcaagcat cctcaaacac atgaaacagc 1320

attgcattgt gctgctgcat ctccatatcc caaaagaaag caaatatgtg aactgttgct 1380

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<210> SEQ ID NO 12
<211> LENGTH: 2039
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 12

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tgctgctgcc cttgacttcc tgcataccaa aggcattgct catcgtgatc tgaaaccaga 120

aaatatattg tgtgaatctc cagaaaaggt gtctccagtg aaaatctgtg actttgactt 180

gggcagtggg atgaaactga acaactcctg tacccccata accacaccag agctgaccac 240

cccatgtggc tctgcagaat acatggcccc tgaggtagtg gaggtcttca cggaccaggc 300

cacattctac gacaagcgct gtgacctgtg gagcctgggc gtggtcctct acatcatgct 360

gagtggctac ccacccttcg tgggtcactg cggggccgac tgtggctggg accggggcga 420

ggtctgcagg gtgtgccaga acaagctgtt tgaaagcatc caggaaggca agtatgagtt 480

tcctgacaag gactgggcac acatctccag tgaagccaaa gacctcatct ccaagctcct 540

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<210> SEQ ID NO 13
<211> LENGTH: 766
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 13

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acccacggtt ggtgctcaaa taccagagaa gatccaaaag gccttcgatg atattgccaa 180

atacttctct aaggaagagt gggaaaagat gaaagcctcg gagaaaatct tctatgtgta 240

tatgaagaga aagtatgagg ctatgactaa actaggtttc aaggccaccc tcccaccttt 300

catgtgtaat aaacgggccg aagacttcca ggggaatgat ttggataatg accctaaccg 360

tgggaatcag gttgaacgtc ctcagatgac tttcggcagg ctccagggaa tctccccgaa 420

gatcatgccc aagaagccag cagaggaagg aaatgattcg gaggaagtgc cagaagcatc 480

tggcccacaa aatgatggga aagagctgtg ccccccggga aaaccaacta cctctgagaa 540

gattcacgag agatctggac ccaaaagggg ggaacatgcc tggacccaca gactgcgtga 600

gagaaaacag ctggtgattt atgaagagat cagcgaccct gaggaagatg acgagtaact 660

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catgggcatg gctgcggacc cctcgtcatc aggtgcatag caagtg 766

<210> SEQ ID NO 14
<211> LENGTH: 4204
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 14

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gctcagccag gcatcaactt caggaccctg agggatgacc gaaggccccg cccacccacc 180

cccaactccc ccgaccccac caggatctac agcctcagga cccccgtccc aatccttacc 240

ccttgcccca tcaccatctt catgcttacc tccacccccа tccgatcccc atccaggcag 300

aatccagttc caccctgcc cggaacccag ggtagtaccg ttgccaggat gtgacgccac 360

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accccgccga cccccgccgc tttagccacg gggaactctg gggacagagc ttaatgtggc 660

cagggcaggg ctggttagaa gaggtcaggg cccacgctgt ggcaggaatc aaggtcagga 720

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gtgc 4204

<210> SEQ ID NO 15
<211> LENGTH: 752
<212> TYPE: DNA
<213> ORGANISM: Homo sapien

<400> SEQUENCE: 15

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ttcctgatgg cccaggggggc aatgctggcg gcccaggaga ggcgggtgcc acgggcggca 180

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<210> SEQ ID NO 16
<211> LENGTH: 1967
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

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Val Asp Ala Glu Gly Pro Val Val Glu Lys Ile Met Ser Ser Arg Ser
        35                  40                  45

Val Lys Lys Gln Lys Glu Ser Gly Glu Glu Val Glu Ile Glu Glu Phe
    50                  55                  60

Tyr Val Lys Tyr Lys Asn Phe Ser Tyr Leu His Cys Gln Trp Ala Ser
65                  70                  75                  80

Ile Glu Asp Leu Glu Lys Asp Lys Arg Ile Gln Gln Lys Ile Lys Arg
                85                  90                  95

Phe Lys Ala Lys Gln Gly Gln Asn Lys Phe Leu Ser Glu Ile Glu Asp
            100                 105                 110

Glu Leu Phe Asn Pro Asp Tyr Val Glu Val Asp Arg Ile Met Asp Phe
        115                 120                 125

Ala Arg Ser Thr Asp Asp Arg Gly Glu Pro Val Thr His Tyr Leu Val
    130                 135                 140

Lys Trp Cys Ser Leu Pro Tyr Glu Asp Ser Thr Trp Glu Arg Arg Gln
145                 150                 155                 160

Asp Ile Asp Gln Ala Lys Ile Glu Glu Phe Glu Lys Leu Met Ser Arg
                165                 170                 175

Glu Pro Glu Thr Glu Arg Val Glu Arg Pro Pro Ala Asp Asp Trp Lys
            180                 185                 190

Lys Ser Glu Ser Ser Arg Glu Tyr Lys Asn Asn Asn Lys Leu Arg Glu
        195                 200                 205

Tyr Gln Leu Glu Gly Val Asn Trp Leu Leu Phe Asn Trp Tyr Asn Met
    210                 215                 220

Arg Asn Cys Ile Leu Ala Asp Glu Met Gly Leu Gly Lys Thr Ile Gln
225                 230                 235                 240

Ser Ile Thr Phe Leu Tyr Glu Ile Tyr Leu Lys Gly Ile His Gly Pro
                245                 250                 255

Phe Leu Val Ile Ala Pro Leu Ser Thr Ile Pro Asn Trp Glu Arg Glu
            260                 265                 270

Phe Arg Thr Trp Thr Glu Leu Asn Val Val Val Tyr His Gly Ser Gln
        275                 280                 285

Ala Ser Arg Arg Thr Ile Gln Leu Tyr Glu Met Tyr Phe Lys Asp Pro
    290                 295                 300

Gln Gly Arg Val Ile Lys Gly Ser Tyr Lys Phe His Ala Ile Ile Thr
305                 310                 315                 320

Thr Phe Glu Met Ile Leu Thr Asp Cys Pro Glu Leu Arg Asn Ile Pro
                325                 330                 335

Trp Arg Cys Val Val Ile Asp Glu Ala His Arg Leu Lys Asn Arg Asn
            340                 345                 350

Cys Lys Leu Leu Glu Gly Leu Lys Met Met Asp Leu Glu His Lys Val
        355                 360                 365

Leu Leu Thr Gly Thr Pro Leu Gln Asn Thr Val Glu Glu Leu Phe Ser
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Leu Leu His Phe Leu Glu Pro Ser Arg Phe Pro Ser Glu Thr Thr Phe
385                 390                 395                 400
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Gln Ala Ile Leu Lys Pro Met Met Leu Arg Arg Leu Lys Glu Asp Val
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Glu Lys Asn Leu Ala Pro Lys Glu Glu Thr Ile Ile Glu Val Glu Leu
        435                 440                 445

Thr Asn Ile Gln Lys Lys Tyr Tyr Arg Ala Ile Leu Glu Lys Asn Phe
    450                 455                 460

Thr Phe Leu Ser Lys Gly Gly Gly Gln Ala Asn Val Pro Asn Leu Leu
465                 470                 475                 480

Asn Thr Met Met Glu Leu Arg Lys Cys Cys Asn His Pro Tyr Leu Ile
                485                 490                 495

Asn Gly Ala Glu Glu Lys Ile Leu Glu Glu Phe Lys Glu Thr His Asn
            500                 505                 510

Ala Glu Ser Pro Asp Phe Gln Leu Gln Ala Met Ile Gln Ala Ala Gly
        515                 520                 525

Lys Leu Val Leu Ile Asp Lys Leu Leu Pro Lys Leu Lys Ala Gly Gly
    530                 535                 540

His Arg Val Leu Ile Phe Ser Gln Met Val Arg Cys Leu Asp Ile Leu
545                 550                 555                 560

Glu Asp Tyr Leu Ile Gln Arg Arg Tyr Pro Tyr Glu Arg Ile Asp Gly
                565                 570                 575

Arg Val Arg Gly Asn Leu Arg Gln Ala Ala Ile Asp Arg Phe Ser Lys
            580                 585                 590

Pro Asp Ser Asp Arg Phe Val Phe Leu Leu Cys Thr Arg Ala Gly Gly
        595                 600                 605

Leu Gly Ile Asn Leu Thr Ala Ala Asp Thr Cys Ile Ile Phe Asp Ser
    610                 615                 620

Asp Trp Asn Pro Gln Asn Asp Leu Gln Ala Gln Ala Arg Cys His Arg
625                 630                 635                 640

Ile Gly Gln Ser Lys Ser Val Lys Ile Tyr Arg Leu Ile Thr Arg Asn
                645                 650                 655

Ser Tyr Glu Arg Glu Met Phe Asp Lys Ala Ser Leu Lys Leu Gly Leu
            660                 665                 670

Asp Lys Ala Val Leu Gln Ser Met Ser Gly Arg Glu Asn Ala Thr Asn
        675                 680                 685

Gly Val Gln Gln Leu Ser Lys Lys Glu Ile Glu Asp Leu Leu Arg Lys
    690                 695                 700

Gly Ala Tyr Gly Ala Leu Met Asp Glu Glu Asp Glu Gly Ser Lys Phe
705                 710                 715                 720

Cys Glu Glu Asp Ile Asp Gln Ile Leu Leu Arg Arg Thr His Thr Ile
                725                 730                 735

Thr Ile Glu Ser Glu Gly Lys Gly Ser Thr Phe Ala Lys Ala Ser Phe
            740                 745                 750

Val Ala Ser Gly Asn Arg Thr Asp Ile Ser Leu Asp Asp Pro Asn Phe
        755                 760                 765

Trp Gln Lys Trp Ala Lys Lys Ala Glu Leu Asp Ile Asp Ala Leu Asn
    770                 775                 780

Gly Arg Asn Asn Leu Val Ile Asp Thr Pro Arg Val Arg Lys Gln Thr
785                 790                 795                 800

Arg Leu Tyr Ser Ala Val Lys Glu Asp Glu Leu Met Glu Phe Ser Asp
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               805                 810                 815

Leu Glu Ser Asp Ser Glu Glu Lys Pro Cys Ala Lys Pro Arg Arg Pro
           820                 825                 830

Gln Asp Lys Ser Gln Gly Tyr Ala Arg Ser Glu Cys Phe Arg Val Glu
       835                 840                 845

Lys Asn Leu Leu Val Tyr Gly Trp Gly Arg Trp Thr Asp Ile Leu Ser
   850                 855                 860

His Gly Arg Tyr Lys Arg Gln Leu Thr Glu Gln Asp Val Glu Thr Ile
865                 870                 875                 880

Cys Arg Thr Ile Leu Val Tyr Cys Leu Asn His Tyr Lys Gly Asp Glu
               885                 890                 895

Asn Ile Lys Ser Phe Ile Trp Asp Leu Ile Thr Pro Thr Ala Asp Gly
           900                 905                 910

Gln Thr Arg Ala Leu Val Asn His Ser Gly Leu Ser Ala Pro Val Pro
       915                 920                 925

Arg Gly Arg Lys Gly Lys Lys Val Lys Ala Gln Ser Thr Gln Pro Val
   930                 935                 940

Val Gln Asp Ala Asp Trp Leu Ala Ser Cys Asn Pro Asp Ala Leu Phe
945                 950                 955                 960

Gln Glu Asp Ser Tyr Lys Lys His Leu Lys His His Cys Asn Lys Val
               965                 970                 975

Leu Leu Arg Val Arg Met Leu Tyr Tyr Leu Arg Gln Glu Val Ile Gly
           980                 985                 990

Asp Gln Ala Asp Lys Ile Leu Glu  Gly Ala Asp Ser Ser  Glu Ala Asp
       995                 1000                1005

Val Trp  Ile Pro Glu Pro Phe  His Ala Glu Val Pro  Ala Asp Trp
   1010                1015                1020

Trp Asp  Lys Glu Ala Asp Lys  Ser Leu Leu Ile Gly  Val Phe Lys
   1025                1030                1035

His Gly  Tyr Glu Lys Tyr Asn  Ser Met Arg Ala Asp  Pro Ala Leu
   1040                1045                1050

Cys Phe  Leu Glu Arg Val Gly  Met Pro Asp Ala Lys  Ala Ile Ala
   1055                1060                1065

Ala Glu  Gln Arg Gly Thr Asp  Met Leu Ala Asp Gly  Gly Asp Gly
   1070                1075                1080

Gly Glu  Phe Asp Arg Glu Asp  Glu Asp Pro Glu Tyr  Lys Pro Thr
   1085                1090                1095

Arg Thr  Pro Phe Lys Asp Glu  Ile Asp Glu Phe Ala  Asn Ser Pro
   1100                1105                1110

Ser Glu  Asp Lys Glu Glu Ser  Met Glu Ile His Ala  Thr Gly Lys
   1115                1120                1125

His Ser  Glu Ser Asn Ala Glu  Leu Gly Gln Leu Tyr  Trp Pro Asn
   1130                1135                1140

Thr Ser  Thr Leu Thr Thr Arg  Leu Arg Arg Leu Ile  Thr Ala Tyr
   1145                1150                1155

Gln Arg  Ser Tyr Lys Arg Gln  Gln Met Arg Gln Glu  Ala Leu Met
   1160                1165                1170

Lys Thr  Asp Arg Arg Arg Arg  Arg Pro Arg Glu Glu  Val Arg Ala
   1175                1180                1185

Leu Glu  Ala Glu Arg Glu Ala  Ile Ile Ser Glu Lys  Arg Gln Lys
   1190                1195                1200
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Trp Thr  Arg Arg Glu Glu Ala  Asp Phe Tyr Arg Val  Val Ser Thr
    1205                 1210                 1215

Phe Gly  Val Ile Phe Asp Pro  Val Lys Gln Gln Phe  Asp Trp Asn
    1220                 1225                 1230

Gln Phe  Arg Ala Phe Ala Arg  Leu Asp Lys Lys Ser  Asp Glu Ser
    1235                 1240                 1245

Leu Glu  Lys Tyr Phe Ser Cys  Phe Val Ala Met Cys  Arg Arg Val
    1250                 1255                 1260

Cys Arg  Met Pro Val Lys Pro  Asp Asp Glu Pro Pro  Asp Leu Ser
    1265                 1270                 1275

Ser Ile  Ile Glu Pro Ile Thr  Glu Glu Arg Ala Ser  Arg Thr Leu
    1280                 1285                 1290

Tyr Arg  Ile Glu Leu Leu Arg  Lys Ile Arg Glu Gln  Val Leu His
    1295                 1300                 1305

His Pro  Gln Leu Gly Glu Arg  Leu Lys Leu Cys Gln  Pro Ser Leu
    1310                 1315                 1320

Asp Leu  Pro Glu Trp Trp Glu  Cys Gly Arg His Asp  Arg Asp Leu
    1325                 1330                 1335

Leu Val  Gly Ala Ala Lys His  Gly Val Ser Arg Thr  Asp Tyr His
    1340                 1345                 1350

Ile Leu  Asn Asp Pro Glu Leu  Ser Phe Leu Asp Ala  His Lys Asn
    1355                 1360                 1365

Phe Ala  Gln Asn Arg Gly Ala  Gly Asn Thr Ser Ser  Leu Asn Pro
    1370                 1375                 1380

Leu Ala  Val Gly Phe Val Gln  Thr Pro Pro Val Ile  Ser Ser Ala
    1385                 1390                 1395

His Ile  Gln Asp Glu Arg Val  Leu Glu Gln Ala Glu  Gly Lys Val
    1400                 1405                 1410

Glu Glu  Pro Glu Asn Pro Ala  Ala Lys Glu Lys Cys  Glu Gly Lys
    1415                 1420                 1425

Glu Glu  Glu Glu Glu Thr Asp  Gly Ser Gly Lys Glu  Ser Lys Gln
    1430                 1435                 1440

Glu Cys  Glu Ala Glu Ala Ser  Ser Val Lys Asn Glu  Leu Lys Gly
    1445                 1450                 1455

Val Glu  Val Gly Ala Asp Thr  Gly Ser Lys Ser Ile  Ser Glu Lys
    1460                 1465                 1470

Gly Ser  Glu Glu Asp Glu Glu  Glu Lys Leu Glu Asp  Asp Asp Lys
    1475                 1480                 1485

Ser Glu  Glu Ser Ser Gln Pro  Glu Ala Gly Ala Val  Ser Arg Gly
    1490                 1495                 1500

Lys Asn  Phe Asp Glu Glu Ser  Asn Ala Ser Met Ser  Thr Ala Arg
    1505                 1510                 1515

Asp Glu  Thr Arg Asp Gly Phe  Tyr Met Glu Asp Gly  Asp Pro Ser
    1520                 1525                 1530

Val Ala  Gln Leu Leu His Glu  Arg Thr Phe Ala Phe  Ser Phe Trp
    1535                 1540                 1545

Pro Lys  Asp Arg Val Met Ile  Asn Arg Leu Asp Asn  Ile Cys Glu
    1550                 1555                 1560

Ala Val  Leu Lys Gly Lys Trp  Pro Val Asn Arg Arg  Gln Met Phe
    1565                 1570                 1575
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Asp Phe  Gln Gly Leu Ile Pro  Gly Tyr Thr Pro Thr  Thr Val Asp
    1580                1585                1590

Ser Pro  Leu Gln Lys Arg Ser  Phe Ala Glu Leu Ser  Met Val Gly
    1595                1600                1605

Gln Ala  Ser Ile Ser Gly Ser  Glu Asp Ile Thr Thr  Ser Pro Gln
    1610                1615                1620

Leu Ser  Lys Glu Asp Ala Leu  Asn Leu Ser Val Pro  Arg Gln Arg
    1625                1630                1635

Arg Arg  Arg Arg Arg Lys Ile  Glu Ile Glu Ala Glu  Arg Ala Ala
    1640                1645                1650

Lys Arg  Arg Asn Leu Met Glu  Met Val Ala Gln Leu  Arg Glu Ser
    1655                1660                1665

Gln Val  Val Ser Glu Asn Gly  Gln Glu Lys Val Val  Asp Leu Ser
    1670                1675                1680

Lys Ala  Ser Arg Glu Ala Thr  Ser Ser Thr Ser Asn  Phe Ser Ser
    1685                1690                1695

Leu Ser  Ser Lys Phe Ile Leu  Pro Asn Val Ser Thr  Pro Val Ser
    1700                1705                1710

Asp Ala  Phe Lys Thr Gln Met  Glu Leu Leu Gln Ala  Gly Leu Ser
    1715                1720                1725

Arg Thr  Pro Thr Arg His Leu  Leu Asn Gly Ser Leu  Val Asp Gly
    1730                1735                1740

Glu Pro  Pro Met Lys Arg Arg  Arg Gly Arg Arg Lys  Asn Val Glu
    1745                1750                1755

Gly Leu  Asp Leu Leu Phe Met  Ser His Lys Arg Thr  Ser Leu Ser
    1760                1765                1770

Ala Glu  Asp Ala Glu Val Thr  Lys Ala Phe Glu Glu  Asp Ile Glu
    1775                1780                1785

Thr Pro  Pro Thr Arg Asn Ile  Pro Ser Pro Gly Gln  Leu Asp Pro
    1790                1795                1800

Asp Thr  Arg Ile Pro Val Ile  Asn Leu Glu Asp Gly  Thr Arg Leu
    1805                1810                1815

Val Gly  Glu Asp Ala Pro Lys  Asn Lys Asp Leu Val  Glu Trp Leu
    1820                1825                1830

Lys Leu  His Pro Thr Tyr Thr  Val Asp Met Pro Ser  Tyr Val Pro
    1835                1840                1845

Lys Asn  Ala Asp Val Leu Phe  Ser Ser Phe Gln Lys  Pro Lys Gln
    1850                1855                1860

Lys Arg  His Arg Cys Arg Asn  Pro Asn Lys Leu Asp  Ile Asn Thr
    1865                1870                1875

Leu Thr  Gly Glu Glu Arg Val  Pro Val Val Asn Lys  Arg Asn Gly
    1880                1885                1890

Lys Lys  Met Gly Gly Ala Met  Ala Pro Pro Met Lys  Asp Leu Pro
    1895                1900                1905

Arg Trp  Leu Glu Glu Asn Pro  Glu Phe Ala Val Ala  Pro Asp Trp
    1910                1915                1920

Thr Asp  Ile Val Lys Gln Ser  Gly Phe Val Pro Glu  Ser Met Phe
    1925                1930                1935

Asp Arg  Leu Leu Thr Gly Pro  Val Val Arg Gly Glu  Gly Ala Ser
    1940                1945                1950

Arg Arg  Gly Arg Arg Pro Lys  Ser Glu Ile Ala Arg  Ala Ala
```

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1955 1960 1965

<210> SEQ ID NO 17
<211> LENGTH: 109
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: (84)..(84)
<223> OTHER INFORMATION: x = any amino acid
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: (100)..(100)
<223> OTHER INFORMATION: x = any amino acid

<400> SEQUENCE: 17

Arg Pro Ser Leu Pro Arg Ala Leu Pro Ala Ala Pro His Glu Arg Ser
1 5 10 15

Pro Ala Arg Pro Gly Ser Val Gly Gly Gly Ala Pro Pro Met Leu Leu
20 25 30

Gln Pro Ala Pro Cys Ala Pro Ser Ala Gly Phe Pro Arg Pro Leu Ala
35 40 45

Ala Pro Gly Ala Met His Leu Phe Ala Glu Gly His His Val His Gln
50 55 60

Asp Leu Arg Gly Arg Pro Ala Val Pro His Tyr Arg Arg Leu Ala Gln
65 70 75 80

Glu Val Leu Xaa Gly Leu Arg Arg His Leu Arg Arg Pro Trp Ser Ser
85 90 95

Pro Thr Ala Xaa Arg Ala Ser Pro Ala Ala Thr Ala Ser
100 105

<210> SEQ ID NO 18
<211> LENGTH: 897
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

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

His Ser Leu Pro Gln His Pro Lys Cys Trp Gly Ala His His Ala Ser
20 25 30

Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Pro Pro Gly Thr Pro Pro
35 40 45

Ser Tyr Lys Leu Pro Leu Pro Gly Pro Tyr Asp Ser Arg Asp Asp Phe
50 55 60

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

Leu Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg
85 90 95

Lys Asp Gly Thr Val Ile Ser Thr Phe Lys Lys Arg Ala Val Glu Ile
100 105 110

Thr Gly Ala Gly Pro Gly Ala Ser Ser Val Cys Asn Ser Ala Pro Gly
115 120 125

Ser Gly Pro Ser Ser Pro Asn Ser Ser His Ser Thr Ile Ala Glu Asn
130 135 140

Gly Phe Thr Gly Ser Val Pro Asn Ile Pro Thr Glu Met Leu Pro Gln
145 150 155 160

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His Arg Ala Leu Pro Leu Asp Ser Ser Pro Asn Gln Phe Ser Leu Tyr
                165                 170                 175

Thr Ser Pro Ser Leu Pro Asn Ile Ser Leu Gly Leu Gln Ala Thr Val
            180                 185                 190

Thr Val Thr Asn Ser His Leu Thr Ala Ser Pro Lys Leu Ser Thr Gln
        195                 200                 205

Gln Glu Ala Glu Arg Gln Ala Leu Gln Ser Leu Arg Gln Gly Gly Thr
    210                 215                 220

Leu Thr Gly Lys Phe Met Ser Thr Ser Ser Ile Pro Gly Cys Leu Leu
225                 230                 235                 240

Gly Val Ala Leu Glu Gly Asp Gly Ser Pro His Gly His Ala Ser Leu
                245                 250                 255

Leu Gln His Val Leu Leu Leu Glu Gln Ala Arg Gln Gln Ser Thr Leu
            260                 265                 270

Ile Ala Val Pro Leu His Gly Gln Ser Pro Leu Val Thr Gly Glu Arg
        275                 280                 285

Val Ala Thr Ser Met Arg Thr Val Gly Lys Leu Pro Arg His Arg Pro
    290                 295                 300

Leu Ser Arg Thr Gln Ser Ser Pro Leu Pro Gln Ser Pro Gln Ala Leu
305                 310                 315                 320

Gln Gln Leu Val Met Gln Gln Gln His Gln Gln Phe Leu Glu Lys Gln
                325                 330                 335

Lys Gln Gln Gln Leu Gln Leu Gly Lys Ile Leu Thr Lys Thr Gly Glu
            340                 345                 350

Leu Pro Arg Gln Pro Thr Thr His Pro Glu Glu Thr Glu Glu Glu Leu
        355                 360                 365

Thr Glu Gln Gln Glu Val Leu Leu Gly Glu Gly Ala Leu Thr Met Pro
    370                 375                 380

Arg Glu Gly Ser Thr Glu Ser Glu Ser Thr Gln Glu Asp Leu Glu Glu
385                 390                 395                 400

Glu Asp Glu Glu Glu Asp Gly Glu Glu Glu Glu Asp Cys Ile Gln Val
                405                 410                 415

Lys Asp Glu Glu Gly Glu Ser Gly Ala Glu Glu Gly Pro Asp Leu Glu
            420                 425                 430

Glu Pro Gly Ala Gly Tyr Lys Lys Leu Phe Ser Asp Ala Gln Pro Leu
        435                 440                 445

Gln Pro Leu Gln Val Tyr Gln Ala Pro Leu Ser Leu Ala Thr Val Pro
    450                 455                 460

His Gln Ala Leu Gly Arg Thr Gln Ser Ser Pro Ala Ala Pro Gly Gly
465                 470                 475                 480

Met Lys Asn Pro Pro Asp Gln Pro Val Lys His Leu Phe Thr Thr Ser
                485                 490                 495

Val Val Tyr Asp Thr Phe Met Leu Lys His Gln Cys Met Cys Gly Asn
            500                 505                 510

Thr His Val His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser
        515                 520                 525

Arg Leu Gln Glu Thr Gly Leu Leu Ser Lys Cys Glu Arg Ile Arg Gly
    530                 535                 540

Arg Lys Ala Thr Leu Asp Glu Ile Gln Thr Val His Ser Glu Tyr His
545                 550                 555                 560
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Thr Leu Leu Tyr Gly Thr Ser Pro Leu Asn Arg Gln Lys Leu Asp Ser
                565                 570                 575

Lys Lys Leu Leu Gly Pro Ile Ser Gln Lys Met Tyr Ala Val Leu Pro
            580                 585                 590

Cys Gly Gly Ile Gly Val Asp Ser Asp Thr Val Trp Asn Glu Met His
        595                 600                 605

Ser Ser Ser Ala Val Arg Met Ala Val Gly Cys Leu Leu Glu Leu Ala
    610                 615                 620

Phe Lys Val Ala Ala Gly Glu Leu Lys Asn Gly Phe Ala Ile Ile Arg
625                 630                 635                 640

Pro Pro Gly His His Ala Glu Glu Ser Thr Ala Met Gly Phe Cys Phe
                645                 650                 655

Phe Asn Ser Val Ala Ile Thr Ala Lys Leu Leu Gln Gln Lys Leu Asn
            660                 665                 670

Val Gly Lys Val Leu Ile Val Asp Trp Asp Ile His His Gly Asn Gly
        675                 680                 685

Thr Gln Gln Ala Phe Tyr Asn Asp Pro Ser Val Leu Tyr Ile Ser Leu
    690                 695                 700

His Arg Tyr Asp Asn Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Glu
705                 710                 715                 720

Glu Val Gly Gly Gly Pro Gly Val Gly Tyr Asn Val Asn Val Ala Trp
                725                 730                 735

Thr Gly Gly Val Asp Pro Pro Ile Gly Asp Val Glu Tyr Leu Thr Ala
            740                 745                 750

Phe Arg Thr Val Val Met Pro Ile Ala His Glu Phe Ser Pro Asp Val
        755                 760                 765

Val Leu Val Ser Ala Gly Phe Asp Ala Val Glu Gly His Leu Ser Pro
    770                 775                 780

Leu Gly Gly Tyr Ser Val Thr Ala Arg Cys Phe Gly His Leu Thr Arg
785                 790                 795                 800

Gln Leu Met Thr Leu Ala Gly Gly Arg Val Val Leu Ala Leu Glu Gly
                805                 810                 815

Gly His Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser
            820                 825                 830

Ala Leu Leu Ser Val Lys Leu Gln Pro Leu Asp Glu Ala Val Leu Gln
        835                 840                 845

Gln Lys Pro Asn Ile Asn Ala Val Ala Thr Leu Glu Lys Val Ile Glu
    850                 855                 860

Ile Gln Ser Lys His Trp Ser Cys Val Gln Lys Phe Ala Ala Gly Leu
865                 870                 875                 880

Gly Arg Ser Leu Arg Gly Ala Gln Ala Gly Glu Thr Glu Glu Ala Glu
                885                 890                 895

Met
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<210> SEQ ID NO 19
<211> LENGTH: 890
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

```
Met Phe Asp Tyr Met Asp Cys Glu Leu Lys Leu Ser Glu Ser Val Phe
1               5                   10                  15
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Arg Gln Leu Asn Thr Ala Ile Ala Val Ser Gln Met Ser Ser Gly Gln
            20                  25                  30

Cys Arg Leu Ala Pro Leu Ile Gln Val Ile Gln Asp Cys Ser His Leu
        35                  40                  45

Tyr His Tyr Thr Val Lys Leu Leu Phe Lys Leu His Ser Cys Leu Pro
    50                  55                  60

Ala Asp Thr Leu Gln Gly His Arg Asp Arg Phe His Glu Gln Phe His
65                  70                  75                  80

Ser Leu Arg Asn Phe Phe Arg Arg Ala Ser Asp Met Leu Tyr Phe Lys
                85                  90                  95

Arg Leu Ile Gln Ile Pro Arg Leu Pro Glu Gly Pro Pro Asn Phe Leu
            100                 105                 110

Arg Ala Ser Ala Leu Ala Glu His Ile Lys Pro Val Val Val Ile Pro
        115                 120                 125

Glu Glu Ala Pro Glu Asp Glu Glu Pro Glu Asn Leu Ile Glu Ile Ser
    130                 135                 140

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

Gln Thr Phe Gly Pro Pro Asn Gly Ser Val Lys Asp Asp Arg Asp Leu
                165                 170                 175

Gln Ile Glu Ser Leu Lys Arg Glu Val Glu Met Leu Arg Ser Glu Leu
            180                 185                 190

Glu Lys Ile Lys Leu Glu Ala Gln Arg Tyr Ile Ala Gln Leu Lys Ser
        195                 200                 205

Gln Val Asn Ala Leu Glu Gly Glu Leu Glu Glu Gln Arg Lys Gln Lys
    210                 215                 220

Gln Lys Ala Leu Val Asp Asn Glu Gln Leu Arg His Glu Leu Ala Gln
225                 230                 235                 240

Leu Arg Ala Ala Gln Leu Glu Gly Glu Arg Ser Gln Gly Leu Arg Glu
                245                 250                 255

Glu Ala Glu Arg Lys Ala Ser Ala Thr Glu Ala Arg Tyr Asn Lys Leu
            260                 265                 270

Lys Glu Lys His Ser Glu Leu Val His Val His Ala Glu Leu Leu Arg
        275                 280                 285

Lys Asn Ala Asp Thr Ala Lys Gln Leu Thr Val Thr Gln Gln Ser Gln
    290                 295                 300

Glu Glu Val Ala Arg Val Lys Glu Gln Leu Ala Phe Gln Val Glu Gln
305                 310                 315                 320

Val Lys Arg Glu Ser Glu Leu Lys Leu Glu Glu Lys Ser Asp Gln Leu
                325                 330                 335

Glu Lys Leu Lys Arg Glu Leu Glu Ala Lys Ala Gly Glu Leu Ala Arg
            340                 345                 350

Ala Gln Glu Ala Leu Ser His Thr Glu Gln Ser Lys Ser Glu Leu Ser
        355                 360                 365

Ser Arg Leu Asp Thr Leu Ser Ala Glu Lys Asp Ala Leu Ser Gly Ala
    370                 375                 380

Val Arg Gln Arg Glu Ala Asp Leu Leu Ala Ala Gln Ser Leu Val Arg
385                 390                 395                 400

Glu Thr Glu Ala Ala Leu Ser Arg Glu Gln Gln Arg Ser Ser Gln Glu
                405                 410                 415

Gln Gly Glu Leu Gln Gly Arg Leu Ala Glu Arg Glu Ser Gln Glu Gln
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            420                 425                 430

Gly Leu Arg Gln Arg Leu Leu Asp Glu Gln Phe Ala Val Leu Arg Gly
        435                 440                 445

Ala Ala Ala Glu Ala Ala Gly Ile Leu Gln Asp Ala Val Ser Lys Leu
    450                 455                 460

Asp Asp Pro Leu His Leu Arg Cys Thr Ser Ser Pro Asp Tyr Leu Val
465                 470                 475                 480

Ser Arg Ala Gln Glu Ala Leu Asp Ala Val Ser Thr Leu Glu Glu Gly
                485                 490                 495

His Ala Gln Tyr Leu Thr Ser Leu Ala Asp Ala Ser Ala Leu Val Ala
            500                 505                 510

Ala Leu Thr Arg Phe Ser His Leu Ala Ala Asp Thr Ile Ile Asn Gly
        515                 520                 525

Gly Ala Thr Ser His Leu Ala Pro Thr Asp Pro Ala Asp Arg Leu Ile
    530                 535                 540

Asp Thr Cys Arg Glu Cys Gly Ala Arg Ala Leu Glu Leu Met Gly Gln
545                 550                 555                 560

Leu Gln Asp Gln Gln Ala Leu Arg His Met Gln Ala Ser Leu Val Arg
                565                 570                 575

Thr Pro Leu Gln Gly Ile Leu Gln Leu Gly Gln Glu Leu Lys Pro Lys
            580                 585                 590

Ser Leu Asp Val Arg Gln Glu Glu Leu Gly Ala Val Val Asp Lys Glu
        595                 600                 605

Met Ala Ala Thr Ser Ala Ala Ile Glu Asp Ala Val Arg Arg Ile Glu
    610                 615                 620

Asp Met Met Asn Gln Ala Arg His Ala Ser Ser Gly Val Lys Leu Glu
625                 630                 635                 640

Val Asn Glu Arg Ile Leu Asn Ser Cys Thr Asp Leu Met Lys Ala Ile
                645                 650                 655

Arg Leu Leu Val Thr Thr Ser Thr Ser Leu Gln Lys Glu Ile Val Glu
            660                 665                 670

Ser Gly Arg Gly Ala Ala Thr Gln Gln Glu Phe Tyr Ala Lys Asn Ser
        675                 680                 685

Arg Trp Thr Glu Gly Leu Ile Ser Ala Ser Lys Ala Val Gly Trp Gly
    690                 695                 700

Ala Thr Gln Leu Val Glu Ala Ala Asp Lys Val Val Leu His Thr Gly
705                 710                 715                 720

Lys Tyr Glu Glu Leu Ile Val Cys Ser His Glu Ile Ala Ala Ser Thr
                725                 730                 735

Ala Gln Leu Val Ala Ala Ser Lys Val Lys Ala Asn Lys His Ser Pro
            740                 745                 750

His Leu Ser Arg Leu Gln Glu Cys Ser Arg Thr Val Asn Glu Arg Ala
        755                 760                 765

Ala Asn Val Val Ala Ser Thr Lys Ser Gly Gln Glu Gln Ile Glu Asp
    770                 775                 780

Arg Asp Thr Met Asp Phe Ser Gly Leu Ser Leu Ile Lys Leu Lys Lys
785                 790                 795                 800

Gln Glu Met Glu Thr Gln Val Arg Val Leu Glu Leu Glu Lys Thr Leu
                805                 810                 815

Glu Ala Glu Arg Met Arg Leu Gly Glu Leu Arg Lys Gln His Tyr Val
            820                 825                 830
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```
Leu Ala Gly Ala Ser Gly Ser Pro Gly Glu Glu Val Ala Ile Arg Pro
        835                 840                 845

Ser Thr Ala Pro Arg Ser Val Thr Thr Lys Lys Pro Pro Leu Ala Gln
    850                 855                 860

Lys Pro Ser Val Ala Pro Arg Gln Asp His Gln Leu Asp Lys Lys Asp
865                 870                 875                 880

Gly Ile Tyr Pro Ala Gln Leu Val Asn Tyr
                885                 890


<210> SEQ ID NO 20
<211> LENGTH: 725
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

Met Ala Met Asp Ser Ser Leu Gln Ala Arg Leu Phe Pro Gly Leu Ala
1               5                   10                  15

Ile Lys Ile Gln Arg Ser Asn Gly Leu Ile His Ser Ala Asn Val Arg
            20                  25                  30

Thr Val Asn Leu Glu Lys Ser Cys Val Ser Val Glu Trp Ala Glu Gly
        35                  40                  45

Gly Ala Thr Lys Gly Lys Glu Ile Asp Phe Asp Asp Val Ala Ala Ile
    50                  55                  60

Asn Pro Glu Leu Leu Gln Leu Leu Pro Leu His Pro Lys Asp Asn Leu
65                  70                  75                  80

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

Asn Ser Lys Ile Pro Ala Pro Lys Glu Ser Leu Arg Ser Arg Ser Thr
            100                 105                 110

Arg Met Ser Thr Val Ser Glu Leu Arg Ile Thr Ala Gln Glu Asn Asp
        115                 120                 125

Met Glu Val Glu Leu Pro Ala Ala Ala Asn Ser Arg Lys Gln Phe Ser
    130                 135                 140

Val Pro Pro Ala Pro Thr Arg Pro Ser Cys Pro Ala Val Ala Glu Ile
145                 150                 155                 160

Pro Leu Arg Met Val Ser Glu Glu Met Glu Glu Gln Val His Ser Ile
                165                 170                 175

Arg Gly Ser Ser Ser Ala Asn Pro Val Asn Ser Val Arg Arg Lys Ser
            180                 185                 190

Cys Leu Val Lys Glu Val Glu Lys Met Lys Asn Lys Arg Glu Glu Lys
        195                 200                 205

Lys Ala Gln Asn Ser Glu Met Arg Met Lys Arg Ala Gln Glu Tyr Asp
    210                 215                 220

Ser Ser Phe Pro Asn Trp Glu Phe Ala Arg Met Ile Lys Glu Phe Arg
225                 230                 235                 240

Ala Thr Leu Glu Cys His Pro Leu Thr Met Thr Asp Pro Ile Glu Glu
                245                 250                 255

His Arg Ile Cys Val Cys Val Arg Lys Arg Pro Leu Asn Lys Gln Glu
            260                 265                 270

Leu Ala Lys Lys Glu Ile Asp Val Ile Ser Ile Pro Ser Lys Cys Leu
        275                 280                 285

Leu Leu Val His Glu Pro Lys Leu Lys Val Asp Leu Thr Lys Tyr Leu
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-continued

```
    290                 295                 300

Glu Asn Gln Ala Phe Cys Phe Asp Phe Ala Phe Asp Glu Thr Ala Ser
305                 310                 315                 320

Asn Glu Val Val Tyr Arg Phe Thr Ala Arg Pro Leu Val Gln Thr Ile
                325                 330                 335

Phe Glu Gly Gly Lys Ala Thr Cys Phe Ala Tyr Gly Gln Thr Gly Ser
            340                 345                 350

Gly Lys Thr His Thr Met Gly Gly Asp Leu Ser Gly Lys Ala Gln Asn
        355                 360                 365

Ala Ser Lys Gly Ile Tyr Ala Met Ala Ser Arg Asp Val Phe Leu Leu
    370                 375                 380

Lys Asn Gln Pro Cys Tyr Arg Lys Leu Gly Leu Glu Val Tyr Val Thr
385                 390                 395                 400

Phe Phe Glu Ile Tyr Asn Gly Lys Leu Phe Asp Leu Leu Asn Lys Lys
                405                 410                 415

Ala Lys Leu Arg Val Leu Glu Asp Gly Lys Gln Gln Val Gln Val Val
            420                 425                 430

Gly Leu Gln Glu His Leu Val Asn Ser Ala Asp Asp Val Ile Lys Met
        435                 440                 445

Leu Asp Met Gly Ser Ala Cys Arg Thr Ser Gly Gln Thr Phe Ala Asn
    450                 455                 460

Ser Asn Ser Ser Arg Ser His Ala Cys Phe Gln Ile Ile Leu Arg Ala
465                 470                 475                 480

Lys Gly Arg Met His Gly Lys Phe Ser Leu Val Asp Leu Ala Gly Asn
                485                 490                 495

Glu Arg Gly Ala Asp Thr Ser Ser Ala Asp Arg Gln Thr Arg Met Glu
            500                 505                 510

Gly Ala Glu Ile Asn Lys Ser Leu Leu Ala Leu Lys Glu Cys Ile Arg
        515                 520                 525

Ala Leu Gly Gln Asn Lys Ala His Thr Pro Phe Arg Glu Ser Lys Leu
    530                 535                 540

Thr Gln Val Leu Arg Asp Ser Phe Ile Gly Glu Asn Ser Arg Thr Cys
545                 550                 555                 560

Met Ile Ala Thr Ile Ser Pro Gly Ile Ser Ser Cys Glu Tyr Thr Leu
                565                 570                 575

Asn Thr Leu Arg Tyr Ala Asp Arg Val Lys Glu Leu Ser Pro His Ser
            580                 585                 590

Gly Pro Ser Gly Glu Gln Leu Ile Gln Met Glu Thr Glu Glu Met Glu
        595                 600                 605

Ala Cys Ser Asn Gly Ala Leu Ile Pro Gly Asn Leu Ser Lys Glu Glu
    610                 615                 620

Glu Glu Leu Ser Ser Gln Met Ser Ser Phe Asn Glu Ala Met Thr Gln
625                 630                 635                 640

Ile Arg Glu Leu Glu Glu Lys Ala Met Glu Glu Leu Lys Glu Ile Ile
                645                 650                 655

Gln Gln Gly Pro Asp Trp Leu Glu Leu Ser Glu Met Thr Glu Gln Pro
            660                 665                 670

Asp Tyr Asp Leu Glu Thr Phe Val Asn Lys Ala Glu Ser Ala Leu Ala
        675                 680                 685

Gln Gln Ala Lys His Phe Ser Ala Leu Arg Asp Val Ile Lys Ala Leu
    690                 695                 700
```

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```
Arg Leu Ala Met Gln Leu Glu Glu Gln Ala Ser Arg Gln Ile Ser Ser
705                 710                 715                 720

Lys Lys Arg Pro Gln
                725
```

<210> SEQ ID NO 21
<211> LENGTH: 752
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

```
Arg Val Lys Ala Thr Leu Ser Glu Arg Lys Ile Gly Asp Ser Cys Asp
1               5                   10                  15

Lys Asp Leu Pro Leu Lys Phe Cys Glu Phe Pro Gln Lys Thr Ile Met
            20                  25                  30

Pro Gly Phe Lys Thr Thr Val Tyr Val Ser His Ile Asn Asp Leu Ser
        35                  40                  45

Asp Phe Tyr Val Gln Leu Ile Glu Asp Glu Ala Glu Ile Ser His Leu
    50                  55                  60

Ser Glu Arg Leu Asn Ser Val Lys Thr Arg Pro Glu Tyr Tyr Val Gly
65                  70                  75                  80

Pro Pro Leu Gln Arg Gly Asp Met Ile Cys Ala Val Phe Pro Glu Asp
                85                  90                  95

Asn Leu Trp Tyr Arg Ala Val Ile Lys Glu Gln Gln Pro Asn Asp Leu
            100                 105                 110

Leu Ser Val Gln Phe Ile Asp Tyr Gly Asn Val Ser Val Val His Thr
        115                 120                 125

Asn Lys Ile Gly Arg Leu Asp Leu Val Asn Ala Ile Leu Pro Gly Leu
    130                 135                 140

Cys Ile His Cys Ser Leu Gln Gly Phe Glu Val Pro Asp Asn Lys Asn
145                 150                 155                 160

Ser Lys Lys Met Met His Tyr Phe Ser Gln Arg Thr Ser Glu Ala Ala
                165                 170                 175

Ile Arg Cys Glu Phe Val Lys Phe Gln Asp Arg Trp Glu Val Ile Leu
            180                 185                 190

Ala Asp Glu His Gly Ile Ile Ala Asp Asp Met Ile Ser Arg Tyr Ala
        195                 200                 205

Leu Ser Glu Lys Ser Gln Val Glu Leu Ser Thr Gln Val Ile Lys Ser
    210                 215                 220

Ala Ser Ser Lys Ser Val Asn Lys Ser Asp Ile Asp Thr Ser Val Phe
225                 230                 235                 240

Leu Asn Trp Tyr Asn Pro Glu Lys Lys Met Ile Arg Ala Tyr Ala Thr
                245                 250                 255

Val Ile Asp Gly Pro Glu Tyr Phe Trp Cys Gln Phe Ala Asp Thr Glu
            260                 265                 270

Lys Leu Gln Cys Leu Glu Val Glu Val Gln Thr Ala Gly Glu Gln Val
        275                 280                 285

Ala Asp Arg Arg Asn Cys Ile Pro Cys Pro Tyr Ile Gly Asp Pro Cys
    290                 295                 300

Ile Val Arg Tyr Arg Glu Asp Gly His Tyr Tyr Arg Ala Leu Ile Thr
305                 310                 315                 320

Asn Ile Cys Glu Asp Tyr Leu Val Ser Val Arg Leu Val Asp Phe Gly
```

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```
                325                 330                 335

Asn Ile Glu Asp Cys Val Asp Pro Lys Ala Leu Trp Ala Ile Pro Ser
            340                 345                 350

Glu Leu Leu Ser Val Pro Met Gln Ala Phe Pro Cys Cys Leu Ser Gly
        355                 360                 365

Phe Asn Ile Ser Glu Gly Leu Cys Ser Gln Glu Gly Asn Asp Tyr Phe
    370                 375                 380

Tyr Glu Ile Ile Thr Glu Asp Val Leu Glu Ile Thr Ile Leu Glu Ile
385                 390                 395                 400

Arg Arg Asp Val Cys Asp Ile Pro Leu Ala Ile Val Asp Leu Lys Ser
                405                 410                 415

Lys Gly Lys Ser Ile Asn Glu Lys Met Glu Lys Tyr Ser Lys Thr Gly
            420                 425                 430

Ile Lys Ser Ala Leu Pro Tyr Glu Asn Ile Asp Ser Glu Ile Lys Gln
        435                 440                 445

Thr Leu Gly Ser Tyr Asn Leu Asp Val Gly Leu Lys Lys Leu Ser Asn
    450                 455                 460

Lys Ala Val Gln Asn Lys Ile Tyr Met Glu Gln Gln Thr Asp Glu Leu
465                 470                 475                 480

Ala Glu Ile Thr Glu Lys Asp Val Asn Ile Ile Gly Thr Lys Pro Ser
                485                 490                 495

Asn Phe Arg Asp Pro Lys Thr Asp Asn Ile Cys Glu Gly Phe Glu Asn
            500                 505                 510

Pro Cys Lys Asp Lys Ile Asp Thr Glu Glu Leu Glu Gly Glu Leu Glu
        515                 520                 525

Cys His Leu Val Asp Lys Ala Glu Phe Asp Asp Lys Tyr Leu Ile Thr
    530                 535                 540

Gly Phe Asn Thr Leu Leu Pro His Ala Asn Glu Thr Lys Glu Ile Leu
545                 550                 555                 560

Glu Leu Asn Ser Leu Glu Val Pro Leu Ser Pro Asp Asp Glu Ser Lys
                565                 570                 575

Glu Phe Leu Glu Leu Glu Ser Ile Glu Leu Gln Asn Ser Leu Val Val
            580                 585                 590

Asp Glu Glu Lys Gly Glu Leu Ser Pro Val Pro Pro Asn Val Pro Leu
        595                 600                 605

Ser Gln Glu Cys Val Thr Lys Gly Ala Met Glu Leu Phe Thr Leu Gln
    610                 615                 620

Leu Pro Leu Ser Cys Glu Ala Glu Lys Gln Pro Glu Leu Glu Leu Pro
625                 630                 635                 640

Thr Ala Gln Leu Pro Leu Asp Asp Lys Met Asp Pro Leu Ser Leu Gly
                645                 650                 655

Val Ser Gln Lys Ala Gln Glu Ser Met Cys Thr Glu Asp Met Arg Lys
            660                 665                 670

Ser Ser Cys Val Glu Ser Phe Asp Asp Gln Arg Arg Met Ser Leu His
        675                 680                 685

Leu His Gly Ala Asp Cys Asp Pro Lys Thr Gln Asn Glu Met Asn Ile
    690                 695                 700

Cys Glu Glu Glu Phe Val Glu Tyr Lys Asn Arg Asp Ala Ile Ser Ala
705                 710                 715                 720

Leu Met Pro Phe Ser Leu Arg Lys Lys Ala Val Met Glu Ala Ser Thr
                725                 730                 735
```

-continued

Ile Met Val Tyr Gln Ile Ile Phe Gln Asn Tyr Arg Thr Pro Thr Leu
740 745 750

<210> SEQ ID NO 22
<211> LENGTH: 286
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Ala Glu Val Lys Thr Pro Phe Asp Leu Ala Lys Ala Gln Glu Asn Ser
1 5 10 15

Asn Ser Val Lys Lys Lys Thr Lys Phe Val Asn Leu Tyr Thr Arg Glu
20 25 30

Arg Gln Asp Arg Leu Ala Val Leu Leu Pro Gly Arg His Pro Cys Asp
35 40 45

Cys Leu Gly Gln Lys His Lys Leu Ile Asn Asn Cys Leu Ile Cys Gly
50 55 60

Arg Ile Val Cys Glu Gln Glu Gly Ser Gly Pro Cys Leu Phe Cys Gly
65 70 75 80

Thr Leu Val Cys Thr His Glu Glu Gln Asp Ile Leu Gln Arg Asp Ser
85 90 95

Asn Lys Ser Gln Lys Leu Leu Lys Lys Leu Met Ser Gly Val Glu Asn
100 105 110

Ser Gly Lys Val Asp Ile Ser Thr Lys Asp Leu Leu Pro His Gln Glu
115 120 125

Leu Arg Ile Lys Ser Gly Leu Glu Lys Ala Ile Lys His Lys Asp Lys
130 135 140

Leu Leu Glu Phe Asp Arg Thr Ser Ile Arg Arg Thr Gln Val Ile Asp
145 150 155 160

Asp Glu Ser Asp Tyr Phe Ala Ser Asp Ser Asn Gln Trp Leu Ser Lys
165 170 175

Leu Glu Arg Glu Thr Leu Gln Lys Arg Glu Glu Glu Leu Arg Glu Leu
180 185 190

Arg His Ala Ser Arg Leu Ser Lys Lys Val Thr Ile Asp Phe Ala Gly
195 200 205

Arg Lys Ile Leu Glu Glu Glu Asn Ser Leu Ala Glu Tyr His Ser Arg
210 215 220

Leu Asp Glu Thr Ile Gln Ala Ile Ala Asn Gly Thr Leu Asn Gln Pro
225 230 235 240

Leu Thr Lys Leu Asp Arg Ser Ser Glu Glu Pro Leu Gly Val Leu Val
245 250 255

Asn Pro Asn Met Tyr Gln Ser Pro Pro Gln Trp Leu Thr Thr Gln Val
260 265 270

Gln Pro His Arg Arg Arg Leu Ser Val Leu Gln Asp Leu Asp
275 280 285

<210> SEQ ID NO 23
<211> LENGTH: 197
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn Asp Pro Leu
1 5 10 15

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```
Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu Pro Ile Arg
            20                  25                  30

Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val Thr Asn His
        35                  40                  45

Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn Glu Gln Pro
    50                  55                  60

Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser Ala Ser Asp
65                  70                  75                  80

Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys Gly Leu Gln
                85                  90                  95

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

Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln Val Ser Ala
        115                 120                 125

Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser Gln Pro Leu
    130                 135                 140

Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys Gln Glu Glu
145                 150                 155                 160

Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu Met Ala Asp
                165                 170                 175

Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile Glu Met Asp
            180                 185                 190

Ser Gly Asp Glu Ala
        195


<210> SEQ ID NO 24
<211> LENGTH: 353
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: UNSURE
<222> LOCATION: (76)..(76)
<223> OTHER INFORMATION: X = any amino acid

<400> SEQUENCE: 24

Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln
1               5                   10                  15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu
            20                  25                  30

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp
        35                  40                  45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro
    50                  55                  60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Xaa Thr Ser Ser Ser
65                  70                  75                  80

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

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly
            100                 105                 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro
        115                 120                 125

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln
    130                 135                 140
```

-continued

```
Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met
145                 150                 155                 160

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys
                165                 170                 175

Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln
            180                 185                 190

His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp
        195                 200                 205

Arg Asn Thr Phe Arg His Ser Val Val Val Pro Cys Glu Pro Pro Glu
    210                 215                 220

Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser
225                 230                 235                 240

Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr
                245                 250                 255

Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val
            260                 265                 270

His Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn
        275                 280                 285

Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr
    290                 295                 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys
305                 310                 315                 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu
                325                 330                 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp
            340                 345                 350

Ala


<210> SEQ ID NO 25
<211> LENGTH: 545
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

Met Glu Thr Pro Ser Gln Arg Arg Ala Thr Arg Ser Gly Ala Gln Ala
1               5                   10                  15

Ser Ser Thr Pro Leu Ser Pro Thr Arg Ile Thr Arg Leu Gln Glu Lys
            20                  25                  30

Glu Asp Leu Gln Glu Leu Asn Asp Arg Leu Ala Val Tyr Ile Asp Arg
        35                  40                  45

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

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

Tyr Glu Ala Glu Leu Gly Asp Ala Arg Lys Thr Leu Asp Ser Val Ala
                85                  90                  95

Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys Val Arg Glu Glu
            100                 105                 110

Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu Gly Asp Leu Ile
        115                 120                 125

Ala Ala Gln Ala Arg Leu Lys Asp Leu Glu Ala Leu Leu Asn Ser Lys
    130                 135                 140
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-continued

```
Glu Ala Ala Leu Ser Thr Ala Leu Ser Glu Lys Arg Thr Leu Glu Gly
145                 150                 155                 160

Glu Leu His Asp Leu Arg Gly Gln Val Ala Lys Leu Glu Ala Ala Leu
                165                 170                 175

Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp
            180                 185                 190

Ala Glu Asn Arg Leu Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys
        195                 200                 205

Asn Ile Tyr Ser Glu Glu Leu Arg Glu Thr Lys Arg Arg His Glu Thr
    210                 215                 220

Arg Leu Val Glu Ile Asp Asn Gly Lys Gln Arg Glu Phe Glu Ser Arg
225                 230                 235                 240

Leu Ala Asp Ala Leu Gln Glu Leu Arg Ala Gln His Glu Asp Gln Val
                245                 250                 255

Glu Gln Tyr Lys Lys Glu Leu Glu Lys Thr Tyr Ser Ala Lys Leu Asp
            260                 265                 270

Asn Ala Arg Gln Ser Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala
        275                 280                 285

His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp Ser Leu Ser Ala
    290                 295                 300

Gln Leu Ser Gln Leu Gln Lys Gln Leu Ala Ala Lys Glu Ala Lys Leu
305                 310                 315                 320

Arg Asp Leu Glu Asp Ser Leu Ala Arg Glu Arg Asp Thr Ser Arg Arg
                325                 330                 335

Leu Leu Ala Glu Lys Glu Arg Glu Met Ala Glu Met Arg Ala Arg Met
            340                 345                 350

Gln Gln Gln Leu Asp Glu Tyr Gln Glu Leu Leu Asp Ile Lys Leu Ala
        355                 360                 365

Leu Asp Met Glu Ile His Ala Tyr Arg Lys Leu Leu Glu Gly Glu Glu
    370                 375                 380

Glu Arg Leu Arg Leu Ser Pro Ser Pro Thr Ser Gln Arg Ser Arg Gly
385                 390                 395                 400

Arg Ala Ser Ser His Ser Ser Gln Thr Gln Gly Gly Gly Ser Val Thr
                405                 410                 415

Lys Lys Arg Lys Leu Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln
            420                 425                 430

His Ala Arg Thr Ser Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu
        435                 440                 445

Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu Asp Gln Ser Met
    450                 455                 460

Gly Asn Trp Gln Ile Lys Arg Gln Asn Gly Asp Asp Pro Leu Leu Thr
465                 470                 475                 480

Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly Gln Val Val Thr
                485                 490                 495

Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu
            500                 505                 510

Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr
        515                 520                 525

Ala Leu Ile Asn Ser Thr Gly Glu Glu Val Ala Met Arg Lys Leu Val
    530                 535                 540

Arg
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545

<210> SEQ ID NO 26
<211> LENGTH: 1227
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

Gln Gly Ala Gln Arg Gly Ala Arg Val Gly Ala Ala Met Gly Leu Arg
1 5 10 15

Arg Ser Gly Asp Ser Arg Glu Pro Ser Gly Pro Gly Pro Glu Arg Val
20 25 30

Phe Ser Gly Gly Pro Arg Pro Pro Ala Arg Gly Ala Gly Ala Pro Ala
35 40 45

Pro Val Ala Gly Ala Val Ala Gly Cys Gly Gly Gly Gln Asp His Val
50 55 60

Gly Ser Pro Leu Arg Arg Arg Gly Ser Gly Leu Arg Asp Ala Ala Ala
65 70 75 80

Glu Ala Val Glu Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys Arg Asn
85 90 95

Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys Val Asn
100 105 110

Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Phe Ala Ala
115 120 125

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

Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His Asn Ala
145 150 155 160

Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg His Gly
165 170 175

Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu His Glu
180 185 190

Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu Gln His
195 200 205

Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala Leu Asp
210 215 220

Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr Lys Lys
225 230 235 240

Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys Met Met
245 250 255

Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp Gly Arg
260 265 270

Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val Lys Ile
275 280 285

Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys
290 295 300

Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu
305 310 315 320

Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala Met Asp
325 330 335

Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn Arg Val
340 345 350

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Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr Leu Leu
        355                 360                 365

Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro Gln Leu
    370                 375                 380

Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu Gln Ala
385                 390                 395                 400

Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser Leu Glu
                405                 410                 415

Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Leu His Cys
            420                 425                 430

Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu Leu Leu
        435                 440                 445

Leu Arg Lys Gly Ala Asn Ile Asn Glu Lys Thr Lys Glu Phe Leu Thr
    450                 455                 460

Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Val Val Glu Val
465                 470                 475                 480

Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu Gly Gln
                485                 490                 495

Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr Cys Arg
            500                 505                 510

Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu Gln Gly
        515                 520                 525

Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu Leu Gln
    530                 535                 540

Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu Leu Glu
545                 550                 555                 560

Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys Thr Val
                565                 570                 575

Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr Pro Leu
            580                 585                 590

His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr Leu Leu
        595                 600                 605

Gln His Gly Ala Asp Val His Ala Lys Asp Lys Gly Gly Leu Val Pro
    610                 615                 620

Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu Leu Leu
625                 630                 635                 640

Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys Phe Thr
                645                 650                 655

Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys Lys Leu
            660                 665                 670

Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp Gly Asn
        675                 680                 685

Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln Asp Leu
    690                 695                 700

Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Gly Cys Leu
705                 710                 715                 720

Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys Arg Asp
                725                 730                 735

Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn
            740                 745                 750

Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp Val Asn
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        755                 760                 765

Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala Ser Tyr
    770                 775                 780

Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala Cys Val
785                 790                 795                 800

Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala Ala Gln
                805                 810                 815

Lys Gly Arg Thr Gln Leu Cys Ala Leu Leu Leu Ala His Gly Ala Asp
            820                 825                 830

Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu Val Ser
        835                 840                 845

Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro Ser Ala
    850                 855                 860

Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg Ser Pro
865                 870                 875                 880

Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro Ser Ser
                885                 890                 895

Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe Ser Glu
            900                 905                 910

Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser Ser Leu
        915                 920                 925

Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln Phe Val
    930                 935                 940

Arg Asn Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg Glu Gln
945                 950                 955                 960

Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu Lys Glu
                965                 970                 975

Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys Gly Val
            980                 985                 990

Glu Arg Leu Ile Ser Gly Gln Gln  Gly Leu Asn Pro Tyr  Leu Thr Leu
        995                 1000                1005

Asn Thr  Ser Gly Ser Gly Thr  Ile Leu Ile Asp Leu  Ser Pro Asp
    1010                1015                1020

Asp Lys  Glu Phe Gln Ser Val  Glu Glu Glu Met Gln  Ser Thr Val
    1025                1030                1035

Arg Glu  His Arg Asp Gly Gly  His Ala Gly Gly Ile  Phe Asn Arg
    1040                1045                1050

Tyr Asn  Ile Leu Lys Ile Gln  Lys Val Cys Asn Lys  Lys Leu Trp
    1055                1060                1065

Glu Arg  Tyr Thr His Arg Arg  Lys Glu Val Ser Glu  Glu Asn His
    1070                1075                1080

Asn His  Ala Asn Glu Arg Met  Leu Phe His Gly Ser  Pro Phe Val
    1085                1090                1095

Asn Ala  Ile Ile His Lys Gly  Phe Asp Glu Arg His  Ala Tyr Ile
    1100                1105                1110

Gly Gly  Met Phe Gly Ala Gly  Ile Tyr Phe Ala Glu  Asn Ser Ser
    1115                1120                1125

Lys Ser  Asn Gln Tyr Val Tyr  Gly Ile Gly Gly Gly  Thr Gly Val
    1130                1135                1140

Gln Phe  Thr Lys Thr Asp Leu  Val Thr Phe Ala Thr  Ala Ala Ala
    1145                1150                1155
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Leu Leu  Pro Gly Asn Leu Gly  Lys Val Phe Pro Ala  Val Gln Cys
    1160                 1165                 1170

Asn Glu  Asn Gly Thr Ser Pro  Pro Gly His His Ser  Val Thr Gly
    1175                 1180                 1185

Arg Pro  Ser Val Asn Gly Leu  Ala Leu Ala Glu Tyr  Val Ile Tyr
    1190                 1195                 1200

Arg Gly  Glu Gln Ala Tyr Pro  Glu Tyr Leu Ile Thr  Tyr Gln Ile
    1205                 1210                 1215

Met Arg  Pro Glu Gly Met Val  Asp Gly
    1220                 1225


<210> SEQ ID NO 27
<211> LENGTH: 290
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

His Ile Gln Lys Gln Lys His Phe Asn Glu Arg Glu Ala Ser Arg Val
1               5                  10                  15

Val Arg Asp Val Ala Ala Ala Leu Asp Phe Leu His Thr Lys Gly Ile
            20                  25                  30

Ala His Arg Asp Leu Lys Pro Glu Asn Ile Leu Cys Glu Ser Pro Glu
        35                  40                  45

Lys Val Ser Pro Val Lys Ile Cys Asp Phe Asp Leu Gly Ser Gly Met
    50                  55                  60

Lys Leu Asn Asn Ser Cys Thr Pro Ile Thr Thr Pro Glu Leu Thr Thr
65                  70                  75                  80

Pro Cys Gly Ser Ala Glu Tyr Met Ala Pro Glu Val Val Glu Val Phe
                85                  90                  95

Thr Asp Gln Ala Thr Phe Tyr Asp Lys Arg Cys Asp Leu Trp Ser Leu
            100                 105                 110

Gly Val Val Leu Tyr Ile Met Leu Ser Gly Tyr Pro Pro Phe Val Gly
        115                 120                 125

His Cys Gly Ala Asp Cys Gly Trp Asp Arg Gly Glu Val Cys Arg Val
    130                 135                 140

Cys Gln Asn Lys Leu Phe Glu Ser Ile Gln Glu Gly Lys Tyr Glu Phe
145                 150                 155                 160

Pro Asp Lys Asp Trp Ala His Ile Ser Ser Glu Ala Lys Asp Leu Ile
                165                 170                 175

Ser Lys Leu Leu Val Arg Asp Ala Lys Gln Lys Leu Ser Ala Ala Gln
            180                 185                 190

Val Leu Gln His Pro Trp Val Gln Gly Gln Ala Pro Glu Lys Gly Leu
        195                 200                 205

Pro Thr Pro Gln Val Leu Gln Arg Asn Ser Ser Thr Met Asp Leu Thr
    210                 215                 220

Leu Phe Ala Ala Glu Ala Ile Ala Leu Asn Arg Gln Leu Ser Gln His
225                 230                 235                 240

Glu Glu Asn Glu Leu Ala Glu Glu Pro Glu Ala Leu Ala Asp Gly Leu
                245                 250                 255

Cys Ser Met Lys Leu Ser Pro Pro Cys Lys Ser Arg Leu Ala Arg Arg
            260                 265                 270

Arg Ala Leu Ala Gln Ala Gly Arg Gly Glu Asn Arg Ser Pro Pro Thr
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        275                 280                 285

Ala Leu
    290


<210> SEQ ID NO 28
<211> LENGTH: 188
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

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

Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
            20                  25                  30

Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
        35                  40                  45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
    50                  55                  60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
65                  70                  75                  80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
                85                  90                  95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
            100                 105                 110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
        115                 120                 125

Ala Ser Gly Pro Gln Asn Asp Gly Lys Glu Leu Cys Pro Pro Gly Lys
    130                 135                 140

Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
145                 150                 155                 160

Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile
                165                 170                 175

Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu
            180                 185


<210> SEQ ID NO 29
<211> LENGTH: 314
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

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1               5                   10                  15

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
            20                  25                  30

Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val
        35                  40                  45

Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser
    50                  55                  60

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
65                  70                  75                  80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
                85                  90                  95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
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            100                 105                 110

Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
        115                 120                 125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
    130                 135                 140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu
145                 150                 155                 160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr
                165                 170                 175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
            180                 185                 190

Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile
        195                 200                 205

Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
    210                 215                 220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly
225                 230                 235                 240

Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu
                245                 250                 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
            260                 265                 270

Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
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His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
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His Glu Trp Val Leu Arg Glu Gly Glu Glu
305                 310


<210> SEQ ID NO 30
<211> LENGTH: 180
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
1               5                   10                  15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
            20                  25                  30

Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
        35                  40                  45

Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
    50                  55                  60

His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
65                  70                  75                  80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
                85                  90                  95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
            100                 105                 110

Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
        115                 120                 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
    130                 135                 140
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Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
145                 150                 155                 160

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
                165                 170                 175

Gly Gln Arg Arg
            180
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We claim:

1. A method for diagnosing colon cancer in a subject comprising:

obtaining a biological sample from a subject,

contacting the sample with at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, and

determining specific binding between the colon cancer-associated polypeptides and agents in the sample, wherein the presence of specific binding is diagnostic for colon cancer in the subject.

2. The method of claim 1, wherein the sample is blood.

3. The method of claim 1, wherein the biological sample is contacted with at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

4. The method of claim 1, wherein the agents are antibodies or antigen-binding fragments thereof.

5. The method of claim 1, further comprising:

contacting the biological sample with a colon cancer-associated polypeptide other than those encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

6. A method for diagnosing colon cancer in a subject comprising:

obtaining a biological sample from a subject,

contacting the sample with antibodies or antigen-binding fragments thereof, that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, and

determining specific binding between the antibodies or antigen-binding fragments thereof and colon cancer-associated polypeptides in the sample, wherein the presence of specific binding is diagnostic for colon cancer in the subject.

7. The method of claim 6, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

8. The sample of claim 7, wherein the tissue is colorectal tissue.

9. The method of claim 6, wherein the biological sample is contacted with antibodies or antigen-binding fragments thereof, that bind specifically to at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

10. The method of claim 6, further comprising:

contacting the biological sample with an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide other than those encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

11. The method of claim 6, wherein the antibodies are monoclonal or polyclonal antibodies.

12. The method of claim 6, wherein the antibodies are chimeric, human, or humanized antibodies.

13. The method of claim 6, wherein the antibodies are single chain antibodies.

14. The method of claim 6, wherein the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

15. A method for determining onset, progression, or regression, of colon cancer in a subject, comprising:

obtaining from a subject a first biological sample,

contacting the first sample with at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected form the group consisting of SEQ ID NOs:1-15,

determining specific binding between agents in the first sample and the at least two different colon cancer-associated polypeptides,

obtaining from a subject a second biological sample,

contacting the second biological sample with at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected form the group consisting of SEQ ID NOs:1-15,

determining specific binding between agents in the second sample and the at least two different colon cancer-associated polypeptides, and

comparing the determination of binding in the first sample to the determination of specific binding in the second sample as a determination of the onset, progression, or regression of the colon cancer.

16. The method of claim 15, wherein the sample is a blood sample.

17. The method of claim 15, wherein binding is determined between the agents and at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated

polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

18. The method of claim 15, wherein the agents are antibodies or antigen-binding fragments thereof.

19. The method of claim 15, further comprising:

determining binding between the agents and a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

20. A method for determining onset, progression, or regression, of colon cancer in a subject, comprising:

obtaining from a subject a first biological sample,

contacting the first sample with antibodies or antigen-binding fragments thereof, that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15,

determining specific binding between colon cancer-associated polypeptides in the first sample and the antibodies or antigen-binding fragments thereof,

obtaining from a subject a second biological sample, contacting the second sample with antibodies or antigen-binding fragments thereof, that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15,

determining specific binding between colon cancer-associated polypeptides in the second sample and the antibodies or antigen-binding fragments thereof, and

comparing the determination of specific binding in the first sample to the determination of specific binding in the second sample as a determination of the onset, progression, or regression of colon cancer.

21. The method of claim 20, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

22. The sample of claim 21, wherein the tissue is colorectal tissue.

23. The method of claim 20, wherein binding is determined between the colon cancer-associated polypeptides and antibodies or antigen-binding fragments thereof, that bind specifically to least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

24. The method of claim 20, further comprising:

determining binding between the colon cancer-associated polypeptide and an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide other than those encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

25. The method of claim 20, wherein the antibodies are monoclonal or polyclonal antibodies.

26. The method of claim 20, wherein the antibodies are chimeric, human, or humanized antibodies.

27. The method of claim 20, wherein the antibodies are single chain antibodies.

28. The method of claim 20, wherein the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

29. A method for selecting a course of treatment of a subject having or suspected of having colon cancer, comprising:

obtaining from the subject a biological sample,

contacting the sample with at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15,

determining specific binding between agents in the sample that are differentially expressed in different types of cancer, and the colon cancer-associated polypeptides, and

selecting a course of treatment appropriate to the cancer of the subject.

30. The method of claim 29, wherein the treatment is administering antibodies that specifically bind to the colon cancer-associated polypeptides.

31. The method of claim 30, wherein the antibodies are labeled with one or more cytotoxic agents.

32. The method of claim 29, wherein the sample is a blood sample.

33. The method of claim 29, wherein the agents are antibodies or antigen-binding fragments thereof.

34. The method of claim 29, wherein the sample is contacted with at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

35. The method of claim 29, further comprising:

contacting the sample with a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

36. A method for selecting a course of treatment of a subject having or suspected of having colon cancer, comprising:

obtaining from the subject a biological sample,

contacting the sample with antibodies or antigen-binding fragments thereof that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15,

determining specific binding between colon cancer-associated polypeptides in the sample that are differentially expressed in different types of cancer, and the antibodies or antigen-binding fragments thereof, and

selecting a course of treatment appropriate to the cancer of the subject.

37. The method of claim 36, wherein the treatment is administering antibodies that specifically bind to the colon cancer-associated polypeptides.

38. The method of claim 37, wherein the antibodies are labeled with one or more cytotoxic agents.

39. The method of claim 36, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

40. The sample of claim 39, wherein the tissue is colorectal tissue.

41. The method of claim 36, wherein the sample is contacted with antibodies or antigen-binding fragments thereof, that bind specifically to least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

42. The method of claim 36, further comprising:

contacting the sample with an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

43. The method of claim 37, wherein the antibodies are monoclonal or polyclonal antibodies.

44. The method of claim 37, wherein the antibodies are chimeric, human, or humanized antibodies.

45. The method of claim 37, wherein the antibodies are single chain antibodies.

46. The method of claim 37, wherein the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

47. A kit for the diagnosis of colon cancer in a subject, comprising:

at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs:1-15, one or more control antigens, and instructions for the use of the polypeptides in the diagnosis of colon cancer.

48. The kit of claim 47, wherein the colon cancer-associated polypeptides are bound to a substrate.

49. The kit of claim 47, wherein the kit comprises at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

50. The kit of claim 47, wherein the kit further comprises a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

51. A kit for the diagnosis of colon cancer in a subject, comprising:

antibodies or antigen-binding fragments thereof that bind specifically to at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15, one or more control agents, and instructions for the use of the agents in the diagnosis of colon cancer.

52. The kit of claim 51, wherein the one or more agents are antibodies or antigen-binding fragments thereof.

53. The kit of claim 51, wherein the one or more agents are bound to a substrate.

54. The kit of claim 51, wherein the kit comprises antibodies or antigen-binding fragments thereof, that bind specifically to least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

55. The kit of claim 51, wherein the kit further comprises an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

56. A protein microarray comprising at least two different colon cancer-associated polypeptides, wherein the colon cancer-associated polypeptides are encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs:1-15, fixed to a solid substrate.

57. The protein microarray of claim 56, wherein the microarray comprises at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

58. The protein microarray of claim 56, further comprising a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

59. The protein microarray of claim 56, further comprising at least one control polypeptide molecule.

60. A protein microarray comprising antibodies or antigen-binding fragments thereof, that specifically bind at least two different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs:1-15, fixed to a solid substrate.

61. The protein microarray of claim 60, wherein the microarray comprises antibodies or antigen-binding fragments thereof, that bind specifically to least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different colon cancer-associated polypeptides encoded by nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

62. The protein microarray of claim 60, further comprising an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide other than those encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

63. The protein microarray of claim 60, further comprising at least one control polypeptide molecule.

64. The protein microarray of claim 60, wherein the antibodies are monoclonal or polyclonal antibodies.

65. The protein microarray of claim 60, wherein the antibodies are chimeric, human, or humanized antibodies.

66. The protein microarray of claim 60, wherein the antibodies are single chain antibodies.

67. The protein microarray of claim 60, wherein the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

68. A nucleic acid microarray comprising at least two nucleic acids selected from the group consisting of SEQ ID NOs:1-15, fixed to a solid substrate.

69. The nucleic acid microarray of claim 68, wherein the microarray comprises at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 different nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

70. The nucleic acid microarray of claim 68, further comprising a nucleic acid molecule other than those selected from the group consisting of SEQ ID NOs:1-15.

71. The nucleic acid microarray of claim 68, further comprising at least one control nucleic acid molecule.

72. A method for diagnosing colon cancer in a subject comprising:

obtaining from the subject a biological sample, and

determining the expression of at least two colon cancer-associated nucleic acid molecules or expression products thereof in the sample, wherein the nucleic acid molecules comprise a nucleotide sequence selected from the group consisting of: SEQ ID NO: 1-15, wherein the expression is diagnosis of the colon cancer in the subject.

73. The method of claim 72, wherein expression is determined for at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 nucleic acid molecules comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

74. The method of claim 72, further comprising:

determining expression of a colon cancer-associated nucleic acid molecule other than those comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

75. The method of claim 72, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

76. The sample of claim 75, wherein the tissue is colorectal tissue.

77. The method of claim 72, wherein the expression of colon cancer-associated nucleic acid molecules is determined by a method selected from the group consisting of nucleic acid hybridization and nucleic acid amplification.

78. The method of claim 77, wherein the hybridization is performed using a nucleic acid microarray.

79. A method for determining onset, progression, or regression, of colon cancer in a subject comprising:

obtaining from a subject a first biological sample,

determining a level of expression of at least two colon cancer-associated nucleic acid molecules or expression products thereof in the first sample, wherein the nucleic acid molecules are selected from the group consisting of: SEQ ID NOs: 1-15,

obtaining from the subject a second biological sample,

determining a level of expression of at least two colon cancer-associated nucleic acid molecules or expression products thereof in the second sample, wherein the nucleic acid molecules are selected from the group consisting of: SEQ ID NOs: 1-15, and

comparing the level of expression in the first sample to the level of expression in the second sample as a determination of the onset, progression, or regression of the colon cancer.

80. The method of claim 79, wherein expression is determined for at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 nucleic acid molecules selected from the group consisting of SEQ ID NOs:1-15.

81. The method of claim 79, further comprising:

determining expression for a colon cancer-associated nucleic acid molecule other than those comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-15.

82. The method of claim 79, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

83. The sample of claim 82, wherein the tissue is colorectal tissue.

84. The method of claim 79, wherein the expression of colon cancer-associated nucleic acid molecules is determined by a method selected from the group consisting of nucleic acid hybridization and nucleic acid amplification.

85. The method of claim 84, wherein the hybridization is performed using a nucleic acid microarray.

86. A method for diagnosing cancer in a subject comprising:

obtaining a biological sample from a subject,

contacting the sample with a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, and

determining specific binding between the colon cancer-associated polypeptide and agents in the sample, wherein the presence of specific binding is diagnostic for cancer in the subject.

87. The method of claim 86, wherein the sample is blood.

88. The method of claim 86, wherein the agents are antibodies or antigen-binding fragments thereof.

89. The method of claim 86, wherein the cancer is colon cancer.

90. A method for diagnosing cancer in a subject comprising:

obtaining a biological sample from a subject,

contacting the sample with an antibody or antigen-binding fragment thereof, that binds specifically to a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6, and

determining specific binding between the antibody or antigen-binding fragment thereof and the colon cancer-associated polypeptide in the sample, wherein the presence of specific binding is diagnostic for cancer in the subject.

91. The method of claim 90, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

92. The sample of claim 91, wherein the tissue is colorectal tissue.

93. The method of claim 90, wherein the antibodies are monoclonal or polyclonal antibodies.

94. The method of claim 90, wherein the antibodies are chimeric, human, or humanized antibodies.

95. The method of claim 90, wherein the antibodies are single chain antibodies.

96. The method of claim 90, wherein the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

97. The method of claim 90, wherein the cancer is colon cancer.

98. A method for determining onset, progression, or regression, of cancer in a subject, comprising:

obtaining from a subject a first biological sample,

contacting the first sample with a colon cancer associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6,

determining specific binding between agents in the first sample and the colon cancer-associated,

obtaining from a subject a second biological sample,

contacting the second sample with a colon cancer associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6,

determining specific binding between agents in the second sample and the colon cancer-associated polypeptide, and

comparing the determination of binding in the first sample to the determination of specific binding in the second sample as a determination of the onset, progression, or regression of cancer.

99. The method of claim 98, wherein the sample is a blood sample.

100. The method of claim 98, wherein the agents are antibodies or antigen-binding fragments thereof.

101. The method of claim 98, wherein the cancer is colon cancer.

102. A method for determining onset, progression, or regression, of cancer in a subject, comprising:

obtaining from a subject a first biological sample,

contacting the first sample with antibodies or antigen-binding fragments thereof, that bind specifically to a colon cancer-associated polypeptides encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6,

determining specific binding between colon cancer-associated polypeptides in the first sample and the antibodies or antigen-fragments thereof,

obtaining from a subject a second biological sample,

contacting the second sample with antibodies or antigen-binding fragments thereof, that bind specifically to a colon cancer-associated polypeptides encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6,

determining specific binding between colon cancer-associated polypeptides in the second sample and the antibodies or antigen-binding fragments thereof, and

comparing the determination of specific binding in the first sample to the determination of specific binding in the second sample as a determination of the onset, progression, or regression of cancer.

103. The method of claim 102, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

104. The sample of claim 103, wherein the tissue is colorectal tissue.

105. The method of claim 102, wherein the antibodies are monoclonal or polyclonal antibodies.

106. The method of claim 102, wherein the antibodies are chimeric, human, or humanized antibodies.

107. The method of claim 102, wherein the antibodies are single chain antibodies.

108. The method of claim 102, wherein the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

109. The method of claim 102, wherein the cancer is colon cancer.

110. A method for selecting a course of treatment of a subject having or suspected of having cancer, comprising:

obtaining from the subject a biological sample,

contacting the sample with a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6,

determining specific binding between agents in the sample that are differentially expressed in different types of cancer, and the colon cancer-associated polypeptide, and

selecting a course of treatment appropriate to the cancer of the subject.

111. The method of claim 110, wherein the treatment is administering antibodies that specifically bind to the colon cancer-associated polypeptide.

112. The method of claim 111, wherein the antibodies are labeled with one or more cytotoxic agents.

113. The method of claim 110, wherein the sample is a blood sample.

114. The method of claim 110, wherein the agents are antibodies or antigen-binding fragments thereof.

115. The method of claim 110, wherein the cancer is colon cancer.

116. A method for selecting a course of treatment of a subject having or suspected of having cancer, comprising:

obtaining from the subject a biological sample,

contacting the sample with antibodies or antigen-binding fragments thereof that bind specifically to a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6,

determining specific binding between colon cancer-associated polypeptides in the sample that are differentially expressed in different types of cancer, and the antibodies or antigen-binding fragments thereof, and

selecting a course of treatment appropriate to the cancer of the subject.

117. The method of claim 116, wherein the treatment is administering antibodies that specifically bind to the colon cancer-associated polypeptide.

118. The method of claim 117, wherein the antibodies are labeled with one or more cytotoxic agents.

119. The method of claim 116, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

120. The sample of claim 119, wherein the tissue is colorectal tissue.

121. The method of claim 116, wherein the antibodies are monoclonal or polyclonal antibodies.

122. The method of claim 116, wherein the antibodies are chimeric, human, or humanized antibodies.

123. The method of claim 116, wherein the antibodies are single chain antibodies.

124. The method of claim 116, wherein the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

125. The method of claim 116, wherein the cancer is colon cancer.

126. A kit for the diagnosis of cancer in a subject, comprising:

a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs: 1, 2, 5, and 6; one or more control antigens; and instructions for the use of the polypeptide and control antigens in the diagnosis of cancer.

127. The kit of claim 126, wherein the colon cancer-associated polypeptide is bound to a substrate.

128. The kit of claim 126, wherein the cancer is colon cancer.

129. A kit for the diagnosis of cancer in a subject, comprising:

antibodies or antigen-binding fragments thereof that bind specifically to a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1, 2, 5, and 6; one or more control agents; and instructions for the use of the antibodies, antigen-binding fragments, and agents in the diagnosis of cancer.

130. The kit of claim 129, wherein the one or more agents are antibodies or antigen-binding fragments thereof.

131. The kit of claim 129, wherein the one or more agents are bound to a substrate.

132. The kit of claim 129, wherein the cancer is colon cancer.

133. A protein microarray comprising a colon cancer-associated polypeptide, wherein the colon cancer-associated polypeptide is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs: 1, 2, 5, and 6, fixed to a solid substrate.

134. The protein microarray of claim 133, further comprising at least one control polypeptide molecule.

135. A protein microarray comprising antibodies or antigen-binding fragments thereof, that specifically bind a colon cancer-associated polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of: SEQ ID NOs:1, 2, 5, and 6, fixed to a solid substrate.

136. The protein microarray of claim 135, further comprising at least one control polypeptide molecule.

137. The protein microarray of claim 135, wherein the antibodies are monoclonal or polyclonal antibodies.

138. The protein microarray of claim 135, wherein the antibodies are chimeric, human, or humanized antibodies.

139. The protein microarray of claim 135, wherein the antibodies are single chain antibodies.

140. The protein microarray of claim 135, wherein the antigen-binding fragments are $F(ab')_2$, Fab, Fd, or Fv fragments.

141. A nucleic acid microarray comprising a nucleic acid selected from the group consisting of SEQ ID NOs: 1, 2, 5, and 6, fixed to a solid substrate.

142. The nucleic acid microarray of claim 141, further comprising at least one control nucleic acid molecule.

143. A method for diagnosing cancer in a subject comprising:

obtaining from the subject a biological sample, and

determining the expression of a colon cancer-associated nucleic acid molecule or expression product thereof in the sample, wherein the nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of: SEQ ID NO: 1, 2, 5, and 6, wherein the expression is diagnostic of cancer in the subject.

144. The method of claim 143, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

145. The sample of claim 144, wherein the tissue is colorectal tissue.

146. The method of claim 143, wherein the expression of colon cancer-associated nucleic acid molecules is determined by a method selected from the group consisting of nucleic acid hybridization and nucleic acid amplification.

147. The method of claim 146, wherein the hybridization is performed using a nucleic acid microarray.

148. The method of claim 143, wherein the cancer is colon cancer.

149. A method for determining onset, progression, or regression, of cancer in a subject comprising:

obtaining from a subject a first biological sample,

determining a level of expression of a colon cancer-associated nucleic acid molecule or expression products thereof in the first sample, wherein the nucleic acid molecule is selected from the group consisting of: SEQ ID NOs: 1, 2, 5, and 6,

obtaining from the subject a second biological sample,

determining a level of expression of a colon cancer-associated nucleic acid molecule or expression product thereof in the second sample, wherein the nucleic acid molecule is selected from the group consisting of: SEQ ID NOs: 1, 2, 5, and 6, and

comparing the level of expression in the first sample to the level of expression in the second sample as a determination of the onset, progression, or regression of the cancer.

150. The method of claim 149, wherein the sample is selected from the group consisting of: tissue, stool, cells, blood, and mucus.

151. The sample of claim 150, wherein the tissue is colorectal tissue.

152. The method of claim 149, wherein the expression of colon cancer-associated nucleic acid molecules is determined by a method selected from the group consisting of nucleic acid hybridization and nucleic acid amplification.

153. The method of claim 152, wherein the hybridization is performed using a nucleic acid microarray.

154. The method of claim 149, wherein the cancer is colon cancer.

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专利名称(译)	结肠癌抗原组		
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摘要(译)

本发明提供了用于诊断癌症（包括结肠癌）的方法，其基于鉴定某些结肠癌相关多肽作为在结肠癌中引发免疫应答的抗原。鉴定的抗原可用作诊断结肠癌的标志物，并用于跟踪结肠癌的治疗过程。

TABLE 1

Colon Cancer Serology
Reactivity of 75 sera from colon cancer patients versus 15 antigens comprising, none of which react with normal sera (0/75, assayed by spot blot as described).

Sera Number	Reactive NY-antigens
COF1	Negative
COF2	Negative
COF3	Negative
COF4	Negative
COF5	Negative
COF6	CO61 + + +
COF7	CO26 + + + +, ESO-1 + + + +, CO61 + + + +
COF8	Negative
COF9	REN32 + + +
COF10	p53 + + +, CO58 + +
COF11	TNKL +, ESO-1 + + + +
COF12	CO94 + +
COF13	Negative
COF14	Negative
COF15	SSX-2 + +
COF16	CO45 + +, CO42 + +
COF17	Negative
COF18	Negative
COF19	Negative
COF20	Negative
COF21	CO58 +
COF22	TNKL + +, CO45 + +, CO42 + +
COF23	CO41 + +
CO24	Negative
CO25	Negative
CO26	TNKL + + +
CO27	CO45 + + + +