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(54) **Titre : ACIDES NUCLEIQUES ET PROTEINES CORRESPONDANTES INTITULEES 191P4D12(b) UTILISES DANS LE TRAITEMENT ET LA DETECTION DU CANCER**
(54) **Title: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED 191P4D12(b) USEFUL IN TREATMENT AND DETECTION OF CANCER**

191P4D12(b) SSH sequence of 223 nucleotides. (SEQ ID NO: 1)

```
  1 GATCACTAAT TCAAGGCTCT TCTGGATGTT TCTCTGGGTT GGGGCTGGAG TTCAATGAGG
 61 TTTATTTTTA GCTGGCCCAC CCAGATACAC TCAGCCAGAA TACCTAGATT TAGTACCCAA
121 ACTCTTCTTA GTCTGAAATC TGCTGGATTT CTGGCCTAAG GGAGAGGCTC CCATCCTTCG
181 TTCCCCAGCC AGCCTAGGAC TTCGAATGTG GAGCCTGAAG ATC
```

(57) **Abrégé/Abstract:**
A novel gene 191P4D12(b) and its encoded protein, and variants thereof, are described wherein 191P4D12(b) exhibits tissue specific expression in normal adult tissue, and is aberrantly expressed in the cancers listed in Table I. Consequently, 191P4D12(b)

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(73) **Propriétaires(suite)/Owners(continued):**AGENSYS, INC., US

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(57) **Abrégé(suite)/Abstract(continued):**
provides a diagnostic, prognostic, prophylactic and/or therapeutic target for cancer. The 191P4D12(b) gene or fragment thereof, or its encoded protein, or variants thereof, or a fragment thereof, can be used to elicit a humoral or cellular immune response; antibodies or T cells reactive with 191P4D12(b) can be used in active or passive immunization.

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(54) Title: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED 191P4D12(b) USEFUL IN TREATMENT AND DETECTION OF CANCER

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(57) Abstract: A novel gene 191P4D12(b) and its encoded protein, and variants thereof, are described wherein 191P4D12(b) exhibits tissue specific expression in normal adult tissue, and is aberrantly expressed in the cancers listed in Table I. Consequently, 191P4D12(b) provides a diagnostic, prognostic, prophylactic and/or therapeutic target for cancer. The 191P4D12(b) gene or fragment thereof, or its encoded protein, or variants thereof, or a fragment thereof, can be used to elicit a humoral or cellular immune response; antibodies or T cells reactive with 191P4D12(b) can be used in active or passive immunization.

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JUMBO APPLICATIONS / PATENTS

THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE THAN ONE VOLUME.

THIS IS VOLUME __1___ OF __3___

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NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED 191P4D12(b) USEFUL IN TREATMENT AND DETECTION OF CANCER

STATEMENT OF RIGHTS TO INVENTIONS MADE UNDER FEDERALLY SPONSORED RESEARCH

Not applicable.

FIELD OF THE INVENTION

The invention described herein relates to genes and their encoded proteins, termed 191P4D12(b), expressed in certain cancers, and to diagnostic and therapeutic methods and compositions useful in the management of cancers that express 191P4D12(b).

BACKGROUND OF THE INVENTION

Cancer is the second leading cause of human death next to coronary disease. Worldwide, millions of people die from cancer every year. In the United States alone, as reported by the American Cancer Society, cancer causes the death of well over a half-million people annually, with over 1.2 million new cases diagnosed per year. While deaths from heart disease have been declining significantly, those resulting from cancer generally are on the rise. In the early part of the next century, cancer is predicted to become the leading cause of death.

Worldwide, several cancers stand out as the leading killers. In particular, carcinomas of the lung, prostate, breast, colon, pancreas, and ovary represent the primary causes of cancer death. These and virtually all other carcinomas share a common lethal feature. With very few exceptions, metastatic disease from a carcinoma is fatal. Moreover, even for those cancer patients who initially survive their primary cancers, common experience has shown that their lives are dramatically altered. Many cancer patients experience strong anxieties driven by the awareness of the potential for recurrence or treatment failure. Many cancer patients experience physical debilitations following treatment. Furthermore, many cancer patients experience a recurrence.

Worldwide, prostate cancer is the fourth most prevalent cancer in men. In North America and Northern Europe, it is by far the most common cancer in males and is the second leading cause of cancer death in men. In the United States alone, well over 30,000 men die annually of this disease - second only to lung cancer. Despite the magnitude of these figures, there is still no effective treatment for metastatic prostate cancer. Surgical prostatectomy, radiation therapy, hormone ablation therapy, surgical castration and chemotherapy continue to be the main treatment modalities. Unfortunately, these treatments are ineffective for many and are often associated with undesirable consequences.

On the diagnostic front, the lack of a prostate tumor marker that can accurately detect early-stage, localized tumors remains a significant limitation in the diagnosis and management of this disease. Although the serum prostate specific antigen (PSA) assay has been a very useful tool, however its specificity and general utility is widely regarded as lacking in several important respects.

Progress in identifying additional specific markers for prostate cancer has been improved by the generation of prostate cancer xenografts that can recapitulate different stages of the disease in mice. The LAPC (Los Angeles Prostate Cancer) xenografts are prostate cancer xenografts that have survived passage in severe combined immune deficient (SCID) mice and have exhibited the capacity to mimic the transition from androgen dependence to androgen independence (Klein *et al.*, 1997, Nat. Med. 3:402). More recently identified prostate cancer markers include PCTA-1 (Su *et al.*, 1996, Proc. Natl. Acad. Sci. USA 93: 7252), prostate-specific membrane (PSM) antigen (Pinto *et al.*, Clin Cancer Res 1996 Sep 2 (9): 1445-51), STEAP (Hubert, *et al.*, Proc Natl Acad Sci U S A. 1999 Dec 7; 96(25): 14523-8) and prostate stem cell antigen (PSCA) (Reiter *et al.*, 1998, Proc. Natl. Acad. Sci. USA 95: 1735).

While previously identified markers such as PSA, PSM, PCTA and PSCA have facilitated efforts to diagnose and treat prostate cancer, there is need for the identification of additional markers and therapeutic targets for prostate and related cancers in order to further improve diagnosis and therapy.

Renal cell carcinoma (RCC) accounts for approximately 3 percent of adult malignancies. Once adenomas reach a diameter of 2 to 3 cm, malignant potential exists. In the adult, the two principal malignant renal tumors are renal cell adenocarcinoma and transitional cell carcinoma of the renal pelvis or ureter. The incidence of renal cell adenocarcinoma is estimated at more than 29,000 cases in the United States, and more than 11,600 patients died of this disease in 1998. Transitional cell carcinoma is less frequent, with an incidence of approximately 500 cases per year in the United States.

Surgery has been the primary therapy for renal cell adenocarcinoma for many decades. Until recently, metastatic disease has been refractory to any systemic therapy. With recent developments in systemic therapies, particularly immunotherapies, metastatic renal cell carcinoma may be approached aggressively in appropriate patients with a possibility of durable responses. Nevertheless, there is a remaining need for effective therapies for these patients.

Of all new cases of cancer in the United States, bladder cancer represents approximately 5 percent in men (fifth most common neoplasm) and 3 percent in women (eighth most common neoplasm). The incidence is increasing slowly, concurrent with an increasing older population. In 1998, there was an estimated 54,500 cases, including 39,500 in men and 15,000 in women. The age-adjusted incidence in the United States is 32 per 100,000 for men and eight per 100,000 in women. The historic male/female ratio of 3:1 may be decreasing related to smoking patterns in women. There were an estimated 11,000 deaths from bladder cancer in 1998 (7,800 in men and 3,900 in women). Bladder cancer incidence and mortality strongly increase with age and will be an increasing problem as the population becomes more elderly.

Most bladder cancers recur in the bladder. Bladder cancer is managed with a combination of transurethral resection of the bladder (TUR) and intravesical chemotherapy or immunotherapy. The multifocal and recurrent nature of bladder cancer points out the limitations of TUR. Most muscle-invasive cancers are not cured by TUR alone. Radical cystectomy and urinary diversion is the most effective means to eliminate the cancer but carry an undeniable impact on urinary and sexual function. There continues to be a significant need for treatment modalities that are beneficial for bladder cancer patients.

An estimated 130,200 cases of colorectal cancer occurred in 2000 in the United States, including 93,800 cases of colon cancer and 36,400 of rectal cancer. Colorectal cancers are the third most common cancers in men and women. Incidence rates declined significantly during 1992-1996 (-2.1% per year). Research suggests that these declines have been due to increased screening and polyp removal, preventing progression of polyps to invasive cancers. There were an estimated 56,300 deaths (47,700 from colon cancer, 8,600 from rectal cancer) in 2000, accounting for about 11% of all U.S. cancer deaths.

At present, surgery is the most common form of therapy for colorectal cancer, and for cancers that have not spread, it is frequently curative. Chemotherapy, or chemotherapy plus radiation, is given before or after surgery to most patients whose cancer has deeply perforated the bowel wall or has spread to the lymph nodes. A permanent colostomy

(creation of an abdominal opening for elimination of body wastes) is occasionally needed for colon cancer and is infrequently required for rectal cancer. There continues to be a need for effective diagnostic and treatment modalities for colorectal cancer.

There were an estimated 164,100 new cases of lung and bronchial cancer in 2000, accounting for 14% of all U.S. cancer diagnoses. The incidence rate of lung and bronchial cancer is declining significantly in men, from a high of 86.5 per 100,000 in 1984 to 70.0 in 1996. In the 1990s, the rate of increase among women began to slow. In 1996, the incidence rate in women was 42.3 per 100,000.

Lung and bronchial cancer caused an estimated 156,900 deaths in 2000, accounting for 28% of all cancer deaths. During 1992–1996, mortality from lung cancer declined significantly among men (-1.7% per year) while rates for women were still significantly increasing (0.9% per year). Since 1987, more women have died each year of lung cancer than breast cancer, which, for over 40 years, was the major cause of cancer death in women. Decreasing lung cancer incidence and mortality rates most likely resulted from decreased smoking rates over the previous 30 years; however, decreasing smoking patterns among women lag behind those of men. Of concern, although the declines in adult tobacco use have slowed, tobacco use in youth is increasing again.

Treatment options for lung and bronchial cancer are determined by the type and stage of the cancer and include surgery, radiation therapy, and chemotherapy. For many localized cancers, surgery is usually the treatment of choice. Because the disease has usually spread by the time it is discovered, radiation therapy and chemotherapy are often needed in combination with surgery. Chemotherapy alone or combined with radiation is the treatment of choice for small cell lung cancer; on this regimen, a large percentage of patients experience remission, which in some cases is long lasting. There is however, an ongoing need for effective treatment and diagnostic approaches for lung and bronchial cancers.

An estimated 182,800 new invasive cases of breast cancer were expected to occur among women in the United States during 2000. Additionally, about 1,400 new cases of breast cancer were expected to be diagnosed in men in 2000. After increasing about 4% per year in the 1980s, breast cancer incidence rates in women have leveled off in the 1990s to about 110.6 cases per 100,000.

In the U.S. alone, there were an estimated 41,200 deaths (40,800 women, 400 men) in 2000 due to breast cancer. Breast cancer ranks second among cancer deaths in women. According to the most recent data, mortality rates declined significantly during 1992–1996 with the largest decreases in younger women, both white and black. These decreases were probably the result of earlier detection and improved treatment.

Taking into account the medical circumstances and the patient's preferences, treatment of breast cancer may involve lumpectomy (local removal of the tumor) and removal of the lymph nodes under the arm; mastectomy (surgical removal of the breast) and removal of the lymph nodes under the arm; radiation therapy; chemotherapy; or hormone therapy. Often, two or more methods are used in combination. Numerous studies have shown that, for early stage disease, long-term survival rates after lumpectomy plus radiotherapy are similar to survival rates after modified radical mastectomy. Significant advances in reconstruction techniques provide several options for breast reconstruction after mastectomy. Recently, such reconstruction has been done at the same time as the mastectomy.

Local excision of ductal carcinoma *in situ* (DCIS) with adequate amounts of surrounding normal breast tissue may prevent the local recurrence of the DCIS. Radiation to the breast and/or tamoxifen may reduce the chance of DCIS occurring in the remaining breast tissue. This is important because DCIS, if left untreated, may develop into invasive breast cancer. Nevertheless, there are serious side effects or sequelae to these treatments. There is, therefore, a need for efficacious breast cancer treatments.

There were an estimated 23,100 new cases of ovarian cancer in the United States in 2000. It accounts for 4% of all cancers among women and ranks second among gynecologic cancers. During 1992–1996, ovarian cancer incidence

rates were significantly declining. Consequent to ovarian cancer, there were an estimated 14,000 deaths in 2000. Ovarian cancer causes more deaths than any other cancer of the female reproductive system.

Surgery, radiation therapy, and chemotherapy are treatment options for ovarian cancer. Surgery usually includes the removal of one or both ovaries, the fallopian tubes (salpingo-oophorectomy), and the uterus (hysterectomy). In some very early tumors, only the involved ovary will be removed, especially in young women who wish to have children. In advanced disease, an attempt is made to remove all intra-abdominal disease to enhance the effect of chemotherapy. There continues to be an important need for effective treatment options for ovarian cancer.

There were an estimated 28,300 new cases of pancreatic cancer in the United States in 2000. Over the past 20 years, rates of pancreatic cancer have declined in men. Rates among women have remained approximately constant but may be beginning to decline. Pancreatic cancer caused an estimated 28,200 deaths in 2000 in the United States. Over the past 20 years, there has been a slight but significant decrease in mortality rates among men (about –0.9% per year) while rates have increased slightly among women.

Surgery, radiation therapy, and chemotherapy are treatment options for pancreatic cancer. These treatment options can extend survival and/or relieve symptoms in many patients but are not likely to produce a cure for most. There is a significant need for additional therapeutic and diagnostic options for pancreatic cancer.

SUMMARY OF THE INVENTION

The present invention relates to a gene, designated 191P4D12(b), that has now been found to be over-expressed in the cancer(s) listed in Table I. Northern blot expression analysis of 191P4D12(b) gene expression in normal tissues shows a restricted expression pattern in adult tissues. The nucleotide (Figure 2) and amino acid (Figure 2, and Figure 3) sequences of 191P4D12(b) are provided. The tissue-related profile of 191P4D12(b) in normal adult tissues, combined with the over-expression observed in the tissues listed in Table I, shows that 191P4D12(b) is aberrantly over-expressed in at least some cancers, and thus serves as a useful diagnostic, prophylactic, prognostic, and/or therapeutic target for cancers of the tissue(s) such as those listed in Table I.

The invention provides polynucleotides corresponding or complementary to all or part of the 191P4D12(b) genes, mRNAs, and/or coding sequences, preferably in isolated form, including polynucleotides encoding 191P4D12(b)-related proteins and fragments of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more than 25 contiguous amino acids; at least 30, 35, 40, 45, 50, 55, 60, 65, 70, 80, 85, 90, 95, 100 or more than 100 contiguous amino acids of a 191P4D12(b)-related protein, as well as the peptides/proteins themselves; DNA, RNA, DNA/RNA hybrids, and related molecules, polynucleotides or oligonucleotides complementary or having at least a 90% homology to the 191P4D12(b) genes or mRNA sequences or parts thereof, and polynucleotides or oligonucleotides that hybridize to the 191P4D12(b) genes, mRNAs, or to 191P4D12(b)-encoding polynucleotides. Also provided are means for isolating cDNAs and the genes encoding 191P4D12(b). Recombinant DNA molecules containing 191P4D12(b) polynucleotides, cells transformed or transduced with such molecules, and host-vector systems for the expression of 191P4D12(b) gene products are also provided. The invention further provides antibodies that bind to 191P4D12(b) proteins and polypeptide fragments thereof, including polyclonal and monoclonal antibodies, murine and other mammalian antibodies, chimeric antibodies, humanized and fully human antibodies, and antibodies labeled with a detectable marker or therapeutic agent. In certain embodiments, there is a *proviso* that the entire nucleic acid sequence of Figure 2 is not encoded and/or the entire amino acid sequence of Figure 2 is not prepared. In certain embodiments, the entire nucleic acid sequence of Figure 2 is encoded and/or the entire amino acid sequence of Figure 2 is prepared, either of which are in respective human unit dose forms.

The invention further provides methods for detecting the presence and status of 191P4D12(b) polynucleotides and proteins in various biological samples, as well as methods for identifying cells that express 191P4D12(b). A typical embodiment of

this invention provides methods for monitoring 191P4D12(b) gene products in a tissue or hematology sample having or suspected of having some form of growth dysregulation such as cancer.

The invention further provides various immunogenic or therapeutic compositions and strategies for treating cancers that express 191P4D12(b) such as cancers of tissues listed in Table I, including therapies aimed at inhibiting the transcription, translation, processing or function of 191P4D12(b) as well as cancer vaccines. In one aspect, the invention provides compositions, and methods comprising them, for treating a cancer that expresses 191P4D12(b) in a human subject wherein the composition comprises a carrier suitable for human use and a human unit dose of one or more than one agent that inhibits the production or function of 191P4D12(b). Preferably, the carrier is a uniquely human carrier. In another aspect of the invention, the agent is a moiety that is immunoreactive with 191P4D12(b) protein. Non-limiting examples of such moieties include, but are not limited to, antibodies (such as single chain, monoclonal, polyclonal, humanized, chimeric, or human antibodies), functional equivalents thereof (whether naturally occurring or synthetic), and combinations thereof. The antibodies can be conjugated to a diagnostic or therapeutic moiety. In another aspect, the agent is a small molecule as defined herein.

In another aspect, the agent comprises one or more than one peptide which comprises a cytotoxic T lymphocyte (CTL) epitope that binds an HLA class I molecule in a human to elicit a CTL response to 191P4D12(b) and/or one or more than one peptide which comprises a helper T lymphocyte (HTL) epitope which binds an HLA class II molecule in a human to elicit an HTL response. The peptides of the invention may be on the same or on one or more separate polypeptide molecules. In a further aspect of the invention, the agent comprises one or more than one nucleic acid molecule that expresses one or more than one of the CTL or HTL response stimulating peptides as described above. In yet another aspect of the invention, the one or more than one nucleic acid molecule may express a moiety that is immunologically reactive with 191P4D12(b) as described above. The one or more than one nucleic acid molecule may also be, or encodes, a molecule that inhibits production of 191P4D12(b). Non-limiting examples of such molecules include, but are not limited to, those complementary to a nucleotide sequence essential for production of 191P4D12(b) (e.g. antisense sequences or molecules that form a triple helix with a nucleotide double helix essential for 191P4D12(b) production) or a ribozyme effective to lyse 191P4D12(b) mRNA.

Note that to determine the starting position of any peptide set forth in Tables VIII-XXI and XXII to XLIX (collectively HLA Peptide Tables) respective to its parental protein, e.g., variant 1, variant 2, etc., reference is made to three factors: the particular variant, the length of the peptide in an HLA Peptide Table, and the Search Peptides in Table VII. Generally, a unique Search Peptide is used to obtain HLA peptides of a particular for a particular variant. The position of each Search Peptide relative to its respective parent molecule is listed in Table VII. Accordingly, if a Search Peptide begins at position "X", one must add the value "X - 1" to each position in Tables VIII-XXI and XXII to XLIX to obtain the actual position of the HLA peptides in their parental molecule. For example, if a particular Search Peptide begins at position 150 of its parental molecule, one must add 150 - 1, i.e., 149 to each HLA peptide amino acid position to calculate the position of that amino acid in the parent molecule.

One embodiment of the invention comprises an HLA peptide, that occurs at least twice in Tables VIII-XXI and XXII to XLIX collectively, or an oligonucleotide that encodes the HLA peptide. Another embodiment of the invention comprises an HLA peptide that occurs at least once in Tables VIII-XXI and at least once in tables XXII to XLIX, or an oligonucleotide that encodes the HLA peptide.

Another embodiment of the invention is antibody epitopes, which comprise a peptide regions, or an oligonucleotide encoding the peptide region, that has one two, three, four, or five of the following characteristics:

i) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Hydrophilicity profile of Figure 5;

ii) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or less than 0.5, 0.4, 0.3, 0.2, 0.1, or having a value equal to 0.0, in the Hydropathicity profile of Figure 6;

iii) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Percent Accessible Residues profile of Figure 7;

iv) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Average Flexibility profile of Figure 8; or

v) a peptide region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Beta-turn profile of Figure 9.

In another embodiment, there is provided a peptide selected from the group consisting of:

a) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 3;

b) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 5;

c) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 7;

d) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 9;

e) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 11;

f) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 13;

g) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 15;

h) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 17;

i) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 19;

j) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 21;

k) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 23;

l) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 25;

m) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 27;

n) a peptide of eight, nine, ten or eleven contiguous amino acids of SEQ ID NO: 29;

o) a peptide of Tables VIII-XXI; p) a peptide of Tables XXII-XLV; and q) a peptide of Tables XLVI to XLIX. The peptide may be at least 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% homologous to an entire amino acid sequence of a peptide described herein. The peptide may be a CTL polypeptide or an analog thereof or an antibody peptide epitope.

In another embodiment, there is provided a peptide related to at least one peptide selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment there is provided a polynucleotide or a polynucleotide complementary thereto that encodes a peptide described herein. The polynucleotide may comprise a sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 4; SEQ ID NO: 6; SEQ ID NO: 8; SEQ ID NO: 10; SEQ ID NO: 12; SEQ ID NO: 14; SEQ ID NO: 16; SEQ ID NO: 18; SEQ ID NO: 20; SEQ ID NO: 22; SEQ ID NO: 24; SEQ ID NO: 27; and SEQ ID NO: 28.

In another embodiment, there is provided an antibody or fragment thereof that specifically binds to at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29 produced by a transgenic animal or a hybridoma. The antibody may be monoclonal, or a human antibody, a humanized antibody, or a chimeric antibody.

In another embodiment, there is provided a method of generating a mammalian immune response directed to at least one peptide selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, the method comprising: exposing cells of the mammal's immune system, *in vitro*, to a portion of a) a 191P4D12(b)-related protein and/or b) a nucleotide sequence that encodes said protein.

In another embodiment, there is provided a method of generating an immune response, the method comprising: providing a 191P4D12(b)-related protein that comprises at least one T cell or at least one B cell epitope; and contacting, *in vitro*, the epitope with a mammalian immune system T cell or B cell respectively, whereby the T cell or B cell is

activated. The immune system cell may be a B cell, and whereby the activated B cell generates antibodies that specifically bind to the 191P4D12(b)-related protein. The immune system cell may be a T cell that is a cytotoxic T cell (CTL) and whereby the activated CTL kills an autologous cell that expresses the 191P4D12(b)-related protein. The immune system cell may be a T cell that is a helper T cell (HTL) and whereby the activated HTL secretes cytokines that facilitate the cytotoxic activity of a cytotoxic T cell (CTL) or the antibody-producing activity of a B cell.

In another embodiment, there is provided a method for detecting the presence of a 191P4D12(b)-related protein or a 191P4D12(b)-related polynucleotide in a sample, the method comprising: contacting the same with a substance that specifically binds to the 191P4D12(b)-related protein or to the 191P4D12(b)-related polynucleotide, respectively, and, determining that there is a complex of the substance with the 191P4D12(b)-related protein with a substance with the 191P4D12(b)-related polynucleotide, respectively.

In another embodiment, there is provided a method for detecting the presence of a 191P4D12(b)-related protein in a sample, the method comprising: contacting the sample with an antibody or fragment thereof which specifically bind to the 191P4D12(b)-related protein; and determining that there is a complex of the antibody or fragment thereof and the 191P4E12(b)-related protein.

In another embodiment, there is provided a method for detecting the presence of mRNA encoding at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29 in a sample comprising: producing cDNA from the sample by reverse transcription using at least one primer; amplifying the cDNA so produced using 191P4D12(b)-related polynucleotides as sense and antisense primers wherein the 191P4D12(b) polynucleotides used at the sense and antisense primers serve to amplify 191P4D12(b) cDNA; and detecting the presence of the amplified 191P4D12(b) cDNA.

In another embodiment, there is provided a method for monitoring one or more 191P4D12(b) gene products in a biological sample, the method comprising: determining the status of one or more 191P4D12(b) gene products expressed by cells in a tissue sample from an individual; comparing the status so determined to the status of one or more 191P4D12(b) gene products in a corresponding normal sample ; and, identifying the presence of one or more aberrant gene products of 191P4D12(b) in the sample relative to the normal sample. The gene products may be a 191P4D12(b) mRNA or a 191P4D12(b) protein, and whereby the presence of one or more elevated gene products in the test sample relative to the normal tissue sample indicates the presence or status of a cancer.

In another embodiment, there is provided a method of delivering a cytotoxic agent or a diagnostic agent to a cell, *in vitro*, that expresses at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, said method comprising: providing the cytotoxic agent or the diagnostic agent conjugated to an antibody or fragment thereof; and, exposing the cell to the antibody-agent or fragment-agent conjugate.

In another embodiment, there is provided a compound capable of modulating the status of a cell that expresses a protein selected from the group consisting of SEQ ID NO. 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29 selected from the group consisting of: a) a substance that modulates the status of a protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29; and b) a molecule that is modulated by a protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided a method of inhibiting growth of cancer cells, *in vitro*, that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, the method comprising administering to the cells a composition described herein.

In another embodiment, there is provided a method of inhibiting growth of cancer cells, *in vitro*, that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, the method comprising administering to said cells an antibody or fragment thereof, which specifically bind to a 191P4D12(b) - related protein.

In another embodiment, there is provided a method of inhibiting growth of cancer cells, *in vitro*, that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, the method comprising administering to said cells a 191P4D12(b)-related protein.

In another embodiment, there is provided a method of inhibiting growth of cancer cells, *in vitro*, that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, the method comprising administering to said cells a polynucleotide comprising a 191P4D12 (b)-related protein coding sequence or a polynucleotide complementary to a polynucleotide having a 191P4D12(b)-related protein coding sequence.

In another embodiment, there is provided a method of inhibiting growth of cancer

cells, *in vitro*, that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, the method comprising administering to said cells a ribozyme that cleaves a polynucleotide that encodes at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided a method of inhibiting growth of cancer cells, *in vitro*, that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, and a particular HLA molecule, the method comprising administering to said cells human T cells wherein said T cells specifically recognize a peptide subsequence of at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29 in the context of the particular HLA molecule.

In another embodiment, there is provided a method of inhibiting growth of cancer cells, *in vitro*, that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, the method comprising administering a vector that delivers a single chain monoclonal antibody coding sequence, whereby the encoded single chain antibody is expressed intracellularly within cancer cells, *in vitro*, that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided use of a 191P4D12(b)-related protein that comprises at least one T cell or at least one B cell epitope for generating an immune response or for preparation of a medicament for generating an immune response. The immune response may be an activated B cell generates that antibodies that specifically bind to the 191P4D12(b)-related protein. The immune response is an activated cytotoxic T cell (CTL) that kills an autologous cell that expresses the 191P4D12(b)-related protein. The immune response may be an activated helper T cell (HTL) that secretes cytokines that facilitate the cytotoxic activity of a cytotoxic T cell (CTL) or the antibody-producing activity of a B cell.

In another embodiment, there is provided use of a composition described herein for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29. The use may be for preparation of a medicament for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided use of an antibody or fragment thereof, which specifically bind to a 191P4D12(b)-related protein for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29. The use may be for preparation of a medicament for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided use of a 191P4D12(b)-related protein for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29. The use may be for preparation of a medicament for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided use of a polynucleotide comprising a 191P4D12(b)-related protein coding sequence or a polynucleotide complementary to a polynucleotide having a 191P4D12(b)-related protein coding sequence for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29. The use may be fore preparation of a medicament for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided use of a ribozyme that cleaves a polynucleotide that encodes at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29 for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29. The use may be for preparation of a medicament for

inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided use of a human T cell that specifically recognizes a peptide subsequence of at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29 in the context of a particular HLA molecule for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, and the particular HLA molecule. The use may be for preparation of a medicament for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29, and the particular HLA molecule.

In another embodiment, there is provided use of a vector that delivers a single chain monoclonal antibody coding sequence, whereby the encoded single chain antibody is expressed intracellularly within cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29 for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9; SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29. The use may be for preparation of a medicament for inhibiting growth of cancer cells that express at least one protein selected from the group consisting of SEQ ID NO: 3, SEQ ID NO: 5; SEQ ID NO: 7; SEQ ID NO: 9;

SEQ ID NO: 11; SEQ ID NO: 13; SEQ ID NO: 15; SEQ ID NO: 17; SEQ ID NO: 19; SEQ ID NO: 21; SEQ ID NO: 23; SEQ ID NO: 25; SEQ ID NO: 27; and SEQ ID NO: 29.

In another embodiment, there is provided a vector that encodes a polynucleotide described herein or a polynucleotide complementary thereto. The vector may be a viral vector or an adenovirus vector.

The invention disclosed and claimed herein relates to a method for determining if there is dysregulated cellular growth in a human subject, comprising: (a) contacting a test sample from a human subject suspected of having cancer with a probe that is capable of specifically binding to a 191P4D12(b)-related gene product, wherein the 191P4D12(b)-related gene product is an mRNA comprising the sequence set forth in SEQ ID NO: 2, SEQ ID NO:4, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 or SEQ ID NO:26, or a protein comprising the sequence set forth in SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 or SEQ ID NO:27, respectively; (b) determining the level of expression of the 191P4D12(b)-related gene product in the test sample; and (c) comparing the level so determined to the expression level of the 191P4D12(b)-related gene product in a normal tissue sample of the same tissue type as the test sample, whereby an increase in the 191P4D12(b)-related gene product in the test sample relative to the normal tissue sample indicates dysregulated cellular growth in said test sample from an organ selected from the group consisting of bladder, lung, kidney, pancreas, colon, prostate, cervix, and ovary.

The invention disclosed and claimed herein also relates to a method for determining susceptibility to developing cancer, comprising: (a) contacting a test sample from a human subject suspected of having cancer with a probe that is capable of specifically binding to a 191P4D12(b) mRNA or a 191P4D12(b) protein, wherein the 191P4D12(b) mRNA comprising the sequence set forth in SEQ ID NO: 2, SEQ ID NO:4, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 or SEQ ID NO:26, and the 191P4D12(b) protein comprising the sequence set forth in SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 or SEQ ID NO:27, respectively; (b) determining the level of expression of the 191P4D12(b) mRNA or the 191P4D12(b) protein in the test sample; and (c) comparing the level so determined to the expression level of the 191P4D12(b) mRNA or the 191P4D12(b) protein in a normal tissue sample of the same tissue type as the test sample, whereby an increase in the 191P4D12(b) mRNA or the 191P4D12(b) protein in the test sample relative to the normal tissue sample indicates susceptibility to developing cancer in said test sample from an organ selected from the group consisting of bladder, lung, kidney, pancreas, colon, prostate, cervix, and ovary.

The invention disclosed and claimed herein also relates to use of an antibody or antigen binding fragment thereof that specifically binds to a protein comprising the amino acid sequence of SEQ ID NO: 3 for inhibiting growth of a tumor cell that expresses the protein, wherein the antibody or antigen binding fragment is conjugated to a cytotoxic agent, and wherein the cell is from a tissue source selected from the group consisting of prostate, bladder, lung, pancreas, and breast cancer.

The invention disclosed and claimed herein also relates to use of antibody-agent conjugate comprising: an antibody or antigen binding fragment thereof that binds specifically to a protein comprising the amino acid sequence of SEQ ID NO: 3; and a cytotoxic agent conjugated to the antibody or fragment, for inhibiting growth of a tumor cell that expresses the protein, wherein the cell is from a tissue source selected from the group consisting of prostate, bladder, lung, pancreas, and breast cancer.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1. The 191P4D12(b) SSH sequence of 223 nucleotides.

Figure 2. A) The cDNA and amino acid sequence of 191P4D12(b) variant 1 (also called "191P4D12(b) v.1" or "191P4D12(b) variant 1") is shown in Figure 2A. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

B) The cDNA and amino acid sequence of 191P4D12(b) variant 2 (also called "191P4D12(b) v.2") is shown in Figure 2B. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

C) The cDNA and amino acid sequence of 191P4D12(b) variant 3 (also called "191P4D12(b) v.3") is shown in Figure 2C. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

D) The cDNA and amino acid sequence of 191P4D12(b) variant 4 (also called "191P4D12(b) v.4") is shown in Figure 2D. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

E) The cDNA and amino acid sequence of 191P4D12(b) variant 5 (also called "191P4D12(b) v.5") is shown in Figure 2E. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

F) The cDNA and amino acid sequence of 191P4D12(b) variant 6 (also called "191P4D12(b) v.6") is shown in Figure 2F. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 789-1676 including the stop codon.

G) The cDNA and amino acid sequence of 191P4D12(b) variant 7 (also called "191P4D12(b) v.7") is shown in Figure 2G. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1721 including the stop codon.

H) The cDNA and amino acid sequence of 191P4D12(b) variant 8 (also called "191P4D12(b) v.8") is shown in Figure 2H. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

I) The cDNA and amino acid sequence of 191P4D12(b) variant 9 (also called "191P4D12(b) v.9") is shown in Figure 2I. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 708-1121 including the stop codon.

J) The cDNA and amino acid sequence of 191P4D12(b) variant 10 (also called "191P4D12(b) v.10") is shown in Figure 2J. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

K) The cDNA and amino acid sequence of 191P4D12(b) variant 11 (also called "191P4D12(b) v.11") is shown in Figure 2K. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

L) The cDNA and amino acid sequence of 191P4D12(b) variant 12 (also called "191P4D12(b) v.12") is shown in Figure 2L. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

M) The cDNA and amino acid sequence of 191P4D12(b) variant 13 (also called "191P4D12(b) v.13") is shown in Figure 2M. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 264-1799 including the stop codon.

N) The cDNA and amino acid sequence of 191P4D12(b) variant 14 (also called "191P4D12(b) v.14") is shown in Figure 2N. The codon for the start methionine is underlined. The open reading frame extends from nucleic acid 708-1121 including the stop codon.

Figure 3.

A) The amino acid sequence of 191P4D12(b) v.1 is shown in Figure 3A; it has 510 amino acids.

B) The amino acid sequence of 191P4D12(b) v.2 is shown in Figure 3B; it has 510 amino acids.

C) The amino acid sequence of 191P4D12(b) v.6 is shown in Figure 3C; it has 295 amino acids.

D) The amino acid sequence of 191P4D12(b) v.7 is shown in Figure 3D; it has 485 amino acids.

E) The amino acid sequence of 191P4D12(b) v.10 is shown in Figure 3E; it has 510 amino acids.

F) The amino acid sequence of 191P4D12(b) v.11 is shown in Figure 3F; it has 510 amino acids.

G) The amino acid sequence of 191P4D12(b) v.12 is shown in Figure 3G; it has 510 amino acids.

H) The amino acid sequence of 191P4D12(b) v.13 is shown in Figure 3H; it has 511 amino acids.

I) The amino acid sequence of 191P4D12(b) v.9 is shown in Figure 3I; it has 137 amino acids.

J) The amino acid sequence of 191P4D12(b) v.14 is shown in Figure 3J; it has 137 amino acids.

As used herein, a reference to 191P4D12(b) includes all variants thereof, including those shown in Figures 2, 3, 10, and 11, unless the context clearly indicates otherwise.

Figure 4. Alignment of 191P4D12(b) with known homologs. Figure 4(A) Alignment of 191P4D12(b)with human Ig superfamily receptor LNIR (gi 14714574). Figure 4(B) Alignment of 191P4D12(b) with mouse nectin 4 (gi 18874521).

Figure 5. Hydrophilicity amino acid profile of 191P4D12(b)v.1, v.7, and v.9 determined by computer algorithm sequence analysis using the method of Hopp and Woods (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828) accessible on the Protscale website
through the ExPasy molecular biology server.

Figure 6. Hydropathicity amino acid profile of 191P4D12(b)v.1, v.7, and v.9 determined by computer algorithm sequence analysis using the method of Kyte and Doolittle (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132) accessible on the ProtScale website through the ExPasy molecular biology server.

Figure 7. Percent accessible residues amino acid profile of 191P4D12(b)v.1, v.7, and v.9 determined by computer algorithm sequence analysis using the method of Janin (Janin J., 1979 Nature 277:491-492) accessed on the ProtScale website through the ExPasy molecular biology server.

Figure 8. Average flexibility amino acid profile of 191P4D12(b)v.1, v.7, and v.9 determined by computer algorithm sequence analysis using the method of Bhaskaran and Ponnuswamy (Bhaskaran R., and Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255) accessed on the ProtScale website through the ExPasy molecular biology server.

Figure 9. Beta-turn amino acid profile of 191P4D12(b)v.1, v.7, and v.9 determined by computer algorithm sequence analysis using the method of Deleage and Roux (Deleage, G„ Roux B. 1987 Protein Engineering 1:289-294) accessed on the ProtScale website located on the World Wide Web through the ExPasy molecular biology server.

Figure 10. Schematic alignment of SNP variants of 191P4D12(b). Variants 191P4D12(b) v.2 through v.5 and v.10 through v.12 are variants with single nucleotide differences. Compared with v.1, v.13 had an insertion of three bases (GCA) between 1262 and1263 and added one amino acid "A" to the protein. Variant v.14 was a SNP variant of transcript variant v.9, corresponding to the SNP at 2688 of v.1. Though these SNP variants were shown separately, they could also occur in any combinations and in any transcript variants, as shown in Fig. 12, that contained the base pairs. Numbers correspond to those of 191P4D12(b) v.1. Black box shows the same sequence as 191P4D12(b) v.1. SNPs are indicated above the box.

Figure 11. Schematic alignment of protein variants of 191P4D12(b). Protein variants correspond to nucleotide variants. Nucleotide variants 191P4D12(b) v.3, v.4, v.5 and v.8 coded for the same protein as v.1. Nucleotide variants 191P4D12(b) v.6, v.7, v.8 and v.9 were splice variants of v.1, as shown in Figure 12. Variant v.9 translated to a totally different protein than other variants, with two isoforms that different from each other by one amino acid at 64: A or D. Variant v.13 had an insertion of one amino acid "A" at 334. Single amino acid differences were indicated above the boxes. Black boxes represent the same sequence as 191P4D12(b) v.1. Numbers underneath the box correspond to 191P4D12(b) v.1.

Figure 12. Exon compositions of transcript variants of 191P4D12(b). Variant 191P4D12(b) v.6, v.7, v.8 and v.9 are transcript variants of v.1. Variants v.6, v.7 and v.8 spliced out 202-321, 1497-1571 and 2951-3013 of v.1, respectively. Variant v.9 was part of the last exon of v.1. The order of the potential exons on the human genome is shown at the bottom. Poly A tails were not shown in the figure. Ends of exons are shown above the boxes. Numbers in "( )" underneath the boxes correspond to those of 191P4D12(b) v.1. Lengths of introns and exons are not proportional.

Figure 13. Secondary structure and transmembrane domains prediction for 191P4D12(b) protein variants. The secondary structure of 191P4D12(b) protein variants 1 (SEQ ID NO:127), v6 (SEQ ID NO:128), v7 (SEQ ID NO:129), and v9 (SEQ ID NO:130) (Figures 13A-D respectively) were predicted using the HNN - Hierarchical Neural Network method (Guermeur, 1997) accessed from the ExPasy molecular biology server. This method predicts the presence and location of alpha helices, extended strands, and random coils from the primary protein sequence.

The percent of the protein in a given secondary structure is also listed. Figures **13E**, **13G**, **13I**, **13K**: Schematic representations of the probability of existence of transmembrane regions and orientation of 191P4D12(b) variants 1, 6, 7, and 9, respectively, based on the TMpred algorithm of Hofmann and Stoffel which utilizes TMBASE (K. Hofmann, W. Stoffel. TMBASE - A database of membrane spanning protein segments Biol. Chem. Hoppe-Seyler 374: 166, 1993). Figures **13F**, **13H**, **13J**, **13L**. Schematic representations of the probability of the existence of transmembrane regions and the extracellular and intracellular orientation of 191P4D12(b) variants 1, 6, 7, and 9, respectively, based on the TMHMM algorithm of Sonnhammer, von Heijne, and Krogh (Erik LL Sonnhammer, Gunnarvon Heijne, and Anders Krogh: A hidden Markov model for predicting transmembrane helices in protein sequences. In Proc. of Sixth Int. Conf. on Intelligent Systems for

Molecular Biology, p 175-182 Ed J. Glasgow, T. Littlejohn, F. Major, R. Lathrop, D. Sankoff, and C. Sensen Menlo Park, CA: AAAI Press, 1998). The TMpred and TMHMM algorithms are accessed from the ExPasy molecular biology server .

Figure 14. 191P4D12(b) Expression by RT-PCR. First strand cDNA was prepared from (A) vital pool 1 (liver, lung and kidney), vital pool 2 (pancreas, colon and stomach), normal kidney, prostate cancer pool, bladder cancer pool, colon cancer pool, lung cancer pool, breast cancer pool and cancer metastasis pool; (B) prostate cancer metastasis to lymph node, prostate cancer pool, bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, ovary cancer pool, breast cancer pool, cancer metastasis pool, pancreas cancer pool, and LAPC prostate xenograft pool. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 191P4D12(b), was performed at 26 and 30 cycles of amplification. In (A) results show strong expression of 191P4D12(b) in bladder cancer pool. Expression of 191P4D12(b) was also detected in prostate cancer pool, colon cancer pool, lung cancer pool, breast cancer pool and cancer metastasis pool but very weakly in vital pool 1 and vital pool 2. In (B) results show strong expression of 191P4D12(b) in prostate, bladder, kidney, colon, lung, ovary, breast, cancer metastasis, and pancreas cancer specimens.

Figure 15. Expression of 191P4D12(b) in normal tissues. Two multiple tissue northern blots (Clontech) both with 2 ug of mRNA/lane were probed with the 191P4D12(b) sequence. Size standards in kilobases (kb) are indicated on the side. Results show expression of an approximately 4kb transcript in placenta and very weakly in prostate but not in any other normal tissue tested. A smaller 191P4D12(b) transcript of approximately 2.5kb was detected in heart and skeletal muscle.

Figure 16. Expression of 191P4D12(b) in Patient Cancer Specimens and Normal Tissues. RNA was extracted from a pool of 3 bladder cancer patient specimens, as well as from normal prostate (NP), normal bladder (NB), normal kidney (NK), normal colon (NC), normal lung (NL), normal breast (NBr), normal ovary (NO), and normal pancreas (NPa). Northern blot with 10 ug of total RNA/lane was probed with 191P4D12(b) SSH sequence. Size standards in kilobases (kb) are indicated on the side. The 191P4D12(b) transcript was detected in the bladder cancer specimens, but not in the normal tissues tested.

Figure 17. Expression of 191P4D12(b) in Bladder Cancer Patient Specimens. RNA was extracted from bladder cancer cell lines (CL), normal bladder (N), and bladder cancer patient tumors (T). Northern blots with 10 ug of total RNA were probed with the 191P4D12(b) SSH fragment. Size standards in kilobases are on the side. Results show expression of the approximately 4kb 191P4D12(b) transcript in the bladder tumor tissues but not in normal bladder. A smaller transcript was detected in the HT1197 cell line but not in the other cancer cell lines tested.

Figure 18. Expression of 191P4D12(b) in Prostate Cancer Xenografts. RNA was extracted from normal prostate, and from the prostate cancer xenografts LAPC-4AD, LAPC-4AI, LAPC-9AD, and LAPC-9AI. Northern blots with 10 ug of total RNA were probed with the 191P4D12(b) SSH fragment. Size standards in kilobases are on the side. Results show expression of the approximately 4kb 191P4D12(b) transcript in all the LAPC xenograft tissues but not in normal prostate.

Figure 19. Expression of 191P4D12(b) in Cervical Cancer Patient Specimens. RNA was extracted from normal cervix, Hela cancer cell line, and 3 cervix cancer patient tumors (T). Northern blots with 10 ug of total RNA were probed with the 191P4D12(b) SSH fragment. Size standards in kilobases are on the side. Results show expression of the approximately 4kb 191P4D12(b) transcript in 2 out of 3 cervix tumors but not in normal cervix nor in the Hela cell line.

Figure 20. Expression of 191P4D12(b) in Lung Cancer Patient Specimens. RNA was extracted from lung cancer cell lines (CL), normal lung (N), bladder cancer patient tumors (T), and normal adjacent tissue (Nat). Northern blots with 10 ug of total RNA were probed with the 191P4D12(b). Size standards in kilobases are on the side. Results show expression of the approximately 4kb 191P4D12(b) transcript in the lung tumor tissues but not in normal lung nor in the cell lines tested.

Figure 21. Figure 21A. 191P4D12(b) Expression in Lung Cancer. First strand cDNA was prepared from a panel of lung cancer specimens. Normalization was performed by PCR using primers to actin. Semi-quantitative PCR, using

primers to 191P4D12(b) SSH fragment, was performed at 26 and 30 cycles of amplification. Expression level was recorded as 0 = no expression detected; 1 = weak expression, 2 = moderate expression; 3 = strong expression. Results show expression of 191P4D12(b) in 97% of the 31 lung cancer patient specimens tested. **Figure 21B.** 191P4D12(b) Expression in Bladder Cancer. First strand cDNA was prepared from a panel of bladder cancer specimens. Normalization was performed by PCR using primers to actin. Semi-quantitative PCR, using primers to 191P4D12(b) SSH fragment, was performed at 26 and 30 cycles of amplification. Expression level was recorded as 0 = no expression detected; 1 = weak expression, 2 = moderate expression; 3 = strong expression. Results show expression of 191P4D12(b) in 94% of the 18 bladder cancer patient specimens tested. **Figure 21C.** 191P4D12(b) Expression in Prostate Cancer. First strand cDNA was prepared from a panel of prostate cancer specimens, and four LAPC prostate cancer xenografts. Normalization was performed by PCR using primers to actin. Semi-quantitative PCR, using primers to 191P4D12(b) SSH fragment, was performed at 26 and 30 cycles of amplification. Expression level was recorded as 0 = no expression detected; 1 = weak expression, 2 = moderate expression; 3 = strong expression. Results show expression of 191P4D12(b) in 100% of the 20 prostate cancer patient specimens tested, and in all 4 prostate cancer xenografts. **Figure 21D.** 191P4D12(b) Expression in Colon Cancer. First strand cDNA was prepared from a panel of colon cancer specimens. Normalization was performed by PCR using primers to actin. Semi-quantitative PCR, using primers to 191P4D12(b) SSH fragment, was performed at 26 and 30 cycles of amplification. Expression level was recorded as 0 = no expression detected; 1 = weak expression, 2 = moderate expression; 3 = strong expression. Results show expression of 191P4D12(b) in 100% of the 22 colon cancer patient specimens tested. **Figure 21E.** 191P4D12(b) Expression in Uterus Cancer. First strand cDNA was prepared from a panel of uterus cancer specimens. Normalization was performed by PCR using primers to actin. Semi-quantitative PCR, using primers to 191P4D12(b) SSH fragment, was performed at 26 and 30 cycles of amplification. Expression level was recorded as 0 = no expression detected; 1 = weak expression, 2 = moderate expression; 3 = strong expression. Results show expression of 191P4D12(b) in 100% of the 12 uterus cancer patient specimens tested. **Figure 21F.** 191P4D12(b) Expression in Cervical Cancer. First strand cDNA was prepared from a panel of cervix cancer specimens. Normalization was performed by PCR using primers to actin. Semi-quantitative PCR, using primers to 191P4D12(b) SSH fragment, was performed at 26 and 30 cycles of amplification. Expression level was recorded as 0 = no expression detected; 1 = weak expression, 2 = moderate expression; 3 = strong expression. Results show expression of 191P4D12(b) in 100% of the 14 cervix cancer patient specimens tested.

Figure 22. Transient Expression of 191P4D12(b) in Transfected 293T Cells. 293T cells were transfected with either 191P4D12(b) .pTag5, 191P4D12(b).pcDNA3.1/mychis or pcDNA3.1/mychis vector control. Forty hours later, cell lysates and supernatant were collected. Samples were run on an SDS-PAGE acrylamide gel, blotted and stained with anti-his antibody. The blot was developed using the ECL chemiluminescence kit and visualized by autoradiography. Results show expression from 191P4D12(b).pTag5 plasmid of 191P4D12(b) extracellular domain in the lysate (Lane 2) and secretion in the culture supernatant (Lane 1). Also, expression of 191P4D12(b) was detected from in the lysates of 191P4D12(b).pcDNA3.1/mychis transfected cells (Lane 3), but not from the control pcDNA3.1/mychis (Lane 4).

Figure 23. Expression of 191P4D12(b) in Transduced Cells Following Retroviral Gene Transfer. 3T3 cells were transduced with the pSRa retroviral vector encoding the 191P4D12(b) gene. Following selection with neomycin, the cells were expanded and RNA was extracted. Northern blot with 10 ug of total RNA/lane was probed with the 191P4D12(b) SSH sequence. Size standards in kilobases (kb) are indicated on the side. Results show expression of the 191P4D12(b) transcript driven from the retroviral LTR, which migrates slower than the endogenous 4 kb 191P4D12(b) transcript detected in the positive control LAPC-4AD.

DETAILED DESCRIPTION OF THE INVENTION

Outline of Sections

I.) Definitions:

Unless otherwise defined, all terms of art, notations and other scientific terms or terminology used herein are intended to have the meanings commonly understood by those of skill in the art to which this invention pertains. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion

of such definitions herein should not necessarily be construed to represent a substantial difference over what is generally understood in the art. Many of the techniques and procedures described or referenced herein are well understood and commonly employed using conventional methodology by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2nd. edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. As appropriate, procedures involving the use of commercially available kits and reagents are generally carried out in accordance with manufacturer defined protocols and/or parameters unless otherwise noted.

The terms "advanced prostate cancer", "locally advanced prostate cancer", "advanced disease" and "locally advanced disease" mean prostate cancers that have extended through the prostate capsule, and are meant to include stage C disease under the American Urological Association (AUA) system, stage C1 - C2 disease under the Whitmore-Jewett system, and stage T3 - T4 and N+ disease under the TNM (tumor, node, metastasis) system. In general, surgery is not recommended for patients with locally advanced disease, and these patients have substantially less favorable outcomes compared to patients having clinically localized (organ-confined) prostate cancer. Locally advanced disease is clinically identified by palpable evidence of induration beyond the lateral border of the prostate, or asymmetry or induration above the prostate base. Locally advanced prostate cancer is presently diagnosed pathologically following radical prostatectomy if the tumor invades or penetrates the prostatic capsule, extends into the surgical margin, or invades the seminal vesicles.

"Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence 191P4D12(b) (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence 191P4D12(b). In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

The term "analog" refers to a molecule which is structurally similar or shares similar or corresponding attributes with another molecule (e.g. a 191P4D12(b)-related protein). For example, an analog of a 191P4D12(b) protein can be specifically bound by an antibody or T cell that specifically binds to 191P4D12(b).

The term "antibody" is used in the broadest sense. Therefore, an "antibody" can be naturally occurring or man-made such as monoclonal antibodies produced by conventional hybridoma technology. Anti-191P4D12(b) antibodies comprise monoclonal and polyclonal antibodies as well as fragments containing the antigen-binding domain and/or one or more complementarity determining regions of these antibodies.

An "antibody fragment" is defined as at least a portion of the variable region of the immunoglobulin molecule that binds to its target, i.e., the antigen-binding region. In one embodiment it specifically covers single anti-191P4D12(b) antibodies and clones thereof (including agonist, antagonist and neutralizing antibodies) and anti-191P4D12(b) antibody compositions with polyepitopic specificity.

The term "codon optimized sequences" refers to nucleotide sequences that have been optimized for a particular host species by replacing any codons having a usage frequency of less than about 20%. Nucleotide sequences that have been optimized for expression in a given host species by elimination of spurious polyadenylation sequences, elimination of exon/intron splicing signals, elimination of transposon-like repeats and/or optimization of GC content in addition to codon optimization are referred to herein as an "expression enhanced sequences."

A "combinatorial library" is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a

polypeptide compound). Numerous chemical compounds are synthesized through such combinatorial mixing of chemical building blocks (Gallop et al., J. Med. Chem. 37(9): 1233-1251 (1994)).

Preparation and screening of combinatorial libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka, Pept. Prot. Res. 37:487-493 (1991), Houghton et al., Nature, 354:84-88 (1991)), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio- oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs et al., Proc. Nat. Acad. Sci. USA 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara et al., J. Amer. Chem. Soc. 114:6568 (1992)), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann et al., J. Amer. Chem. Soc. 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen et al., J. Amer. Chem. Soc. 116:2661 (1994)), oligocarbamates (Cho, et al., Science 261:1303 (1993)), and/or peptidyl phosphonates (Campbell et al., J. Org. Chem. 59:658 (1994)). See, generally, Gordon et al., J. Med. Chem. 37:1385 (1994), nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn et al., Nature Biotechnology 14(3): 309-314 (1996), and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al., Science 274:1520-1522 (1996), and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum, C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506, 337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 NIPS, 390 NIPS, Advanced Chem Tech, Louisville KY; Symphony, Rainin, Woburn, MA; 433A, Applied Biosystems, Foster City, CA; 9050, Plus, Millipore, Bedford, NIA). A number of well-known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations such as the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate H, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, NJ; Asinex, Moscow, RU; Tripos, Inc., St. Louis, MO; ChemStar, Ltd, Moscow, RU; 3D Pharmaceuticals, Exton, PA; Martek Biosciences, Columbia, MD; etc.).

The term "cytotoxic agent" refers to a substance that inhibits or prevents the expression activity of cells, function of cells and/or causes destruction of cells. The term is intended to include radioactive isotopes chemotherapeutic agents, and toxins such as small molecule toxins or enzymatically active toxins of bacterial, fungal, plant or animal origin, including fragments and/or variants thereof. Examples of cytotoxic agents include, but are not limited to auristatins, auromycins, maytansinoids, yttrium, bismuth, ricin, ricin A-chain, combrestatin, duocarmycins, dolostatins, doxorubicin, daunorubicin, taxol, cisplatin, cc1065, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin, diphtheria toxin, Pseudomonas exotoxin (PE) A, PE40, abrin, abrin A chain, modeccin A chain, alpha-sarcin, gelonin, mitogellin, retstrictocin, phenomycin, enomycin, curicin, crotin, calicheamicin, *Sapaonaria officinalis* inhibitor, and glucocorticoid and other chemotherapeutic agents, as well as radioisotopes such as At^{211}, I^{131}, I^{125}, Y^{90}, Re^{186}, Re^{188}, Sm^{153}, $Bi^{212 \text{ or } 213}$, P^{32} and radioactive isotopes of Lu including Lu^{177}. Antibodies may also be conjugated to an anti-cancer pro-drug activating enzyme capable of converting the pro-drug to its active form.

The "gene product" is sometimes referred to herein as a protein or mRNA. For example, a "gene product of the invention" is sometimes referred to herein as a "cancer amino acid sequence", "cancer protein", "protein of a cancer listed in

Table I", a "cancer mRNA", "mRNA of a cancer listed in Table I", etc. In one embodiment, the cancer protein is encoded by a nucleic acid of Figure 2. The cancer protein can be a fragment, or alternatively, be the full-length protein to the fragment encoded by the nucleic acids of Figure 2. In one embodiment, a cancer amino acid sequence is used to determine sequence identity or similarity. In another embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of Figure 2. In another embodiment, the sequences are sequence variants as further described herein.

"High throughput screening" assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins; U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays); while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Amersham Biosciences, Piscataway, NJ; Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA; etc.). These systems typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

The term "homolog" refers to a molecule which exhibits homology to another molecule, by for example, having sequences of chemical residues that are the same or similar at corresponding positions.

"Human Leukocyte Antigen" or "HLA" is a human class I or class II Major Histocompatibility Complex (MHC) protein (*see, e.g.*, Stites, *et al.*, IMMUNOLOGY, 8TH ED., Lange Publishing, Los Altos, CA (1994).

The terms "hybridize", "hybridizing", "hybridizes" and the like, used in the context of polynucleotides, are meant to refer to conventional hybridization conditions, preferably such as hybridization in 50% formamide/6XSSC/0.1% SDS/100 μg/ml ssDNA, in which temperatures for hybridization are above 37 degrees C and temperatures for washing in 0.1XSSC/0.1% SDS are above 55 degrees C.

The phrases "isolated" or "biologically pure" refer to material which is substantially or essentially free from components which normally accompany the material as it is found in its native state. Thus, isolated peptides in accordance with the invention preferably do not contain materials normally associated with the peptides in their *in situ* environment. For example, a polynucleotide is said to be "isolated" when it is substantially separated from contaminant polynucleotides that correspond or are complementary to genes other than the 191P4D12(b) genes or that encode polypeptides other than 191P4D12(b) gene product or fragments thereof. A skilled artisan can readily employ nucleic acid isolation procedures to obtain an isolated 191P4D12(b) polynuclectide. A protein is said to be "isolated," for example, when physical, mechanical or chemical methods are employed to remove the 191P4D12(b) proteins from cellular constituents that are normally associated with the protein. A skilled artisan can readily employ standard purification methods to obtain an isolated 191P4D12(b) protein. Alternatively, an isolated protein can be prepared by chemical means.

The term "mammal" refers to any organism classified as a mammal, including mice, rats, rabbits, dogs, cats, cows, horses and humans. In one embodiment of the invention, the mammal is a mouse. In another embodiment of the invention, the mammal is a human.

The terms "metastatic prostate cancer" and "metastatic disease" mean prostate cancers that have spread to regional lymph nodes or to distant sites, and are meant to include stage D disease under the AUA system and stage

TxNxM+ under the TNM system. As is the case with locally advanced prostate cancer, surgery is generally not indicated for patients with metastatic disease, and hormonal (androgen ablation) therapy is a preferred treatment modality. Patients with metastatic prostate cancer eventually develop an androgen-refractory state within 12 to 18 months of treatment initiation. Approximately half of these androgen-refractory patients die within 6 months after developing that status. The most common site for prostate cancer metastasis is bone. Prostate cancer bone metastases are often osteoblastic rather than osteolytic (i.e., resulting in net bone formation). Bone metastases are found most frequently in the spine, followed by the femur, pelvis, rib cage, skull and humerus. Other common sites for metastasis include lymph nodes, lung, liver and brain. Metastatic prostate cancer is typically diagnosed by open or laparoscopic pelvic lymphadenectomy, whole body radionuclide scans, skeletal radiography, and/or bone lesion biopsy.

The term "modulator" or "test compound" or "drug candidate" or grammatical equivalents as used herein describe any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequences, or effects of cancer sequences (e.g., signaling, gene expression, protein interaction, etc.) In one aspect, a modulator will neutralize the effect of a cancer protein of the invention. By "neutralize" is meant that an activity of a protein is inhibited or blocked, along with the consequent effect on the cell. In another aspect, a modulator will neutralize the effect of a gene, and its corresponding protein, of the invention by normalizing levels of said protein. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein, or downstream effector pathways. In one embodiment, the modulator suppresses a cancer phenotype, e.g. to a normal tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures is run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

Modulators, drug candidates or test compounds encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 Daltons. Preferred small molecules are less than 2000, or less than 1500 or less than 1000 or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Modulators also comprise biomolecules such as peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs or combinations thereof. Particularly preferred are peptides. One class of modulators are peptides, for example of from about five to about 35 amino acids, with from about five to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. Preferably, the cancer modulatory protein is soluble, includes a non-transmembrane region, and/or, has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, i.e., to cysteine. In one embodiment, a cancer protein of the invention is conjugated to an immunogenic agent as discussed herein. In one embodiment, the cancer protein is conjugated to BSA. The peptides of the invention, e.g., of preferred lengths, can be linked to each other or to other amino acids to create a longer peptide/protein. The modulatory peptides can be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. In a preferred embodiment, peptide/protein-based modulators are antibodies, and fragments thereof, as defined herein.

Modulators of cancer can also be nucleic acids. Nucleic acid modulating agents can be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes can be used in an approach analogous to that outlined above for proteins.

The term "monoclonal antibody" refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the antibodies comprising the population are identical except for possible naturally occurring mutations that are present in minor amounts.

A "motif", as in biological motif of a 191P4D12(b)-related protein, refers to any pattern of amino acids forming part of the primary sequence of a protein, that is associated with a particular function (e.g. protein-protein interaction, protein-DNA interaction, etc) or modification (e.g. that is phosphorylated, glycosylated or amidated), or localization (e.g. secretory sequence, nuclear localization sequence, etc.) or a sequence that is correlated with being immunogenic, either humorally or cellularly. A motif can be either contiguous or capable of being aligned to certain positions that are generally correlated with a certain function or property. In the context of HLA motifs, "motif" refers to the pattern of residues in a peptide of defined length, usually a peptide of from about 8 to about 13 amino acids for a class I HLA motif and from about 6 to about 25 amino acids for a class II HLA motif, which is recognized by a particular HLA molecule. Peptide motifs for HLA binding are typically different for each protein encoded by each human HLA allele and differ in the pattern of the primary and secondary anchor residues.

A "pharmaceutical excipient" comprises a material such as an adjuvant, a carrier, pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservative, and the like.

"Pharmaceutically acceptable" refers to a non-toxic, inert, and/or composition that is physiologically compatible with humans or other mammals.

The term "polynucleotide" means a polymeric form of nucleotides of at least 10 bases or base pairs in length, either ribonucleotides or deoxynucleotides or a modified form of either type of nucleotide, and is meant to include single and double stranded forms of DNA and/or RNA. In the art, this term if often used interchangeably with "oligonucleotide". A polynucleotide can comprise a nucleotide sequence disclosed herein wherein thymidine (T), as shown for example in Figure 2, can also be uracil (U); this definition pertains to the differences between the chemical structures of DNA and RNA, in particular the observation that one of the four major bases in RNA is uracil (U) instead of thymidine (T).

The term "polypeptide" means a polymer of at least about 4, 5, 6, 7, or 8 amino acids. Throughout the specification, standard three letter or single letter designations for amino acids are used. In the art, this term is often used interchangeably with "peptide" or "protein".

An HLA "primary anchor residue" is an amino acid at a specific position along a peptide sequence which is understood to provide a contact point between the immunogenic peptide and the HLA molecule. One to three, usually two, primary anchor residues within a peptide of defined length generally defines a "motif" for an immunogenic peptide. These residues are understood to fit in close contact with peptide binding groove of an HLA molecule, with their side chains buried in specific pockets of the binding groove. In one embodiment, for example, the primary anchor residues for an HLA class I molecule are located at position 2 (from the amino terminal position) and at the carboxyl terminal position of a 8, 9, 10, 11, or 12 residue peptide epitope in accordance with the invention. Alternatively, in another embodiment, the primary anchor residues of a peptide binds an HLA class II molecule are spaced relative to each other, rather than to the termini of a peptide, where the peptide is generally of at least 9 amino acids in length. The primary anchor positions for each motif and supermotif are set forth in Table IV. For example, analog peptides can be created by altering the presence or absence of particular residues in the primary and/or secondary anchor positions shown in Table IV. Such analogs are used to modulate the binding affinity and/or population coverage of a peptide comprising a particular HLA motif or supermotif.

"Radioisotopes" include, but are not limited to the following (non-limiting exemplary uses are also set forth):

Examples of Medical Isotopes:

Isotope	Description of use
Actinium-225	See Thorium-229 (Th-229)

(AC-225)	
Actinium-227 (AC-227)	Parent of Radium-223 (Ra-223) which is an alpha emitter used to treat metastases in the skeleton resulting from cancer (i.e., breast and prostate cancers), and cancer radioimmunotherapy
Bismuth-212 (Bi-212)	See Thorium-228 (Th-228)
Bismuth-213 (Bi-213)	See Thorium-229 (Th-229)
Cadmium-109 (Cd-109)	Cancer detection
Cobalt-60 (Co-60)	Radiation source for radiotherapy of cancer, for food irradiators, and for sterilization of medical supplies
Copper-64 (Cu-64)	A positron emitter used for cancer therapy and SPECT imaging
Copper-67 (Cu-67)	Beta/gamma emitter used in cancer radioimmunotherapy and diagnostic studies (i.e., breast and colon cancers, and lymphoma)
Dysprosium-166 (Dy-166)	Cancer radioimmunotherapy
Erbium-169 (Er-169)	Rheumatoid arthritis treatment, particularly for the small joints associated with fingers and toes
Europium-152 (Eu-152)	Radiation source for food irradiation and for sterilization of medical supplies
Europium-154 (Eu-154)	Radiation source for food irradiation and for sterilization of medical supplies
Gadolinium-153 (Gd-153)	Osteoporosis detection and nuclear medical quality assurance devices
Gold-198 (Au-198)	Implant and intracavity therapy of ovarian, prostate, and brain cancers
Holmium-166 (Ho-166)	Multiple myeloma treatment in targeted skeletal therapy, cancer radioimmunotherapy, bone marrow ablation, and rheumatoid arthritis treatment
Iodine-125 (I-125)	Osteoporosis detection, diagnostic imaging, tracer drugs, brain cancer treatment, radiolabeling, tumor imaging, mapping of receptors in the brain, interstitial radiation therapy, brachytherapy for treatment of prostate cancer, determination of glomerular filtration rate (GFR), determination of plasma volume, detection of deep vein thrombosis of the legs
Iodine-131 (I-131)	Thyroid function evaluation, thyroid disease detection, treatment of thyroid cancer as well as other non-malignant thyroid diseases (i.e., Graves disease, goiters, and hyperthyroidism), treatment of leukemia, lymphoma, and other forms of cancer (e.g., breast cancer) using radioimmunotherapy
Iridium-192 (Ir-192)	Brachytherapy, brain and spinal cord tumor treatment, treatment of blocked arteries (i.e., arteriosclerosis and restenosis), and implants for breast and prostate tumors
Lutetium-177 (Lu-177)	Cancer radioimmunotherapy and treatment of blocked arteries (i.e., arteriosclerosis and restenosis)
Molybdenum-99 (Mo-99)	Parent of Technetium-99m (Tc-99m) which is used for imaging the brain, liver, lungs, heart, and other organs. Currently, Tc-99m is the most widely used radioisotope used for diagnostic imaging of various cancers and diseases involving the brain, heart, liver, lungs; also used in detection of deep vein thrombosis of the legs
Osmium-194 (Os-194)	Cancer radioimmunotherapy
Palladium-103 (Pd-103)	Prostate cancer treatment
Platinum-195m (Pt-195m)	Studies on biodistribution and metabolism of cisplatin, a chemotherapeutic drug
Phosphorus-32	Polycythemia rubra vera (blood cell disease) and leukemia treatment, bone cancer

(P-32)	diagnosis/treatment; colon, pancreatic, and liver cancer treatment; radiolabeling nucleic acids for in vitro research, diagnosis of superficial tumors, treatment of blocked arteries (i.e., arteriosclerosis and restenosis), and intracavity therapy
Phosphorus-33 (P-33)	Leukemia treatment, bone disease diagnosis/treatment, radiolabeling, and treatment of blocked arteries (i.e., arteriosclerosis and restenosis)
Radium-223 (Ra-223)	See Actinium-227 (Ac-227)
Rhenium-186 (Re-186)	Bone cancer pain relief, rheumatoid arthritis treatment, and diagnosis and treatment of lymphoma and bone, breast, colon, and liver cancers using radioimmunotherapy
Rhenium-188 (Re-188)	Cancer diagnosis and treatment using radioimmunotherapy, bone cancer pain relief, treatment of rheumatoid arthritis, and treatment of prostate cancer
Rhodium-105 (Rh-105)	Cancer radioimmunotherapy
Samarium-145 (Sm-145)	Ocular cancer treatment
Samarium-153 (Sm-153)	Cancer radioimmunotherapy and bone cancer pain relief
Scandium-47 (Sc-47)	Cancer radioimmunotherapy and bone cancer pain relief
Selenium-75 (Se-75)	Radiotracer used in brain studies, imaging of adrenal cortex by gamma-scintigraphy, lateral locations of steroid secreting tumors, pancreatic scanning, detection of hyperactive parathyroid glands, measure rate of bile acid loss from the endogenous pool
Strontium-85 (Sr-85)	Bone cancer detection and brain scans
Strontium-89 (Sr-89)	Bone cancer pain relief, multiple myeloma treatment, and osteoblastic therapy
Technetium-99m (Tc-99m)	See Molybdenum-99 (Mo-99)
Thorium-228 (Th-228)	Parent of Bismuth-212 (Bi-212) which is an alpha emitter used in cancer radioimmunotherapy
Thorium-229 (Th-229)	Parent of Actinium-225 (Ac-225) and grandparent of Bismuth-213 (Bi-213) which are alpha emitters used in cancer radioimmunotherapy
Thulium-170 (Tm-170)	Gamma source for blood irradiators, energy source for implanted medical devices
Tin-117m (Sn-117m)	Cancer immunotherapy and bone cancer pain relief
Tungsten-188 (W-188)	Parent for Rhenium-188 (Re-188) which is used for cancer diagnostics/treatment, bone cancer pain relief, rheumatoid arthritis treatment, and treatment of blocked arteries (i.e., arteriosclerosis and restenosis)
Xenon-127 (Xe-127)	Neuroimaging of brain disorders, high resolution SPECT studies, pulmonary function tests, and cerebral blood flow studies
Ytterbium-175 (Yb-175)	Cancer radioimmunotherapy
Yttrium-90 (Y-90)	Microseeds obtained from irradiating Yttrium-89 (Y-89) for liver cancer treatment
Yttrium-91 (Y-91)	A gamma-emitting label for Yttrium-90 (Y-90) which is used for cancer radioimmunotherapy (i.e., lymphoma, breast, colon, kidney, lung, ovarian, prostate, pancreatic, and inoperable liver cancers)

By "randomized" or grammatical equivalents as herein applied to nucleic acids and proteins is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. These random peptides (or nucleic acids, discussed herein) can incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, a library is "fully randomized," with no sequence preferences or constants at any position. In another embodiment, the library is a "biased random" library. That is, some positions within the sequence either are held constant, or are selected from a limited number of possibilities. For example, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

A "recombinant" DNA or RNA molecule is a DNA or RNA molecule that has been subjected to molecular manipulation *in vitro*.

Non-limiting examples of small molecules include compounds that bind or interact with 191P4D12(b), ligands including hormones, neuropeptides, chemokines, odorants, phospholipids, and functional equivalents thereof that bind and preferably inhibit 191P4D12(b) protein function. Such non-limiting small molecules preferably have a molecular weight of less than about 10 kDa, more preferably below about 9, about 8, about 7, about 6, about 5 or about 4 kDa. In certain embodiments, small molecules physically associate with, or bind, 191P4D12(b) protein; are not found in naturally occurring metabolic pathways; and/or are more soluble in aqueous than non-aqueous solutions

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured nucleic acid sequences to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature that can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel *et al.*, Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, are identified by, but not limited to, those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50 mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42 °C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42 °C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium. citrate) and 50% formamide at 55 °C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55 °C. "Moderately stringent conditions" are described by, but not limited to, those in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x

Denhardt's solution, 10% dextran sulfate, and 20 mg/mL denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

An HLA "supermotif" is a peptide binding specificity shared by HLA molecules encoded by two or more HLA alleles. Overall phenotypic frequencies of HLA-supertypes in different ethnic populations are set forth in Table IV (F). The non-limiting constituents of various supetypes are as follows:

A2: A*0201, A*0202, A*0203, A*0204, A* 0205, A*0206, A*6802, A*6901, A*0207

A3: A3, A11, A31, A*3301, A*6801, A*0301, A*1101, A*3101

B7: B7, B*3501-03, B*51, B*5301, B*5401, B*5501, B*5502, B*5601, B*6701, B*7801, B*0702, B*5101, B*5602

B44: B*3701, B*4402, B*4403, B*60 (B*4001), B61 (B*4006)

A1: A*0102, A*2604, A*3601, A*4301, A*8001

A24: A*24, A*30, A*2403, A*2404, A*3002, A*3003

B27: B*1401-02, B*1503, B*1509, B*1510, B*1518, B*3801-02, B*3901, B*3902, B*3903-04, B*4801-02, B*7301, B*2701-08

B58: B*1516, B*1517, B*5701, B*5702, B58

B62: B*4601, B52, B*1501 (B62), B*1502 (B75), B*1513 (B77)

Calculated population coverage afforded by different HLA-supertype combinations are set forth in Table IV (G).

As used herein "to treat" or "therapeutic" and grammatically related terms, refer to any improvement of any consequence of disease, such as prolonged survival, less morbidity, and/or a lessening of side effects which are the byproducts of an alternative therapeutic modality; full eradication of disease is not required.

A "transgenic animal" (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A "transgene" is a DNA that is integrated into the genome of a cell from which a transgenic animal develops.

As used herein, an HLA or cellular immune response "vaccine" is a composition that contains or encodes one or more peptides of the invention. There are numerous embodiments of such vaccines, such as a cocktail of one or more individual peptides; one or more peptides of the invention comprised by a polyepitopic peptide; or nucleic acids that encode such individual peptides or polypeptides, *e.g.*, a minigene that encodes a polyepitopic peptide. The "one or more peptides" can include any whole unit integer from 1-150 or more, e.g., at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, or 150 or more peptides of the invention. The peptides or polypeptides can optionally be modified, such as by lipidation, addition of targeting or other sequences. HLA class I peptides of the invention can be admixed with, or linked to, HLA class II peptides, to facilitate activation of both cytotoxic T lymphocytes and helper T lymphocytes. HLA vaccines can also comprise peptide-pulsed antigen presenting cells, *e.g.*, dendritic cells.

The term "variant" refers to a molecule that exhibits a variation from a described type or norm, such as a protein that has one or more different amino acid residues in the corresponding position(s) of a specifically described protein (e.g. the 191P4D12(b) protein shown in Figure 2 or Figure 3. An analog is an example of a variant protein. Splice isoforms and single nucleotides polymorphisms (SNPs) are further examples of variants.

The "191P4D12(b)-related proteins" of the invention include those specifically identified herein, as well as allelic variants, conservative substitution variants, analogs and homologs that can be isolated/generated and characterized without undue experimentation following the methods outlined herein or readily available in the art. Fusion proteins that combine parts of different 191P4D12(b) proteins or fragments thereof, as well as fusion proteins of a 191P4D12(b) protein and a heterologous

polypeptide are also included. Such 191P4D12(b) proteins are collectively referred to as the 191P4D12(b)-related proteins, the proteins of the invention, or 191P4D12(b). The term "191P4D12(b)-related protein" refers to a polypeptide fragment or a 191P4D12(b) protein sequence of 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or more than 25 amino acids; or, at least 30, 35, 40, 45, 50, 55, 60, 65, 70, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 525, 550, 575, or 576 or more amino acids.

II.) 191P4D12(b) Polynucleotides

One aspect of the invention provides polynucleotides corresponding or complementary to all or part of a 191P4D12(b) gene, mRNA, and/or coding sequence, preferably in isolated form, including polynucleotides encoding a 191P4D12(b)-related protein and fragments thereof, DNA, RNA, DNA/RNA hybrid, and related molecules, polynucleotides or oligonucleotides complementary to a 191P4D12(b) gene or mRNA sequence or a part thereof, and polynucleotides or oligonucleotides that hybridize to a 191P4D12(b) gene, mRNA, or to a 191P4D12(b) encoding polynucleotide (collectively, "191P4D12(b) polynucleotides"). In all instances when referred to in this section, T can also be U in Figure 2.

Embodiments of a 191P4D12(b) polynucleotide include: a 191P4D12(b) polynucleotide having the sequence shown in Figure 2, the nucleotide sequence of 191P4D12(b) as shown in Figure 2 wherein T is U; at least 10 contiguous nucleotides of a polynucleotide having the sequence as shown in Figure 2; or, at least 10 contiguous nucleotides of a polynucleotide having the sequence as shown in Figure 2 where T is U. For example, embodiments of 191P4D12(b) nucleotides comprise, without limitation:

(I) a polynucleotide comprising, consisting essentially of, or consisting of a sequence as shown in Figure 2, wherein T can also be U;

(II) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2A, from nucleotide residue number 264 through nucleotide residue number 1796, including the stop codon, wherein T can also be U;

(III) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2B, from nucleotide residue number 264 through nucleotide residue number 1796, including the stop codon, wherein T can also be U;

(IV) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2C, from nucleotide residue number 264 through nucleotide residue number 1796, including the a stop codon, wherein T can also be U;

(V) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2D, from nucleotide residue number 264 through nucleotide residue number 1796, including the stop codon, wherein T can also be U;

(VI) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2E, from nucleotide residue number 264 through nucleotide residue number 1796, including the stop codon, wherein T can also be U;

(VII) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2F, from nucleotide residue number 789 through nucleotide residue number 1676, including the stop codon, wherein T can also be U;

(VIII) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2G, from nucleotide residue number 264 through nucleotide residue number 1721, including the stop codon, wherein T can also be U;

(IX) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2H, from nucleotide residue number 264 through nucleotide residue number 1796, including the stop codon, wherein T can also be U;

(X) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2I, from nucleotide residue number 708 through nucleotide residue number 1121, including the stop codon, wherein T can also be U;

(XI) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2J, from nucleotide residue number 264 through nucleotide residue number 1796, including the stop codon, wherein T can also be U;

(XII) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2K, from nucleotide residue number 264 through nucleotide residue number 1796, including the stop codon, wherein T can also be U;

(XIII) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2L, from nucleotide residue number 264 through nucleotide residue number 1796, including the stop codon, wherein T can also be U;

(XIV) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2M, from nucleotide residue number 264 through nucleotide residue number 1799, including the stop codon, wherein T can also be U;

(XV) a polynucleotide comprising, consisting essentially of, or consisting of the sequence as shown in Figure 2N, from nucleotide residue number 708 through nucleotide residue number 1121, including the stop codon, wherein T can also be U;

(XVI) a polynucleotide that encodes a 191P4D12(b)-related protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% homologous to an entire amino acid sequence shown in Figure 2A-N;

(XVII) a polynucleotide that encodes a 191P4D12(b)-related protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identical to an entire amino acid sequence shown in Figure 2A-N;

(XVIII) a polynucleotide that encodes at least one peptide set forth in Tables VIII-XXI and XXII-XLIX;

(XIX) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figures 3A-B and 3E-G in any whole number increment up to 510 that includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XX) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3A-B and 3E-G in any whole number increment up to 510 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,

19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXI) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3A-B and 3E-G in any whole number increment up to 510 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3A-B and 3E-G in any whole number increment up to 510 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXIII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3A-B and 3E-G in any whole number increment up to 510 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XXIV) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3C in any whole number increment up to 295 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XXV) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3C in any whole number increment up to 295 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXVI) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3C in any whole number increment up to 295 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXVII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3C in any whole number increment up to 295 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXVIII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3C in any whole

number increment up to 295 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9

(XXIX) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3D in any whole number increment up to 485 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XXX) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3D in any whole number increment up to 485 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXXI) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3D in any whole number increment up to 485 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXXII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3D in any whole number increment up to 485 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXXIII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3D in any whole number increment up to 485 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9

(XXXIV) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3H in any whole number increment up to 511 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XXXV) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3H in any whole number increment up to 511 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXXVI) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3H in any whole number increment up to 511 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXXVII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3H in any whole number increment up to 511 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXXVIII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3H in any whole number increment up to 511 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9

(XXXIX) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3I-J in any whole number increment up to 137 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XL) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27; 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3I-J in any whole number increment up to 137 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XLI) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3I-J in any whole number increment up to 137 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XLII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3I-J in any whole number increment up to 137 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XLIII) a polynucleotide that encodes a peptide region of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a peptide of Figure 3I-J in any whole number increment up to 137 that includes 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9

(XLIV) a polynucleotide that is fully complementary to a polynucleotide of any one of (I)-(XLIII).

(XLV) a peptide that is encoded by any of (I) to (XLIV); and

(XLVI) a composition comprising a polynucleotide of any of (I)-(XLIII) or peptide of (XLV) together with a pharmaceutical excipient and/or in a human unit dose form.

(XLVII) a method of using a polynucleotide of any (I)-(XLIV) or peptide of (XLV) or a composition of (XLVI) in a method to modulate a cell expressing 191P4D12(b),

(XLVIII) a method of using a polynucleotide of any (I)-(XLIV) or peptide of (XLV) or a composition of (XLVI) in a method to diagnose, prophylax, prognose, or treat an individual who bears a cell expressing 191P4D12(b)

(XLIX) a method of using a polynucleotide of any (I)-(XLIV) or peptide of (XLV) or a composition of (XLVI) in a method to diagnose, prophylax, prognose, or treat an individual who bears a cell expressing 191P4D12(b), said cell from a cancer of a tissue listed in Table I;

(L) a method of using a polynucleotide of any (I)-(XLIV) or peptide of (XLV) or a composition of (XLVI) in a method to diagnose, prophylax, prognose, or treat a a cancer;

(LI) a method of using a polynucleotide of any (I)-(XLIV) or peptide of (XLV) or a composition of (XLVI) in a method to diagnose, prophylax, prognose, or treat a a cancer of a tissue listed in Table I; and,

(LII) a method of using a polynucleotide of any (I)-(XLIV) or peptide of (XLV) or a composition of (XLVI) in a method to identify or characterize a modulator of a cell expressing 191P4D12(b).

As used herein, a range is understood to disclose specifically all whole unit positions thereof.

Typical embodiments of the invention disclosed herein include 191P4D12(b) polynucleotides that encode specific portions of 191P4D12(b) mRNA sequences (and those which are complementary to such sequences) such as those that encode the proteins and/or fragments thereof, for example: .

(a) 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 505 or 510 more contiguous amino acids of 191P4D12(b) variant 1; the maximal lengths relevant for other variants are: variant 2, 510 amino acids; variant 6, 295 amino acids, variant 7, 485 amino acids, variant 10, 510 amino acids, variant 11, 510 amoni acids, variant 12, 510 amoni acids, variant 13, 511 amino acids, variant 9, 137 amino acids, and variant 14, 137 amino acids.

For example, representative embodiments of the invention disclosed herein include: polynucleotides and their encoded peptides themselves encoding about amino acid 1 to about amino acid 10 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 10 to about amino acid 20 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 20 to about amino acid 30 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 30 to about amino acid 40 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 40 to about amino acid 50 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 50 to about amino acid 60 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 60 to about amino acid 70 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 70 to about amino acid 80 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 80 to about amino acid 90 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, polynucleotides encoding about amino acid 90 to about amino acid 100 of the 191P4D12(b) protein shown in Figure 2 or Figure 3, in increments of about 10 amino

acids, ending at the carboxyl terminal amino acid set forth in Figure 2 or Figure 3. Accordingly, polynucleotides encoding portions of the amino acid sequence (of about 10 amino acids), of amino acids, 100 through the carboxyl terminal amino acid of the 191P4D12(b) protein are embodiments of the invention. Wherein it is understood that each particular amino acid position discloses that position plus or minus five amino acid residues.

Polynucleotides encoding relatively long portions of a 191P4D12(b) protein are also within the scope of the invention. For example, polynucleotides encoding from about amino acid 1 (or 20 or 30 or 40 etc.) to about amino acid 20, (or 30, or 40 or 50 etc.) of the 191P4D12(b) protein "or variant" shown in Figure 2 or Figure 3 can be generated by a variety of techniques well known in the art. These polynucleotide fragments can include any portion of the 191P4D12(b) sequence as shown in Figure 2.

Additional illustrative embodiments of the invention disclosed herein include 191P4D12(b) polynucleotide fragments encoding one or more of the biological motifs contained within a 191P4D12(b) protein "or variant" sequence, *including one or more of the motif-bearing subsequences of a 191P4D12(b) protein "or variant" set forth in Tables VIII-XXI* and XXII-XLIX. In another embodiment, typical polynucleotide fragments of the invention encode one or more of the regions of 191P4D12(b) protein or variant that exhibit homology to a known molecule. In another embodiment of the invention, typical polynucleotide fragments can encode one or more of the 191P4D12(b) protein or variant N-glycosylation sites, cAMP and cGMP-dependent protein kinase phosphorylation sites, casein kinase II phosphorylation sites or N-myristoylation site and amidation sites.

Note that to determine the starting position of any peptide set forth in Tables VIII-XXI and Tables XXII to XLIX (collectively HLA Peptide Tables) respective to its parental protein, e.g., variant 1, variant 2, etc., reference is made to three factors: the particular variant, the length of the peptide in an HLA Peptide Table, and the Search Peptides listed in Table VII. Generally, a unique Search Peptide is used to obtain HLA peptides for a particular variant. The position of each Search Peptide relative to its respective parent molecule is listed in Table VII. Accordingly, if a Search Peptide begins at position "X", one must add the value "X minus 1" to each position in Tables VIII-XXI and Tables XXII-IL to obtain the actual position of the HLA peptides in their parental molecule. For example if a particular Search Peptide begins at position 150 of its parental molecule, one must add 150 - 1, i.e., 149 to each HLA peptide amino acid position to calculate the position of that amino acid in the parent molecule.

II.A.) Uses of 191P4D12(b) Polynucleotides

II.A.1.) Monitoring of Genetic Abnormalities

The polynucleotides of the preceding paragraphs have a number of different specific uses. The human 191P4D12(b) gene maps to the chromosomal location set forth in the Example entitled "Chromosomal Mapping of 191P4D12(b)." For example, because the 191P4D12(b) gene maps to this chromosome, polynucleotides that encode different regions of the 191P4D12(b) proteins are used to characterize cytogenetic abnormalities of this chromosomal locale, such as abnormalities that are identified as being associated with various cancers. In certain genes, a variety of chromosomal abnormalities including rearrangements have been identified as frequent cytogenetic abnormalities in a number of different cancers (see e.g. Krajinovic *et al.*, Mutat. Res. 382(3-4): 81-83 (1998); Johansson *et al.*, Blood 86(10): 3905-3914 (1995) and Finger *et al.*, P.N.A.S. 85(23): 9158-9162 (1988)). Thus, polynucleotides encoding specific regions of the 191P4D12(b) proteins provide new tools that can be used to delineate, with greater precision than previously possible, cytogenetic abnormalities in the chromosomal region that encodes 191P4D12(b) that may contribute to the malignant phenotype. In this context, these polynucleotides satisfy a need in the art for expanding the sensitivity of chromosomal screening in order to identify more subtle and less common chromosomal abnormalities (see e.g. Evans *et al.*, Am. J. Obstet. Gynecol 171(4): 1055-1057 (1994)).

Furthermore, as 191P4D12(b) was shown to be highly expressed in prostate and other cancers, 191P4D12(b) polynucleotides are used in methods assessing the status of 191P4D12(b) gene products in normal versus cancerous tissues. Typically, polynucleotides that encode specific regions of the 191P4D12(b) proteins are used to assess the presence of perturbations (such as deletions, insertions, point mutations, or alterations resulting in a loss of an antigen etc.) in specific regions of the 191P4D12(b) gene, such as regions containing one or more motifs. Exemplary assays include both RT-PCR assays as well as single-strand conformation polymorphism (SSCP) analysis (see, e.g., Marrogi *et al.*, J. Cutan. Pathol. 26(8): 369-378 (1999), both of which utilize polynucleotides encoding specific regions of a protein to examine these regions within the protein.

II.A.2.) Antisense Embodiments

Other specifically contemplated nucleic acid related embodiments of the invention disclosed herein are genomic DNA, cDNAs, ribozymes, and antisense molecules, as well as nucleic acid molecules based on an alternative backbone, or including alternative bases, whether derived from natural sources or synthesized, and include molecules capable of inhibiting the RNA or protein expression of 191P4D12(b). For example, antisense molecules can be RNAs or other molecules, including peptide nucleic acids (PNAs) or non-nucleic acid molecules such as phosphorothioate derivatives that specifically bind DNA or RNA in a base pair-dependent manner. A skilled artisan can readily obtain these classes of nucleic acid molecules using the 191P4D12(b) polynucleotides and polynucleotide sequences disclosed herein.

Antisense technology entails the administration of exogenous oligonucleotides that bind to a target polynucleotide located within the cells. The term "antisense" refers to the fact that such oligonucleotides are complementary to their intracellular targets, e.g., 191P4D12(b). See for example, Jack Cohen, Oligodeoxynucleotides, Antisense Inhibitors of Gene Expression, CRC Press, 1989; and Synthesis 1:1-5 (1988). The 191P4D12(b) antisense oligonucleotides of the present invention include derivatives such as S-oligonucleotides (phosphorothioate derivatives or S-oligos, see, Jack Cohen, supra), which exhibit enhanced cancer cell growth inhibitory action. S-oligos (nucleoside phosphorothioates) are isoelectronic analogs of an oligonucleotide (O-oligo) in which a nonbridging oxygen atom of the phosphate group is replaced by a sulfur atom. The S-oligos of the present invention can be prepared by treatment of the corresponding O-oligos with 3H-1,2-benzodithiol-3-one-1,1-dioxide, which is a sulfur transfer reagent. See, *e.g.*, Iyer, R. P. *et al.*, J. Org. Chem. 55:4693-4698 (1990); and Iyer, R. P. *et al.*, J. Am. Chem. Soc. 112:1253-1254 (1990). Additional 191P4D12(b) antisense oligonucleotides of the present invention include morpholino antisense oligonucleotides known in the art (see, e.g., Partridge *et al.*, 1996, Antisense & Nucleic Acid Drug Development 6: 169-175).

The 191P4D12(b) antisense oligonucleotides of the present invention typically can be RNA or DNA that is complementary to and stably hybridizes with the first 100 5' codons or last 100 3' codons of a 191P4D12(b) genomic sequence or the corresponding mRNA. Absolute complementarity is not required, although high degrees of complementarity are preferred. Use of an oligonucleotide complementary to this region allows for the selective hybridization to 191P4D12(b) mRNA and not to mRNA specifying other regulatory subunits of protein kinase. In one embodiment, 191P4D12(b) antisense oligonucleotides of the present invention are 15 to 30-mer fragments of the antisense DNA molecule that have a sequence that hybridizes to 191P4D12(b) mRNA. Optionally, 191P4D12(b) antisense oligonucleotide is a 30-mer oligonucleotide that is complementary to a region in the first 10 5' codons or last 10 3' codons of 191P4D12(b). Alternatively, the antisense molecules are modified to employ ribozymes in the inhibition of 191P4D12(b) expression, see, e.g., L. A. Couture & D. T. Stinchcomb; *Trends Genet* 12: 510-515 (1996).

II.A.3.) Primers and Primer Pairs

Further specific embodiments of these nucleotides of the invention include primers and primer pairs, which allow the specific amplification of polynucleotides of the invention or of any specific parts thereof, and probes that selectively or specifically hybridize to nucleic acid molecules of the invention or to any part thereof. Probes can be labeled with a

detectable marker, such as, for example, a radioisotope, fluorescent compound, bioluminescent compound, a chemiluminescent compound, metal chelator or enzyme. Such probes and primers are used to detect the presence of a 191P4D12(b) polynucleotide in a sample and as a means for detecting a cell expressing a 191P4D12(b) protein.

Examples of such probes include polypeptides comprising all or part of the human 191P4D12(b) cDNA sequence shown in Figure 2. Examples of primer pairs capable of specifically amplifying 191P4D12(b) mRNAs are also described in the Examples. As will be understood by the skilled artisan, a great many different primers and probes can be prepared based on the sequences provided herein and used effectively to amplify and/or detect a 191P4D12(b) mRNA.

The 191P4D12(b) polynucleotides of the invention are useful for a variety of purposes, including but not limited to their use as probes and primers for the amplification and/or detection of the 191P4D12(b) gene(s), mRNA(s), or fragments thereof; as reagents for the diagnosis and/or prognosis of prostate cancer and other cancers; as coding sequences capable of directing the expression of 191P4D12(b) polypeptides; as tools for modulating or inhibiting the expression of the 191P4D12(b) gene(s) and/or translation of the 191P4D12(b) transcript(s); and as therapeutic agents.

The present invention includes the use of any probe as described herein to identify and isolate a 191P4D12(b) or 191P4D12(b) related nucleic acid sequence from a naturally occurring source, such as humans or other mammals, as well as the isolated nucleic acid sequence *per se*, which would comprise all or most of the sequences found in the probe used.

II.A.4.) Isolation of 191P4D12(b)-Encoding Nucleic Acid Molecules

The 191P4D12(b) cDNA sequences described herein enable the isolation of other polynucleotides encoding 191P4D12(b) gene product(s), as well as the isolation of polynucleotides encoding 191P4D12(b) gene product homologs, alternatively spliced isoforms, allelic variants, and mutant forms of a 191P4D12(b) gene product as well as polynucleotides that encode analogs of 191P4D12(b)-related proteins. Various molecular cloning methods that can be employed to isolate full length cDNAs encoding a 191P4D12(b) gene are well known (see, for example, Sambrook, J. *et al.*, Molecular Cloning: A Laboratory Manual, 2d edition, Cold Spring Harbor Press, New York, 1989; Current Protocols in Molecular Biology. Ausubel *et al.*, Eds., Wiley and Sons, 1995). For example, lambda phage cloning methodologies can be conveniently employed, using commercially available cloning systems (e.g., Lambda ZAP Express, Stratagene). Phage clones containing 191P4D12(b) gene cDNAs can be identified by probing with a labeled 191P4D12(b) cDNA or a fragment thereof. For example, in one embodiment, a 191P4D12(b) cDNA (e.g., Figure 2) or a portion thereof can be synthesized and used as a probe to retrieve overlapping and full-length cDNAs corresponding to a 191P4D12(b) gene. A 191P4D12(b) gene itself can be isolated by screening genomic DNA libraries, bacterial artificial chromosome libraries (BACs), yeast artificial chromosome libraries (YACs), and the like, with 191P4D12(b) DNA probes or primers.

II.A.5.) Recombinant Nucleic Acid Molecules and Host-Vector Systems

The invention also provides recombinant DNA or RNA molecules containing a 191P4D12(b) polynucleotide, a fragment, analog or homologue thereof, including but not limited to phages, plasmids, phagemids, cosmids, YACs, BACs, as well as various viral and non-viral vectors well known in the art, and cells transformed or transfected with such recombinant DNA or RNA molecules. Methods for generating such molecules are well known (see, for example, Sambrook *et al.*, 1989, supra).

The invention further provides a host-vector system comprising a recombinant DNA molecule containing a 191P4D12(b) polynucleotide, fragment, analog or homologue thereof within a suitable prokaryotic or eukaryotic host cell. Examples of suitable eukaryotic host cells include a yeast cell, a plant cell, or an animal cell, such as a mammalian cell or an insect cell (e.g., a baculovirus-infectible cell such as an Sf9 or HighFive cell). Examples of suitable mammalian cells include various prostate cancer cell lines such as DU145 and TsuPr1, other transfectable or transducible prostate cancer cell lines, primary cells (PrEC), as well as a number of mammalian cells routinely used for the expression of recombinant proteins (e.g., COS, CHO, 293, 293T cells). More particularly, a polynucleotide comprising the coding sequence of 191P4D12(b) or a

fragment, analog or homolog thereof can be used to generate 191P4D12(b) proteins or fragments thereof using any number of host-vector systems routinely used and widely known in the art.

A wide range of host-vector systems suitable for the expression of 191P4D12(b) proteins or fragments thereof are available, see for example, Sambrook *et al.*, 1989, supra; Current Protocols in Molecular Biology, 1995, supra). Preferred vectors for mammalian expression include but are not limited to pcDNA 3.1 myc-His-tag (Invitrogen) and the retroviral vector pSRαtkneo (Muller *et al.*, 1991, MCB 11:1785). Using these expression vectors, 191P4D12(b) can be expressed in several prostate cancer and non-prostate cell lines, including for example 293, 293T, rat-1, NIH 3T3 and TsuPr1. The host-vector systems of the invention are useful for the production of a 191P4D12(b) protein or fragment thereof. Such host-vector systems can be employed to study the functional properties of 191P4D12(b) and 191P4D12(b) mutations or analogs.

Recombinant human 191P4D12(b) protein or an analog or homolog or fragment thereof can be produced by mammalian cells transfected with a construct encoding a 191P4D12(b)-related nucleotide. For example, 293T cells can be transfected with an expression plasmid encoding 191P4D12(b) or fragment, analog or homolog thereof, a 191P4D12(b)-related protein is expressed in the 293T cells, and the recombinant 191P4D12(b) protein is isolated using standard purification methods (e.g., affinity purification using anti-191P4D12(b) antibodies). In another embodiment, a 191P4D12(b) coding sequence is subcloned into the retroviral vector pSRαMSVtkneo and used to infect various mammalian cell lines, such as NIH 3T3, TsuPr1, 293 and rat-1 in order to establish 191P4D12(b) expressing cell lines. Various other expression systems well known in the art can also be employed. Expression constructs encoding a leader peptide joined in frame to a 191P4D12(b) coding sequence can be used for the generation of a secreted form of recombinant 191P4D12(b) protein.

As discussed herein, redundancy in the genetic code permits variation in 191P4D12(b) gene sequences. In particular, it is known in the art that specific host species often have specific codon preferences, and thus one can adapt the disclosed sequence as preferred for a desired host. For example, preferred analog codon sequences typically have rare codons (i.e., codons having a usage frequency of less than about 20% in known sequences of the desired host) replaced with higher frequency codons. Codon preferences for a specific species are calculated, for example, by utilizing codon usage tables available on the INTERNET.

Additional sequence modifications are known to enhance protein expression in a cellular host. These include elimination of sequences encoding spurious polyadenylation signals, exon/intron splice site signals, transposon-like repeats, and/or other such well-characterized sequences that are deleterious to gene expression. The GC content of the sequence is adjusted to levels average for a given cellular host, as calculated by reference to known genes expressed in the host cell. Where possible, the sequence is modified to avoid predicted hairpin secondary mRNA structures. Other useful modifications include the addition of a translational initiation consensus sequence at the start of the open reading frame, as described in Kozak, *Mol. Cell Biol.*, 9:5073-5080 (1989). Skilled artisans understand that the general rule that eukaryotic ribosomes initiate translation exclusively at the 5' proximal AUG codon is abrogated only under rare conditions (see, e.g., Kozak PNAS 92(7): 2662-2666, (1995) and Kozak NAR 15(20): 8125-8148 (1987)).

III.) 191P4D12(b)-related Proteins

Another aspect of the present invention provides 191P4D12(b)-related proteins. Specific embodiments of 191P4D12(b) proteins comprise a polypeptide having all or part of the amino acid sequence of human 191P4D12(b) as shown in Figure 2 or Figure 3. Alternatively, embodiments of 191P4D12(b) proteins comprise variant, homolog or analog polypeptides that have alterations in the amino acid sequence of 191P4D12(b) shown in Figure 2 or Figure 3.

Embodiments of a 191P4D12(b) polypeptide include: a 191P4D12(b) polypeptide having a sequence shown in Figure 2, a peptide sequence of a 191P4D12(b) as shown in Figure 2 wherein T is U; at least 10 contiguous nucleotides of a polypeptide having the sequence as shown in Figure 2; or, at least 10 contiguous peptides of a polypeptide having the

sequence as shown in Figure 2 where T is U. For example, embodiments of 191P4D12(b) peptides comprise, without limitation:

(I) a protein comprising, consisting essentially of, or consisting of an amino acid sequence as shown in Figure 2A-N or Figure 3A-J;

(II) a 191P4D12(b)-related protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% homologous to an entire amino acid sequence shown in Figure 2A-N or 3A-J;

(III) a 191P4D12(b)-related protein that is at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identical to an entire amino acid sequence shown in Figure 2A-N or 3A-J;

(IV) a protein that comprises at least one peptide set forth in Tables VIII to XLIX, optionally with a *proviso* that it is not an entire protein of Figure 2;

(V) a protein that comprises at least one peptide set forth in Tables VIII-XXI, collectively, which peptide is also set forth in Tables XXII to XLIX, collectively, optionally with a *proviso* that it is not an entire protein of Figure 2;

(VI) a protein that comprises at least two peptides selected from the peptides set forth in Tables VIII-XLIX, optionally with a *proviso* that it is not an entire protein of Figure 2;

(VII) a protein that comprises at least two peptides selected from the peptides set forth in Tables VIII to XLIX collectively, with a *proviso* that the protein is not a contiguous sequence from an amino acid sequence of Figure 2;

(VIII) a protein that comprises at least one peptide selected from the peptides set forth in Tables VIII-XXI; and at least one peptide selected from the peptides set forth in Tables XXII to XLIX, with a *proviso* that the protein is not a contiguous sequence from an amino acid sequence of Figure 2;

(IX) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3A-B or 3E-G, in any whole number increment up to 510 respectively that includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(X) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3A-B or 3E-G, in any whole number increment up to 510 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XI) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3A-B or 3E-G, in any whole number increment up to 510 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3A-B or 3E-G, in any whole number increment up to 510 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,

18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XIII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, amino acids of a protein of Figure 3A-B or 3E-G in any whole number increment up to 510 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XIV) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3C, in any whole number increment up to 295 respectively that includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XV) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3C, in any whole number increment up to 295 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XVI) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3C, in any whole number increment up to 295 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XVII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3C, in any whole number increment up to 295 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XVIII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, amino acids of a protein of Figure 3C in any whole number increment up to 295 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XIX) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3D, in any whole number increment up to 485 respectively that includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XX) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3D, in any whole number increment up

to 485 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXI) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3D, in any whole number increment up to 485 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3D, in any whole number increment up to 485 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXIII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, amino acids of a protein of Figure 3D in any whole number increment up to 485 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XXIV) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3H, in any whole number increment up to 511 respectively that includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XXV) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3H, in any whole number increment up to 511 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXVI) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3H, in any whole number increment up to 511 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXVII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3H, in any whole number increment up to 511 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXVIII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, amino acids of a protein of Figure 3H in any whole number increment up to 511 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XXIX) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3I-J, in any whole number increment up to 137 respectively that includes at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Hydrophilicity profile of Figure 5;

(XXX) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3I-J, in any whole number increment up to 137 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value less than 0.5 in the Hydropathicity profile of Figure 6;

(XXXI) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3I-J, in any whole number increment up to 137 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Percent Accessible Residues profile of Figure 7;

(XXXII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acids of a protein of Figure 3I-J, in any whole number increment up to 137 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Average Flexibility profile of Figure 8;

(XXXIII) a polypeptide comprising at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, amino acids of a protein of Figure 3I-J in any whole number increment up to 137 respectively that includes at least at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35 amino acid position(s) having a value greater than 0.5 in the Beta-turn profile of Figure 9;

(XXXIV) a peptide that occurs at least twice in Tables VIII-XXI and XXII to XLIX, collectively;

(XXXV) a peptide that occurs at least three times in Tables VIII-XXI and XXII to XLIX, collectively;

(XXXVI) a peptide that occurs at least four times in Tables VIII-XXI and XXII to XLIX, collectively;

(XXXVII) a peptide that occurs at least five times in Tables VIII-XXI and XXII to XLIX, collectively;

(XXXVIII) a peptide that occurs at least once in Tables VIII-XXI, and at least once in tables XXII to XLIX;

(XXXIX) a peptide that occurs at least once in Tables VIII-XXI, and at least twice in tables XXII to XLIX;

(XL) a peptide that occurs at least twice in Tables VIII-XXI, and at least once in tables XXII to XLIX;

(XLI) a peptide that occurs at least twice in Tables VIII-XXI, and at least twice in tables XXII to XLIX;

(XLII) a peptide which comprises one two, three, four, or five of the following characteristics, or an oligonucleotide encoding such peptide:

i) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Hydrophilicity profile of Figure 5;

ii) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or less than 0.5, 0.4, 0.3, 0.2, 0.1, or having a value equal to 0.0, in the Hydropathicity profile of Figure 6;

iii) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Percent Accessible Residues profile of Figure 7;

iv) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Average Flexibility profile of Figure 8; or,

v) a region of at least 5 amino acids of a particular peptide of Figure 3, in any whole number increment up to the full length of that protein in Figure 3, that includes an amino acid position having a value equal to or greater than 0.5, 0.6, 0.7, 0.8, 0.9, or having a value equal to 1.0, in the Beta-turn profile of Figure 9;

(XLIII) a composition comprising a peptide of (I)-(XLII) or an antibody or binding region thereof together with a pharmaceutical excipient and/or in a human unit dose form.

(XLIV) a method of using a peptide of (I)-(XLII), or an antibody or binding region thereof or a composition of (XLIII) in a method to modulate a cell expressing 191P4D12(b),

(XLV) a method of using a peptide of (I)-(XLII) or an antibody or binding region thereof or a composition of (XLIII) in a method to diagnose, prophylax, prognose, or treat an individual who bears a cell expressing 191P4D12(b)

(XLVI) a method of using a peptide of (I)-(XLII) or an antibody or binding region thereof or a composition (XIIII) in a method to diagnose, prophylax, prognose, or treat an individual who bears a cell expressing 191P4D12(b), said cell from a cancer of a tissue listed in Table I;

(XLVII) a method of using a peptide of (I)-(XLII) or an antibody or binding region thereof or a composition of (XLIII) in a method to diagnose, prophylax, prognose, or treat a a cancer;

(XLVIII) a method of using a peptide of (I)-(XLII) or an antibody or binding region thereof or a composition of (XLIII) in a method to diagnose, prophylax, prognose, or treat a a cancer of a tissue listed in Table I; and,

(XLIX) a method of using a a peptide of (I)-(XLII) or an antibody or binding region thereof or a composition (XLIII) in a method to identify or characterize a modulator of a cell expressing 191P4D12(b).

As used herein, a range is understood to specifically disclose all whole unit positions thereof.

Typical embodiments of the invention disclosed herein include 191P4D12(b) polynucleotides that encode specific portions of 191P4D12(b) mRNA sequences (and those which are complementary to such sequences) such as those that encode the proteins and/or fragments thereof, for example:

(a) 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 225, 250, 275, 300, 325, 350, 375, 400, 425, 450, 475, 500, 505, or 510 or more contiguous amino acids of 191P4D12(b) variant 1; the maximal lengths relevant for other variants are: variant 2, 510 amino acids; variant 6, 295 amino acids, variant 7, 485 amino acids, variant 10, 510 amino acids, variant 11, 510 amino acids, variant 12, 510 amino acids, variant 13, 511 amino acids, variant 9, 137 amino acids, and variant 14, 137 amino acids..

In general, naturally occurring allelic variants of human 191P4D12(b) share a high degree of structural identity and homology (e.g., 90% or more homology). Typically, allelic variants of a 191P4D12(b) protein contain conservative amino acid substitutions within the 191P4D12(b) sequences described herein or contain a substitution of an amino acid from a corresponding position in a homologue of 191P4D12(b). One class of 191P4D12(b) allelic variants are proteins that share a high degree of homology with at least a small region of a particular 191P4D12(b) amino acid sequence, but further contain a radical departure from the sequence, such as a non-conservative substitution, truncation, insertion or frame shift. In comparisons of protein sequences, the terms, similarity, identity, and homology each have a distinct meaning as appreciated in the field of genetics. Moreover, orthology and paralogy can be important concepts describing the relationship of members of a given protein family in one organism to the members of the same family in other organisms.

Amino acid abbreviations are provided in Table II. Conservative amino acid substitutions can frequently be made in a protein without altering either the conformation or the function of the protein. Proteins of the invention can comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 conservative substitutions. Such changes include substituting any of isoleucine (I), valine (V), and leucine (L) for any other of these hydrophobic amino acids; aspartic acid (D) for glutamic acid (E) and vice versa; glutamine (Q) for asparagine (N) and vice versa; and serine (S) for threonine (T) and vice versa. Other substitutions can also be considered conservative, depending on the environment of the particular amino acid and its role in the three-dimensional structure of the protein. For example, glycine (G) and alanine (A) can frequently be interchangeable, as can alanine (A) and valine (V). Methionine (M), which is relatively hydrophobic, can frequently be interchanged with leucine and isoleucine, and sometimes with valine. Lysine (K) and arginine (R) are frequently interchangeable in locations in which the significant feature of the amino acid residue is its charge and the differing pK's of these two amino acid residues are not significant. Still other changes can be considered "conservative" in particular environments (see, e.g. Table III herein; pages 13-15 "Biochemistry" 2nd ED. Lubert Stryer ed (Stanford University); Henikoff *et al.*, PNAS 1992 Vol 89 10915-10919; Lei *et al.*, J Biol Chem 1995 May 19; 270(20):11882-6).

Embodiments of the invention disclosed herein include a wide variety of art-accepted variants or analogs of 191P4D12(b) proteins such as polypeptides having amino acid insertions, deletions and substitutions. 191P4D12(b) variants can be made using methods known in the art such as site-directed mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis (Carter *et al., Nucl. Acids Res., 13*:4331 (1986); Zoller *et al., Nucl. Acids Res., 10*:6487 (1987)), cassette mutagenesis (Wells *et al.*, Gene, 34:315 (1985)), restriction selection mutagenesis (Wells *et al., Philos. Trans. R. Soc. London SerA*, 317:415 (1986)) or other known techniques can be performed on the cloned DNA to produce the 191P4D12(b) variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence that is involved in a specific biological activity such as a protein-protein interaction. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions (Creighton, *The Proteins,*

(W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)). If alanine substitution does not yield adequate amounts of variant, an isosteric amino acid can be used.

As defined herein, 191P4D12(b) variants, analogs or homologs, have the distinguishing attribute of having at least one epitope that is "cross reactive" with a 191P4D12(b) protein having an amino acid sequence of Figure 3. As used in this sentence, "cross reactive" means that an antibody or T cell that specifically binds to a 191P4D12(b) variant also specifically binds to a 191P4D12(b) protein having an amino acid sequence set forth in Figure 3. A polypeptide ceases to be a variant of a protein shown in Figure 3, when it no longer contains any epitope capable of being recognized by an antibody or T cell that specifically binds to the starting 191P4D12(b) protein. Those skilled in the art understand that antibodies that recognize proteins bind to epitopes of varying size, and a grouping of the order of about four or five amino acids, contiguous or not, is regarded as a typical number of amino acids in a minimal epitope. See, e.g., Nair *et al.*, J. Immunol 2000 165(12): 6949-6955; Hebbes *et al.*, Mol Immunol (1989) 26(9):865-73; Schwartz *et al.*, J Immunol (1985) 135(4):2598-608.

Other classes of 191P4D12(b)-related protein variants share 70%, 75%, 80%, 85% or 90% or more similarity with an amino acid sequence of Figure 3, or a fragment thereof. Another specific class of 191P4D12(b) protein variants or analogs comprises one or more of the 191P4D12(b) biological motifs described herein or presently known in the art. Thus, encompassed by the present invention are analogs of 191P4D12(b) fragments (nucleic or amino acid) that have altered functional (e.g. immunogenic) properties relative to the starting fragment. It is to be appreciated that motifs now or which become part of the art are to be applied to the nucleic or amino acid sequences of Figure 2 or Figure 3.

As discussed herein, embodiments of the claimed invention include polypeptides containing less than the full amino acid sequence of a 191P4D12(b) protein shown in Figure 2 or Figure 3. For example, representative embodiments of the invention comprise peptides/proteins having any 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more contiguous amino acids of a 191P4D12(b) protein shown in Figure 2 or Figure 3.

Moreover, representative embodiments of the invention disclosed herein include polypeptides consisting of about amino acid 1 to about amino acid 10 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 10 to about amino acid 20 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 20 to about amino acid 30 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 30 to about amino acid 40 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 40 to about amino acid 50 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 50 to about amino acid 60 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 60 to about amino acid 70 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 70 to about amino acid 80 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 80 to about amino acid 90 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, polypeptides consisting of about amino acid 90 to about amino acid 100 of a 191P4D12(b) protein shown in Figure 2 or Figure 3, etc. throughout the entirety of a 191P4D12(b) amino acid sequence. Moreover, polypeptides consisting of about amino acid 1 (or 20 or 30 or 40 etc.) to about amino acid 20, (or 130, or 140 or 150 etc.) of a 191P4D12(b) protein shown in Figure 2 or Figure 3 are embodiments of the invention. It is to be appreciated that the starting and stopping positions in this paragraph refer to the specified position as well as that position plus or minus 5 residues.

191P4D12(b)-related proteins are generated using standard peptide synthesis technology or using chemical cleavage methods well known in the art. Alternatively, recombinant methods can be used to generate nucleic acid molecules that encode a 191P4D12(b)-related protein. In one embodiment, nucleic acid molecules provide a means to generate defined fragments of a 191P4D12(b) protein (or variants, homologs or analogs thereof).

III.A.) Motif-bearing Protein Embodiments

Additional illustrative embodiments of the invention disclosed herein include 191P4D12(b) polypeptides comprising the amino acid residues of one or more of the biological motifs contained within a 191P4D12(b) polypeptide sequence set forth in Figure 2 or Figure 3. Various motifs are known in the art, and a protein can be evaluated for the presence of such motifs by a number of publicly available Internet sites.

Motif bearing subsequences of all 191P4D12(b) variant proteins are set forth and identified in Tables VIII-XXI and XXII-XLIX.

Table V sets forth several frequently occurring motifs based on pfam searches.

The columns of Table V list (1) motif name abbreviation, (2) percent identity found amongst the different member of the motif family, (3) motif name or description and (4) most common function; location information is included if the motif is relevant for location.

Polypeptides comprising one or more of the 191P4D12(b) motifs discussed above are useful in elucidating the specific characteristics of a malignant phenotype in view of the observation that the 191P4D12(b) motifs discussed above are associated with growth dysregulation and because 191P4D12(b) is overexpressed in certain cancers (See, e.g., Table I). Casein kinase II, cAMP and camp-dependent protein kinase, and Protein Kinase C, for example, are enzymes known to be associated with the development of the malignant phenotype (see e.g. Chen *et al.*, Lab Invest., 78(2): 165-174 (1998); Gaiddon *et al.*, Endocrinology 136(10): 4331-4338 (1995); Hall *et al.*, Nucleic Acids Research 24(6): 1119-1126 (1996); Peterziel *et al.*, Oncogene 18(46): 6322-6329 (1999) and O'Brian, Oncol. Rep. 5(2): 305-309 (1998)). Moreover, both glycosylation and myristoylation are protein modifications also associated with cancer and cancer progression (see e.g. Dennis *et al.*, Biochem. Biophys. Acta 1473(1):21-34 (1999); Raju *et al.*, Exp. Cell Res. 235(1): 145-154 (1997)). Amidation is another protein modification also associated with cancer and cancer progression (see e.g. Treston *et al.*, J. Natl. Cancer Inst. Monogr. (13): 169-175 (1992)).

In another embodiment, proteins of the invention comprise one or more of the immunoreactive epitopes identified in accordance with art-accepted methods, such as the peptides set forth in Tables VIII-XXI and XXII-XLIX. CTL epitopes can be determined using specific algorithms to identify peptides within a 191P4D12(b) protein that are capable of optimally binding to specified HLA alleles (e.g., Table IV; Epimatrix™ and Epimer™, Brown University).

Moreover, processes for identifying peptides that have sufficient binding affinity for HLA molecules and which are correlated with being immunogenic epitopes, are well known in the art, and are carried out without undue experimentation. In addition, processes for identifying peptides that are immunogenic epitopes, are well known in the art, and are carried out without undue experimentation either *in vitro* or *in vivo*.

Also known in the art are principles for creating analogs of such epitopes in order to modulate immunogenicity. For example, one begins with an epitope that bears a CTL or HTL motif (see, e.g., the HLA Class I and HLA Class II motifs/supermotifs of Table IV). The epitope is analoged by substituting out an amino acid at one of the specified positions, and replacing it with another amino acid specified for that position. For example, on the basis of residues defined in Table IV, one can substitute out a deleterious residue in favor of any other residue, such as a preferred residue; substitute a less-preferred residue with a preferred residue; or substitute an originally-occurring preferred residue with another preferred residue. Substitutions can occur at primary anchor positions or at other positions in a peptide; see, e.g., Table IV.

A variety of references reflect the art regarding the identification and generation of epitopes in a protein of interest as well as analogs thereof. See, for example, WO 97/33602 to Chesnut *et al.*; Sette, Immunogenetics 1999 50(3-4): 201-

212; Sette *et al.*, J. Immunol. 2001 166(2): 1389-1397; Sidney *et al.*, Hum. Immunol. 1997 58(1): 12-20; Kondo *et al.*, Immunogenetics 1997 45(4): 249-258; Sidney *et al.*, J. Immunol. 1996 157(8): 3480-90; and Falk *et al.*, Nature 351: 290-6 (1991); Hunt *et al.*, Science 255:1261-3 (1992); Parker *et al.*, J. Immunol. 149:3580-7 (1992); Parker *et al.*, J. Immunol. 152:163-75 (1994)); Kast *et al.*, 1994 152(8): 3904-12; Borras-Cuesta *et al.*, Hum. Immunol. 2000 61(3): 266-278; Alexander *et al.*, J. Immunol. 2000 164(3); 164(3): 1625-1633; Alexander *et al.*, PMID: 7895164, UI: 95202582; O'Sullivan *et al.*, J. Immunol. 1991 147(8): 2663-2669; Alexander *et al.*, Immunity 1994 1(9): 751-761 and Alexander *et al.*, Immunol. Res. 1998 18(2): 79-92.

Related embodiments of the invention include polypeptides comprising combinations of the different motifs set forth in Table VI, and/or, one or more of the predicted CTL epitopes of Tables VIII-XXI and XXII-XLIX, and/or, one or more of the predicted HTL epitopes of Tables XLVI-XLIX, and/or, one or more of the T cell binding motifs known in the art. Preferred embodiments contain no insertions, deletions or substitutions either within the motifs or within the intervening sequences of the polypeptides. In addition, embodiments which include a number of either N-terminal and/or C-terminal amino acid residues on either side of these motifs may be desirable (to, for example, include a greater portion of the polypeptide architecture in which the motif is located). Typically, the number of N-terminal and/or C-terminal amino acid residues on either side of a motif is between about 1 to about 100 amino acid residues, preferably 5 to about 50 amino acid residues.

191P4D12(b)-related proteins are embodied in many forms, preferably in isolated form. A purified 191P4D12(b) protein molecule will be substantially free of other proteins or molecules that impair the binding of 191P4D12(b) to antibody, T cell or other ligand. The nature and degree of isolation and purification will depend on the intended use. Embodiments of a 191P4D12(b)-related proteins include purified 191P4D12(b)-related proteins and functional, soluble 191P4D12(b)-related proteins. In one embodiment, a functional, soluble 191P4D12(b) protein or fragment thereof retains the ability to be bound by antibody, T cell or other ligand.

The invention also provides 191P4D12(b) proteins comprising biologically active fragments of a 191P4D12(b) amino acid sequence shown in Figure 2 or Figure 3. Such proteins exhibit properties of the starting 191P4D12(b) protein, such as the ability to elicit the generation of antibodies that specifically bind an epitope associated with the starting 191P4D12(b) protein; to be bound by such antibodies; to elicit the activation of HTL or CTL; and/or, to be recognized by HTL or CTL that also specifically bind to the starting protein.

191P4D12(b)-related polypeptides that contain particularly interesting structures can be predicted and/or identified using various analytical techniques well known in the art, including, for example, the methods of Chou-Fasman, Garnier-Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis, or based on immunogenicity. Fragments that contain such structures are particularly useful in generating subunit-specific anti-191P4D12(b) antibodies or T cells or in identifying cellular factors that bind to 191P4D12(b). For example, hydrophilicity profiles can be generated, and immunogenic peptide fragments identified, using the method of Hopp, T.P. and Woods, K.R., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828. Hydropathicity profiles can be generated, and immunogenic peptide fragments identified, using the method of Kyte, J. and Doolittle, R.F., 1982, J. Mol. Biol. 157:105-132. Percent (%) Accessible Residues profiles can be generated, and immunogenic peptide fragments identified, using the method of Janin J., 1979, Nature 277:491-492. Average Flexibility profiles can be generated, and immunogenic peptide fragments identified, using the method of Bhaskaran R., Ponnuswamy P.K., 1988, Int. J. Pept. Protein Res. 32:242-255. Beta-turn profiles can be generated, and immunogenic peptide fragments identified, using the method of Deleage, G., Roux B., 1987, Protein Engineering 1:289-294.

CTL epitopes can be determined using specific algorithms to identify peptides within a 191P4D12(b) protein that are capable of optimally binding to specified HLA alleles (e.g., by using the SYFPEITHI site

; the listings in Table IV(A)-(E); Epimatrix™ and Epimer™, Brown University

; and BIMAS). Illustrating this, peptide epitopes from 191P4D12(b)

that are presented in the context of human MHC Class I molecules, e.g., HLA-A1, A2, A3, A11, A24, B7 and B35 were predicted (see, e.g., Tables VIII-XXI, XXII-XLIX). Specifically, the complete amino acid sequence of the 191P4D12(b) protein and relevant portions of other variants, i.e., for HLA Class I predictions 9 flanking residues on either side of a point mutation or exon juction, and for HLA Class II predictions 14 flanking residues on either side of a point mutation or exon junction corresponding to that variant, were entered into the HLA Peptide Motif Search algorithm found in the Bioinformatics and Molecular Analysis Section (BIMAS) web site ; in addition to the site SYFPEITHI.

The HLA peptide motif search algorithm was developed by Dr. Ken Parker based on binding of specific peptide sequences in the groove of HLA Class I molecules, in particular HLA-A2 (see, e.g., Falk *et al.*, Nature 351: 290-6 (1991); Hunt *et al.*, Science 255:1261-3 (1992); Parker *et al.*, J. Immunol. 149:3580-7 (1992); Parker *et al.*, J. Immunol. 152:163-75 (1994)). This algorithm allows location and ranking of 8-mer, 9-mer, and 10-mer peptides from a complete protein sequence for predicted binding to HLA-A2 as well as numerous other HLA Class I molecules. Many HLA class I binding peptides are 8-, 9-, 10 or 11-mers. For example, for Class I HLA-A2, the epitopes preferably contain a leucine (L) or methionine (M) at position 2 and a valine (V) or leucine (L) at the C-terminus (see, e.g., Parker *et al.*, J. Immunol. 149:3580-7 (1992)). Selected results of 191P4D12(b) predicted binding peptides are shown in Tables VIII-XXI and XXII-XLIX herein. In Tables VIII-XXI and XXII-XLVII, selected candidates, 9-mers and 10-mers, for each family member are shown along with their location, the amino acid sequence of each specific peptide, and an estimated binding score. In Tables XLVI-XLIX, selected candidates, 15-mers, for each family member are shown along with their location, the amino acid sequence of each specific peptide, and an estimated binding score. The binding score corresponds to the estimated half time of dissociation of complexes containing the peptide at 37°C at pH 6.5. Peptides with the highest binding score are predicted to be the most tightly bound to HLA Class I on the cell surface for the greatest period of time and thus represent the best immunogenic targets for T-cell recognition.

Actual binding of peptides to an HLA allele can be evaluated by stabilization of HLA expression on the antigen-processing defective cell line T2 (see, e.g., Xue *et al.*, Prostate 30:73-8 (1997) and Peshwa *et al.*, Prostate 36:129-38 (1998)). Immunogenicity of specific peptides can be evaluated *in vitro* by stimulation of CD8+ cytotoxic T lymphocytes (CTL) in the presence of antigen presenting cells such as dendritic cells.

It is to be appreciated that every epitope predicted by the BIMAS site, Epimer™ and Epimatrix™ sites, or specified by the HLA class I or class II motifs available in the art or which become part of the art such as set forth in Table IV (or determined using the SYFPEITHI website, or BIMAS) are to be "applied" to a 191P4D12(b) protein in accordance with the invention. As used in this context "applied" means that a 191P4D12(b) protein is evaluated, e.g., visually or by computer-based patterns finding methods, as appreciated by those of skill in the relevant art. Every subsequence of a 191P4D12(b) protein of 8, 9, 10, or 11 amino acid residues that bears an HLA Class I motif, or a subsequence of 9 or more amino acid residues that bear an HLA Class II motif are within the scope of the invention.

III.B.) Expression of 191P4D12(b)-related Proteins

In an embodiment described in the examples that follow, 191P4D12(b) can be conveniently expressed in cells (such as 293T cells) transfected with a commercially available expression vector such as a CMV-driven expression vector encoding 191P4D12(b) with a C-terminal 6XHis and MYC tag (pcDNA3.1/mycHIS, Invitrogen or Tag5, GenHunter Corporation, Nashville TN). The Tag5 vector provides an IgGK secretion signal that can be used to facilitate the production of a secreted 191P4D12(b) protein in transfected cells. The secreted HIS-tagged 191P4D12(b) in the culture media can be purified, e.g., using a nickel column using standard techniques.

III.C.) Modifications of 191P4D12(b)-related Proteins

Modifications of 191P4D12(b)-related proteins such as covalent modifications are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a 191P4D12(b) polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of a 191P4D12(b) protein. Another type of covalent modification of a 191P4D12(b) polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of a protein of the invention. Another type of covalent modification of 191P4D12(b) comprises linking a 191P4D12(b) polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The 191P4D12(b)-related proteins of the present invention can also be modified to form a chimeric molecule comprising 191P4D12(b) fused to another, heterologous polypeptide or amino acid sequence. Such a chimeric molecule can be synthesized chemically or recombinantly. A chimeric molecule can have a protein of the invention fused to another tumor-associated antigen or fragment thereof. Alternatively, a protein in accordance with the invention can comprise a fusion of fragments of a 191P4D12(b) sequence (amino or nucleic acid) such that a molecule is created that is not, through its length, directly homologous to the amino or nucleic acid sequences shown in Figure 2 or Figure 3. Such a chimeric molecule can comprise multiples of the same subsequence of 191P4D12(b). A chimeric molecule can comprise a fusion of a 191P4D12(b)-related protein with a polyhistidine epitope tag, which provides an epitope to which immobilized nickel can selectively bind, with cytokines or with growth factors. The epitope tag is generally placed at the amino- or carboxyl-terminus of a 191P4D12(b) protein. In an alternative embodiment, the chimeric molecule can comprise a fusion of a 191P4D12(b)-related protein with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a 191P4D12(b) polypeptide in place of at least one variable region within an Ig molecule. In a preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CHI, CH2 and CH3 regions of an IgGl molecule. For the production of immunoglobulin fusions see, e.g., U.S. Patent No. 5,428,130 issued June 27, 1995.

III.D.) Uses of 191P4D12(b)-related Proteins

The proteins of the invention have a number of different specific uses. As 191P4D12(b) is highly expressed in prostate and other cancers, 191P4D12(b)-related proteins are used in methods that assess the status of 191P4D12(b) gene products in normal versus cancerous tissues, thereby elucidating the malignant phenotype. Typically, polypeptides from specific regions of a 191P4D12(b) protein are used to assess the presence of perturbations (such as deletions, insertions, point mutations etc.) in those regions (such as regions containing one or more motifs). Exemplary assays utilize antibodies or T cells targeting 191P4D12(b)-related proteins comprising the amino acid residues of one or more of the biological motifs contained within a 191P4D12(b) polypeptide sequence in order to evaluate the characteristics of this region in normal versus cancerous tissues or to elicit an immune response to the epitope. Alternatively, 191P4D12(b)-related proteins that contain the amino acid residues of one or more of the biological motifs in a 191P4D12(b) protein are used to screen for factors that interact with that region of 191P4D12(b).

191P4D12(b) protein fragments/subsequences are particularly useful in generating and characterizing domain-specific antibodies (e.g., antibodies recognizing an extracellular or intracellular epitope of a 191P4D12(b) protein), for identifying agents or cellular factors that bind to 191P4D12(b) or a particular structural domain thereof, and in various therapeutic and diagnostic contexts, including but not limited to diagnostic assays, cancer vaccines and methods of preparing such vaccines.

Proteins encoded by the 191P4D12(b) genes, or by analogs, homologs or fragments thereof, have a variety of uses, including but not limited to generating antibodies and in methods for identifying ligands and other agents and cellular constituents that bind to a 191P4D12(b) gene product. Antibodies raised against a 191P4D12(b) protein or fragment thereof are useful in diagnostic and prognostic assays, and imaging methodologies in the management of human cancers characterized by expression of 191P4D12(b) protein, such as those listed in Table I. Such antibodies can be expressed intracellularly and used in methods of treating patients with such cancers. 191P4D12(b)-related nucleic acids or proteins are also used in generating HTL or CTL responses.

Various immunological assays useful for the detection of 191P4D12(b) proteins are used, including but not limited to various types of radioimmunoassays, enzyme-linked immunosorbent assays (ELISA), enzyme-linked immunofluorescent assays (ELIFA), immunocytochemical methods, and the like. Antibodies can be labeled and used as immunological imaging reagents capable of detecting 191P4D12(b)-expressing cells (e.g., in radioscintigraphic imaging methods). 191P4D12(b) proteins are also particularly useful in generating cancer vaccines, as further described herein.

IV.) 191P4D12(b) Antibodies

Another aspect of the invention provides antibodies that bind to 191P4D12(b)-related proteins. Preferred antibodies specifically bind to a 191P4D12(b)-related protein and do not bind (or bind weakly) to peptides or proteins that are not 191P4D12(b)-related proteins under physiological conditions. In this context, examples of physiological conditions include: 1) phosphate buffered saline; 2) Tris-buffered saline containing 25mM Tris and 150 mM NaCl; or normal saline (0.9% NaCl); 4) animal serum such as human serum; or, 5) a combination of any of 1) through 4); these reactions preferably taking place at pH 7.5, alternatively in a range of pH 7.0 to 8.0, or alternatively in a range of pH 6.5 to 8.5; also, these reactions taking place at a temperature between 4°C to 37°C. For example, antibodies that bind 191P4D12(b) can bind 191P4D12(b)-related proteins such as the homologs or analogs thereof.

191P4D12(b) antibodies of the invention are particularly useful in cancer (see, e.g., Table I) diagnostic and prognostic assays, and imaging methodologies. Similarly, such antibodies are useful in the treatment, diagnosis, and/or prognosis of other cancers, to the extent 191P4D12(b) is also expressed or overexpressed in these other cancers. Moreover, intracellularly expressed antibodies (e.g., single chain antibodies) are therapeutically useful in treating cancers in which the expression of 191P4D12(b) is involved, such as advanced or metastatic prostate cancers.

The invention also provides various immunological assays useful for the detection and quantification of 191P4D12(b) and mutant 191P4D12(b)-related proteins. Such assays can comprise one or more 191P4D12(b) antibodies capable of recognizing and binding a 191P4D12(b)-related protein, as appropriate. These assays are performed within various immunological assay formats well known in the art, including but not limited to various types of radioimmunoassays, enzyme-linked immunosorbent assays (ELISA), enzyme-linked immunofluorescent assays (ELIFA), and the like.

Immunological non-antibody assays of the invention also comprise T cell immunogenicity assays (inhibitory or stimulatory) as well as major histocompatibility complex (MHC) binding assays.

In addition, immunological imaging methods capable of detecting prostate cancer and other cancers expressing 191P4D12(b) are also provided by the invention, including but not limited to radioscintigraphic imaging methods using labeled 191P4D12(b) antibodies. Such assays are clinically useful in the detection, monitoring, and prognosis of 191P4D12(b) expressing cancers such as prostate cancer.

191P4D12(b) antibodies are also used in methods for purifying a 191P4D12(b)-related protein and for isolating 191P4D12(b) homologues and related molecules. For example, a method of purifying a 191P4D12(b)-related protein comprises incubating a 191P4D12(b) antibody, which has been coupled to a solid matrix, with a lysate or other solution containing a 191P4D12(b)-related protein under conditions that permit the 191P4D12(b) antibody to bind to the 191P4D12(b)-related protein;

washing the solid matrix to eliminate impurities; and eluting the 191P4D12(b)-related protein from the coupled antibody. Other uses of 191P4D12(b) antibodies in accordance with the invention include generating anti-idiotypic antibodies that mimic a 191P4D12(b) protein.

Various methods for the preparation of antibodies are well known in the art. For example, antibodies can be prepared by immunizing a suitable mammalian host using a 191P4D12(b)-related protein, peptide, or fragment, in isolated or immunoconjugated form (Antibodies: A Laboratory Manual, CSH Press, Eds., Harlow, and Lane (1988); Harlow, Antibodies, Cold Spring Harbor Press, NY (1989)). In addition, fusion proteins of 191P4D12(b) can also be used, such as a 191P4D12(b) GST-fusion protein. In a particular embodiment, a GST fusion protein comprising all or most of the amino acid sequence of Figure 2 or Figure 3 is produced, then used as an immunogen to generate appropriate antibodies. In another embodiment, a 191P4D12(b)-related protein is synthesized and used as an immunogen.

In addition, naked DNA immunization techniques known in the art are used (with or without purified 191P4D12(b)-related protein or 191P4D12(b) expressing cells) to generate an immune response to the encoded immunogen (for review, see Donnelly *et al.*, 1997, Ann. Rev. Immunol. 15: 617-648).

The amino acid sequence of a 191P4D12(b) protein as shown in Figure 2 or Figure 3 can be analyzed to select specific regions of the 191P4D12(b) protein for generating antibodies. For example, hydrophobicity and hydrophilicity analyses of a 191P4D12(b) amino acid sequence are used to identify hydrophilic regions in the 191P4D12(b) structure. Regions of a 191P4D12(b) protein that show immunogenic structure, as well as other regions and domains, can readily be identified using various other methods known in the art, such as Chou-Fasman, Garnier-Robson, Kyte-Doolittle, Eisenberg, Karplus-Schultz or Jameson-Wolf analysis. Hydrophilicity profiles can be generated using the method of Hopp, T.P. and Woods, K.R., 1981, Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828. Hydropathicity profiles can be generated using the method of Kyte, J. and Doolittle, R.F., 1982, J. Mol. Biol. 157:105-132. Percent (%) Accessible Residues profiles can be generated using the method of Janin J., 1979, Nature 277:491-492. Average Flexibility profiles can be generated using the method of Bhaskaran R., Ponnuswamy P.K., 1988, Int. J. Pept. Protein Res. 32:242-255. Beta-turn profiles can be generated using the method of Deleage, G., Roux B., 1987, Protein Engineering 1:289-294. Thus, each region identified by any of these programs or methods is within the scope of the present invention. Methods for the generation of 191P4D12(b) antibodies are further illustrated by way of the examples provided herein. Methods for preparing a protein or polypeptide for use as an immunogen are well known in the art. Also well known in the art are methods for preparing immunogenic conjugates of a protein with a carrier, such as BSA, KLH or other carrier protein. In some circumstances, direct conjugation using, for example, carbodiimide reagents are used; in other instances linking reagents such as those supplied by Pierce Chemical Co., Rockford, IL, are effective. Administration of a 191P4D12(b) immunogen is often conducted by injection over a suitable time period and with use of a suitable adjuvant, as is understood in the art. During the immunization schedule, titers of antibodies can be taken to determine adequacy of antibody formation.

191P4D12(b) monoclonal antibodies can be produced by various means well known in the art. For example, immortalized cell lines that secrete a desired monoclonal antibody are prepared using the standard hybridoma technology of Kohler and Milstein or modifications that immortalize antibody-producing B cells, as is generally known. Immortalized cell lines that secrete the desired antibodies are screened by immunoassay in which the antigen is a 191P4D12(b)-related protein. When the appropriate immortalized cell culture is identified, the cells can be expanded and antibodies produced either from *in vitro* cultures or from ascites fluid.

The antibodies or fragments of the invention can also be produced, by recombinant means. Regions that bind specifically to the desired regions of a 191P4D12(b) protein can also be produced in the context of chimeric or complementarity-determining region (CDR) grafted antibodies of multiple species origin. Humanized or human 191P4D12(b) antibodies can also be produced, and are preferred for use in therapeutic contexts. Methods for humanizing murine and other non-human antibodies,

by substituting one or more of the non-human antibody CDRs for corresponding human antibody sequences, are well known (see for example, Jones *et al.*, 1986, Nature 321: 522-525; Riechmann *et al.*, 1988, Nature 332: 323-327; Verhoeyen *et al.*, 1988, Science 239: 1534-1536). See also, Carter *et al.*, 1993, Proc. Natl. Acad. Sci. USA 89: 4285 and Sims *et al.*, 1993, J. Immunol. 151: 2296.

Methods for producing fully human monoclonal antibodies include phage display and transgenic methods (for review, see Vaughan *et al.*, 1998, Nature Biotechnology 16: 535-539). Fully human 191P4D12(b) monoclonal antibodies can be generated using cloning technologies employing large human Ig gene combinatorial libraries (i.e., phage display) (Griffiths and Hoogenboom, Building an *in vitro* immune system: human antibodies from phage display libraries. In: Protein Engineering of Antibody Molecules for Prophylactic and Therapeutic Applications in Man, Clark, M. (Ed.), Nottingham Academic, pp 45-64 (1993); Burton and Barbas, Human Antibodies from combinatorial libraries. Id., pp 65-82). Fully human 191P4D12(b) monoclonal antibodies can also be produced using transgenic mice engineered to contain human immunoglobulin gene loci as described in PCT Patent Application WO98/24893, Kucherlapati and Jakobovits *et al.*, published December 3, 1997 (see also, Jakobovits, 1998, Exp. Opin. Invest. Drugs 7(4): 607-614; U.S. patents 6,162,963 issued 19 December 2000; 6,150,584 issued 12 November 2000; and, 6,114598 issued 5 September 2000). This method avoids the *in vitro* manipulation required with phage display technology and efficiently produces high affinity authentic human antibodies.

Reactivity of 191P4D12(b) antibodies with a 191P4D12(b)-related protein can be established by a number of well known means, including Western blot, immunoprecipitation, ELISA, and FACS analyses using, as appropriate, 191P4D12(b)-related proteins, 191P4D12(b)-expressing cells or extracts thereof. A 191P4D12(b) antibody or fragment thereof can be labeled with a detectable marker or conjugated to a second molecule. Suitable detectable markers include, but are not limited to, a radioisotope, a fluorescent compound, a bioluminescent compound, chemiluminescent compound, a metal chelator or an enzyme. Further, bi-specific antibodies specific for two or more 191P4D12(b) epitopes are generated using methods generally known in the art. Homodimeric antibodies can also be generated by cross-linking techniques known in the art (e.g., Wolff *et al.*, Cancer Res. 53: 2560-2565).

V.) 191P4D12(b) Cellular Immune Responses

The mechanism by which T cells recognize antigens has been delineated. Efficacious peptide epitope vaccine compositions of the invention induce a therapeutic or prophylactic immune responses in very broad segments of the world-wide population. For an understanding of the value and efficacy of compositions of the invention that induce cellular immune responses, a brief review of immunology-related technology is provided.

A complex of an HLA molecule and a peptidic antigen acts as the ligand recognized by HLA-restricted T cells (Buus, S. *et al.*, *Cell* 47:1071, 1986; Babbitt, B. P. *et al.*, *Nature* 317:359, 1985; Townsend, A. and Bodmer, H., *Annu. Rev. Immunol.* 7:601, 1989; Germain, R. N., *Annu. Rev. Immunol.* 11:403, 1993). Through the study of single amino acid substituted antigen analogs and the sequencing of endogenously bound, naturally processed peptides, critical residues that correspond to motifs required for specific binding to HLA antigen molecules have been identified and are set forth in Table IV (see also, e.g., Southwood, *et al.*, *J. Immunol.* 160:3363, 1998; Rammensee, *et al.*, *Immunogenetics* 41:178, 1995; Rammensee *et al.*, SYFPEITHI ; Sette, A. and Sidney, J. *Curr. Opin. Immunol.* 10:478, 1998; Engelhard, V. H., *Curr. Opin. Immunol.* 6:13, 1994; Sette, A. and Grey, H. M., *Curr. Opin. Immunol.* 4:79, 1992; Sinigaglia, F. and Hammer, J. *Curr. Biol.* 6:52, 1994; Ruppert *et al.*, *Cell* 74:929-937, 1993; Kondo *et al.*, *J. Immunol.* 155:4307-4312, 1995; Sidney *et al.*, *J. Immunol.* 157:3480-3490, 1996; Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; Sette, A. and Sidney, J. *Immunogenetics 1999 Nov; 50(3-4):201-12,* Review).

Furthermore, x-ray crystallographic analyses of HLA-peptide complexes have revealed pockets within the peptide binding cleft/groove of HLA molecules which accommodate, in an allele-specific mode, residues borne by peptide ligands;

these residues in turn determine the HLA binding capacity of the peptides in which they are present. (*See, e.g.*, Madden, D.R. *Annu. Rev. Immunol.* 13:587, 1995; Smith, *et al.*, *Immunity* 4:203, 1996; Fremont *et al.*, *Immunity* 8:305, 1998; Stern *et al.*, *Structure* 2:245, 1994; Jones, E.Y. *Curr. Opin. Immunol.* 9:75, 1997; Brown, J. H. *et al.*, *Nature* 364:33, 1993; Guo, H. C. *et al.*, *Proc. Natl. Acad. Sci. USA* 90:8053, 1993; Guo, H. C. *et al.*, *Nature* 360:364, 1992; Silver, M. L. *et al.*, *Nature* 360:367, 1992; Matsumura, M. *et al.*, *Science* 257:927, 1992; Madden *et al.*, *Cell* 70:1035, 1992; Fremont, D. H. *et al.*, *Science* 257:919, 1992; Saper, M. A. , Bjorkman, P. J. and Wiley, D. C., *J. Mol. Biol.* 219:277, 1991.)

Accordingly, the definition of class I and class II allele-specific HLA binding motifs, or class I or class II supermotifs allows identification of regions within a protein that are correlated with binding to particular HLA antigen(s).

Thus, by a process of HLA motif identification, candidates for epitope-based vaccines have been identified; such candidates can be further evaluated by HLA-peptide binding assays to determine binding affinity and/or the time period of association of the epitope and its corresponding HLA molecule. Additional confirmatory work can be performed to select, amongst these vaccine candidates, epitopes with preferred characteristics in terms of population coverage, and/or immunogenicity.

Various strategies can be utilized to evaluate cellular immunogenicity, including:

1) Evaluation of primary T cell cultures from normal individuals (*see, e.g.*, Wentworth, P. A. *et al.*, *Mol. Immunol.* 32:603, 1995; Celis, E. *et al.*, *Proc. Natl. Acad. Sci. USA* 91:2105, 1994; Tsai, V. *et al.*, *J. Immunol.* 158:1796, 1997; Kawashima, I. *et al.*, *Human Immunol.* 59:1, 1998). This procedure involves the stimulation of peripheral blood lymphocytes (PBL) from normal subjects with a test peptide in the presence of antigen presenting cells *in vitro* over a period of several weeks. T cells specific for the peptide become activated during this time and are detected using, *e.g.*, a lymphokine- or ^{51}Cr-release assay involving peptide sensitized target cells.

2) Immunization of HLA transgenic mice (*see, e.g.*, Wentworth, P. A. *et al.*, *J. Immunol.* 26:97, 1996; Wentworth, P. A. *et al.*, *Int. Immunol.* 8:651, 1996; Alexander, J. *et al.*, *J. Immunol.* 159:4753, 1997). For example, in such methods peptides in incomplete Freund's adjuvant are administered subcutaneously to HLA transgenic mice. Several weeks following immunization, splenocytes are removed and cultured *in vitro* in the presence of test peptide for approximately one week. Peptide-specific T cells are detected using, *e.g.*, a ^{51}Cr-release assay involving peptide sensitized target cells and target cells expressing endogenously generated antigen.

3) Demonstration of recall T cell responses from immune individuals who have been either effectively vaccinated and/or from chronically ill patients (*see, e.g.*, Rehermann, B. *et al.*, *J. Exp. Med.* 181:1047, 1995; Doolan, D. L. *et al.*, *Immunity* 7:97, 1997; Bertoni, R. *et al.*, *J. Clin. Invest.* 100:503, 1997; Threlkeld, S. C. *et al.*, *J. Immunol.* 159:1648, 1997; Diepolder, H. M. *et al.*, *J. Virol.* 71:6011, 1997). Accordingly, recall responses are detected by culturing PBL from subjects that have been exposed to the antigen due to disease and thus have generated an immune response "naturally", or from patients who were vaccinated against the antigen. PBL from subjects are cultured *in vitro* for 1-2 weeks in the presence of test peptide plus antigen presenting cells (APC) to allow activation of "memory" T cells, as compared to "naive" T cells. At the end of the culture period, T cell activity is detected using assays including ^{51}Cr release involving peptide-sensitized targets, T cell proliferation, or lymphokine release.

VI.) 191P4D12(b) Transgenic Animals

Nucleic acids that encode a 191P4D12(b)-related protein can also be used to generate either transgenic animals or "knock out" animals that, in turn, are useful in the development and screening of therapeutically useful reagents. In accordance with established techniques, cDNA encoding 191P4D12(b) can be used to clone genomic DNA that encodes 191P4D12(b). The cloned genomic sequences can then be used to generate transgenic animals containing cells that express DNA that encode 191P4D12(b). Methods for generating transgenic animals, particularly animals such as mice or

rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 issued 12 April 1988, and 4,870,009 issued 26 September 1989. Typically, particular cells would be targeted for 191P4D12(b) transgene incorporation with tissue-specific enhancers.

Transgenic animals that include a copy of a transgene encoding 191P4D12(b) can be used to examine the effect of increased expression of DNA that encodes 191P4D12(b). Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this aspect of the invention, an animal is treated with a reagent and a reduced incidence of a pathological condition, compared to untreated animals that bear the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of 191P4D12(b) can be used to construct a 191P4D12(b) "knock out" animal that has a defective or altered gene encoding 191P4D12(b) as a result of homologous recombination between the endogenous gene encoding 191P4D12(b) and altered genomic DNA encoding 191P4D12(b) introduced into an embryonic cell of the animal. For example, cDNA that encodes 191P4D12(b) can be used to clone genomic DNA encoding 191P4D12(b) in accordance with established techniques. A portion of the genomic DNA encoding 191P4D12(b) can be deleted or replaced with another gene, such as a gene encoding a selectable marker that can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector (see, e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected (see, e.g., Li *et al.*, Cell, 69:915 (1992)). The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras (see, e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal, and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knock out animals can be characterized, for example, for their ability to defend against certain pathological conditions or for their development of pathological conditions due to absence of a 191P4D12(b) polypeptide.

VII.) Methods for the Detection of 191P4D12(b)

Another aspect of the present invention relates to methods for detecting 191P4D12(b) polynucleotides and 191P4D12(b)-related proteins, as well as methods for identifying a cell that expresses 191P4D12(b). The expression profile of 191P4D12(b) makes it a diagnostic marker for metastasized disease. Accordingly, the status of 191P4D12(b) gene products provides information useful for predicting a variety of factors including susceptibility to advanced stage disease, rate of progression, and/or tumor aggressiveness. As discussed in detail herein, the status of 191P4D12(b) gene products in patient samples can be analyzed by a variety protocols that are well known in the art including immunohistochemical analysis, the variety of Northern blotting techniques including *in situ* hybridization, RT-PCR analysis (for example on laser capture micro-dissected samples), Western blot analysis and tissue array analysis.

More particularly, the invention provides assays for the detection of 191P4D12(b) polynucleotides in a biological sample, such as serum, bone, prostate, and other tissues, urine, semen, cell preparations, and the like. Detectable 191P4D12(b) polynucleotides include, for example, a 191P4D12(b) gene or fragment thereof, 191P4D12(b) mRNA, alternative splice variant 191P4D12(b) mRNAs, and recombinant DNA or RNA molecules that contain a 191P4D12(b) polynucleotide. A number of methods for amplifying and/or detecting the presence of 191P4D12(b) polynucleotides are well known in the art and can be employed in the practice of this aspect of the invention.

In one embodiment, a method for detecting a 191P4D12(b) mRNA in a biological sample comprises producing cDNA from the sample by reverse transcription using at least one primer; amplifying the cDNA so produced using a 191P4D12(b) polynucleotides as sense and antisense primers to amplify 191P4D12(b) cDNAs therein; and detecting the presence of the amplified 191P4D12(b) cDNA. Optionally, the sequence of the amplified 191P4D12(b) cDNA can be determined.

In another embodiment, a method of detecting a 191P4D12(b) gene in a biological sample comprises first isolating genomic DNA from the sample; amplifying the isolated genomic DNA using 191P4D12(b) polynucleotides as sense and antisense primers; and detecting the presence of the amplified 191P4D12(b) gene. Any number of appropriate sense and antisense probe combinations can be designed from a 191P4D12(b) nucleotide sequence (see, e.g., Figure 2) and used for this purpose.

The invention also provides assays for detecting the presence of a 191P4D12(b) protein in a tissue or other biological sample such as serum, semen, bone, prostate, urine, cell preparations, and the like. Methods for detecting a 191P4D12(b)-related protein are also well known and include, for example, immunoprecipitation, immunohistochemical analysis, Western blot analysis, molecular binding assays, ELISA, ELIFA and the like. For example, a method of detecting the presence of a 191P4D12(b)-related protein in a biological sample comprises first contacting the sample with a 191P4D12(b) antibody, a 191P4D12(b)-reactive fragment thereof, or a recombinant protein containing an antigen-binding region of a 191P4D12(b) antibody; and then detecting the binding of 191P4D12(b)-related protein in the sample.

Methods for identifying a cell that expresses 191P4D12(b) are also within the scope of the invention. In one embodiment, an assay for identifying a cell that expresses a 191P4D12(b) gene comprises detecting the presence of 191P4D12(b) mRNA in the cell. Methods for the detection of particular mRNAs in cells are well known and include, for example, hybridization assays using complementary DNA probes (such as *in situ* hybridization using labeled 191P4D12(b) riboprobes, Northern blot and related techniques) and various nucleic acid amplification assays (such as RT-PCR using complementary primers specific for 191P4D12(b), and other amplification type detection methods, such as, for example, branched DNA, SISBA, TMA and the like). Alternatively, an assay for identifying a cell that expresses a 191P4D12(b) gene comprises detecting the presence of 191P4D12(b)-related protein in the cell or secreted by the cell. Various methods for the detection of proteins are well known in the art and are employed for the detection of 191P4D12(b)-related proteins and cells that express 191P4D12(b)-related proteins.

191P4D12(b) expression analysis is also useful as a tool for identifying and evaluating agents that modulate 191P4D12(b) gene expression. For example, 191P4D12(b) expression is significantly upregulated in prostate cancer, and is expressed in cancers of the tissues listed in Table I. Identification of a molecule or biological agent that inhibits 191P4D12(b) expression or over-expression in cancer cells is of therapeutic value. For example, such an agent can be identified by using a screen that quantifies 191P4D12(b) expression by RT-PCR, nucleic acid hybridization or antibody binding.

VIII.) Methods for Monitoring the Status of 191P4D12(b)-related Genes and Their Products

Oncogenesis is known to be a multistep process where cellular growth becomes progressively dysregulated and cells progress from a normal physiological state to precancerous and then cancerous states (see, e.g., Alers *et al.*, Lab Invest. 77(5): 437-438 (1997) and Isaacs *et al.*, Cancer Surv. 23: 19-32 (1995)). In this context, examining a biological sample for evidence of dysregulated cell growth (such as aberrant 191P4D12(b) expression in cancers) allows for early detection of such aberrant physiology, before a pathologic state such as cancer has progressed to a stage that therapeutic options are more limited and or the prognosis is worse. In such examinations, the status of 191P4D12(b) in a biological sample of interest can be compared, for example, to the status of 191P4D12(b) in a corresponding normal sample (e.g. a sample from that individual or alternatively another individual that is not affected by a pathology). An alteration in the status of 191P4D12(b) in the biological sample (as compared to the normal sample) provides evidence of dysregulated cellular

growth. In addition to using a biological sample that is not affected by a pathology as a normal sample, one can also use a predetermined normative value such as a predetermined normal level of mRNA expression (see, e.g., Grever *et al.*, J. Comp. Neurol. 1996 Dec 9; 376(2): 306-14 and U.S. Patent No. 5,837,501) to compare 191P4D12(b) status in a sample.

The term "status" in this context is used according to its art accepted meaning and refers to the condition or state of a gene and its products. Typically, skilled artisans use a number of parameters to evaluate the condition or state of a gene and its products. These include, but are not limited to the location of expressed gene products (including the location of 191P4D12(b) expressing cells) as well as the level, and biological activity of expressed gene products (such as 191P4D12(b) mRNA, polynucleotides and polypeptides). Typically, an alteration in the status of 191P4D12(b) comprises a change in the location of 191P4D12(b) and/or 191P4D12(b) expressing cells and/or an increase in 191P4D12(b) mRNA and/or protein expression.

191P4D12(b) status in a sample can be analyzed by a number of means well known in the art, including without limitation, immunohistochemical analysis, *in situ* hybridization, RT-PCR analysis on laser capture micro-dissected samples, Western blot analysis, and tissue array analysis. Typical protocols for evaluating the status of a 191P4D12(b) gene and gene products are found, for example in Ausubel *et al.* eds., 1995, Current Protocols In Molecular Biology, Units 2 (Northern Blotting), 4 (Southern Blotting), 15 (Immunoblotting) and 18 (PCR Analysis). Thus, the status of 191P4D12(b) in a biological sample is evaluated by various methods utilized by skilled artisans including, but not limited to genomic Southern analysis (to examine, for example perturbations in a 191P4D12(b) gene), Northern analysis and/or PCR analysis of 191P4D12(b) mRNA (to examine, for example alterations in the polynucleotide sequences or expression levels of 191P4D12(b) mRNAs), and, Western and/or immunohistochemical analysis (to examine, for example alterations in polypeptide sequences, alterations in polypeptide localization within a sample, alterations in expression levels of 191P4D12(b) proteins and/or associations of 191P4D12(b) proteins with polypeptide binding partners). Detectable 191P4D12(b) polynucleotides include, for example, a 191P4D12(b) gene or fragment thereof, 191P4D12(b) mRNA, alternative splice variants, 191P4D12(b) mRNAs, and recombinant DNA or RNA molecules containing a 191P4D12(b) polynucleotide.

The expression profile of 191P4D12(b) makes it a diagnostic marker for local and/or metastasized disease, and provides information on the growth or oncogenic potential of a biological sample. In particular, the status of 191P4D12(b) provides information useful for predicting susceptibility to particular disease stages, progression, and/or tumor aggressiveness. The invention provides methods and assays for determining 191P4D12(b) status and diagnosing cancers that express 191P4D12(b), such as cancers of the tissues listed in Table I. For example, because 191P4D12(b) mRNA is so highly expressed in prostate and other cancers relative to normal prostate tissue, assays that evaluate the levels of 191P4D12(b) mRNA transcripts or proteins in a biological sample can be used to diagnose a disease associated with 191P4D12(b) dysregulation, and can provide prognostic information useful in defining appropriate therapeutic options.

The expression status of 191P4D12(b) provides information including the presence, stage and location of dysplastic, precancerous and cancerous cells, predicting susceptibility to various stages of disease, and/or for gauging tumor aggressiveness. Moreover, the expression profile makes it useful as an imaging reagent for metastasized disease. Consequently, an aspect of the invention is directed to the various molecular prognostic and diagnostic methods for examining the status of 191P4D12(b) in biological samples such as those from individuals suffering from, or suspected of suffering from a pathology characterized by dysregulated cellular growth, such as cancer.

As described above, the status of 191P4D12(b) in a biological sample can be examined by a number of well-known procedures in the art. For example, the status of 191P4D12(b) in a biological sample taken from a specific location in the body can be examined by evaluating the sample for the presence or absence of 191P4D12(b) expressing cells (e.g. those that express 191P4D12(b) mRNAs or proteins). This examination can provide evidence of dysregulated cellular growth, for example, when 191P4D12(b)-expressing cells are found in a biological sample that does not normally contain such cells (such as a lymph node), because such alterations in the status of 191P4D12(b) in a biological sample are often associated

with dysregulated cellular growth. Specifically, one indicator of dysregulated cellular growth is the metastases of cancer cells from an organ of origin (such as the prostate) to a different area of the body (such as a lymph node). In this context, evidence of dysregulated cellular growth is important for example because occult lymph node metastases can be detected in a substantial proportion of patients with prostate cancer, and such metastases are associated with known predictors of disease progression (see, e.g., Murphy *et al.*, Prostate 42(4): 315-317 (2000);Su *et al.*, Semin. Surg. Oncol. 18(1): 17-28 (2000) and Freeman *et al.*, J Urol 1995 Aug 154(2 Pt 1):474-8).

In one aspect, the invention provides methods for monitoring 191P4D12(b) gene products by determining the status of 191P4D12(b) gene products expressed by cells from an individual suspected of having a disease associated with dysregulated cell growth (such as hyperplasia or cancer) and then comparing the status so determined to the status of 191P4D12(b) gene products in a corresponding normal sample. The presence of aberrant 191P4D12(b) gene products in the test sample relative to the normal sample provides an indication of the presence of dysregulated cell growth within the cells of the individual.

In another aspect, the invention provides assays useful in determining the presence of cancer in an individual, comprising detecting a significant increase in 191P4D12(b) mRNA or protein expression in a test cell or tissue sample relative to expression levels in the corresponding normal cell or tissue. The presence of 191P4D12(b) mRNA can, for example, be evaluated in tissues including but not limited to those listed in Table I. The presence of significant 191P4D12(b) expression in any of these tissues is useful to indicate the emergence, presence and/or severity of a cancer, since the corresponding normal tissues do not express 191P4D12(b) mRNA or express it at lower levels.

In a related embodiment, 191P4D12(b) status is determined at the protein level rather than at the nucleic acid level. For example, such a method comprises determining the level of 191P4D12(b) protein expressed by cells in a test tissue sample and comparing the level so determined to the level of 191P4D12(b) expressed in a corresponding normal sample. In one embodiment, the presence of 191P4D12(b) protein is evaluated, for example, using immunohistochemical methods. 191P4D12(b) antibodies or binding partners capable of detecting 191P4D12(b) protein expression are used in a variety of assay formats well known in the art for this purpose.

In a further embodiment, one can evaluate the status of 191P4D12(b) nucleotide and amino acid sequences in a biological sample in order to identify perturbations in the structure of these molecules. These perturbations can include insertions, deletions, substitutions and the like. Such evaluations are useful because perturbations in the nucleotide and amino acid sequences are observed in a large number of proteins associated with a growth dysregulated phenotype (see, e.g., Marrogi *et al.*, 1999, J. Cutan. Pathol. 26(8):369-378). For example, a mutation in the sequence of 191P4D12(b) may be indicative of the presence or promotion of a tumor. Such assays therefore have diagnostic and predictive value where a mutation in 191P4D12(b) indicates a potential loss of function or increase in tumor growth.

A wide variety of assays for observing perturbations in nucleotide and amino acid sequences are well known in the art. For example, the size and structure of nucleic acid or amino acid sequences of 191P4D12(b) gene products are observed by the Northern, Southern, Western, PCR and DNA sequencing protocols discussed herein. In addition, other methods for observing perturbations in nucleotide and amino acid sequences such as single strand conformation polymorphism analysis are well known in the art (see, e.g., U.S. Patent Nos. 5,382,510 issued 7 September 1999, and 5,952,170 issued 17 January 1995).

Additionally, one can examine the methylation status of a 191P4D12(b) gene in a biological sample. Aberrant demethylation and/or hypermethylation of CpG islands in gene 5' regulatory regions frequently occurs in immortalized and transformed cells, and can result in altered expression of various genes. For example, promoter hypermethylation of the pi-class glutathione S-transferase (a protein expressed in normal prostate but not expressed in >90% of prostate carcinomas) appears to permanently silence transcription of this gene and is the most frequently detected genomic alteration in prostate carcinomas (De Marzo *et al.*, Am. J. Pathol. 155(6): 1985-1992 (1999)). In addition, this alteration is present in at least 70%

of cases of high-grade prostatic intraepithelial neoplasia (PIN) (Brooks *et al.*, Cancer Epidemiol. Biomarkers Prev., 1998, 7:531-536). In another example, expression of the LAGE-I tumor specific gene (which is not expressed in normal prostate but is expressed in 25-50% of prostate cancers) is induced by deoxy-azacytidine in lymphoblastoid cells, suggesting that tumoral expression is due to demethylation (Lethe *et al.*, Int. J. Cancer 76(6): 903-908 (1998)). A variety of assays for examining methylation status of a gene are well known in the art. For example, one can utilize, in Southern hybridization approaches, methylation-sensitive restriction enzymes that cannot cleave sequences that contain methylated CpG sites to assess the methylation status of CpG islands. In addition, MSP (methylation specific PCR) can rapidly profile the methylation status of all the CpG sites present in a CpG island of a given gene. This procedure involves initial modification of DNA by sodium bisulfite (which will convert all unmethylated cytosines to uracil) followed by amplification using primers specific for methylated versus unmethylated DNA. Protocols involving methylation interference can also be found for example in Current Protocols In Molecular Biology, Unit 12, Frederick M. Ausubel *et al.* eds., 1995.

Gene amplification is an additional method for assessing the status of 191P4D12(b). Gene amplification is measured in a sample directly, for example, by conventional Southern blotting or Northern blotting to quantitate the transcription of mRNA (Thomas, 1980, Proc. Natl. Acad. Sci. USA, 77:5201-5205), dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies are employed that recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn are labeled and the assay carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Biopsied tissue or peripheral blood can be conveniently assayed for the presence of cancer cells using for example, Northern, dot blot or RT-PCR analysis to detect 191P4D12(b) expression. The presence of RT-PCR amplifiable 191P4D12(b) mRNA provides an indication of the presence of cancer. RT-PCR assays are well known in the art. RT-PCR detection assays for tumor cells in peripheral blood are currently being evaluated for use in the diagnosis and management of a number of human solid tumors. In the prostate cancer field, these include RT-PCR assays for the detection of cells expressing PSA and PSM (Verkaik *et al.*, 1997, Urol. Res. 25:373-384; Ghossein *et al.*, 1995, J. Clin. Oncol. 13:1195-2000; Heston *et al.*, 1995, Clin. Chem. 41:1687-1688).

A further aspect of the invention is an assessment of the susceptibility that an individual has for developing cancer. In one embodiment, a method for predicting susceptibility to cancer comprises detecting 191P4D12(b) mRNA or 191P4D12(b) protein in a tissue sample, its presence indicating susceptibility to cancer, wherein the degree of 191P4D12(b) mRNA expression correlates to the degree of susceptibility. In a specific embodiment, the presence of 191P4D12(b) in prostate or other tissue is examined, with the presence of 191P4D12(b) in the sample providing an indication of prostate cancer susceptibility (or the emergence or existence of a prostate tumor). Similarly, one can evaluate the integrity 191P4D12(b) nucleotide and amino acid sequences in a biological sample, in order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like. The presence of one or more perturbations in 191P4D12(b) gene products in the sample is an indication of cancer susceptibility (or the emergence or existence of a tumor).

The invention also comprises methods for gauging tumor aggressiveness. In one embodiment, a method for gauging aggressiveness of a tumor comprises determining the level of 191P4D12(b) mRNA or 191P4D12(b) protein expressed by tumor cells, comparing the level so determined to the level of 191P4D12(b) mRNA or 191P4D12(b) protein expressed in a corresponding normal tissue taken from the same individual or a normal tissue reference sample, wherein the degree of 191P4D12(b) mRNA or 191P4D12(b) protein expression in the tumor sample relative to the normal sample indicates the degree of aggressiveness. In a specific embodiment, aggressiveness of a tumor is evaluated by determining the extent to which 191P4D12(b) is expressed in the tumor cells, with higher expression levels indicating more aggressive tumors. Another embodiment is the evaluation of the integrity of 191P4D12(b) nucleotide and amino acid sequences in a biological sample, in

order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like. The presence of one or more perturbations indicates more aggressive tumors.

Another embodiment of the invention is directed to methods for observing the progression of a malignancy in an individual over time. In one embodiment, methods for observing the progression of a malignancy in an individual over time comprise determining the level of 191P4D12(b) mRNA or 191P4D12(b) protein expressed by cells in a sample of the tumor, comparing the level so determined to the level of 191P4D12(b) mRNA or 191P4D12(b) protein expressed in an equivalent tissue sample taken from the same individual at a different time, wherein the degree of 191P4D12(b) mRNA or 191P4D12(b) protein expression in the tumor sample over time provides information on the progression of the cancer. In a specific embodiment, the progression of a cancer is evaluated by determining 191P4D12(b) expression in the tumor cells over time, where increased expression over time indicates a progression of the cancer. Also, one can evaluate the integrity 191P4D12(b) nucleotide and amino acid sequences in a biological sample in order to identify perturbations in the structure of these molecules such as insertions, deletions, substitutions and the like, where the presence of one or more perturbations indicates a progression of the cancer.

The above diagnostic approaches can be combined with any one of a wide variety of prognostic and diagnostic protocols known in the art. For example, another embodiment of the invention is directed to methods for observing a coincidence between the expression of 191P4D12(b) gene and 191P4D12(b) gene products (or perturbations in 191P4D12(b) gene and 191P4D12(b) gene products) and a factor that is associated with malignancy, as a means for diagnosing and prognosticating the status of a tissue sample. A wide variety of factors associated with malignancy can be utilized, such as the expression of genes associated with malignancy (e.g. PSA, PSCA and PSM expression for prostate cancer etc.) as well as gross cytological observations (see, e.g., Bocking *et al.*, 1984, Anal. Quant. Cytol. 6(2):74-88; Epstein, 1995, Hum. Pathol. 26(2):223-9; Thorson *et al.*, 1998, Mod. Pathol. 11(6):543-51; Baisden *et al.*, 1999, Am. J. Surg. Pathol. 23(8):918-24). Methods for observing a coincidence between the expression of 191P4D12(b) gene and 191P4D12(b) gene products (or perturbations in 191P4D12(b) gene and 191P4D12(b) gene products) and another factor that is associated with malignancy are useful, for example, because the presence of a set of specific factors that coincide with disease provides information crucial for diagnosing and prognosticating the status of a tissue sample.

In one embodiment, methods for observing a coincidence between the expression of 191P4D12(b) gene and 191P4D12(b) gene products (or perturbations in 191P4D12(b) gene and 191P4D12(b) gene products) and another factor associated with malignancy entails detecting the overexpression of 191P4D12(b) mRNA or protein in a tissue sample, detecting the overexpression of PSA mRNA or protein in a tissue sample (or PSCA or PSM expression), and observing a coincidence of 191P4D12(b) mRNA or protein and PSA mRNA or protein overexpression (or PSCA or PSM expression). In a specific embodiment, the expression of 191P4D12(b) and PSA mRNA in prostate tissue is examined, where the coincidence of 191P4D12(b) and PSA mRNA overexpression in the sample indicates the existence of prostate cancer, prostate cancer susceptibility or the emergence or status of a prostate tumor.

Methods for detecting and quantifying the expression of 191P4D12(b) mRNA or protein are described herein, and standard nucleic acid and protein detection and quantification technologies are well known in the art. Standard methods for the detection and quantification of 191P4D12(b) mRNA include *in situ* hybridization using labeled 191P4D12(b) riboprobes, Northern blot and related techniques using 191P4D12(b) polynucleotide probes, RT-PCR analysis using primers specific for 191P4D12(b), and other amplification type detection methods, such as, for example, branched DNA, SISBA, TMA and the like. In a specific embodiment, semi-quantitative RT-PCR is used to detect and quantify 191P4D12(b) mRNA expression. Any number of primers capable of amplifying 191P4D12(b) can be used for this purpose, including but not limited to the various primer sets specifically described herein. In a specific embodiment, polyclonal or monoclonal antibodies specifically reactive with the wild-type 191P4D12(b) protein can be used in an immunohistochemical assay of biopsied tissue.

IX.) Identification of Molecules That Interact With 191P4D12(b)

The 191P4D12(b) protein and nucleic acid sequences disclosed herein allow a skilled artisan to identify proteins, small molecules and other agents that interact with 191P4D12(b), as well as pathways activated by 191P4D12(b) via any one of a variety of art accepted protocols. For example, one can utilize one of the so-called interaction trap systems (also referred to as the "two-hybrid assay"). In such systems, molecules interact and reconstitute a transcription factor which directs expression of a reporter gene, whereupon the expression of the reporter gene is assayed. Other systems identify protein-protein interactions *in vivo* through reconstitution of a eukaryotic transcriptional activator, see, e.g., U.S. Patent Nos. 5,955,280 issued 21 September 1999, 5,925,523 issued 20 July 1999, 5,846,722 issued 8 December 1998 and 6,004,746 issued 21 December 1999. Algorithms are also available in the art for genome-based predictions of protein function (see, e.g., Marcotte, *et al.*, Nature 402: 4 November 1999, 83-86).

Alternatively one can screen peptide libraries to identify molecules that interact with 191P4D12(b) protein sequences. In such methods, peptides that bind to 191P4D12(b) are identified by screening libraries that encode a random or controlled collection of amino acids. Peptides encoded by the libraries are expressed as fusion proteins of bacteriophage coat proteins, the bacteriophage particles are then screened against the 191P4D12(b) protein(s).

Accordingly, peptides having a wide variety of uses, such as therapeutic, prognostic or diagnostic reagents, are thus identified without any prior information on the structure of the expected ligand or receptor molecule. Typical peptide libraries and screening methods that can be used to identify molecules that interact with 191P4D12(b) protein sequences are disclosed for example in U.S. Patent Nos. 5,723,286 issued 3 March 1998 and 5,733,731 issued 31 March 1998.

Alternatively, cell lines that express 191P4D12(b) are used to identify protein-protein interactions mediated by 191P4D12(b). Such interactions can be examined using immunoprecipitation techniques (see, e.g., Hamilton B.J., *et al.* Biochem. Biophys. Res. Commun. 1999, 261:646-51). 191P4D12(b) protein can be immunoprecipitated from 191P4D12(b)-expressing cell lines using anti-191P4D12(b) antibodies. Alternatively, antibodies against His-tag can be used in a cell line engineered to express fusions of 191P4D12(b) and a His-tag (vectors mentioned above). The immunoprecipitated complex can be examined for protein association by procedures such as Western blotting, ^{35}S-methionine labeling of proteins, protein microsequencing, silver staining and two-dimensional gel electrophoresis.

Small molecules and ligands that interact with 191P4D12(b) can be identified through related embodiments of such screening assays. For example, small molecules can be identified that interfere with protein function, including molecules that interfere with 191P4D12(b)'s ability to mediate phosphorylation and de-phosphorylation, interaction with DNA or RNA molecules as an indication of regulation of cell cycles, second messenger signaling or tumorigenesis. Similarly, small molecules that modulate 191P4D12(b)-related ion channel, protein pump, or cell communication functions are identified and used to treat patients that have a cancer that expresses 191P4D12(b) (see, e.g., Hille, B., Ionic Channels of Excitable Membranes 2nd Ed., Sinauer Assoc., Sunderland, MA, 1992). Moreover, ligands that regulate 191P4D12(b) function can be identified based on their ability to bind 191P4D12(b) and activate a reporter construct. Typical methods are discussed for example in U.S. Patent No. 5,928,868 issued 27 July 1999, and include methods for forming hybrid ligands in which at least one ligand is a small molecule. In an illustrative embodiment, cells engineered to express a fusion protein of 191P4D12(b) and a DNA-binding protein are used to co-express a fusion protein of a hybrid ligand/small molecule and a cDNA library transcriptional activator protein. The cells further contain a reporter gene, the expression of which is conditioned on the proximity of the first and second fusion proteins to each other, an event that occurs only if the hybrid ligand binds to target sites on both hybrid proteins. Those cells that express the reporter gene are selected and the unknown small molecule or the unknown ligand is identified. This method provides a means of identifying modulators, which activate or inhibit 191P4D12(b).

An embodiment of this invention comprises a method of screening for a molecule that interacts with a 191P4D12(b) amino acid sequence shown in Figure 2 or Figure 3, comprising the steps of contacting a population of molecules with a 191P4D12(b) amino acid sequence, allowing the population of molecules and the 191P4D12(b) amino acid sequence to interact under conditions that facilitate an interaction, determining the presence of a molecule that interacts with the 191P4D12(b) amino acid sequence, and then separating molecules that do not interact with the 191P4D12(b) amino acid sequence from molecules that do. In a specific embodiment, the method further comprises purifying, characterizing and identifying a molecule that interacts with the 191P4D12(b) amino acid sequence. The identified molecule can be used to modulate a function performed by 191P4D12(b). In a preferred embodiment, the 191P4D12(b) amino acid sequence is contacted with a library of peptides.

X.) Therapeutic Methods and Compositions

The identification of 191P4D12(b) as a protein that is normally expressed in a restricted set of tissues, but which is also expressed in cancers such as those listed in Table I, opens a number of therapeutic approaches to the treatment of such cancers.

Of note, targeted antitumor therapies have been useful even when the targeted protein is expressed on normal tissues, even vital normal organ tissues. A vital organ is one that is necessary to sustain life, such as the heart or colon. A non-vital organ is one that can be removed whereupon the individual is still able to survive. Examples of non-vital organs are ovary, breast, and prostate.

For example, Herceptin® is an FDA approved pharmaceutical that has as its active ingredient an antibody which is immunoreactive with the protein variously known as HER2, HER2/neu, and erb-b-2. It is marketed by Genentech and has been a commercially successful antitumor agent. Herceptin sales reached almost $400 million in 2002. Herceptin is a treatment for HER2 positive metastatic breast cancer. However, the expression of HER2 is not limited to such tumors. The same protein is expressed in a number of normal tissues. In particular, it is known that HER2/neu is present in normal kidney and heart, thus these tissues are present in all human recipients of Herceptin. The presence of HER2/neu in normal kidney is also confirmed by Latif, Z., et al., *B.J.U. International* (2002) 89:5-9. As shown in this article (which evaluated whether renal cell carcinoma should be a preferred indication for anti-HER2 antibodies such as Herceptin) both protein and mRNA are produced in benign renal tissues. Notably, HER2/neu protein was strongly overexpressed in benign renal tissue. Despite the fact that HER2/neu is expressed in such vital tissues as heart and kidney, Herceptin is a very useful, FDA approved, and commercially successful drug. The effect of Herceptin on cardiac tissue, i.e., "cardiotoxicity," has merely been a side effect to treatment. When patients were treated with Herceptin alone, significant cardiotoxicity occurred in a very low percentage of patients.

Of particular note, although kidney tissue is indicated to exhibit normal expression, possibly even higher expression than cardiac tissue, kidney has no appreciable Herceptin side effect whatsoever. Moreover, of the diverse array of normal tissues in which HER2 is expressed, there is very little occurrence of any side effect. Only cardiac tissue has manifested any appreciable side effect at all. A tissue such as kidney, where HER2/neu expression is especially notable, has not been the basis for any side effect.

Furthermore, favorable therapeutic effects have been found for antitumor therapies that target epidermal growth factor receptor (EGFR). EGFR is also expressed in numerous normal tissues. There have been very limited side effects in normal tissues following use of anti-EGFR therapeutics.

Thus, expression of a target protein in normal tissue, even vital normal tissue, does not defeat the utility of a targeting agent for the protein as a therapeutic for certain tumors in which the protein is also overexpressed.

Accordingly, therapeutic approaches that inhibit the activity of a 191P4D12(b) protein are useful for patients suffering from a cancer that expresses 191P4D12(b). These therapeutic approaches generally fall into two classes. One class comprises various methods for inhibiting the binding or association of a 191P4D12(b) protein with its binding partner or with other proteins. Another class comprises a variety of methods for inhibiting the transcription of a 191P4D12(b) gene or translation of 191P4D12(b) mRNA.

X.A.) Anti-Cancer Vaccines

The invention provides cancer vaccines comprising a 191P4D12(b)-related protein or 191P4D12(b)-related nucleic acid. In view of the expression of 191P4D12(b), cancer vaccines prevent and/or treat 191P4D12(b)-expressing cancers with minimal or no effects on non-target tissues. The use of a tumor antigen in a vaccine that generates humoral and/or cell-mediated immune responses as anti-cancer therapy is well known in the art and has been employed in prostate cancer using human PSMA and rodent PAP immunogens (Hodge *et al.*, 1995, Int. J. Cancer 63:231-237; Fong *et al.*, 1997, J. Immunol. 159:3113-3117).

Such methods can be readily practiced by employing a 191P4D12(b)-related protein, or a 191P4D12(b)-encoding nucleic acid molecule and recombinant vectors capable of expressing and presenting the 191P4D12(b) immunogen (which typically comprises a number of antibody or T cell epitopes). Skilled artisans understand that a wide variety of vaccine systems for delivery of immunoreactive epitopes are known in the art (see, e.g., Heryln *et al.*, Ann Med 1999 Feb 31(1):66-78; Maruyama *et al.*, Cancer Immunol Immunother 2000 Jun 49(3):123-32) Briefly, such methods of generating an immune response (e.g. humoral and/or cell-mediated) in a mammal, comprise the steps of: exposing the mammal's immune system to an immunoreactive epitope (e.g. an epitope present in a 191P4D12(b) protein shown in Figure 3 or analog or homolog thereof) so that the mammal generates an immune response that is specific for that epitope (e.g. generates antibodies that specifically recognize that epitope). In a preferred method, a 191P4D12(b) immunogen contains a biological motif, see e.g., Tables VIII-XXI and XXII-XLIX, or a peptide of a size range from 191P4D12(b) indicated in Figure 5, Figure 6, Figure 7, Figure 8, and Figure 9.

The entire 191P4D12(b) protein, immunogenic regions or epitopes thereof can be combined and delivered by various means. Such vaccine compositions can include, for example, lipopeptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991: Alonso *et al.*, *Vaccine* 12:299-306, 1994; Jones *et al.*, *Vaccine* 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (*see, e.g.*, Takahashi *et al.*, *Nature* 344:873-875, 1990; Hu *et al.*, *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (*see e.g.*, Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. *et al.*, *Nature* 320:535, 1986; Hu, S. L. *et al.*, *Nature* 320:537, 1986; Kieny, M.-P. *et al.*, *AIDS Bio/Technology* 4:790, 1986; Top, F. H. *et al.*, *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. *et al.*, *Virology* 175:535, 1990), particles of viral or synthetic origin (*e.g.*, Kofler, N. *et al.*, *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. *et al.*, *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. *et al.*, *Vaccine* 11:293, 1993), liposomes (Reddy, R. *et al.*, *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. *et al.*, *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. *et al.*, In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. *et al.*, *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

In patients with 191P4D12(b)-associated cancer, the vaccine compositions of the invention can also be used in conjunction with other treatments used for cancer, *e.g.*, surgery, chemotherapy, drug therapies, radiation therapies, *etc.* including use in combination with immune adjuvants such as IL-2, IL-12, GM-CSF, and the like.

Cellular Vaccines:

CTL epitopes can be determined using specific algorithms to identify peptides within 191P4D12(b) protein that bind corresponding HLA alleles (see e.g., Table IV; Epimer™ and Epimatrix™, Brown University

; and, BIMAS, ; · SYFPEITHI).

In a preferred embodiment, a 191P4D12(b) immunogen contains one or more amino acid sequences identified using techniques well known in the art, such as the sequences shown in Tables VIII-XXI and XXII-XLIX or a peptide of 8, 9, 10 or 11 amino acids specified by an HLA Class I motif/supermotif (e.g., Table IV (A), Table IV (D), or Table IV (E)) and/or a peptide of at least 9 amino acids that comprises an HLA Class II motif/supermotif (e.g., Table IV (B) or Table IV (C)). As is appreciated in the art, the HLA Class I binding groove is essentially closed ended so that peptides of only a particular size range can fit into the groove and be bound, generally HLA Class I epitopes are 8, 9, 10, or 11 amino acids long. In contrast, the HLA Class II binding groove is essentially open ended; therefore a peptide of about 9 or more amino acids can be bound by an HLA Class II molecule. Due to the binding groove differences between HLA Class I and II, HLA Class I motifs are length specific, i.e., position two of a Class I motif is the second amino acid in an amino to carboxyl direction of the peptide. The amino acid positions in a Class II motif are relative only to each other, not the overall peptide, i.e., additional amino acids can be attached to the amino and/or carboxyl termini of a motif-bearing sequence. HLA Class II epitopes are often 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids long, or longer than 25 amino acids.

Antibody-based Vaccines

A wide variety of methods for generating an immune response in a mammal are known in the art (for example as the first step in the generation of hybridomas). Methods of generating an immune response in a mammal comprise exposing the mammal's immune system to an immunogenic epitope on a protein (e.g. a 191P4D12(b) protein) so that an immune response is generated. A typical embodiment consists of a method for generating an immune response to 191P4D12(b) in a host, by contacting the host with a sufficient amount of at least one 191P4D12(b) B cell or cytotoxic T-cell epitope or analog thereof; and at least one periodic interval thereafter re-contacting the host with the 191P4D12(b) B cell or cytotoxic T-cell epitope or analog thereof. A specific embodiment consists of a method of generating an immune response against a 191P4D12(b)-related protein or a man-made multiepitopic peptide comprising: administering 191P4D12(b) immunogen (e.g. a 191P4D12(b) protein or a peptide fragment thereof, a 191P4D12(b) fusion protein or analog etc.) in a vaccine preparation to a human or another mammal. Typically, such vaccine preparations further contain a suitable adjuvant (see, e.g., U.S. Patent No. 6,146,635) or a universal helper epitope such as a PADRE™ peptide (Epimmune Inc., San Diego, CA; see, e.g., Alexander *et al.*, J. Immunol. 2000 164(3); 164(3): 1625-1633; Alexander *et al.*, Immunity 1994 1(9): 751-761 and Alexander *et al.*, Immunol. Res. 1998 18(2): 79-92). An alternative method comprises generating an immune response in an individual against a 191P4D12(b) immunogen by: administering *in vivo* to muscle or skin of the individual's body a DNA molecule that comprises a DNA sequence that encodes a 191P4D12(b) immunogen, the DNA sequence operatively linked to regulatory sequences which control the expression of the DNA sequence; wherein the DNA molecule is taken up by cells, the DNA sequence is expressed in the cells and an immune response is generated against the immunogen (see, e.g., U.S. Patent No. 5,962,428). Optionally a genetic vaccine facilitator such as anionic lipids; saponins; lectins; estrogenic compounds; hydroxylated lower alkyls; dimethyl sulfoxide; and urea is also administered. In addition, an antiidiotypic antibody can be administered that mimics 191P4D12(b), in order to generate a response to the target antigen.

Nucleic Acid Vaccines:

Vaccine compositions of the invention include nucleic acid-mediated modalities. DNA or RNA that encode protein(s) of the invention can be administered to a patient. Genetic immunization methods can be employed to generate prophylactic or therapeutic humoral and cellular immune responses directed against cancer cells expressing 191P4D12(b). Constructs comprising DNA encoding a 191P4D12(b)-related protein/immunogen and appropriate regulatory sequences can be injected directly into muscle or skin of an individual, such that the cells of the muscle or skin take-up the construct and express the encoded 191P4D12(b) protein/immunogen. Alternatively, a vaccine comprises a 191P4D12(b)-related protein. Expression of the 191P4D12(b)-related protein immunogen results in the generation of prophylactic or therapeutic humoral and cellular immunity against cells that bear a 191P4D12(b) protein. Various prophylactic and therapeutic genetic immunization techniques known in the art can be used.

Nucleic acid-based delivery is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, proteins of the invention can be expressed via viral or bacterial vectors. Various viral gene delivery systems that can be used in the practice of the invention include, but are not limited to, vaccinia, fowlpox, canarypox, adenovirus, influenza, poliovirus, adeno-associated virus, lentivirus, and sindbis virus (see, e.g., Restifo, 1996, Curr. Opin. Immunol. 8:658-663; Tsang *et al.* J. Natl. Cancer Inst. 87:982-990 (1995)). Non-viral delivery systems can also be employed by introducing naked DNA encoding a 191P4D12(b)-related protein into the patient (e.g., intramuscularly or intradermally) to induce an anti-tumor response.

Vaccinia virus is used, for example, as a vector to express nucleotide sequences that encode the peptides of the invention. Upon introduction into a host, the recombinant vaccinia virus expresses the protein immunogenic peptide, and thereby elicits a host immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization of the peptides of the invention, *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein.

Thus, gene delivery systems are used to deliver a 191P4D12(b)-related nucleic acid molecule. In one embodiment, the full-length human 191P4D12(b) cDNA is employed. In another embodiment, 191P4D12(b) nucleic acid molecules encoding specific cytotoxic T lymphocyte (CTL) and/or antibody epitopes are employed.

Ex Vivo Vaccines

Various *ex vivo* strategies can also be employed to generate an immune response. One approach involves the use of antigen presenting cells (APCs) such as dendritic cells (DC) to present 191P4D12(b) antigen to a patient's immune system. Dendritic cells express MHC class I and II molecules, B7 co-stimulator, and IL-12, and are thus highly specialized antigen presenting cells. In prostate cancer, autologous dendritic cells pulsed with peptides of the prostate-specific membrane antigen (PSMA) are being used in a Phase I clinical trial to stimulate prostate cancer patients' immune systems (Tjoa *et al.*, 1996, Prostate 28:65-69; Murphy *et al.*, 1996, Prostate 29:371-380). Thus, dendritic cells can be used to present 191P4D12(b) peptides to T cells in the context of MHC class I or II molecules. In one embodiment, autologous dendritic cells are pulsed with 191P4D12(b) peptides capable of binding to MHC class I and/or class II molecules. In another embodiment, dendritic cells are pulsed with the complete 191P4D12(b) protein. Yet another embodiment involves engineering the overexpression of a 191P4D12(b) gene in dendritic cells using various implementing vectors known in the art, such as adenovirus (Arthur *et al.*, 1997, Cancer Gene Ther. 4:17-25), retrovirus (Henderson *et al.*, 1996, Cancer Res. 56:3763-3770),

lentivirus, adeno-associated virus, DNA transfection (Ribas *et al.*, 1997, Cancer Res. 57:2865-2869), or tumor-derived RNA transfection (Ashley *et al.*, 1997, J. Exp. Med. 186:1177-1182). Cells that express 191P4D12(b) can also be engineered to express immune modulators, such as GM-CSF, and used as immunizing agents.

X.B.) 191P4D12(b) as a Target for Antibody-based Therapy

191P4D12(b) is an attractive target for antibody-based therapeutic strategies. A number of antibody strategies are known in the art for targeting both extracellular and intracellular molecules (see, e.g., complement and ADCC mediated killing as well as the use of intrabodies). Because 191P4D12(b) is expressed by cancer cells of various lineages relative to corresponding normal cells, systemic administration of 191P4D12(b)-immunoreactive compositions are prepared that exhibit excellent sensitivity without toxic, non-specific and/or non-target effects caused by binding of the immunoreactive composition to non-target organs and tissues. Antibodies specifically reactive with domains of 191P4D12(b) are useful to treat 191P4D12(b)-expressing cancers systemically, either as conjugates with a toxin or therapeutic agent, or as naked antibodies capable of inhibiting cell proliferation or function.

191P4D12(b) antibodies can be introduced into a patient such that the antibody binds to 191P4D12(b) and modulates a function, such as an interaction with a binding partner, and consequently mediates destruction of the tumor cells and/or inhibits the growth of the tumor cells. Mechanisms by which such antibodies exert a therapeutic effect can include complement-mediated cytolysis, antibody-dependent cellular cytotoxicity, modulation of the physiological function of 191P4D12(b), inhibition of ligand binding or signal transduction pathways, modulation of tumor cell differentiation, alteration of tumor angiogenesis factor profiles, and/or apoptosis.

Those skilled in the art understand that antibodies can be used to specifically target and bind immunogenic molecules such as an immunogenic region of a 191P4D12(b) sequence shown in Figure 2 or Figure 3. In addition, skilled artisans understand that it is routine to conjugate antibodies to cytotoxic agents (see, e.g., Slevers *et al.* Blood 93:11 3678-3684 (June 1, 1999)). When cytotoxic and/or therapeutic agents are delivered directly to cells, such as by conjugating them to antibodies specific for a molecule expressed by that cell (e.g. 191P4D12(b)), the cytotoxic agent will exert its known biological effect (i.e. cytotoxicity) on those cells.

A wide variety of compositions and methods for using antibody-cytotoxic agent conjugates to kill cells are known in the art. In the context of cancers, typical methods entail administering to an animal having a tumor a biologically effective amount of a conjugate comprising a selected cytotoxic and/or therapeutic agent linked to a targeting agent (e.g. an anti-191P4D12(b) antibody) that binds to a marker (e.g. 191P4D12(b)) expressed, accessible to binding or localized on the cell surfaces. A typical embodiment is a method of delivering a cytotoxic and/or therapeutic agent to a cell expressing 191P4D12(b), comprising conjugating the cytotoxic agent to an antibody that immunospecifically binds to a 191P4D12(b) epitope, and, exposing the cell to the antibody-agent conjugate. Another illustrative embodiment is a method of treating an individual suspected of suffering from metastasized cancer, comprising a step of administering parenterally to said individual a pharmaceutical composition comprising a therapeutically effective amount of an antibody conjugated to a cytotoxic and/or therapeutic agent.

Cancer immunotherapy using anti-191P4D12(b) antibodies can be done in accordance with various approaches that have been successfully employed in the treatment of other types of cancer, including but not limited to colon cancer (Arlen *et al.*, 1998, Crit. Rev. Immunol. 18:133-138), multiple myeloma (Ozaki *et al.*, 1997, Blood 90:3179-3186, Tsunenari *et al.*, 1997, Blood 90:2437-2444), gastric cancer (Kasprzyk *et al.*, 1992, Cancer Res. 52:2771-2776), B-cell lymphoma (Funakoshi *et al.*, 1996, J. Immunother. Emphasis Tumor Immunol. 19:93-101), leukemia (Zhong *et al.*, 1996, Leuk. Res. 20:581-589), colorectal cancer (Moun *et al.*, 1994, Cancer Res. 54:6160-6166; Velders *et al.*, 1995, Cancer Res. 55:4398-4403), and breast cancer (Shepard *et al.*, 1991, J. Clin. Immunol. 11:117-127). Some therapeutic approaches involve

conjugation of naked antibody to a toxin or radioisotope, such as the conjugation of Y^{91} or I^{131} to anti-CD20 antibodies (e.g., Zevalin™, IDEC Pharmaceuticals Corp. or Bexxar™, Coulter Pharmaceuticals), while others involve co-administration of antibodies and other therapeutic agents, such as Herceptin™ (trastuzumab) with paclitaxel (Genentech, Inc.). The antibodies can be conjugated to a therapeutic agent. To treat prostate cancer, for example, 191P4D12(b) antibodies can be administered in conjunction with radiation, chemotherapy or hormone ablation. Also, antibodies can be conjugated to a toxin such as calicheamicin (e.g., Mylotarg™, Wyeth-Ayerst, Madison, NJ, a recombinant humanized IgG_4 kappa antibody conjugated to antitumor antibiotic calicheamicin) or a maytansinoid (e.g., taxane-based Tumor-Activated Prodrug, TAP, platform, ImmunoGen, Cambridge, MA, also see e.g., US Patent 5,416,064).

Although 191P4D12(b) antibody therapy is useful for all stages of cancer, antibody therapy can be particularly appropriate in advanced or metastatic cancers. Treatment with the antibody therapy of the invention is indicated for patients who have received one or more rounds of chemotherapy. Alternatively, antibody therapy of the invention is combined with a chemotherapeutic or radiation regimen for patients who have not received chemotherapeutic treatment. Additionally, antibody therapy can enable the use of reduced dosages of concomitant chemotherapy, particularly for patients who do not tolerate the toxicity of the chemotherapeutic agent very well. Fan et al. (Cancer Res. 53:4637-4642, 1993), Prewett et al. (International J. of Onco. 9:217-224, 1996), and Hancock et al. (Cancer Res. 51:4575-4580, 1991) describe the use of various antibodies together with chemotherapeutic agents.

Although 191P4D12(b) antibody therapy is useful for all stages of cancer, antibody therapy can be particularly appropriate in advanced or metastatic cancers. Treatment with the antibody therapy of the invention is indicated for patients who have received one or more rounds of chemotherapy. Alternatively, antibody therapy of the invention is combined with a chemotherapeutic or radiation regimen for patients who have not received chemotherapeutic treatment. Additionally, antibody therapy can enable the use of reduced dosages of concomitant chemotherapy, particularly for patients who do not tolerate the toxicity of the chemotherapeutic agent very well.

Cancer patients can be evaluated for the presence and level of 191P4D12(b) expression, preferably using immunohistochemical assessments of tumor tissue, quantitative 191P4D12(b) imaging, or other techniques that reliably indicate the presence and degree of 191P4D12(b) expression. Immunohistochemical analysis of tumor biopsies or surgical specimens is preferred for this purpose. Methods for immunohistochemical analysis of tumor tissues are well known in the art.

Anti-191P4D12(b) monoclonal antibodies that treat prostate and other cancers include those that initiate a potent immune response against the tumor or those that are directly cytotoxic. In this regard, anti-191P4D12(b) monoclonal antibodies (mAbs) can elicit tumor cell lysis by either complement-mediated or antibody-dependent cell cytotoxicity (ADCC) mechanisms, both of which require an intact Fc portion of the immunoglobulin molecule for interaction with effector cell Fc receptor sites on complement proteins. In addition, anti-191P4D12(b) mAbs that exert a direct biological effect on tumor growth are useful to treat cancers that express 191P4D12(b). Mechanisms by which directly cytotoxic mAbs act include: inhibition of cell growth, modulation of cellular differentiation, modulation of tumor angiogenesis factor profiles, and the induction of apoptosis. The mechanism(s) by which a particular anti-191P4D12(b) mAb exerts an anti-tumor effect is evaluated using any number of *in vitro* assays that evaluate cell death such as ADCC, ADMMC, complement-mediated cell lysis, and so forth, as is generally known in the art.

In some patients, the use of murine or other non-human monoclonal antibodies, or human/mouse chimeric mAbs can induce moderate to strong immune responses against the non-human antibody. This can result in clearance of the antibody from circulation and reduced efficacy. In the most severe cases, such an immune response can lead to the extensive formation of immune complexes which, potentially, can cause renal failure. Accordingly, preferred monoclonal

antibodies used in the therapeutic methods of the invention are those that are either fully human or humanized and that bind specifically to the target 191P4D12(b) antigen with high affinity but exhibit low or no antigenicity in the patient.

Therapeutic methods of the invention contemplate the administration of single anti-191P4D12(b) mAbs as well as combinations, or cocktails, of different mAbs. Such mAb cocktails can have certain advantages inasmuch as they contain mAbs that target different epitopes, exploit different effector mechanisms or combine directly cytotoxic mAbs with mAbs that rely on immune effector functionality. Such mAbs in combination can exhibit synergistic therapeutic effects. In addition, anti-191P4D12(b) mAbs can be administered concomitantly with other therapeutic modalities, including but not limited to various chemotherapeutic agents, androgen-blockers, immune modulators (e.g., IL-2, GM-CSF), surgery or radiation. The anti-191P4D12(b) mAbs are administered in their "naked" or unconjugated form, or can have a therapeutic agent(s) conjugated to them.

Anti-191P4D12(b) antibody formulations are administered via any route capable of delivering the antibodies to a tumor cell. Routes of administration include, but are not limited to, intravenous, intraperitoneal, intramuscular, intratumor, intradermal, and the like. Treatment generally involves repeated administration of the anti-191P4D12(b) antibody preparation, via an acceptable route of administration such as intravenous injection (IV), typically at a dose in the range of about 0.1, .2, .3, .4, .5, .6, .7, .8, .9., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, or 25 mg/kg body weight. In general, doses in the range of 10-1000 mg mAb per week are effective and well tolerated.

Based on clinical experience with the Herceptin™ mAb in the treatment of metastatic breast cancer, an initial loading dose of approximately 4 mg/kg patient body weight IV, followed by weekly doses of about 2 mg/kg IV of the anti-191P4D12(b) mAb preparation represents an acceptable dosing regimen. Preferably, the initial loading dose is administered as a 90-minute or longer infusion. The periodic maintenance dose is administered as a 30 minute or longer infusion, provided the initial dose was well tolerated. As appreciated by those of skill in the art, various factors can influence the ideal dose regimen in a particular case. Such factors include, for example, the binding affinity and half life of the Ab or mAbs used, the degree of 191P4D12(b) expression in the patient, the extent of circulating shed 191P4D12(b) antigen, the desired steady-state antibody concentration level, frequency of treatment, and the influence of chemotherapeutic or other agents used in combination with the treatment method of the invention, as well as the health status of a particular patient.

Optionally, patients should be evaluated for the levels of 191P4D12(b) in a given sample (e.g. the levels of circulating 191P4D12(b) antigen and/or 191P4D12(b) expressing cells) in order to assist in the determination of the most effective dosing regimen, etc. Such evaluations are also used for monitoring purposes throughout therapy, and are useful to gauge therapeutic success in combination with the evaluation of other parameters (for example, urine cytology and/or ImmunoCyt levels in bladder cancer therapy, or by analogy, serum PSA levels in prostate cancer therapy).

Anti-idiotypic anti-191P4D12(b) antibodies can also be used in anti-cancer therapy as a vaccine for inducing an immune response to cells expressing a 191P4D12(b)-related protein. In particular, the generation of anti-idiotypic antibodies is well known in the art; this methodology can readily be adapted to generate anti-idiotypic anti-191P4D12(b) antibodies that mimic an epitope on a 191P4D12(b)-related protein (see, for example, Wagner *et al.*, 1997, Hybridoma 16: 33-40; Foon *et al.*, 1995, J. Clin. Invest. 96:334-342; Herlyn *et al.*, 1996, Cancer Immunol. Immunother. 43:65-76). Such an anti-idiotypic antibody can be used in cancer vaccine strategies.

X.C.) 191P4D12(b) as a Target for Cellular Immune Responses

Vaccines and methods of preparing vaccines that contain an immunogenically effective amount of one or more HLA-binding peptides as described herein are further embodiments of the invention. Furthermore, vaccines in accordance with the invention encompass compositions of one or more of the claimed peptides. A peptide can be present in a vaccine individually. Alternatively, the peptide can exist as a homopolymer comprising multiple copies of the same peptide, or as a

heteropolymer of various peptides. Polymers have the advantage of increased immunological reaction and, where different peptide epitopes are used to make up the polymer, the additional ability to induce antibodies and/or CTLs that react with different antigenic determinants of the pathogenic organism or tumor-related peptide targeted for an immune response. The composition can be a naturally occurring region of an antigen or can be prepared, *e.g.*, recombinantly or by chemical synthesis.

Carriers that can be used with vaccines of the invention are well known in the art, and include, *e.g.*, thyroglobulin, albumins such as human serum albumin, tetanus toxoid, polyamino acids such as poly L-lysine, poly L-glutamic acid, influenza, hepatitis B virus core protein, and the like. The vaccines can contain a physiologically tolerable (*i.e.*, acceptable) diluent such as water, or saline, preferably phosphate buffered saline. The vaccines also typically include an adjuvant. Adjuvants such as incomplete Freund's adjuvant, aluminum phosphate, aluminum hydroxide, or alum are examples of materials well known in the art. Additionally, as disclosed herein, CTL responses can be primed by conjugating peptides of the invention to lipids, such as tripalmitoyl-S-glycerylcysteinlyseryl- serine (P_3CSS). Moreover, an adjuvant such as a synthetic cytosine-phosphorothiolated-guanine-containing (CpG) oligonucleotides has been found to increase CTL responses 10- to 100-fold. (see, e.g. Davila and Celis, J. Immunol. 165:539-547 (2000))

Upon immunization with a peptide composition in accordance with the invention, via injection, aerosol, oral, transdermal, transmucosal, intrapleural, intrathecal, or other suitable routes, the immune system of the host responds to the vaccine by producing large amounts of CTLs and/or HTLs specific for the desired antigen. Consequently, the host becomes at least partially immune to later development of cells that express or overexpress 191P4D12(b) antigen, or derives at least some therapeutic benefit when the antigen was tumor-associated.

In some embodiments, it may be desirable to combine the class I peptide components with components that induce or facilitate neutralizing antibody and or helper T cell responses directed to the target antigen. A preferred embodiment of such a composition comprises class I and class II epitopes in accordance with the invention. An alternative embodiment of such a composition comprises a class I and/or class II epitope in accordance with the invention, along with a cross reactive HTL epitope such as PADRE™ (Epimmune, San Diego, CA) molecule (described *e.g.*, in U.S. Patent Number 5,736,142).

A vaccine of the invention can also include antigen-presenting cells (APC), such as dendritic cells (DC), as a vehicle to present peptides of the invention. Vaccine compositions can be created *in vitro*, following dendritic cell mobilization and harvesting, whereby loading of dendritic cells occurs *in vitro*. For example, dendritic cells are transfected, *e.g.*, with a minigene in accordance with the invention, or are pulsed with peptides. The dendritic cell can then be administered to a patient to elicit immune responses *in vivo*. Vaccine compositions, either DNA- or peptide-based, can also be administered *in vivo* in combination with dendritic cell mobilization whereby loading of dendritic cells occurs *in vivo*.

Preferably, the following principles are utilized when selecting an array of epitopes for inclusion in a polyepitopic composition for use in a vaccine, or for selecting discrete epitopes to be included in a vaccine and/or to be encoded by nucleic acids such as a minigene. It is preferred that each of the following principles be balanced in order to make the selection. The multiple epitopes to be incorporated in a given vaccine composition may be, but need not be, contiguous in sequence in the native antigen from which the epitopes are derived.

1.) Epitopes are selected which, upon administration, mimic immune responses that have been observed to be correlated with tumor clearance. For HLA Class I this includes 3-4 epitopes that come from at least one tumor associated antigen (TAA). For HLA Class II a similar rationale is employed; again 3-4 epitopes are selected from at least one TAA (see, *e.g.*, Rosenberg *et al.*, *Science* 278:1447-1450). Epitopes from one TAA may be used in combination with epitopes from one or more additional TAAs to produce a vaccine that targets tumors with varying expression patterns of frequently-expressed TAAs.

2.) Epitopes are selected that have the requisite binding affinity established to be correlated with immunogenicity: for HLA Class I an IC_{50} of 500 nM or less, often 200 nM or less; and for Class II an IC_{50} of 1000 nM or less.

3.) Sufficient supermotif bearing-peptides, or a sufficient array of allele-specific motif-bearing peptides, are selected to give broad population coverage. For example, it is preferable to have at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess the breadth, or redundancy of, population coverage.

4.) When selecting epitopes from cancer-related antigens it is often useful to select analogs because the patient may have developed tolerance to the native epitope.

5.) Of particular relevance are epitopes referred to as "nested epitopes." Nested epitopes occur where at least two epitopes overlap in a given peptide sequence. A nested peptide sequence can comprise B cell, HLA class I and/or HLA class II epitopes. When providing nested epitopes, a general objective is to provide the greatest number of epitopes per sequence. Thus, an aspect is to avoid providing a peptide that is any longer than the amino terminus of the amino terminal epitope and the carboxyl terminus of the carboxyl terminal epitope in the peptide. When providing a multi-epitopic sequence, such as a sequence comprising nested epitopes, it is generally important to screen the sequence in order to insure that it does not have pathological or other deleterious biological properties.

6.) If a polyepitopic protein is created, or when creating a minigene, an objective is to generate the smallest peptide that encompasses the epitopes of interest. This principle is similar, if not the same as that employed when selecting a peptide comprising nested epitopes. However, with an artificial polyepitopic peptide, the size minimization objective is balanced against the need to integrate any spacer sequences between epitopes in the polyepitopic protein. Spacer amino acid residues can, for example, be introduced to avoid junctional epitopes (an epitope recognized by the immune system, not present in the target antigen, and only created by the man-made juxtaposition of epitopes), or to facilitate cleavage between epitopes and thereby enhance epitope presentation. Junctional epitopes are generally to be avoided because the recipient may generate an immune response to that non-native epitope. Of particular concern is a junctional epitope that is a "dominant epitope." A dominant epitope may lead to such a zealous response that immune responses to other epitopes are diminished or suppressed.

7.) Where the sequences of multiple variants of the same target protein are present, potential peptide epitopes can also be selected on the basis of their conservancy. For example, a criterion for conservancy may define that the entire sequence of an HLA class I binding peptide or the entire 9-mer core of a class II binding peptide be conserved in a designated percentage of the sequences evaluated for a specific protein antigen.

X.C.1. Minigene Vaccines

A number of different approaches are available which allow simultaneous delivery of multiple epitopes. Nucleic acids encoding the peptides of the invention are a particularly useful embodiment of the invention. Epitopes for inclusion in a minigene are preferably selected according to the guidelines set forth in the previous section. A preferred means of administering nucleic acids encoding the peptides of the invention uses minigene constructs encoding a peptide comprising one or multiple epitopes of the invention.

The use of multi-epitope minigenes is described below and in, Ishioka *et al.*, *J. Immunol.* 162:3915-3925, 1999; An, L. and Whitton, J. L., *J. Virol.* 71:2292, 1997; Thomson, S. A. *et al.*, *J. Immunol.* 157:822, 1996; Whitton, J. L. *et al.*, *J. Virol.* 67:348, 1993; Hanke, R. *et al.*, *Vaccine* 16:426, 1998. For example, a multi-epitope DNA plasmid encoding supermotif- and/or motif-bearing epitopes derived 191P4D12(b), the PADRE® universal helper T cell epitope or multiple HTL epitopes from 191P4D12(b) (see e.g., Tables VIII-XXI and XXII to XLIX), and an endoplasmic reticulum-translocating signal sequence can be engineered. A vaccine may also comprise epitopes that are derived from other TAAs.

The immunogenicity of a multi-epitopic minigene can be confirmed in transgenic mice to evaluate the magnitude of CTL induction responses against the epitopes tested. Further, the immunogenicity of DNA-encoded epitopes *in vivo* can be correlated with the *in vitro* responses of specific CTL lines against target cells transfected with the DNA plasmid. Thus, these experiments can show that the minigene serves to both: 1.) generate a CTL response and 2.) that the induced CTLs recognized cells expressing the encoded epitopes.

For example, to create a DNA sequence encoding the selected epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes may be reverse translated. A human codon usage table can be used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences may be directly adjoined, so that when translated, a continuous polypeptide sequence is created. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequences that can be reverse translated and included in the minigene sequence include: HLA class I epitopes, HLA class II epitopes, antibody epitopes, a ubiquitination signal sequence, and/or an endoplasmic reticulum targeting signal. In addition, HLA presentation of CTL and HTL epitopes may be improved by including synthetic (*e.g.* poly-alanine) or naturally-occurring flanking sequences adjacent to the CTL or HTL epitopes; these larger peptides comprising the epitope(s) are within the scope of the invention.

The minigene sequence may be converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) may be synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides can be joined, for example, using T4 DNA ligase. This synthetic minigene, encoding the epitope polypeptide, can then be cloned into a desired expression vector.

Standard regulatory sequences well known to those of skill in the art are preferably included in the vector to ensure expression in the target cells. Several vector elements are desirable: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an *E. coli* origin of replication; and an *E. coli* selectable marker (*e.g.* ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, *e.g.*, the human cytomegalovirus (hCMV) promoter. *See, e.g.*, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences and sequences for replication in mammalian cells may also be considered for increasing minigene expression.

Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate *E. coli* strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

In addition, immunostimulatory sequences (ISSs or CpGs) appear to play a role in the immunogenicity of DNA vaccines. These sequences may be included in the vector, outside the minigene coding sequence, if desired to enhance immunogenicity.

In some embodiments, a bi-cistronic expression vector which allows production of both the minigene-encoded epitopes and a second protein (included to enhance or decrease immunogenicity) can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (*e.g.*, IL-2, IL-12, GM-CSF), cytokine-inducing molecules (*e.g.*, LeIF), costimulatory molecules, or for HTL responses, pan-DR binding proteins (PADRE™, Epimmune, San Diego, CA). Helper (HTL) epitopes can be joined to intracellular targeting signals and

expressed separately from expressed CTL epitopes; this allows direction of the HTL epitopes to a cell compartment different than that of the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the HLA class II pathway, thereby improving HTL induction. In contrast to HTL or CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (*e.g.* TGF-β) may be beneficial in certain diseases.

Therapeutic quantities of plasmid DNA can be produced for example, by fermentation in *E. coli*, followed by purification. Aliquots from the working cell bank are used to inoculate growth medium, and grown to saturation in shaker flasks or a bioreactor according to well-known techniques. Plasmid DNA can be purified using standard bioseparation technologies such as solid phase anion-exchange resins supplied by QIAGEN, Inc. (Valencia, California). If required, supercoiled DNA can be isolated from the open circular and linear forms using gel electrophoresis or other methods.

Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). This approach, known as "naked DNA," is currently being used for intramuscular (IM) administration in clinical trials. To maximize the immunotherapeutic effects of minigene DNA vaccines, an alternative method for formulating purified plasmid DNA may be desirable. A variety of methods have been described, and new techniques may become available. Cationic lipids, glycolipids, and fusogenic liposomes can also be used in the formulation (see, *e.g.*, as described by WO 93/24640; Mannino & Gould-Fogerite, *BioTechniques* 6(7): 682 (1988); U.S. Pat No. 5,279,833; WO 91/06309; and Felgner, *et al., Proc. Nat'l Acad. Sci. USA* 84:7413 (1987). In addition, peptides and compounds referred to collectively as protective, interactive, non-condensing compounds (PINC) could also be complexed to purified plasmid DNA to influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

Target cell sensitization can be used as a functional assay for expression and HLA class I presentation of minigene-encoded CTL epitopes. For example, the plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used will be dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct *in vitro* transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 (^{51}Cr) labeled and used as target cells for epitope-specific CTL lines; cytolysis, detected by ^{51}Cr release, indicates both production of, and HLA presentation of, minigene-encoded CTL epitopes. Expression of HTL epitopes may be evaluated in an analogous manner using assays to assess HTL activity.

In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human HLA proteins are immunized with the DNA product. The dose and route of administration are formulation dependent (*e.g.*, IM for DNA in PBS, intraperitoneal (i.p.) for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for one week in the presence of peptides encoding each epitope being tested. Thereafter, for CTL effector cells, assays are conducted for cytolysis of peptide-loaded, ^{51}Cr-labeled target cells using standard techniques. Lysis of target cells that were sensitized by HLA loaded with peptide epitopes, corresponding to minigene-encoded epitopes, demonstrates DNA vaccine function for *in vivo* induction of CTLs. Immunogenicity of HTL epitopes is confirmed in transgenic mice in an analogous manner.

Alternatively, the nucleic acids can be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Using this technique, particles comprised solely of DNA are administered. In a further alternative embodiment, DNA can be adhered to particles, such as gold particles.

Minigenes can also be delivered using other bacterial or viral delivery systems well known in the art, *e.g.*, an expression construct encoding epitopes of the invention can be incorporated into a viral vector such as vaccinia.

X.C.2. Combinations of CTL Peptides with Helper Peptides

Vaccine compositions comprising CTL peptides of the invention can be modified, e.g., analoged, to provide desired attributes, such as improved serum half life, broadened population coverage or enhanced immunogenicity.

For instance, the ability of a peptide to induce CTL activity can be enhanced by linking the peptide to a sequence which contains at least one epitope that is capable of inducing a T helper cell response. Although a CTL peptide can be directly linked to a T helper peptide, often CTL epitope/HTL epitope conjugates are linked by a spacer molecule. The spacer is typically comprised of relatively small, neutral molecules, such as amino acids or amino acid mimetics, which are substantially uncharged under physiological conditions. The spacers are typically selected from, *e.g.*, Ala, Gly, or other neutral spacers of nonpolar amino acids or neutral polar amino acids. It will be understood that the optionally present spacer need not be comprised of the same residues and thus may be a hetero- or homo-oligomer. When present, the spacer will usually be at least one or two residues, more usually three to six residues and sometimes 10 or more residues. The CTL peptide epitope can be linked to the T helper peptide epitope either directly or via a spacer either at the amino or carboxy terminus of the CTL peptide. The amino terminus of either the immunogenic peptide or the T helper peptide may be acylated.

In certain embodiments, the T helper peptide is one that is recognized by T helper cells present in a majority of a genetically diverse population. This can be accomplished by selecting peptides that bind to many, most, or all of the HLA class II molecules. Examples of such amino acid bind many HLA Class II molecules include sequences from antigens such as *tetanus toxoid* at positions 830-843 (QYIKANSKFIGITE; SEQ ID NO: 44), *Plasmodium falciparum* circumsporozoite (CS) protein at positions 378-398 (DIEKKIAKMEKASSVFNVVNS; SEQ ID NO: 45), and *Streptococcus* 18kD protein at positions 116-131 (GAVDSILGGVATYGAA; SEQ ID NO: 46). Other examples include peptides bearing a DR 1-4-7 supermotif, or either of the DR3 motifs.

Alternatively, it is possible to prepare synthetic peptides capable of stimulating T helper lymphocytes, in a loosely HLA-restricted fashion, using amino acid sequences not found in nature (*see, e.g.*, PCT publication WO 95/07707). These synthetic compounds called Pan-DR-binding epitopes (*e.g.*, PADRE™, Epimmune, Inc., San Diego, CA) are designed, most preferably, to bind most HLA-DR (human HLA class II) molecules. For instance, a pan-DR-binding epitope peptide having the formula: XKXVAAWTLKAAX (SEQ ID NO: 47), where "X" is either cyclohexylalanine, phenylalanine, or tyrosine, and a is either D-alanine or L-alanine, has been found to bind to most HLA-DR alleles, and to stimulate the response of T helper lymphocytes from most individuals, regardless of their HLA type. An alternative of a pan-DR binding epitope comprises all "L" natural amino acids and can be provided in the form of nucleic acids that encode the epitope.

HTL peptide epitopes can also be modified to alter their biological properties. For example, they can be modified to include D-amino acids to increase their resistance to proteases and thus extend their serum half life, or they can be conjugated to other molecules such as lipids, proteins, carbohydrates, and the like to increase their biological activity. For example, a T helper peptide can be conjugated to one or more palmitic acid chains at either the amino or carboxyl termini.

X.C.3. Combinations of CTL Peptides with T Cell Priming Agents

In some embodiments it may be desirable to include in the pharmaceutical compositions of the invention at least one component which primes B lymphocytes or T lymphocytes. Lipids have been identified as agents capable of priming CTL *in vivo*. For example, palmitic acid residues can be attached to the ε-and α- amino groups of a lysine residue and then linked, *e.g.*, via one or more linking residues such as Gly, Gly-Gly-, Ser, Ser-Ser, or the like, to an immunogenic peptide. The lipidated peptide can then be administered either directly in a micelle or particle, incorporated into a liposome, or emulsified in an adjuvant, *e.g.*, incomplete Freund's adjuvant. In a preferred embodiment, a particularly effective immunogenic composition comprises palmitic acid attached to ε- and α- amino groups of Lys, which is attached via linkage, *e.g.*, Ser-Ser, to the amino terminus of the immunogenic peptide.

As another example of lipid priming of CTL responses, *E. coli* lipoproteins, such as tripalmitoyl-S-glycerylcysteinlyseryl- serine (P_3CSS) can be used to prime virus specific CTL when covalently attached to an appropriate peptide (*see, e.g.*, Deres, *et al., Nature* 342:561, 1989). Peptides of the invention can be coupled to P_3CSS, for example, and the lipopeptide administered to an individual to prime specifically an immune response to the target antigen. Moreover, because the induction of neutralizing antibodies can also be primed with P_3CSS-conjugated epitopes, two such compositions can be combined to more effectively elicit both humoral and cell-mediated responses.

X.C.4. Vaccine Compositions Comprising DC Pulsed with CTL and/or HTL Peptides

An embodiment of a vaccine composition in accordance with the invention comprises *ex vivo* administration of a cocktail of epitope-bearing peptides to PBMC, or isolated DC therefrom, from the patient's blood. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Pharmacia-Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides and prior to reinfusion into patients, the DC are washed to remove unbound peptides. In this embodiment, a vaccine comprises peptide-pulsed DCs which present the pulsed peptide epitopes complexed with HLA molecules on their surfaces.

The DC can be pulsed *ex vivo* with a cocktail of peptides, some of which stimulate CTL responses to 191P4D12(b). Optionally, a helper T cell (HTL) peptide, such as a natural or artificial loosely restricted HLA Class II peptide, can be included to facilitate the CTL response. Thus, a vaccine in accordance with the invention is used to treat a cancer which expresses or overexpresses 191P4D12(b).

X.D. Adoptive Immunotherapy

Antigenic 191P4D12(b)-related peptides are used to elicit a CTL and/or HTL response *ex vivo*, as well. The resulting CTL or HTL cells, can be used to treat tumors in patients that do not respond to other conventional forms of therapy, or will not respond to a therapeutic vaccine peptide or nucleic acid in accordance with the invention. *Ex vivo* CTL or HTL responses to a particular antigen are induced by incubating in tissue culture the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of antigen-presenting cells (APC), such as dendritic cells, and the appropriate immunogenic peptide. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused back into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cell (e.g., a tumor cell). Transfected dendritic cells may also be used as antigen presenting cells.

X.E. Administration of Vaccines for Therapeutic or Prophylactic Purposes

Pharmaceutical and vaccine compositions of the invention are typically used to treat and/or prevent a cancer that expresses or overexpresses 191P4D12(b). In therapeutic applications, peptide and/or nucleic acid compositions are administered to a patient in an amount sufficient to elicit an effective B cell, CTL and/or HTL response to the antigen and to cure or at least partially arrest or slow symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use will depend on, e.g., the particular composition administered, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician.

For pharmaceutical compositions, the immunogenic peptides of the invention, or DNA encoding them, are generally administered to an individual already bearing a tumor that expresses 191P4D12(b). The peptides or DNA encoding them can be administered individually or as fusions of one or more peptide sequences. Patients can be treated with the immunogenic peptides separately or in conjunction with other treatments, such as surgery, as appropriate.

For therapeutic use, administration should generally begin at the first diagnosis of 191P4D12(b)-associated cancer. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter. The embodiment of the vaccine composition (*i.e.*, including, but not limited to embodiments such as peptide cocktails, polyepitopic polypeptides, minigenes, or TAA-specific CTLs or pulsed dendritic cells) delivered to the patient may vary according to the stage of the disease or the patient's health status. For example, in a patient with a tumor that expresses 191P4D12(b), a vaccine comprising 191P4D12(b)-specific CTL may be more efficacious in killing tumor cells in patient with advanced disease than alternative embodiments.

It is generally important to provide an amount of the peptide epitope delivered by a mode of administration sufficient to stimulate effectively a cytotoxic T cell response; compositions which stimulate helper T cell responses can also be given in accordance with this embodiment of the invention.

The dosage for an initial therapeutic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1,000 µg and the higher value is about 10,000; 20,000; 30,000; or 50,000 µg. Dosage values for a human typically range from about 500 µg to about 50,000 µg per 70 kilogram patient. Boosting dosages of between about 1.0 µg to about 50,000 µg of peptide pursuant to a boosting regimen over weeks to months may be administered depending upon the patient's response and condition as determined by measuring the specific activity of CTL and HTL obtained from the patient's blood. Administration should continue until at least clinical symptoms or laboratory tests indicate that the neoplasia, has been eliminated or reduced and for a period thereafter. The dosages, routes of administration, and dose schedules are adjusted in accordance with methodologies known in the art.

In certain embodiments, the peptides and compositions of the present invention are employed in serious disease states, that is, life-threatening or potentially life threatening situations. In such cases, as a result of the minimal amounts of extraneous substances and the relative nontoxic nature of the peptides in preferred compositions of the invention, it is possible and may be felt desirable by the treating physician to administer substantial excesses of these peptide compositions relative to these stated dosage amounts.

The vaccine compositions of the invention can also be used purely as prophylactic agents. Generally the dosage for an initial prophylactic immunization generally occurs in a unit dosage range where the lower value is about 1, 5, 50, 500, or 1000 µg and the higher value is about 10,000; 20,000; 30,000; or 50,000 µg. Dosage values for a human typically range from about 500 µg to about 50,000 µg per 70 kilogram patient. This is followed by boosting dosages of between about 1.0 µg to about 50,000 µg of peptide administered at defined intervals from about four weeks to six months after the initial administration of vaccine. The immunogenicity of the vaccine can be assessed by measuring the specific activity of CTL and HTL obtained from a sample of the patient's blood.

The pharmaceutical compositions for therapeutic treatment are intended for parenteral, topical, oral, nasal, intrathecal, or local (*e.g.* as a cream or topical ointment) administration. Preferably, the pharmaceutical compositions are administered parentally, *e.g.*, intravenously, subcutaneously, intradermally, or intramuscularly. Thus, the invention provides compositions for parenteral administration which comprise a solution of the immunogenic peptides dissolved or suspended in an acceptable carrier, preferably an aqueous carrier.

A variety of aqueous carriers may be used, *e.g.*, water, buffered water, 0.8% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well-known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration.

The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH-adjusting and buffering agents, tonicity adjusting agents, wetting agents, preservatives,

and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, *etc.*

The concentration of peptides of the invention in the pharmaceutical formulations can vary widely, *i.e.*, from less than about 0.1%, usually at or at least about 2% to as much as 20% to 50% or more by weight, and will be selected primarily by fluid volumes, viscosities, *etc.*, in accordance with the particular mode of administration selected.

A human unit dose form of a composition is typically included in a pharmaceutical composition that comprises a human unit dose of an acceptable carrier, in one embodiment an aqueous carrier, and is administered in a volume/quantity that is known by those of skill in the art to be used for administration of such compositions to humans (*see, e.g.*, Remington's Pharmaceutical Sciences, 17th Edition, A. Gennaro, Editor, Mack Publishing Co., Easton, Pennsylvania, 1985). For example a peptide dose for initial immunization can be from about 1 to about 50,000 μg, generally 100-5,000 μg, for a 70 kg patient. For example, for nucleic acids an initial immunization may be performed using an expression vector in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be recombinant fowlpox virus administered at a dose of 5-10^7 to 5x10^9 pfu.

For antibodies, a treatment generally involves repeated administration of the anti-191P4D12(b) antibody preparation, via an acceptable route of administration such as intravenous injection (IV), typically at a dose in the range of about 0.1 to about 10 mg/kg body weight. In general, doses in the range of 10-500 mg mAb per week are effective and well tolerated. Moreover, an initial loading dose of approximately 4 mg/kg patient body weight IV, followed by weekly doses of about 2 mg/kg IV of the anti- 191P4D12(b) mAb preparation represents an acceptable dosing regimen. As appreciated by those of skill in the art, various factors can influence the ideal dose in a particular case. Such factors include, for example, half life of a composition, the binding affinity of an Ab, the immunogenicity of a substance, the degree of 191P4D12(b) expression in the patient, the extent of circulating shed 191P4D12(b) antigen, the desired steady-state concentration level, frequency of treatment, and the influence of chemotherapeutic or other agents used in combination with the treatment method of the invention, as well as the health status of a particular patient. Non-limiting preferred human unit doses are, for example, 500μg - 1mg, 1mg - 50mg, 50mg - 100mg, 100mg - 200mg, 200mg - 300mg, 400mg - 500mg, 500mg - 600mg, 600mg - 700mg, 700mg - 800mg, 800mg - 900mg, 900mg - 1g, or 1mg - 700mg. In certain embodiments, the dose is in a range of 2-5 mg/kg body weight, e.g., with follow on weekly doses of 1-3 mg/kg; 0.5mg, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10mg/kg body weight followed, e.g., in two, three or four weeks by weekly doses; 0.5 - 10mg/kg body weight, e.g., followed in two, three or four weeks by weekly doses; 225, 250, 275, 300, 325, 350, 375, 400mg m^2 of body area weekly; 1-600mg m^2 of body area weekly; 225-400mg m^2 of body area weekly; these does can be followed by weekly doses for 2, 3, 4, 5, 6, 7, 8, 9, 19, 11, 12 or more weeks.

In one embodiment, human unit dose forms of polynucleotides comprise a suitable dosage range or effective amount that provides any therapeutic effect. As appreciated by one of ordinary skill in the art a therapeutic effect depends on a number of factors, including the sequence of the polynucleotide, molecular weight of the polynucleotide and route of administration. Dosages are generally selected by the physician or other health care professional in accordance with a variety of parameters known in the art, such as severity of symptoms, history of the patient and the like. Generally, for a polynucleotide of about 20 bases, a dosage range may be selected from, for example, an independently selected lower limit such as about 0.1, 0.25, 0.5, 1, 2, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400 or 500 mg/kg up to an independently selected upper limit, greater than the lower limit, of about 60, 80, 100, 200, 300, 400, 500, 750, 1000, 1500, 2000, 3000, 4000, 5000, 6000, 7000, 8000, 9000 or 10,000 mg/kg. For example, a dose may be about any of the following: 0.1 to 100 mg/kg, 0.1 to 50 mg/kg, 0.1 to 25 mg/kg, 0.1 to 10 mg/kg, 1 to 500 mg/kg, 100 to 400 mg/kg, 200 to 300 mg/kg, 1 to 100 mg/kg, 100 to 200 mg/kg, 300 to 400 mg/kg, 400 to 500 mg/kg, 500 to 1000 mg/kg, 500 to 5000 mg/kg, or 500 to

10,000 mg/kg. Generally, parenteral routes of administration may require higher doses of polynucleotide compared to more direct application to the nucleotide to diseased tissue, as do polynucleotides of increasing length.

In one embodiment, human unit dose forms of T-cells comprise a suitable dosage range or effective amount that provides any therapeutic effect. As appreciated by one of ordinary skill in the art, a therapeutic effect depends on a number of factors. Dosages are generally selected by the physician or other health care professional in accordance with a variety of parameters known in the art, such as severity of symptoms, history of the patient and the like. A dose may be about 10^4 cells to about 10^6 cells, about 10^6 cells to about 10^8 cells, about 10^8 to about 10^{11} cells, or about 10^8 to about 5×10^{10} cells. A dose may also about 10^6 cells/m^2 to about 10^{10} cells/m^2, or about 10^6 cells/m^2 to about 10^8 cells/m^2 .

Proteins(s) of the invention, and/or nucleic acids encoding the protein(s), can also be administered via liposomes, which may also serve to: 1) target the proteins(s) to a particular tissue, such as lymphoid tissue; 2) to target selectively to diseases cells; or, 3) to increase the half-life of the peptide composition. Liposomes include emulsions, foams, micelles, insoluble monolayers, liquid crystals, phospholipid dispersions, lamellar layers and the like. In these preparations, the peptide to be delivered is incorporated as part of a liposome, alone or in conjunction with a molecule which binds to a receptor prevalent among lymphoid cells, such as monoclonal antibodies which bind to the CD45 antigen, or with other therapeutic or immunogenic compositions. Thus, liposomes either filled or decorated with a desired peptide of the invention can be directed to the site of lymphoid cells, where the liposomes then deliver the peptide compositions. Liposomes for use in accordance with the invention are formed from standard vesicle-forming lipids, which generally include neutral and negatively charged phospholipids and a sterol, such as cholesterol. The selection of lipids is generally guided by consideration of, *e.g.*, liposome size, acid lability and stability of the liposomes in the blood stream. A variety of methods are available for preparing liposomes, as described in, *e.g.*, Szoka, *et al., Ann. Rev. Biophys. Bioeng.* 9:467 (1980), and U.S. Patent Nos. 4,235,871, 4,501,728, 4,837,028, and 5,019,369.

For targeting cells of the immune system, a ligand to be incorporated into the liposome can include, *e.g.*, antibodies or fragments thereof specific for cell surface determinants of the desired immune system cells. A liposome suspension containing a peptide may be administered intravenously, locally, topically, *etc.* in a dose which varies according to, *inter alia*, the manner of administration, the peptide being delivered, and the stage of the disease being treated.

For solid compositions, conventional nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

For aerosol administration, immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are about 0.01%-20% by weight, preferably about 1%-10%. The surfactant must, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from about 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute about 0.1%-20% by weight of the composition, preferably about 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included, as desired, as with, *e.g.*, lecithin for intranasal delivery.

XI.) Diagnostic and Prognostic Embodiments of 191P4D12(b).

As disclosed herein, 191P4D12(b) polynucleotides, polypeptides, reactive cytotoxic T cells (CTL), reactive helper T cells (HTL) and anti-polypeptide antibodies are used in well known diagnostic, prognostic and therapeutic assays that

examine conditions associated with dysregulated cell growth such as cancer, in particular the cancers listed in Table I (see, e.g., both its specific pattern of tissue expression as well as its overexpression in certain cancers as described for example in the Example entitled "Expression analysis of 191P4D12(b) in normal tissues, and patient specimens").

191P4D12(b) can be analogized to a prostate associated antigen PSA, the archetypal marker that has been used by medical practitioners for years to identify and monitor the presence of prostate cancer (see, e.g., Merrill *et al.*, J. Urol. 163(2): 503-5120 (2000); Polascik *et al.*, J. Urol. Aug; 162(2):293-306 (1999) and Fortier *et al.*, J. Nat. Cancer Inst. 91(19): 1635-1640(1999)). A variety of other diagnostic markers are also used in similar contexts including p53 and K-ras (see, e.g., Tulchinsky *et al.*, Int J Mol Med 1999 Jul 4(1):99-102 and Minimoto *et al.*, Cancer Detect Prev 2000;24(1):1-12). Therefore, this disclosure of 191P4D12(b) polynucleotides and polypeptides (as well as 191P4D12(b) polynucleotide probes and anti-191P4D12(b) antibodies used to identify the presence of these molecules) and their properties allows skilled artisans to utilize these molecules in methods that are analogous to those used, for example, in a variety of diagnostic assays directed to examining conditions associated with cancer.

Typical embodiments of diagnostic methods which utilize the 191P4D12(b) polynucleotides, polypeptides, reactive T cells and antibodies are analogous to those methods from well-established diagnostic assays, which employ, e.g., PSA polynucleotides, polypeptides, reactive T cells and antibodies. For example, just as PSA polynucleotides are used as probes (for example in Northern analysis, see, e.g., Sharief *et al.*, Biochem. Mol. Biol. Int. 33(3):567-74(1994)) and primers (for example in PCR analysis, see, e.g., Okegawa *et al.*, J. Urol. 163(4): 1189-1190 (2000)) to observe the presence and/or the level of PSA mRNAs in methods of monitoring PSA overexpression or the metastasis of prostate cancers, the 191P4D12(b) polynucleotides described herein can be utilized in the same way to detect 191P4D12(b) overexpression or the metastasis of prostate and other cancers expressing this gene. Alternatively, just as PSA polypeptides are used to generate antibodies specific for PSA which can then be used to observe the presence and/or the level of PSA proteins in methods to monitor PSA protein overexpression (see, e.g., Stephan *et al.*, Urology 55(4):560-3 (2000)) or the metastasis of prostate cells (see, e.g., Alanen *et al.*, Pathol. Res. Pract. 192(3):233-7 (1996)), the 191P4D12(b) polypeptides described herein can be utilized to generate antibodies for use in detecting 191P4D12(b) overexpression or the metastasis of prostate cells and cells of other cancers expressing this gene.

Specifically, because metastases involves the movement of cancer cells from an organ of origin (such as the lung or prostate gland etc.) to a different area of the body (such as a lymph node), assays which examine a biological sample for the presence of cells expressing 191P4D12(b) polynucleotides and/or polypeptides can be used to provide evidence of metastasis. For example, when a biological sample from tissue that does not normally contain 191P4D12(b)-expressing cells (lymph node) is found to contain 191P4D12(b)-expressing cells such as the 191P4D12(b) expression seen in LAPC4 and LAPC9, xenografts isolated from lymph node and bone metastasis, respectively, this finding is indicative of metastasis.

Alternatively 191P4D12(b) polynucleotides and/or polypeptides can be used to provide evidence of cancer, for example, when cells in a biological sample that do not normally express 191P4D12(b) or express 191P4D12(b) at a different level are found to express 191P4D12(b) or have an increased expression of 191P4D12(b) (see, e.g., the 191P4D12(b) expression in the cancers listed in Table I and in patient samples etc. shown in the accompanying Figures). In such assays, artisans may further wish to generate supplementary evidence of metastasis by testing the biological sample for the presence of a second tissue restricted marker (in addition to 191P4D12(b)) such as PSA, PSCA etc. (see, e.g., Alanen *et al.*, Pathol. Res. Pract. 192(3): 233-237 (1996)).

The use of immunohistochemistry to identify the presence of a 191P4D12(b) polypeptide within a tissue section can indicate an altered state of certain cells within that tissue. It is well understood in the art that the ability of an antibody to localize to a polypeptide that is expressed in cancer cells is a way of diagnosing presence of disease, disease stage,

progression and/or tumor aggressiveness. Such an antibody can also detect an altered distribution of the polypeptide within the cancer cells, as compared to corresponding non-malignant tissue.

The 191P4D12(b) polypeptide and immunogenic compositions are also useful in view of the phenomena of altered subcellular protein localization in disease states. Alteration of cells from normal to diseased state causes changes in cellular morphology and is often associated with changes in subcellular protein localization/distribution. For example, cell membrane proteins that are expressed in a polarized manner in normal cells can be altered in disease, resulting in distribution of the protein in a non-polar manner over the whole cell surface.

The phenomenon of altered subcellular protein localization in a disease state has been demonstrated with MUC1 and Her2 protein expression by use of immunohistochemical means. Normal epithelial cells have a typical apical distribution of MUC1, in addition to some supranuclear localization of the glycoprotein, whereas malignant lesions often demonstrate an apolar staining pattern (Diaz *et al*, The Breast Journal, 7; 40-45 (2001); Zhang *et al*, Clinical Cancer Research, 4; 2669-2676 (1998): Cao, *et al*, The Journal of Histochemistry and Cytochemistry, 45: 1547-1557 (1997)). In addition, normal breast epithelium is either negative for Her2 protein or exhibits only a basolateral distribution whereas malignant cells can express the protein over the whole cell surface (De Potter, *et al*, International Journal of Cancer, 44; 969-974 (1989): McCormick, *et al*, 117; 935-943 (2002)). Alternatively, distribution of the protein may be altered from a surface only localization to include diffuse cytoplasmic expression in the diseased state. Such an example can be seen with MUC1 (Diaz, *et al*, The Breast Journal, 7: 40-45 (2001)).

Alteration in the localization/distribution of a protein in the cell, as detected by immunohistochemical methods, can also provide valuable information concerning the favorability of certain treatment modalities. This last point is illustrated by a situation where a protein may be intracellular in normal tissue, but cell surface in malignant cells; the cell surface location makes the cells favorably amenable to antibody-based diagnostic and treatment regimens. When such an alteration of protein localization occurs for 191P4D12(b), the 191P4D12(b) protein and immune responses related thereto are very useful. Accordingly, the ability to determine whether alteration of subcellular protein localization occurred for 24P4C12 make the 191P4D12(b) protein and immune responses related thereto very useful. Use of the 191P4D12(b) compositions allows those skilled in the art to make important diagnostic and therapeutic decisions.

Immunohistochemical reagents specific to 191P4D12(b) are also useful to detect metastases of tumors expressing 191P4D12(b) when the polypeptide appears in tissues where 191P4D12(b) is not normally produced.

Thus, 191P4D12(b) polypeptides and antibodies resulting from immune responses thereto are useful in a variety of important contexts such as diagnostic, prognostic, preventative and/or therapeutic purposes known to those skilled in the art.

Just as PSA polynucleotide fragments and polynucleotide variants are employed by skilled artisans for use in methods of monitoring PSA, 191P4D12(b) polynucleotide fragments and polynucleotide variants are used in an analogous manner. In particular, typical PSA polynucleotides used in methods of monitoring PSA are probes or primers which consist of fragments of the PSA cDNA sequence. Illustrating this, primers used to PCR amplify a PSA polynucleotide must include less than the whole PSA sequence to function in the polymerase chain reaction. In the context of such PCR reactions, skilled artisans generally create a variety of different polynucleotide fragments that can be used as primers in order to amplify different portions of a polynucleotide of interest or to optimize amplification reactions (see, e.g., Caetano-Anolles, G. Biotechniques 25(3): 472-476, 478-480 (1998); Robertson *et al.*, Methods Mol. Biol. 98:121-154 (1998)). An additional illustration of the use of such fragments is provided in the Example entitled "Expression analysis of 191P4D12(b) in normal tissues, and patient specimens," where a 191P4D12(b) polynucleotide fragment is used as a probe to show the expression of 191P4D12(b) RNAs in cancer cells. In addition, variant polynucleotide sequences are typically used as primers and probes for the corresponding mRNAs in PCR and Northern analyses (see, e.g., Sawai *et al.*, Fetal Diagn. Ther. 1996 Nov-Dec 11(6):407-13 and Current Protocols In Molecular Biology, Volume 2, Unit 2, Frederick M. Ausubel *et al.* eds., 1995)).

Polynucleotide fragments and variants are useful in this context where they are capable of binding to a target polynucleotide sequence (e.g., a 191P4D12(b) polynucleotide shown in Figure 2 or variant thereof) under conditions of high stringency.

Furthermore, PSA polypeptides which contain an epitope that can be recognized by an antibody or T cell that specifically binds to that epitope are used in methods of monitoring PSA. 191P4D12(b) polypeptide fragments and polypeptide analogs or variants can also be used in an analogous manner. This practice of using polypeptide fragments or polypeptide variants to generate antibodies (such as anti-PSA antibodies or T cells) is typical in the art with a wide variety of systems such as fusion proteins being used by practitioners (see, e.g., Current Protocols In Molecular Biology, Volume 2, Unit 16, Frederick M. Ausubel *et al.* eds., 1995). In this context, each epitope(s) functions to provide the architecture with which an antibody or T cell is reactive. Typically, skilled artisans create a variety of different polypeptide fragments that can be used in order to generate immune responses specific for different portions of a polypeptide of interest (see, e.g., U.S. Patent No. 5,840,501 and U.S. Patent No. 5,939,533). For example it may be preferable to utilize a polypeptide comprising one of the 191P4D12(b) biological motifs discussed herein or a motif-bearing subsequence which is readily identified by one of skill in the art based on motifs available in the art. Polypeptide fragments, variants or analogs are typically useful in this context as long as they comprise an epitope capable of generating an antibody or T cell specific for a target polypeptide sequence (e.g. a 191P4D12(b) polypeptide shown in Figure 3).

As shown herein, the 191P4D12(b) polynucleotides and polypeptides (as well as the 191P4D12(b) polynucleotide probes and anti-191P4D12(b) antibodies or T cells used to identify the presence of these molecules) exhibit specific properties that make them useful in diagnosing cancers such as those listed in Table I. Diagnostic assays that measure the presence of 191P4D12(b) gene products, in order to evaluate the presence or onset of a disease condition described herein, such as prostate cancer, are used to identify patients for preventive measures or further monitoring, as has been done so successfully with PSA. Moreover, these materials satisfy a need in the art for molecules having similar or complementary characteristics to PSA in situations where, for example, a definite diagnosis of metastasis of prostatic origin cannot be made on the basis of a test for PSA alone (see, e.g., Alanen *et al.*, Pathol. Res. Pract. 192(3): 233-237 (1996)), and consequently, materials such as 191P4D12(b) polynucleotides and polypeptides (as well as the 191P4D12(b) polynucleotide probes and anti-191P4D12(b) antibodies used to identify the presence of these molecules) need to be employed to confirm a metastases of prostatic origin.

Finally, in addition to their use in diagnostic assays, the 191P4D12(b) polynucleotides disclosed herein have a number of other utilities such as their use in the identification of oncogenetic associated chromosomal abnormalities in the chromosomal region to which the 191P4D12(b) gene maps (see the Example entitled "Chromosomal Mapping of 191P4D12(b)" below). Moreover, in addition to their use in diagnostic assays, the 191P4D12(b)-related proteins and polynucleotides disclosed herein have other utilities such as their use in the forensic analysis of tissues of unknown origin (see, e.g., Takahama K Forensic Sci Int 1996 Jun 28;80(1-2): 63-9).

Additionally, 191P4D12(b)-related proteins or polynucleotides of the invention can be used to treat a pathologic condition characterized by the over-expression of 191P4D12(b). For example, the amino acid or nucleic acid sequence of Figure 2 or Figure 3, or fragments of either, can be used to generate an immune response to a 191P4D12(b) antigen. Antibodies or other molecules that react with 191P4D12(b) can be used to modulate the function of this molecule, and thereby provide a therapeutic benefit.

XII.) Inhibition of 191P4D12(b) Protein Function

The invention includes various methods and compositions for inhibiting the binding of 191P4D12(b) to its binding partner or its association with other protein(s) as well as methods for inhibiting 191P4D12(b) function.

XII.A.) Inhibition of 191P4D12(b) With Intracellular Antibodies

In one approach, a recombinant vector that encodes single chain antibodies that specifically bind to 191P4D12(b) are introduced into 191P4D12(b) expressing cells via gene transfer technologies. Accordingly, the encoded single chain anti-191P4D12(b) antibody is expressed intracellularly, binds to 191P4D12(b) protein, and thereby inhibits its function. Methods for engineering such intracellular single chain antibodies are well known. Such intracellular antibodies, also known as "intrabodies", are specifically targeted to a particular compartment within the cell, providing control over where the inhibitory activity of the treatment is focused. This technology has been successfully applied in the art (for review, see Richardson and Marasco, 1995, TIBTECH vol. 13). Intrabodies have been shown to virtually eliminate the expression of otherwise abundant cell surface receptors (see, e.g., Richardson *et al.*, 1995, Proc. Natl. Acad. Sci. USA 92: 3137-3141; Beerli *et al.*, 1994, J. Biol. Chem. 289: 23931-23936; Deshane *et al.*, 1994, Gene Ther. 1: 332-337).

Single chain antibodies comprise the variable domains of the heavy and light chain joined by a flexible linker polypeptide, and are expressed as a single polypeptide. Optionally, single chain antibodies are expressed as a single chain variable region fragment joined to the light chain constant region. Well-known intracellular trafficking signals are engineered into recombinant polynucleotide vectors encoding such single chain antibodies in order to target precisely the intrabody to the desired intracellular compartment. For example, intrabodies targeted to the endoplasmic reticulum (ER) are engineered to incorporate a leader peptide and, optionally, a C-terminal ER retention signal, such as the KDEL amino acid motif. Intrabodies intended to exert activity in the nucleus are engineered to include a nuclear localization signal. Lipid moieties are joined to intrabodies in order to tether the intrabody to the cytosolic side of the plasma membrane. Intrabodies can also be targeted to exert function in the cytosol. For example, cytosolic intrabodies are used to sequester factors within the cytosol, thereby preventing them from being transported to their natural cellular destination.

In one embodiment, intrabodies are used to capture 191P4D12(b) in the nucleus, thereby preventing its activity within the nucleus. Nuclear targeting signals are engineered into such 191P4D12(b) intrabodies in order to achieve the desired targeting. Such 191P4D12(b) intrabodies are designed to bind specifically to a particular 191P4D12(b) domain. In another embodiment, cytosolic intrabodies that specifically bind to a 191P4D12(b) protein are used to prevent 191P4D12(b) from gaining access to the nucleus, thereby preventing it from exerting any biological activity within the nucleus (e.g., preventing 191P4D12(b) from forming transcription complexes with other factors).

In order to specifically direct the expression of such intrabodies to particular cells, the transcription of the intrabody is placed under the regulatory control of an appropriate tumor-specific promoter and/or enhancer. In order to target intrabody expression specifically to prostate, for example, the PSA promoter and/or promoter/enhancer can be utilized (See, for example, U.S. Patent No. 5,919,652 issued 6 July 1999).

XII.B.) Inhibition of 191P4D12(b) with Recombinant Proteins

In another approach, recombinant molecules bind to 191P4D12(b) and thereby inhibit 191P4D12(b) function. For example, these recombinant molecules prevent or inhibit 191P4D12(b) from accessing/binding to its binding partner(s) or associating with other protein(s). Such recombinant molecules can, for example, contain the reactive part(s) of a 191P4D12(b) specific antibody molecule. In a particular embodiment, the 191P4D12(b) binding domain of a 191P4D12(b) binding partner is engineered into a dimeric fusion protein, whereby the fusion protein comprises two 191P4D12(b) ligand binding domains linked to the Fc portion of a human IgG, such as human IgG1. Such IgG portion can contain, for example, the C_H2 and C_H3 domains and the hinge region, but not the C_H1 domain. Such dimeric fusion proteins are administered in soluble form to patients suffering from a cancer associated with the expression of 191P4D12(b), whereby the dimeric fusion protein specifically binds to 191P4D12(b) and blocks 191P4D12(b) interaction with a binding partner. Such dimeric fusion proteins are further combined into multimeric proteins using known antibody linking technologies.

XII.C.) Inhibition of 191P4D12(b) Transcription or Translation

The present invention also comprises various methods and compositions for inhibiting the transcription of the 191P4D12(b) gene. Similarly, the invention also provides methods and compositions for inhibiting the translation of 191P4D12(b) mRNA into protein.

In one approach, a method of inhibiting the transcription of the 191P4D12(b) gene comprises contacting the 191P4D12(b) gene with a 191P4D12(b) antisense polynucleotide. In another approach, a method of inhibiting 191P4D12(b) mRNA translation comprises contacting a 191P4D12(b) mRNA with an antisense polynucleotide. In another approach, a 191P4D12(b) specific ribozyme is used to cleave a 191P4D12(b) message, thereby inhibiting translation. Such antisense and ribozyme based methods can also be directed to the regulatory regions of the 191P4D12(b) gene, such as 191P4D12(b) promoter and/or enhancer elements. Similarly, proteins capable of inhibiting a 191P4D12(b) gene transcription factor are used to inhibit 191P4D12(b) mRNA transcription. The various polynucleotides and compositions useful in the aforementioned methods have been described above. The use of antisense and ribozyme molecules to inhibit transcription and translation is well known in the art.

Other factors that inhibit the transcription of 191P4D12(b) by interfering with 191P4D12(b) transcriptional activation are also useful to treat cancers expressing 191P4D12(b). Similarly, factors that interfere with 191P4D12(b) processing are useful to treat cancers that express 191P4D12(b). Cancer treatment methods utilizing such factors are also within the scope of the invention.

XII.D.) General Considerations for Therapeutic Strategies

Gene transfer and gene therapy technologies can be used to deliver therapeutic polynucleotide molecules to tumor cells synthesizing 191P4D12(b) (i.e., antisense, ribozyme, polynucleotides encoding intrabodies and other 191P4D12(b) inhibitory molecules). A number of gene therapy approaches are known in the art. Recombinant vectors encoding 191P4D12(b) antisense polynucleotides, ribozymes, factors capable of interfering with 191P4D12(b) transcription, and so forth, can be delivered to target tumor cells using such gene therapy approaches.

The above therapeutic approaches can be combined with any one of a wide variety of surgical, chemotherapy or radiation therapy regimens. The therapeutic approaches of the invention can enable the use of reduced dosages of chemotherapy (or other therapies) and/or less frequent administration, an advantage for all patients and particularly for those that do not tolerate the toxicity of the chemotherapeutic agent well.

The anti-tumor activity of a particular composition (e.g., antisense, ribozyme, intrabody), or a combination of such compositions, can be evaluated using various *in vitro* and *in vivo* assay systems. *In vitro* assays that evaluate therapeutic activity include cell growth assays, soft agar assays and other assays indicative of tumor promoting activity, binding assays capable of determining the extent to which a therapeutic composition will inhibit the binding of 191P4D12(b) to a binding partner, etc.

In vivo, the effect of a 191P4D12(b) therapeutic composition can be evaluated in a suitable animal model. For example, xenogenic prostate cancer models can be used, wherein human prostate cancer explants or passaged xenograft tissues are introduced into immune compromised animals, such as nude or SCID mice (Klein *et al.*, 1997, Nature Medicine 3: 402-408). For example, PCT Patent Application WO98/16628 and U.S. Patent 6,107,540 describe various xenograft models of human prostate cancer capable of recapitulating the development of primary tumors, micrometastasis, and the formation of osteoblastic metastases characteristic of late stage disease. Efficacy can be predicted using assays that measure inhibition of tumor formation, tumor regression or metastasis, and the like.

In vivo assays that evaluate the promotion of apoptosis are useful in evaluating therapeutic compositions. In one embodiment, xenografts from tumor bearing mice treated with the therapeutic composition can be examined for the presence

of apoptotic foci and compared to untreated control xenograft-bearing mice. The extent to which apoptotic foci are found in the tumors of the treated mice provides an indication of the therapeutic efficacy of the composition.

The therapeutic compositions used in the practice of the foregoing methods can be formulated into pharmaceutical compositions comprising a carrier suitable for the desired delivery method. Suitable carriers include any material that when combined with the therapeutic composition retains the anti-tumor function of the therapeutic composition and is generally non-reactive with the patient's immune system. Examples include, but are not limited to, any of a number of standard pharmaceutical carriers such as sterile phosphate buffered saline solutions, bacteriostatic water, and the like (see, generally, Remington's Pharmaceutical Sciences 16th Edition, A. Osal., Ed., 1980).

Therapeutic formulations can be solubilized and administered via any route capable of delivering the therapeutic composition to the tumor site. Potentially effective routes of administration include, but are not limited to, intravenous, parenteral, intraperitoneal, intramuscular, intratumor, intradermal, intraorgan, orthotopic, and the like. A preferred formulation for intravenous injection comprises the therapeutic composition in a solution of preserved bacteriostatic water, sterile unpreserved water, and/or diluted in polyvinylchloride or polyethylene bags containing 0.9% sterile Sodium Chloride for Injection, USP. Therapeutic protein preparations can be lyophilized and stored as sterile powders, preferably under vacuum, and then reconstituted in bacteriostatic water (containing for example, benzyl alcohol preservative) or in sterile water prior to injection.

Dosages and administration protocols for the treatment of cancers using the foregoing methods will vary with the method and the target cancer, and will generally depend on a number of other factors appreciated in the art.

XIII.) Identification, Characterization and Use of Modulators of 191P4D12(b)

Methods to Identify and Use Modulators

In one embodiment, screening is performed to identify modulators that induce or suppress a particular expression profile, suppress or induce specific pathways, preferably generating the associated phenotype thereby. In another embodiment, having identified differentially expressed genes important in a particular state; screens are performed to identify modulators that alter expression of individual genes, either increase or decrease. In another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition, screens are done for genes that are induced in response to a candidate agent. After identifying a modulator (one that suppresses a cancer expression pattern leading to a normal expression pattern, or a modulator of a cancer gene that leads to expression of the gene as in normal tissue) a screen is performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent-treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue, and vice versa. These agent-specific sequences are identified and used by methods described herein for cancer genes or proteins. In particular these sequences and the proteins they encode are used in marking or identifying agent-treated cells. In addition, antibodies are raised against the agent-induced proteins and used to target novel therapeutics to the treated cancer tissue sample.

Modulator-related Identification and Screening Assays:

Gene Expression-related Assays

Proteins, nucleic acids, and antibodies of the invention are used in screening assays. The cancer-associated proteins, antibodies, nucleic acids, modified proteins and cells containing these sequences are used in screening assays,

such as evaluating the effect of drug candidates on a "gene expression profile," expression profile of polypeptides or alteration of biological function. In one embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Davis, GF, et al, J Biol Screen 7:69 (2002); Zlokarnik, et al., Science 279:84-8 (1998); Heid, Genome Res 6:986-94,1996).

The cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins or genes are used in screening assays. That is, the present invention comprises methods for screening for compositions which modulate the cancer phenotype or a physiological function of a cancer protein of the invention. This is done on a gene itself or by evaluating the effect of drug candidates on a "gene expression profile" or biological function. In one embodiment, expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring after treatment with a candidate agent, see Zlokarnik, supra.

A variety of assays are executed directed to the genes and proteins of the invention. Assays are run on an individual nucleic acid or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds are screened for the ability to modulate gene expression or for binding to the cancer protein of the invention. "Modulation" in this context includes an increase or a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue a target value of a 10-fold increase in expression by the test compound is often desired. Modulators that exacerbate the type of gene expression seen in cancer are also useful, e.g., as an upregulated target in further analyses.

The amount of gene expression is monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, a gene product itself is monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques also allow for quantification of expression.

Expression Monitoring to Identify Compounds that Modify Gene Expression

In one embodiment, gene expression monitoring, i.e., an expression profile, is monitored simultaneously for a number of entities. Such profiles will typically involve one or more of the genes of Figure 2. In this embodiment, e.g., cancer nucleic acid probes are attached to biochips to detect and quantify cancer sequences in a particular cell. Alternatively, PCR can be used. Thus, a series, e.g., wells of a microtiter plate, can be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Expression monitoring is performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out in Figure 2. Generally, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins of the invention, bind to a cancer protein of the invention, or interfere with the binding of a cancer protein of the invention and an antibody or other binding partner.

In one embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds," as compounds for screening, or as therapeutics.

In certain embodiments, combinatorial libraries of potential modulators are screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by

identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

As noted above, gene expression monitoring is conveniently used to test candidate modulators (e.g., protein, nucleic acid or small molecule). After the candidate agent has been added and the cells allowed to incubate for a period, the sample containing a target sequence to be analyzed is, e.g., added to a biochip.

If required, the target sequence is prepared using known techniques. For example, a sample is treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

The target sequence can be labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that is detected. Alternatively, the label is a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5, 681,702; 5,597,909; 5,545,730; 5,594,117; 5,591,584; 5,571,670; 5,580,731; 5,571,670; 5,591,584; 5,624,802; 5,635,352; 5,594,118; 5,359,100; 5,124, 246; and 5,681,697. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions are used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allow formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc. These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus, it can be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein can be accomplished in a variety of ways. Components of the reaction can be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g. albumin, detergents, etc. which can be used to facilitate optimal hybridization and detection, and/or reduce nonspecific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target. The assay data are analyzed to determine the expression levels of individual genes, and changes in expression levels as between states, forming a gene expression profile.

Biological Activity-related Assays

The invention provides methods identify or screen for a compound that modulates the activity of a cancer-related gene or protein of the invention. The methods comprise adding a test compound, as defined above, to a cell comprising a cancer protein of the invention. The cells contain a recombinant nucleic acid that encodes a cancer protein of the invention. In another embodiment, a library of candidate agents is tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g. hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e., cell-cell contacts). In another example, the determinations are made at different stages of the cell cycle process. In this way, compounds that modulate genes or proteins of the invention are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein of the invention. Once identified, similar structures are evaluated to identify critical structural features of the compound.

In one embodiment, a method of modulating (e.g., inhibiting) cancer cell division is provided; the method comprises administration of a cancer modulator. In another embodiment, a method of modulating (e.g., inhibiting) cancer is provided; the method comprises administration of a cancer modulator. In a further embodiment, methods of treating cells or individuals with cancer are provided; the method comprises administration of a cancer modulator.

In one embodiment, a method for modulating the status of a cell that expresses a gene of the invention is provided. As used herein status comprises such art-accepted parameters such as growth, proliferation, survival, function, apoptosis, senescence, location, enzymatic activity, signal transduction, etc. of a cell. In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule. A variety of cell growth, proliferation, and metastasis assays are known to those of skill in the art, as described herein.

High Throughput Screening to Identify Modulators

The assays to identify suitable modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

In one embodiment, modulators evaluated in high throughput screening methods are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, are used. In this way, libraries of proteins are made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes, or ligands and receptors.

Use of Soft Agar Growth and Colony Formation to Identify and Characterize Modulators

Normal cells require a solid substrate to attach and grow. When cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, can regenerate normal phenotype and once again require a solid substrate to attach to and grow. Soft agar growth or colony formation in assays are used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A modulator reduces or eliminates the host cells' ability to grow suspended in solid or semisolid media, such as agar.

Techniques for soft agar growth or colony formation in suspension assays are described in Freshney, Culture of Animal Cells a Manual of Basic Technique (3rd ed., 1994). See also, the methods section of Garkavtsev et al. (1996), supra.

Evaluation of Contact Inhibition and Growth Density Limitation to Identify and Characterize Modulators

Normal cells typically grow in a flat and organized pattern in cell culture until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. Transformed cells, however, are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, transformed cells grow to a higher saturation density than corresponding normal cells. This is detected morphologically by the formation of a disoriented monolayer of cells or cells in foci. Alternatively, labeling index with (^{3}H)-thymidine at saturation density is used to measure density limitation of growth, similarly an MTT or Alamar blue assay will reveal proliferation capacity of cells and the the ability of modulators to affect same. See Freshney (1994), supra. Transformed cells, when transfected with tumor suppressor genes, can regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with ^{3}H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (^{3}H)-thymidine is determined by incorporated cpm.

Contact independent growth is used to identify modulators of cancer sequences, which had led to abnormal cellular proliferation and transformation. A modulator reduces or eliminates contact independent growth, and returns the cells to a normal phenotype.

Evaluation of Growth Factor or Serum Dependence to Identify and Characterize Modulators

Transformed cells have lower serum dependence than their normal counterparts (see, e.g., Temin, J. Natl. Cancer Inst. 37:167-175 (1966); Eagle et al., J. Exp. Med 131:836-879 (1970)); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. The degree of growth factor or serum dependence of transformed host cells can be compared with that of control. For example, growth factor or serum dependence of a cell is monitored in methods to identify and characterize compounds that modulate cancer-associated sequences of the invention.

Use of Tumor-specific Marker Levels to Identify and Characterize Modulators

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino, Angiogenesis, Tumor Vascularization, and Potential Interference with Tumor Growth, *in* Biological Responses in Cancer, pp. 178-184 (Mihich (ed.) 1985)). Similarly, Tumor Angiogenesis Factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman, Angiogenesis and Cancer, Sem Cancer Biol. (1992)), while bFGF is released from endothelial tumors (Ensoli, B et al).

Various techniques which measure the release of these factors are described in Freshney (1994), supra. Also, see, Unkless et al., J. Biol. Chem. 249:4295-4305 (1974); Strickland & Beers, J. Biol. Chem. 251:5694-5702 (1976); Whur et al., Br. J. Cancer 42:305 312 (1980); Gullino, Angiogenesis, Tumor Vascularization, and Potential Interference with Tumor Growth, *in* Biological Responses in Cancer, pp. 178-184 (Mihich (ed.) 1985); Freshney, Anticancer Res. 5:111-130 (1985). For example, tumor specific marker levels are monitored in methods to identify and characterize compounds that modulate cancer-associated sequences of the invention.

Invasiveness into Matrigel to Identify and Characterize Modulators

The degree of invasiveness into Matrigel or an extracellular matrix constituent can be used as an assay to identify and characterize compounds that modulate cancer associated sequences. Tumor cells exhibit a positive correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells. Techniques described in Cancer Res. 1999; 59:6010; Freshney (1994), *supra*, can be used. Briefly, the level of invasion of host cells is measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated

histologically by number of cells and distance moved, or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Evaluation of Tumor Growth *In Vivo* to Identify and Characterize Modulators

Effects of cancer-associated sequences on cell growth are tested in transgenic or immune-suppressed organisms. Transgenic organisms are prepared in a variety of art-accepted ways. For example, knock-out transgenic organisms, e.g., mammals such as mice, are made, in which a cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice are made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

To prepare transgenic chimeric animals, e.g., mice, a DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells some of which are derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi et al., Science 244:1288 (1989)). Chimeric mice can be derived according to US Patent 6,365,797, issued 2 April 2002; US Patent 6,107,540 issued 22 August 2000; Hogan et al., Manipulating the Mouse Embryo: A laboratory Manual, Cold Spring Harbor Laboratory (1988) and Teratocarcinomas and Embryonic Stem Cells: A Practical Approach, Robertson, ed., IRL Press, Washington, D.C., (1987).

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, a genetically athymic "nude" mouse (see, e.g., Giovanella et al., J. Natl. Cancer Inst. 52:921 (1974)), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley et al., Br. J. Cancer 38:263 (1978); Selby et al., Br. J. Cancer 41:52 (1980)) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts produce invasive tumors in a high proportion of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing cancer-associated sequences are injected subcutaneously or orthotopically. Mice are then separated into groups, including control groups and treated experimental groups) e.g. treated with a modulator). After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions, or weight) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

In Vitro Assays to Identify and Characterize Modulators

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as Western blotting, ELISA and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e. g., Northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or P-gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured

according to standard techniques known to those of skill in the art (Davis GF, supra; Gonzalez, J. & Negulescu, P. Curr. Opin. Biotechnol. 1998: 9:624).

As outlined above, in vitro screens are done on individual genes and gene products. That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself is performed.

In one embodiment, screening for modulators of expression of specific gene(s) is performed. Typically, the expression of only one or a few genes is evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

Binding Assays to Identify and Characterize Modulators

In binding assays in accordance with the invention, a purified or isolated gene product of the invention is generally used. For example, antibodies are generated to a protein of the invention, and immunoassays are run to determine the amount and/or location of protein. Alternatively, cells comprising the cancer proteins are used in the assays.

Thus, the methods comprise combining a cancer protein of the invention and a candidate compound such as a ligand, and determining the binding of the compound to the cancer protein of the invention. Preferred embodiments utilize the human cancer protein; animal models of human disease of can also be developed and used. Also, other analogous mammalian proteins also can be used as appreciated by those of skill in the art. Moreover, in some embodiments variant or derivative cancer proteins are used.

Generally, the cancer protein of the invention, or the ligand, is non-diffusibly bound to an insoluble support. The support can, e.g., be one having isolated sample receiving areas (a microtiter plate, an array, etc.). The insoluble supports can be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports can be solid or porous and of any convenient shape.

Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharide, nylon, nitrocellulose, or Teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition to the support is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies which do not sterically block either the ligand binding site or activation sequence when attaching the protein to the support, direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or ligand/binding agent to the support, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

Once a cancer protein of the invention is bound to the support, and a test compound is added to the assay. Alternatively, the candidate binding agent is bound to the support and the cancer protein of the invention is then added. Binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc.

Of particular interest are assays to identify agents that have a low toxicity for human cells. A wide variety of assays can be used for this purpose, including proliferation assays, cAMP assays, labeled *in vitro* protein-protein binding assays,

electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

A determination of binding of the test compound (ligand, binding agent, modulator, etc.) to a cancer protein of the invention can be done in a number of ways. The test compound can be labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein of the invention to a solid support, adding a labeled candidate compound (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps can be utilized as appropriate.

In certain embodiments, only one of the components is labeled, e.g., a protein of the invention or ligands labeled. Alternatively, more than one component is labeled with different labels, e.g., I^{125}, for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

Competitive Binding to Identify and Characterize Modulators

In one embodiment, the binding of the "test compound" is determined by competitive binding assay with a "competitor." The competitor is a binding moiety that binds to the target molecule (e.g., a cancer protein of the invention). Competitors include compounds such as antibodies, peptides, binding partners, ligands, etc. Under certain circumstances, the competitive binding between the test compound and the competitor displaces the test compound. In one embodiment, the test compound is labeled. Either the test compound, the competitor, or both, is added to the protein for a time sufficient to allow binding. Incubations are performed at a temperature that facilitates optimal activity, typically between four and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening; typically between zero and one hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In one embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the post-test compound wash solution indicates displacement by the test compound. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor indicates that the test compound binds to the cancer protein with higher affinity than the competitor. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, indicates that the test compound binds to and thus potentially modulates the cancer protein of the invention.

Accordingly, the competitive binding methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins of the invention. In this embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second sample comprises a test compound, the cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. For example the structure of the cancer protein is modeled and used in rational drug design to synthesize agents that interact with that site, agents which generally do not bind to site-modified proteins.

Moreover, such drug candidates that affect the activity of a native cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of such proteins.

Positive controls and negative controls can be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples occurs for a time sufficient to allow for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples can be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents can be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc. which are used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., can be used. The mixture of components is added in an order that provides for the requisite binding.

Use of Polynucleotides to Down-regulate or Inhibit a Protein of the Invention.

Polynucleotide modulators of cancer can be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand-binding molecule, as described in WO 91/04753. Suitable ligand-binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer can be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of a polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Inhibitory and Antisense Nucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of antisense polynucleotide or inhibitory small nuclear RNA (snRNA), i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein of the invention, mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally occurring nucleotides, or synthetic species formed from naturally occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprised by this invention so long as they function effectively to hybridize with nucleotides of the invention. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. Antisense or sense oligonucleotides, according to the present invention,

comprise a fragment generally at least about 12 nucleotides, preferably from about 12 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein &Cohen (Cancer Res. 48:2659 (1988 and van der Krol et al. (BioTechniques 6:958 (1988)).

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto et al., Adv. in Pharmacology 25: 289-317 (1994) for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel et al., Nucl. Acids Res. 18:299-304 (1990); European Patent Publication No. 0360257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., WO 94/26877; Ojwang et al., Proc. Natl. Acad. Sci. USA 90:6340-6344 (1993); Yamada et al., Human Gene Therapy 1:39-45 (1994); Leavitt et al., Proc. Natl. Acad Sci. USA 92:699- 703 (1995); Leavitt et al., Human Gene Therapy 5: 1151-120 (1994); and Yamada et al., Virology 205: 121-126 (1994)).

Use of Modulators in Phenotypic Screening

In one embodiment, a test compound is administered to a population of cancer cells, which have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the modulator is added to the cells in such a manner as to allow the modulator to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, a nucleic acid encoding a proteinaceous agent (i.e., a peptide) is put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used. Once the modulator has been administered to the cells, the cells are washed if desired and are allowed to incubate under preferably physiological conditions for some period. The cells are then harvested and a new gene expression profile is generated. Thus, e.g., cancer tissue is screened for agents that modulate, e.g., induce or suppress, the cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. Similarly, altering a biological function or a signaling pathway is indicative of modulator activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype are devised. With this approach, the drug target need not be known and need not be represented in the original gene/protein expression screening platform, nor does the level of transcript for the target protein need to change. The modulator inhibiting function will serve as a surrogate marker

As outlined above, screens are done to assess genes or gene products. That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself is performed.

Use of Modulators to Affect Peptides of the Invention

Measurements of cancer polypeptide activity, or of the cancer phenotype are performed using a variety of assays. For example, the effects of modulators upon the function of a cancer polypeptide(s) are measured by examining parameters described above. A physiological change that affects activity is used to assess the influence of a test compound on the polypeptides of this invention. When the functional outcomes are determined using intact cells or animals, a variety of effects can be assesses such as, in the case of a cancer associated with solid tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., by

Northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGNIP.

Methods of Identifying Characterizing Cancer-associated Sequences

Expression of various gene sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes are determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining the presence of, all or part, the sequence of at least one endogenous cancer gene in a cell. This is accomplished using any number of sequencing techniques. The invention comprises methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one gene of the invention in the individual. This is generally done in at least one tissue of the individual, e.g., a tissue set forth in Table I, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced gene to a known cancer gene, i.e., a wild-type gene to determine the presence of family members, homologies, mutations or variants. The sequence of all or part of the gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This is done using any number of known homology programs, such as BLAST, Bestfit, etc. The presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number of copies of the cancer gene in the genome. The cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

XIV.) Kits/Articles of Manufacture

For use in the diagnostic and therapeutic applications described herein, kits are also within the scope of the invention. Such kits can comprise a carrier, package, or container that is compartmentalized to receive one or more containers such as vials, tubes, and the like, each of the container(s) comprising one of the separate elements to be used in the method. For example, the container(s) can comprise a probe that is or can be detectably labeled. Such probe can be an antibody or polynucleotide specific for a Figure 2-related protein or a Figure 2 gene or message, respectively. Where the method utilizes nucleic acid hybridization to detect the target nucleic acid, the kit can also have containers containing nucleotide(s) for amplification of the target nucleic acid sequence and/or a container comprising a reporter-means, such as a biotin-binding protein, such as avidin or streptavidin, bound to a reporter molecule, such as an enzymatic, florescent, or radioisotope label. The kit can include all or part of the amino acid sequences in Figure 2 or Figure 3 or analogs thereof, or a nucleic acid molecules that encodes such amino acid sequences.

The kit of the invention will typically comprise the container described above and one or more other containers comprising materials desirable from a commercial and user standpoint, including buffers, diluents, filters, needles, syringes; carrier, package, container, vial and/or tube labels listing contents and/or instructions for use, and package inserts with instructions for use.

A label can be present on the container to indicate that the composition is used for a specific therapy or non-therapeutic application, such as a diagnostic or laboratory application, and can also indicate directions for either *in vivo* or *in vitro* use, such as those described herein. Directions and or other information can also be included on an insert(s) or label(s) which is included with or on the kit.

The terms "kit" and "article of manufacture" can be used as synonyms.

In another embodiment of the invention, an article(s) of manufacture containing compositions, such as amino acid sequence(s), small molecule(s), nucleic acid sequence(s), and/or antibody(s), e.g., materials useful for the diagnosis, prognosis, prophylaxis and/or treatment of neoplasias of tissues such as those set forth in Table I is provided. The article of manufacture typically comprises at least one container and at least one label. Suitable containers include, for example, bottles, vials, syringes, and test tubes. The containers can be formed from a variety of materials such as glass or plastic. The container can hold amino acid sequence(s), small molecule(s), nucleic acid sequence(s), and/or antibody(s), in one embodiment the container holds a polynucleotide for use in examining the mRNA expression profile of a cell,. together with reagents used for this purpose.

The container can alternatively hold a composition which is effective for treating, diagnosis, prognosing or prophylaxing a condition and can have a sterile access port (for example the container can be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle). The active agents in the composition can be an antibody capable of specifically binding 191P4D12(b) and modulating the function of 191P4D12(b).

The label can be on or associated with the container. A label a can be on a container when letters, numbers or other characters forming the label are molded or etched into the container itself; a label can be associated with a container when it is present within a receptacle or carrier that also holds the container, e.g., as a package insert. The label can indicate that the composition is used for diagnosing, treating, prophylaxing or prognosing a condition, such as a neoplasia of a tissue set forth in Table I. The article of manufacture can further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution and/ordextrose solution. It can further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, stirrers, needles, syringes, and/or package inserts with indications and/or instructions for use.

EXAMPLES:

Various aspects of the invention are further described and illustrated by way of the several examples that follow, none of which are intended to limit the scope of the invention.

Example 1: SSH-Generated Isolation of cDNA Fragment of the 191P4D12(b) Gene

To isolate genes that are over-expressed in prostate cancer we used the Suppression Subtractive Hybridization (SSH) procedure using cDNA derived from prostate cancer tissues. The 191P4D12(b) SSH cDNA sequence was derived from bladder tumor minus cDNAs derived from a pool of 9 normal tissues. The 191P4D12(b) cDNA was identified as highly expressed in the bladder cancer.

Materials and Methods

Human Tissues:

The patient cancer and normal tissues were purchased from different sources such as the NDRI (Philadelphia, PA). mRNA for some normal tissues were purchased from Clontech, Palo Alto, CA.

RNA Isolation:

Tissues were homogenized in Trizol reagent (Life Technologies, Gibco BRL) using 10 ml/ g tissue isolate total RNA. Poly A RNA was purified from total RNA using Qiagen's Oligotex mRNA Mini and Midi kits. Total and mRNA were quantified by spectrophotometric analysis (O.D. 260/280 nm) and analyzed by gel electrophoresis.

Oligonucleotides:

The following HPLC purified oligonucleotides were used.

DPNCDN (cDNA synthesis primer):

5'TTTT**GATC**AAGCTT$_{30}$3' (SEQ ID NO: 48)

Adaptor 1:

5'CTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAG3' (SEQ ID NO: 49)

3'GGCCCGTC**CTAG**5' (SEQ ID NO: 50)

Adaptor 2:

5'GTAATACGACTCACTATAGGGCAGCGTGGTCGCGGCCGAG3' (SEQ ID NO: 51)

3'CGGCTC**CTAG**5' (SEQ ID NO: 52)

PCR primer 1:

5'CTAATACGACTCACTATAGGGC3' (SEQ ID NO: 53)

Nested primer (NP)1:

5'TCGAGCGGCCGCCCGGGCAG**GA**3' (SEQ ID NO: 54)

Nested primer (NP)2:

5'AGCGTGGTCGCGGCCGAG**GA**3' (SEQ ID NO: 55)

Suppression Subtractive Hybridization:

Suppression Subtractive Hybridization (SSH) was used to identify cDNAs corresponding to genes that may be differentially expressed in bladder cancer. The SSH reaction utilized cDNA from bladder cancer and normal tissues.

The gene 191P4D12(b) sequence was derived from bladder cancer minus normal tissue cDNA subtraction. The SSH DNA sequence (Figure 1) was identified.

The cDNA derived from of pool of normal tissues was used as the source of the "driver" cDNA, while the cDNA from bladder cancer was used as the source of the "tester" cDNA. Double stranded cDNAs corresponding to tester and driver cDNAs were synthesized from 2 μg of poly(A)$^+$ RNA isolated from the relevant xenograft tissue, as described above, using CLONTECH's PCR-Select cDNA Subtraction Kit and 1 ng of oligonucleotide DPNCDN as primer. First- and second-strand synthesis were carried out as described in the Kit's user manual protocol (CLONTECH Protocol No. PT1117-1, Catalog No. K1804-1). The resulting cDNA was digested with Dpn II for 3 hrs at 37°C. Digested cDNA was extracted with phenol/chloroform (1:1) and ethanol precipitated.

Driver cDNA was generated by combining in a 1:1 ratio Dpn II digested cDNA from the relevant tissue source (see above) with a mix of digested cDNAs derived from the nine normal tissues: stomach, skeletal muscle, lung, brain, liver, kidney, pancreas, small intestine, and heart.

Tester cDNA was generated by diluting 1 μl of Dpn II digested cDNA from the relevant tissue source (see above) (400 ng) in 5 μl of water. The diluted cDNA (2 μl, 160 ng) was then ligated to 2 μl of Adaptor 1 and Adaptor 2 (10 μM), in separate ligation reactions, in a total volume of 10 μl at 16°C overnight, using 400 u of T4 DNA ligase (CLONTECH). Ligation was terminated with 1 μl of 0.2 M EDTA and heating at 72°C for 5 min.

The first hybridization was performed by adding 1.5 μl (600 ng) of driver cDNA to each of two tubes containing 1.5 μl (20 ng) Adaptor 1- and Adaptor 2- ligated tester cDNA. In a final volume of 4 μl, the samples were overlaid with mineral oil, denatured in an MJ Research thermal cycler at 98°C for 1.5 minutes, and then were allowed to hybridize for 8 hrs at 68°C. The two hybridizations were then mixed together with an additional 1 μl of fresh denatured driver cDNA and were allowed to hybridize overnight at 68°C. The second hybridization was then diluted in 200 μl of 20 mM Hepes, pH 8.3, 50 mM NaCl, 0.2 mM EDTA, heated at 70°C for 7 min. and stored at -20°C.

PCR Amplification, Cloning and Sequencing of Gene Fragments Generated from SSH:

To amplify gene fragments resulting from SSH reactions, two PCR amplifications were performed. In the primary PCR reaction 1 µl of the diluted final hybridization mix was added to 1 µl of PCR primer 1 (10 µM), 0.5 µl dNTP mix (10 µM), 2.5 µl 10 x reaction buffer (CLONTECH) and 0.5 µl 50 x Advantage cDNA polymerase Mix (CLONTECH) in a final volume of 25 µl. PCR 1 was conducted using the following conditions: 75°C for 5 min., 94°C for 25 sec., then 27 cycles of 94°C for 10 sec, 66°C for 30 sec, 72°C for 1.5 min. Five separate primary PCR reactions were performed for each experiment. The products were pooled and diluted 1:10 with water. For the secondary PCR reaction, 1 µl from the pooled and diluted primary PCR reaction was added to the same reaction mix as used for PCR 1, except that primers NP1 and NP2 (10 µM) were used instead of PCR primer 1. PCR 2 was performed using 10-12 cycles of 94°C for 10 sec, 68°C for 30 sec, and 72°C for 1.5 minutes. The PCR products were analyzed using 2% agarose gel electrophoresis.

The PCR products were inserted into pCR2.1 using the T/A vector cloning kit (Invitrogen). Transformed *E. coli* were subjected to blue/white and ampicillin selection. White colonies were picked and arrayed into 96 well plates and were grown in liquid culture overnight. To identify inserts, PCR amplification was performed on 1 µl of bacterial culture using the conditions of PCR1 and NP1 and NP2 as primers. PCR products were analyzed using 2% agarose gel electrophoresis.

Bacterial clones were stored in 20% glycerol in a 96 well format. Plasmid DNA was prepared, sequenced, and subjected to nucleic acid homology searches of the GenBank, dBest, and NCI-CGAP databases.

RT-PCR Expression Analysis:

First strand cDNAs can be generated from 1 µg of mRNA with oligo (dT)12-18 priming using the Gibco-BRL Superscript Preamplification system. The manufacturer's protocol was used which included an incubation for 50 min at 42°C with reverse transcriptase followed by RNAse H treatment at 37°C for 20 min. After completing the reaction, the volume can be increased to 200 µl with water prior to normalization. First strand cDNAs from 16 different normal human tissues can be obtained from Clontech.

Normalization of the first strand cDNAs from multiple tissues was performed by using the primers 5'atatcgccgcgctcgtcgtcgacaa3' (SEQ ID NO: 56) and 5'agccacacgcagctcattgtagaagg 3' (SEQ ID NO: 57) to amplify β-actin. First strand cDNA (5 µl) were amplified in a total volume of 50 µl containing 0.4 µM primers, 0.2 µM each dNTPs, 1XPCR buffer (Clontech, 10 mM Tris-HCL, 1.5 mM $MgCl_2$, 50 mM KCl, pH8.3) and 1X Klentaq DNA polymerase (Clontech). Five µl of the PCR reaction can be removed at 18, 20, and 22 cycles and used for agarose gel electrophoresis. PCR was performed using an MJ Research thermal cycler under the following conditions: Initial denaturation can be at 94°C for 15 sec, followed by a 18, 20, and 22 cycles of 94°C for 15, 65°C for 2 min, 72°C for 5 sec. A final extension at 72°C was carried out for 2 min. After agarose gel electrophoresis, the band intensities of the 283 b.p. β-actin bands from multiple tissues were compared by visual inspection. Dilution factors for the first strand cDNAs were calculated to result in equal β-actin band intensities in all tissues after 22 cycles of PCR. Three rounds of normalization can be required to achieve equal band intensities in all tissues after 22 cycles of PCR.

To determine expression levels of the 191P4D12(b) gene, 5 µl of normalized first strand cDNA were analyzed by PCR using 26, and 30 cycles of amplification. Semi-quantitative expression analysis can be achieved by comparing the PCR products at cycle numbers that give light band intensities. The primers used for RT-PCR were designed using the 191P4D12(b) SSH sequence and are listed below:

191P4D12(b).1
5'- GGCTGGAGTTCAATGAGGTTTATTT - 3' (SEQ ID NO: 58)

191P4D12(b).2
5'- TCCAGCAGATTTCAGACTAAGAAGA - 3' (SEQ ID NO: 59)

A typical RT-PCR expression analysis is shown in Figure 14. First strand cDNA was prepared from vital pool 1 (liver, lung and kidney), vital pool 2 (pancreas, colon and stomach), normal kidney, prostate cancer pool, bladder cancer pool, colon cancer pool, lung cancer pool, breast cancer pool and cancer metastasis pool. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 191P4D12(b), was performed at 26 and 30 cycles of amplification. Results show strong expression of 191P4D12(b) in bladder cancer pool. Expression of 191P4D12(b) was also detected in prostate cancer pool, colon cancer pool, lung cancer pool, breast cancer pool and cancer metastasis pool but very weakly in vital pool 1 and vital pool 2.

Example 2: Isolation of Full Length 191P4D12(b) Encoding cDNA

The 191P4D12(b) SSH cDNA sequence was derived from a subtraction consisting of bladder cancer minus a mixture of 9 normal tissues: stomach, skeletal muscle, lung, brain, liver, kidney, pancreas, small intestine and heart. The SSH cDNA sequence of 223 bp (Figure 1) was designated 191P4D12(b).

191P4D12(b) v.1 (clone 1A1) of 3464 bp was cloned from bladder cancer cDNA library, revealing an ORF of 510 amino acids (Figure 2 and Figure 3). Other variants of 191P4D12(b) were also identified and these are listed in Figures 2 and 3.

191P4D12(b) v.1, v.2, v.10, v.11, and v.12 proteins are 510 amino acids in length and differ from each other by one amino acid as shown in Figure 11. 191P4D12(b) v.3, v.4, v.5, and v.8 code for the same protein as 191P4D12(b) v.1. 191P4D12(b) v.6 and v.7 are splice variants and code for proteins of 295 and 485 amino acids, respectively. 191P4D12(b) v.13 clone 9C was cloned from bladder cancer cDNA and has one amino acid insertion at position 334 compared to 191P4D12(b) v.1. 191P4D12(b) v.9 clone BCP1 is a splice variant of 191P4D12(b) v.1 and was cloned from a bladder cancer cDNA library. 191P4D12(b) v.14 is a SNP variant and differs from 191P4D12(b) v.9 by one amino acid as shown in Figure 2.

191P4D12(b) v.1 shows 99% identity over 2744 to the Ig superfamily receptor LNIR (nectin-4), accession number NM_030916. 191P4D12(b) v.9 protein is 100% identical to clone AF218028 with function of inhibiting cancer cell growth.

Example 3: Chromosomal Mapping of 191P4D12(b)

Chromosomal localization can implicate genes in disease pathogenesis. Several chromosome mapping approaches are available including fluorescent *in situ* hybridization (FISH), human/hamster radiation hybrid (RH) panels (Walter et al., 1994; Nature Genetics 7:22; Research Genetics, Huntsville Al), human-rodent somatic cell hybrid panels such as is available from the Cornell Institute (Camden, New Jersey), and genomic viewers utilizing BLAST homologies to sequenced and mapped genomic clones (NCBI, Bethesda, Maryland).

191P4D12(b) maps to chromosome 1q22-q23.2 using 191P4D12(b) sequence and the NCBI BLAST tool located on the World Wide Web.

Example 4: Expression Analysis of 191P4D12(b) in Normal Tissues and Patient Specimens

Expression analysis by RT-PCR demonstrated that 191P4D12(b) is strongly expressed in bladder cancer patient specimens (Figure 14). First strand cDNA was prepared from (A) vital pool 1 (liver, lung and kidney), vital pool 2 (pancreas, colon and stomach), normal kidney, prostate cancer pool, bladder cancer pool, colon cancer pool, lung cancer pool, breast cancer pool and cancer metastasis pool; (B) prostate cancer metastasis to lymph node, prostate cancer pool, bladder cancer pool, kidney cancer pool, colon cancer pool, lung cancer pool, ovary cancer pool, breast cancer pool, cancer metastasis pool, pancreas cancer pool, and LAPC prostate xenograft pool. Normalization was performed by PCR using primers to actin and GAPDH. Semi-quantitative PCR, using primers to 191P4D12(b), was performed at 26 and 30 cycles of amplification. In (A), results show strong expression of 191P4D12(b) in bladder cancer pool. Expression of 191P4D12(b) was also detected in prostate cancer pool, colon cancer pool, lung cancer pool, breast cancer pool and cancer metastasis pool but very weakly

in vital pool 1 and vital pool 2. In (B), results show strong expression of 191P4D12(b) in prostate, bladder, kidney, colon, lung, ovary, breast, cancer metastasis, and pancreas cancer specimens.

Northern blot analysis of 251P5G2 is a technique known to those skilled in the art to detect 251P5G2 protein production. Northern blotting detects relative levels of mRNA expressed from a 251P5G2 gene. Specific mRNA is measured using a nucleic acid hybridization technique and the signal is detected on an autoradiogram. The stronger the signal, the more abundant is the mRNA. For 251P5G2 genes that produce mRNA that contains an open reading frame flanked by a good Kozak translation initiation site and a stop codon, in the vast majority of cases the synthesized mRNA is expressed as a protein.

The level of expression of the 251P5G2 gene is determined in various normal tissues and in various tumor tissues and tumor cell lines using the technique of Northern blotting, which detects production of messenger RNA. It is well known in the art that the production of messenger RNA, that encodes the protein, is a necessary step in the production of the protein itself. Thus, detection of high levels of messenger RNA by, for example, Northern blot, is a way of determining that the protein itself is produced. The Northern blot technique is used as a routine procedure because it does not require the time delays (as compared to Western blotting, immunoblotting or immunohistochemistry) involved in isolating or synthesizing the protein, preparing an immunological composition of the protein, eliciting a humoral immune response, harvesting the antibodies, and verifying the specificity thereof.

The Kozak consensus sequence for translation initiation CCACC*ATG*G, where the ATG start codon is noted, is the sequence with the highest established probability of initiating translation. This was confirmed by Peri and Pandey *Trends in Genetics* (2001) 17: 685-687. The conclusion is consistent with the general knowledge in the art that, with rare exceptions, expression of an mRNA is predictive of expression of its encoded protein. This is particularly true for mRNA with an open reading frame and a Kozak consensus sequence for translation initiation.

It is understood in the art that the absolute levels of messenger RNA present and the amounts of protein produced do not always provide a 1:1 correlation. In those instances where the Northern blot has shown mRNA to be present, it is almost always possible to detect the presence of the corresponding protein in the tissue which provided a positive result in the Northern blot. The levels of the protein compared to the levels of the mRNA may be differential, but generally, cells that exhibit detectable mRNA also exhibit detectable corresponding protein and *vice versa*. This is particularly true where the mRNA has an open reading frame and a good Kozak sequence (See, Peri and Pandey, *supra.)*.

Occasionally those skilled in the art encounter a rare occurrence where there is no detectable protein in the presence of corresponding mRNA. (See, Fu, L., *et al.*, Embo. Journal, 15:4392-4401 (1996)). In many cases, a reported lack of protein expression is due to technical limitations of the protein detection assay. These limitations are readily known to those skilled in the art. These limitations include but are not limited to, available antibodies that only detect denatured protein and not native protein present in a cell and unstable proteins with very short half-life. Short-lived proteins are still functional and have been previously described to induce tumor formation. (See, e.g., Reinstein, *et al.*, Oncogene, 19: 5944-5950). In such situations, when more sensitive detection techniques are performed and/or other antibodies are generated, protein expression is detected. When studies fail to take these principles into account, they are likely to report artifactually lowered correlations of mRNA to protein. Outside of these rare exceptions the use of Northern blot analysis is recognized to those skilled in the art to be predictive and indicative of the detection of 251P5G2 protein production.

Extensive expression of 191P4D12(b) in normal tissues is shown in Figure 15. Two multiple tissue northern blots (Clontech) both with 2 ug of mRNA/lane were probed with the 191P4D12(b) sequence. Size standards in kilobases (kb) are indicated on the side. Results show expression of an approximately 4kb transcript in placenta and very weakly in prostate but not in any other normal tissue tested. A smaller 191P4D12(b) transcript of approximately 2.5kb was detected in heart and skeletal muscle.

Expression of 191P4D12(b) in bladder cancer patient specimens and human normal tissues is shown in Figure 16. RNA was extracted from a pool of 3 bladder cancer patient specimens, as well as from normal prostate (NP), normal bladder (NB), normal kidney (NK), normal colon (NC), normal lung (NL), normal breast (NBr), normal ovary (NO), and normal pancreas (NPa). Northern blot with 10 ug of total RNA/lane was probed with 191P4D12(b) SSH sequence. Size standards in kilobases (kb) are indicated on the side. The 191P4D12(b) transcript was detected in the bladder cancer specimens, but not in the normal tissues tested.

Analysis of individual bladder cancer patient specimens is depicted in Figure 17. RNA was extracted from bladder cancer cell lines (CL), normal bladder (N), and bladder cancer patient tumors (T). Northern blots with 10 ug of total RNA were probed with the 191P4D12(b) SSH fragment. Size standards in kilobases are on the side. Results show expression of the approximately 4kb 191P4D12(b) transcript in the bladder tumor tissues but not in normal bladder. A smaller transcript was detected in the HT1197 cell line but not in the other cancer cell lines tested.

Expression of 191P4D12(b) was also detected in prostate cancer xenograft tissues (Figure 18). RNA was extracted from normal prostate, and from the prostate cancer xenografts LAPC-4AD, LAPC-4AI, LAPC-9AD, and LAPC-9AI. Northern blots with 10 ug of total RNA were probed with the 191P4D12(b) SSH fragment. Size standards in kilobases are on the side. Results show expression of the approximately 4kb 191P4D12(b) transcript in all the LAPC xenograft tissues but not in normal prostate.

Figure 19 shows expression of 191P4D12(b) in cervical cancer patient specimens. RNA was extracted from normal cervix, Hela cancer cell line, and 3 cervix cancer patient tumors (T). Northern blots with 10 ug of total RNA were probed with the 191P4D12(b) SSH fragment. Size standards in kilobases are on the side. Results show expression of the approximately 4kb 191P4D12(b) transcript in 2 out of 3 cervix tumors tested but not in normal cervix nor in the Hela cell line.

191P4D12(b) was also expressed in lung cancer patient specimens (Figure 20). RNA was extracted from lung cancer cell lines (CL), normal lung (N), bladder cancer patient tumors (T), and normal adjacent tissue (Nat). Northern blots with 10 ug of total RNA were probed with the 191P4D12(b). Size standards in kilobases are on the side. Results show expression of the approximately 4kb 191P4D12(b) transcript in the lung tumor tissues but not in normal lung nor in the cell lines tested.

191P4D12(b) expression was tested in a panel of individual patient cancer specimens (Figure 21). First strand cDNA was prepared from a panel of lung cancer specimens (A), bladder cancer specimens (B), prostate cancer specimens (C), colon cancer specimens (D), uterus cancer specimens (E), and cervix cancer specimens (F). Normalization was performed by PCR using primers to actin. Semi-quantitative PCR, using primers to 191P4D12(b) SSH fragment, was performed at 26 and 30 cycles of amplification. Expression level was recorded as 0 = no expression detected; 1 = weak expression, 2 = moderate expression; 3 = strong expression. Results show expression of 191P4D12(b) in 97% of the 31 lung cancer patient specimens tested, 94% of 18 bladder cancer patient specimens, 100% of 20 prostate cancer patient specimens, 100% of 22 colon cancer patient specimens, 100% of 12 uterus cancer patient specimens, and 100% of 14 cervix cancer patient specimens tested.

The restricted expression of 191P4D12(b) in normal tissues and the expression detected in cancer patient specimens suggest that 191P4D12(b) is a potential therapeutic target and a diagnostic marker for human cancers.

Example 5: Transcript Variants of 191P4D12(b)

Transcript variants are variants of mature mRNA from the same gene which arise by alternative transcription or alternative splicing. Alternative transcripts are transcripts from the same gene but start transcription at different points. Splice variants are mRNA variants spliced differently from the same transcript. In eukaryotes, when a multi-exon gene is transcribed from genomic DNA, the initial RNA is spliced to produce functional mRNA, which has only exons and is used for

translation into an amino acid sequence. Accordingly, a given gene can have zero to many alternative transcripts and each transcript can have zero to many splice variants. Each transcript variant has a unique exon makeup, and can have different coding and/or non-coding (5' or 3' end) portions, from the original transcript. Transcript variants can code for similar or different proteins with the same or a similar function or can encode proteins with different functions, and can be expressed in the same tissue at the same time, or in different tissues at the same time, or in the same tissue at different times, or in different tissues at different times. Proteins encoded by transcript variants can have similar or different cellular or extracellular localizations, e.g., secreted versus intracellular.

Transcript variants are identified by a variety of art-accepted methods. For example, alternative transcripts and splice variants are identified by full-length cloning experiment, or by use of full-length transcript and EST sequences. First, all human ESTs were grouped into clusters which show direct or indirect identity with each other. Second, ESTs in the same cluster were further grouped into sub-clusters and assembled into a consensus sequence. The original gene sequence is compared to the consensus sequence(s) or other full-length sequences. Each consensus sequence is a potential splice variant for that gene. Even when a variant is identified that is not a full-length clone, that portion of the variant is very useful for antigen generation and for further cloning of the full-length splice variant, using techniques known in the art.

Moreover, computer programs are available in the art that identify transcript variants based on genomic sequences. Genomic-based transcript variant identification programs include FgenesH (A. Salamov and V. Solovyev, "Ab initio gene finding in Drosophila genomic DNA," Genome Research. 2000 April;10(4):516-22); Grail and GenScan. For a general discussion of splice variant identification protocols see., e.g., Southan, C., A genomic perspective on human proteases, FEBS Lett. 2001 Jun 8; 498(2-3):214-8; de Souza, S.J., *et al.*, Identification of human chromosome 22 transcribed sequences with ORF expressed sequence tags, Proc. Natl Acad Sci U S A. 2000 Nov 7; 97(23):12690-3.

To further confirm the parameters of a transcript variant, a variety of techniques are available in the art, such as full-length cloning, proteomic validation, PCR-based validation, and 5' RACE validation, etc. (see e.g., Proteomic Validation: Brennan, S.O., *et al.*, Albumin banks peninsula: a new termination variant characterized by electrospray mass spectrometry, Biochem Biophys Acta. 1999 Aug 17;1433(1-2):321-6; Ferranti P, *et al.*, Differential splicing of pre-messenger RNA produces multiple forms of mature caprine alpha(s1)-casein, Eur J Biochem. 1997 Oct 1;249(1):1-7. For PCR-based Validation: Wellmann S, *et al.*, Specific reverse transcription-PCR quantification of vascular endothelial growth factor (VEGF) splice variants by LightCycler technology, Clin Chem. 2001 Apr;47(4):654-60; Jia, H.P., *et al.*, Discovery of new human beta-defensins using a genomics-based approach, Gene. 2001 Jan 24; 263(1-2):211-8. For PCR-based and 5' RACE Validation: Brigle, K.E., *et al.*, Organization of the murine reduced folate carrier gene and identification of variant splice forms, Biochem Biophys Acta. 1997 Aug 7; 1353(2): 191-8).

It is known in the art that genomic regions are modulated in cancers. When the genomic region to which a gene maps is modulated in a particular cancer, the alternative transcripts or splice variants of the gene are modulated as well. Disclosed herein is that 191P4D12(b) has a particular expression profile related to cancer. Alternative transcripts and splice variants of 191P4D12(b) may also be involved in cancers in the same or different tissues, thus serving as tumor-associated markers/antigens.

Using the full-length gene and EST sequences, four additional transcript variants were identified, designated as 191P4D12(b) v.6, v.7, v.8 and v.9 as shown in Figure 12. The boundaries of exons in the original transcript, 191P4D12(b) v.1 were shown in Table LI. Compared with 191P4D12(b) v.1, variant v.6 spliced out 202-321 from the first exon of v.1 while variant v.8 spliced out 63 bases from the last exon of v.1. Variant v.7 spliced out exon 8 of v.1. Variant 9 was part of the last exon of v.1. Theoretically, each different combination of exons in spatial order, e.g. exons 2, 3, 5, 7 and 9 of v.1, is a potential splice variant.

Tables LII (a) – (d) through LV (a) – (d) are set forth on a variant-by-variant bases. Tables LII (a) – (d) shows nucleotide sequence of the transcript variants. Tables LIII (a) – (d) shows the alignment of the transcript variant with nucleic acid sequence of 191P4D12(b) v.1. Tables LIV (a) – (d) lays out amino acid translation of the transcript variant for the identified reading frame orientation. Tables LV (a) – (d) displays alignments of the amino acid sequence encoded by the splice variant with that of 191P4D12(b) v.1.

Example 6: Single Nucleotide Polymorphisms of 191P4D12(b)

A Single Nucleotide Polymorphism (SNP) is a single base pair variation in a nucleotide sequence at a specific location. At any given point of the genome, there are four possible nucleotide base pairs: A/T, C/G, G/C and T/A. Genotype refers to the specific base pair sequence of one or more locations in the genome of an individual. Haplotype refers to the base pair sequence of more than one location on the same DNA molecule (or the same chromosome in higher organisms), often in the context of one gene or in the context of several tightly linked genes. SNP that occurs on a cDNA is called cSNP. This cSNP may change amino acids of the protein encoded by the gene and thus change the functions of the protein. Some SNP cause inherited diseases; others contribute to quantitative variations in phenotype and reactions to environmental factors including diet and drugs among individuals. Therefore, SNP and/or combinations of alleles (called haplotypes) have many applications, including diagnosis of inherited diseases, determination of drug reactions and dosage, identification of genes responsible for diseases, and analysis of the genetic relationship between individuals (P. Nowotny, J. M. Kwon and A. M. Goate, " SNP analysis to dissect human traits," Curr. Opin. Neurobiol. 2001 Oct; 11(5):637-641; M. Pirmohamed and B. K. Park, "Genetic susceptibility to adverse drug reactions," Trends Pharmacol. Sci. 2001 Jun; 22(6):298-305; J. H. Riley, C. J. Allan, E. Lai and A. Roses, "The use of single nucleotide polymorphisms in the isolation of common disease genes," Pharmacogenomics. 2000 Feb; 1(1):39-47; R. Judson, J. C. Stephens and A. Windemuth, "The predictive power of haplotypes in clinical response," Pharmacogenomics. 2000 feb; 1(1):15-26).

SNP are identified by a variety of art-accepted methods (P. Bean, "The promising voyage of SNP target discovery," Am. Clin. Lab. 2001 Oct-Nov; 20(9):18-20; K. M. Weiss, "In search of human variation," Genome Res. 1998 Jul; 8(7):691-697; M. M. She, "Enabling large-scale pharmacogenetic studies by high-throughput mutation detection and genotyping technologies," Clin. Chem. 2001 Feb; 47(2):164-172). For example, SNP can be identified by sequencing DNA fragments that show polymorphism by gel-based methods such as restriction fragment length polymorphism (RFLP) and denaturing gradient gel electrophoresis (DGGE). They can also be discovered by direct sequencing of DNA samples pooled from different individuals or by comparing sequences from different DNA samples. With the rapid accumulation of sequence data in public and private databases, one can discover SNP by comparing sequences using computer programs (Z. Gu, L. Hillier and P. Y. Kwok, "Single nucleotide polymorphism hunting in cyberspace," Hum. Mutat. 1998; 12(4):221-225). SNP can be verified and genotype or haplotype of an individual can be determined by a variety of methods including direct sequencing and high throughput microarrays (P. Y. Kwok, "Methods for genotyping single nucleotide polymorphisms," Annu. Rev. Genomics Hum. Genet. 2001; 2:235-258; M. Kokoris, K. Dix, K. Moynihan, J. Mathis, B. Erwin, P. Grass, B. Hines and A. Duesterhoeft, "High-throughput SNP genotyping with the Masscode system," Mol. Diagn. 2000 Dec; 5(4):329-340).
Using the methods described above, seven SNP and one insertion/deletion of three bases were identified in the original transcript, 191P4D12(b) v.1, at positions 420 (T/C), 2184 (G/T), 2341 (G/A), 2688 (C/A), 367 (A/G), 699 (C/A), 1590 (C/T), and insertion of GCA in between 1262 and 1263I. The transcripts or proteins with alternative allele were designated as variant 191P4D12(b) v.2 through v.5 and v.10 through v.13, as shown in Figure 10. Figure 11 shows the schematic alignment of protein variants, corresponding to nucleotide variants. Nucleotide variants that code for the same amino acid sequence as v.1 are not shown in Figure 11. These alleles of the SNP, though shown separately here, can occur in different combinations (haplotypes) and in any one of the transcript variants (such as 191P4D12(b) v.9) that contains the site of the

SNP. The SNP at 2688 of v.1 occurs also in transcript variant v.9 and contributed to one codon change of v.9 at amino acid 64 from Ala to Asp (Figure 11).

Example 7: Production of Recombinant 191P4D12(b) in Prokaryotic Systems

To express recombinant 191P4D12(b) and 191P4D12(b) variants in prokaryotic cells, the full or partial length 191P4D12(b) and 191P4D12(b) variant cDNA sequences are cloned into any one of a variety of expression vectors known in the art. One or more of the following regions of 191P4D12(b) variants are expressed: the full length sequence presented in Figures 2 and 3, or any 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous amino acids from 191P4D12(b), variants, or analogs thereof.

A. *In vitro* transcription and translation constructs:

pCRII: To generate 191P4D12(b) sense and anti-sense RNA probes for RNA *in situ* investigations, pCRII constructs (Invitrogen, Carlsbad CA) are generated encoding either all or fragments of the 191P4D12(b) cDNA. The pCRII vector has Sp6 and T7 promoters flanking the insert to drive the transcription of 191P4D12(b) RNA for use as probes in RNA *in situ* hybridization experiments. These probes are used to analyze the cell and tissue expression of 191P4D12(b) at the RNA level. Transcribed 191P4D12(b) RNA representing the cDNA amino acid coding region of the 191P4D12(b) gene is used in *in vitro* translation systems such as the TnT™ Coupled Reticulolysate System (Promega, Corp., Madison, WI) to synthesize 191P4D12(b) protein.

B. Bacterial Constructs:

pGEX Constructs: To generate recombinant 191P4D12(b) proteins in bacteria that are fused to the Glutathione S-transferase (GST) protein, all or parts of the 191P4D12(b) cDNA protein coding sequence are cloned into the pGEX family of GST-fusion vectors (Amersham Pharmacia Biotech, Piscataway, NJ). These constructs allow controlled expression of recombinant 191P4D12(b) protein sequences with GST fused at the amino-terminus and a six histidine epitope (6X His) at the carboxyl-terminus. The GST and 6X His tags permit purification of the recombinant fusion protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-GST and anti-His antibodies. The 6X His tag is generated by adding 6 histidine codons to the cloning primer at the 3' end, e.g., of the open reading frame (ORF). A proteolytic cleavage site, such as the PreScission™ recognition site in pGEX-6P-1, may be employed such that it permits cleavage of the GST tag from 191P4D12(b)-related protein. The ampicillin resistance gene and pBR322 origin permits selection and maintenance of the pGEX plasmids in *E. coli*.

pMAL Constructs: To generate, in bacteria, recombinant 191P4D12(b) proteins that are fused to maltose-binding protein (MBP), all or parts of the 191P4D12(b) cDNA protein coding sequence are fused to the MBP gene by cloning into the pMAL-c2X and pMAL-p2X vectors (New England Biolabs, Beverly, MA). These constructs allow controlled expression of recombinant 191P4D12(b) protein sequences with MBP fused at the amino-terminus and a 6X His epitope tag at the carboxyl-terminus. The MBP and 6X His tags permit purification of the recombinant protein from induced bacteria with the appropriate affinity matrix and allow recognition of the fusion protein with anti-MBP and anti-His antibodies. The 6X His epitope tag is generated by adding 6 histidine codons to the 3' cloning primer. A Factor Xa recognition site permits cleavage of the pMAL tag from 191P4D12(b). The pMAL-c2X and pMAL-p2X vectors are optimized to express the recombinant protein in the cytoplasm or periplasm respectively. Periplasm expression enhances folding of proteins with disulfide bonds.

pET Constructs: To express 191P4D12(b) in bacterial cells, all or parts of the 191P4D12(b) cDNA protein coding sequence are cloned into the pET family of vectors (Novagen, Madison, WI). These vectors allow tightly controlled expression of recombinant 191P4D12(b) protein in bacteria with and without fusion to proteins that enhance solubility, such as NusA and thioredoxin (Trx), and epitope tags, such as 6X His and S-Tag ™ that aid purification and detection of the

recombinant protein. For example, constructs are made utilizing pET NusA fusion system 43.1 such that regions of the 191P4D12(b) protein are expressed as amino-terminal fusions to NusA.

C. Yeast Constructs:

pESC Constructs: To express 191P4D12(b) in the yeast species *Saccharomyces cerevisiae* for generation of recombinant protein and functional studies, all or parts of the 191P4D12(b) cDNA protein coding sequence are cloned into the pESC family of vectors each of which contain 1 of 4 selectable markers, HIS3, TRP1, LEU2, and URA3 (Stratagene, La Jolla, CA). These vectors allow controlled expression from the same plasmid of up to 2 different genes or cloned sequences containing either Flag™ or Myc epitope tags in the same yeast cell. This system is useful to confirm protein-protein interactions of 191P4D12(b). In addition, expression in yeast yields similar post-translational modifications, such as glycosylations and phosphorylations, that are found when expressed in eukaryotic cells.

pESP Constructs: To express 191P4D12(b) in the yeast species *Saccharomyces pombe*, all or parts of the 191P4D12(b) cDNA protein coding sequence are cloned into the pESP family of vectors. These vectors allow controlled high level of expression of a 191P4D12(b) protein sequence that is fused at either the amino terminus or at the carboxyl terminus to GST which aids purification of the recombinant protein. A Flag™ epitope tag allows detection of the recombinant protein with anti-Flag™ antibody.

Example 8: Production of Recombinant 191P4D12(b) in Higher Eukaryotic Systems

A. Mammalian Constructs:

To express recombinant 191P4D12(b) in eukaryotic cells, the full or partial length 191P4D12(b) cDNA sequences can be cloned into any one of a variety of expression vectors known in the art. One or more of the following regions of 191P4D12(b) are expressed in these constructs, amino acids 1 to 510, or any 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous amino acids from 191P4D12(b) v.1, v.2, v.10, v.11, v.12; amino acids 1 to 511, or any 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous amino acids from 191P4D12(b) v.13, variants, or analogs thereof.

The constructs can be transfected into any one of a wide variety of mammalian cells such as 293T cells. Transfected 293T cell lysates can be probed with the anti-191P4D12(b) polyclonal serum, described herein.

pcDNA4/HisMax Constructs: To express 191P4D12(b) in mammalian cells, a 191P4D12(b) ORF, or portions thereof, of 191P4D12(b) were cloned into pcDNA4/HisMax Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter and the SP16 translational enhancer. The recombinant protein has Xpress™ and six histidine (6X His) epitopes fused to the amino-terminus. The pcDNA4/HisMax vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Zeocin resistance gene allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*.

pcDNA3.1/MycHis Constructs: To express 191P4D12(b) in mammalian cells, a 191P4D12(b) ORF, or portions thereof, of 191P4D12(b) with a consensus Kozak translation initiation site was cloned into pcDNA3.1/MycHis Version A (Invitrogen, Carlsbad, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the myc epitope and 6X His epitope fused to the carboxyl-terminus. The pcDNA3.1/MycHis vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability, along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene can be used, as it allows for selection of mammalian cells expressing the protein and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*. Figure 22

shows expression of 191P4D12(b).pcDNA3.1/MycHis following vector transfection into 293T cells. 293T cells were transfected with either 191P4D12(b).pcDNA3.1/mychis or pcDNA3.1/mychis vector control. Forty hours later cell lysates were collected. Samples were run on an SDS-PAGE acrylamide gel, blotted and stained with anti-his antibody. The blot was developed using the ECL chemiluminescence kit and visualized by autoradiography. Results show expression of 191P4D12(b) in the lysates of 191P4D12(b).pcDNA3.1/mychis transfected cells (Lane 3), but not from the control pcDNA3.1/mychis (Lane 4).

pcDNA3.1/CT-GFP-TOPO Construct: To express 191P4D12(b) in mammalian cells and to allow detection of the recombinant proteins using fluorescence, a 191P4D12(b) ORF, or portions thereof, with a consensus Kozak translation initiation site are cloned into pcDNA3.1/CT-GFP-TOPO (Invitrogen, CA). Protein expression is driven from the cytomegalovirus (CMV) promoter. The recombinant proteins have the Green Fluorescent Protein (GFP) fused to the carboxyl-terminus facilitating non-invasive, *in vivo* detection and cell biology studies. The pcDNA3.1CT-GFP-TOPO vector also contains the bovine growth hormone (BGH) polyadenylation signal and transcription termination sequence to enhance mRNA stability along with the SV40 origin for episomal replication and simple vector rescue in cell lines expressing the large T antigen. The Neomycin resistance gene allows for selection of mammalian cells that express the protein, and the ampicillin resistance gene and ColE1 origin permits selection and maintenance of the plasmid in *E. coli*. Additional constructs with an amino-terminal GFP fusion are made in pcDNA3.1/NT-GFP-TOPO spanning the entire length of a 191P4D12(b) protein.

PAPtag: A 191P4D12(b) ORF, or portions thereof, is cloned into pAPtag-5 (GenHunter Corp. Nashville, TN). This construct generates an alkaline phosphatase fusion at the carboxyl-terminus of a 191P4D12(b) protein while fusing the IgGκ signal sequence to the amino-terminus. Constructs are also generated in which alkaline phosphatase with an amino-terminal IgGκ signal sequence is fused to the amino-terminus of a 191P4D12(b) protein. The resulting recombinant 191P4D12(b) proteins are optimized for secretion into the media of transfected mammalian cells and can be used to identify proteins such as ligands or receptors that interact with 191P4D12(b) proteins. Protein expression is driven from the CMV promoter and the recombinant proteins also contain myc and 6X His epitopes fused at the carboxyl-terminus that facilitates detection and purification. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the recombinant protein and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

pTag5: A 191P4D12(b) v.1 extracellular domain was cloned into pTag-5 plasmid. This vector is similar to pAPtag but without the alkaline phosphatase fusion. This construct generates 191P4D12(b) protein with an amino-terminal IgGκ signal sequence and myc and 6X His epitope tags at the carboxyl-terminus that facilitate detection and affinity purification. The resulting recombinant 191P4D12(b) protein is optimized for secretion into the media of transfected mammalian cells, and is used as immunogen or ligand to identify proteins such as ligands or receptors that interact with the 191P4D12(b) proteins. Protein expression is driven from the CMV promoter. The Zeocin resistance gene present in the vector allows for selection of mammalian cells expressing the protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*. Figure 22 shows expression and secretion of the extracellular domain of 191P4D12(b) following 191P4D12(b).pTag5 vector transfection into 293T cells. 293T cells were transfected with 191P4D12(b) .pTag5. Forty hours later, cell lysate and supernatant were collected. Samples were run on an SDS-PAGE acrylamide gel, blotted and stained with anti-his antibody. The blot was developed using the ECL chemiluminescence kit and visualized by autoradiography. Results show expression from 191P4D12(b).pTag5 plasmid of 191P4D12(b) extracellular domain in the lysate (Lane 2) and secretion in the culture supernatant (Lane 1).

191P4D12(b) ORF, or portions thereof, is also cloned into pTag-5 plasmid.

PsecFc: A 191P4D12(b) ORF, or portions thereof, is also cloned into psecFc. The psecFc vector was assembled by cloning the human immunoglobulin G1 (IgG) Fc (hinge, CH2, CH3 regions) into pSecTag2 (Invitrogen, California). This

construct generates an IgG1 Fc fusion at the carboxyl-terminus of the 191P4D12(b) proteins, while fusing the IgGK signal sequence to N-terminus. 191P4D12(b) fusions utilizing the murine IgG1 Fc region are also used. The resulting recombinant 191P4D12(b) proteins are optimized for secretion into the media of transfected mammalian cells, and can be used as immunogens or to identify proteins such as ligands or receptors that interact with 191P4D12(b) protein. Protein expression is driven from the CMV promoter. The hygromycin resistance gene present in the vector allows for selection of mammalian cells that express the recombinant protein, and the ampicillin resistance gene permits selection of the plasmid in *E. coli*.

pSRα Constructs: To generate mammalian cell lines that express 191P4D12(b) constitutively, 191P4D12(b) ORF, or portions thereof, of 191P4D12(b) were cloned into pSRα constructs. Amphotropic and ecotropic retroviruses were generated by transfection of pSRα constructs into the 293T-10A1 packaging line or co-transfection of pSRα and a helper plasmid (containing deleted packaging sequences) into the 293 cells, respectively. The retrovirus is used to infect a variety of mammalian cell lines, resulting in the integration of the cloned gene, 191P4D12(b), into the host cell-lines. Protein expression is driven from a long terminal repeat (LTR). The Neomycin resistance gene present in the vector allows for selection of mammalian cells that express the protein, and the ampicillin resistance gene and ColE1 origin permit selection and maintenance of the plasmid in *E. coli*. The retroviral vectors can thereafter be used for infection and generation of various cell lines using, for example, PC3, NIH 3T3, TsuPr1, 293 or rat-1 cells.

Figure 23 shows stable expression of 191P4D12(b) following 191P4D12(b).pSRa transduction into 3T3 cells. 3T3 cells were transduced with the pSRa retroviral vector encoding the 191P4D12(b) gene. Following selection with neomycin, the cells were expanded and RNA was extracted. Northern blot with 10 ug of total RNA/lane was probed with the 191P4D12(b) SSH sequence. Size standards in kilobases (kb) are indicated on the side. Results show expression of the 191P4D12(b) transcript driven from the retroviral LTR, which migrates slower than the endogenous 4 kb 191P4D12(b) transcript detected in the positive control LAPC-4AD.

Additional pSRα constructs are made that fuse an epitope tag such as the FLAG™ tag to the carboxyl-terminus of 191P4D12(b) sequences to allow detection using anti-Flag antibodies. For example, the FLAG™ sequence 5' gat tac aag gat gac gac gat aag 3' (SEQ ID NO: 60) is added to cloning primer at the 3' end of the ORF. Additional pSRα constructs are made to produce both amino-terminal and carboxyl-terminal GFP and myc/6X His fusion proteins of the full-length 191P4D12(b) proteins.

Additional Viral Vectors: Additional constructs are made for viral-mediated delivery and expression of 191P4D12(b). High virus titer leading to high level expression of 191P4D12(b) is achieved in viral delivery systems such as adenoviral vectors and herpes amplicon vectors. A 191P4D12(b) coding sequences or fragments thereof are amplified by PCR and subcloned into the AdEasy shuttle vector (Stratagene). Recombination and virus packaging are performed according to the manufacturer's instructions to generate adenoviral vectors. Alternatively, 191P4D12(b) coding sequences or fragments thereof are cloned into the HSV-1 vector (Imgenex) to generate herpes viral vectors. The viral vectors are thereafter used for infection of various cell lines such as PC3, NIH 3T3, 293 or rat-1 cells.

Regulated Expression Systems: To control expression of 191P4D12(b) in mammalian cells, coding sequences of 191P4D12(b), or portions thereof, are cloned into regulated mammalian expression systems such as the T-Rex System (Invitrogen), the GeneSwitch System (Invitrogen) and the tightly-regulated Ecdysone System (Sratagene). These systems allow the study of the temporal and concentration dependent effects of recombinant 191P4D12(b). These vectors are thereafter used to control expression of 191P4D12(b) in various cell lines such as PC3, NIH 3T3, 293 or rat-1 cells.

B. Baculovirus Expression Systems

To generate recombinant 191P4D12(b) proteins in a baculovirus expression system, 191P4D12(b) ORF, or portions thereof, are cloned into the baculovirus transfer vector pBlueBac 4.5 (Invitrogen), which provides a His-tag at the N-terminus. Specifically, pBlueBac-191P4D12(b) is co-transfected with helper plasmid pBac-N-Blue (Invitrogen) into SF9

(*Spodoptera frugiperda*) insect cells to generate recombinant baculovirus (see Invitrogen instruction manual for details). Baculovirus is then collected from cell supernatant and purified by plaque assay.

Recombinant 191P4D12(b) protein is then generated by infection of HighFive insect cells (Invitrogen) with purified baculovirus. Recombinant 191P4D12(b) protein can be detected using anti-191P4D12(b) or anti-His-tag antibody. 191P4D12(b) protein can be purified and used in various cell-based assays or as immunogen to generate polyclonal and monoclonal antibodies specific for 191P4D12(b).

Example 9: Antigenicity Profiles and Secondary Structure

Figure 5(A-C), Figure 6(A-C), Figure 7(A-E), Figure 8(A-C), and Figure 9(A-C) depict graphically five amino acid profiles of 191P4D12(b) variants 1, 7, and 9, each assessment available by accessing the ProtScale website located on the World Wide Web through the ExPasy molecular biology server.

These profiles: Figure 5, Hydrophilicity, (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828); Figure 6, Hydropathicity, (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132); Figure 7, Percentage Accessible Residues (Janin J., 1979 Nature 277:491-492); Figure 8, Average Flexibility, (Bhaskaran R., and Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255); Figure 9, Beta-turn (Deleage, G., Roux B. 1987 Protein Engineering 1:289-294); and optionally others available in the art, such as on the ProtScale website, were used to identify antigenic regions of each of the 191P4D12(b) variant proteins. Each of the above amino acid profiles of 191P4D12(b) variants were generated using the following ProtScale parameters for analysis: 1) A window size of 9; 2) 100% weight of the window edges compared to the window center; and, 3) amino acid profile values normalized to lie between 0 and 1.

Hydrophilicity (Figure 5), Hydropathicity (Figure 6) and Percentage Accessible Residues (Figure 7) profiles were used to determine stretches of hydrophilic amino acids (i.e., values greater than 0.5 on the Hydrophilicity and Percentage Accessible Residues profile, and values less than 0.5 on the Hydropathicity profile). Such regions are likely to be exposed to the aqueous environment, be present on the surface of the protein, and thus available for immune recognition, such as by antibodies.

Average Flexibility (Figure 8) and Beta-turn (Figure 9) profiles determine stretches of amino acids (i.e., values greater than 0.5 on the Beta-turn profile and the Average Flexibility profile) that are not constrained in secondary structures such as beta sheets and alpha helices. Such regions are also more likely to be exposed on the protein and thus accessible to immune recognition, such as by antibodies.

Antigenic sequences of the 191P4D12(b) variant proteins indicated, e.g., by the profiles set forth in Figure 5(A-C), Figure 6(A-C), Figure 7(A-C), Figure 8(A-C), and/or Figure 9(A-C) are used to prepare immunogens, either peptides or nucleic acids that encode them, to generate therapeutic and diagnostic anti-191P4D12(b) antibodies. The immunogen can be any 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50 or more than 50 contiguous amino acids, or the corresponding nucleic acids that encode them, from the 191P4D12(b) protein variants listed in Figures 2 and 3, of which the amino acid profiles are shown in Figure 9, or are identical to the variant sequences that are the same as a variant depicted in figure 9. In particular, peptide immunogens of the invention can comprise, a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Hydrophilicity profiles of Figure 5; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value less than 0.5 in the Hydropathicity profile of Figures 6 ; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Percent Accessible Residues profiles of Figure 7; a peptide region of at least 5 amino acids of Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Average Flexibility profiles on Figure 8 ; and, a peptide region of at least 5 amino acids of

Figures 2 and 3 in any whole number increment that includes an amino acid position having a value greater than 0.5 in the Beta-turn profile of Figures 9 . Peptide immunogens of the invention can also comprise nucleic acids that encode any of the forgoing.

All immunogens of the invention, peptide or nucleic acid, can be embodied in human unit dose form, or comprised by a composition that includes a pharmaceutical excipient compatible with human physiology.

The secondary structure of 191P4D12(b) protein variants 1, 7, and 9, namely the predicted presence and location of alpha helices, extended strands, and random coils, is predicted from the primary amino acid sequence using the HNN - Hierarchical Neural Network method (Guermeur, 1997)
accessed from the ExPasy molecular biology server located on the World Wide Web . The analysis indicates that 191P4D12(b) variant 1 is composed of 24.90% alpha helix, 18.63% extended strand, and 56.47% random coil (Figure 13A). Variant 6 is composed of 28.47% alpha helix, 19.32% extended strand, and 52.20% random coil (Figure 13B). Variant 7 is composed of 26.19% alpha helix, 18.76% extended strand, and 55.05% random coil (Figure 13C). Variant 7 is composed of 56.20% alpha helix, 8.76% extended strand, and 35.04% random coil (Figure 13D).

Analysis for the potential presence of transmembrane domains in the 191P4D12(b) variant proteins was carried out using a variety of transmembrane prediction algorithms accessed from the ExPasy molecular biology server located on the World Wide Web at (.expasy.ch/tools/). Shown graphically in figure 13E and 13F are the results of analysis of variant 1 depicting the presence and location of 1 transmembrane domain using the TMpred program (Figure 13E) and 1 transmembrane domain using the TMHMM program (Figure 13F). Shown graphically in figure 13G and 13H are the results of analysis of variant 6 depicting the presence and location of 1 transmembrane domains using the TMpred program (Figure 13G) and 1 transmembrane domain using the TMHMM program (Figure 13H). Shown graphically in figure 13I and 13J are the results of analysis of variant 7 depicting the presence and location of 1 transmembrane domain using the TMpred program (Figure 13I) and 1 transmembrane domain using the TMHMM program (Figure 13J). Shown graphically in figure 13K and 13L are the results of analysis of variant 9 depicting the presence and location of 2 transmembrane domains using the TMpred program (Figure 1K) and 1 transmembrane domain using the TMHMM program (Figure 13L). The results of each program, namely the amino acids encoding the transmembrane domains are summarized in Table VI and Table L.

Example 10: Generation of 191P4D12(b) Polyclonal Antibodies

Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. In addition to immunizing with a full length 191P4D12(b) protein variant, computer algorithms are employed in design of immunogens that, based on amino acid sequence analysis contain characteristics of being antigenic and available for recognition by the immune system of the immunized host (see the Example entitled "Antigenicity Profiles and Secondary Structures"). Such regions would be predicted to be hydrophilic, flexible, in beta-turn conformations, and be exposed on the surface of the protein (see, e.g., Figure 5(A-C), Figure 6(A & C), Figure 7(A-C), Figure 8(A -C), or Figure 9(A-C) for amino acid profiles that indicate such regions of 191P4D12(b) protein variants).

For example, recombinant bacterial fusion proteins or peptides containing hydrophilic, flexible, beta-turn regions of 191P4D12(b) protein variants are used as antigens to generate polyclonal antibodies in New Zealand White rabbits or monoclonal antibodies as described in Example 11. For example, in 191P4D12(b) variant 1, such regions include, but are not limited to, amino acids 27-39, amino acids 93-109, and amino acids 182-204. In sequence unique to variant 7, such regions include, but are not limited to, amino acids 400-420. In sequence specific for variant 9, such regions include, but are not limited to, amino acids 80-94. It is useful to conjugate the immunizing agent to a protein known to be immunogenic in the

mammal being immunized. Examples of such immunogenic proteins include, but are not limited to, keyhole limpet hemocyanin (KLH), serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. In one embodiment, a peptide encoding amino acids 52-63 of 191P4D12(b) variant 1 and amino acids 179-197 were each conjugated to KLH and used to immunize separate rabbits. Alternatively the immunizing agent may include all or portions of the 191P4D12(b) variant proteins, analogs or fusion proteins thereof. For example, the 191P4D12(b) variant 1 amino acid sequence can be fused using recombinant DNA techniques to any one of a variety of fusion protein partners that are well known in the art, such as glutathione-S-transferase (GST) and HIS tagged fusion proteins. In another embodiment, amino acids 2-349 of 191P4D12(b) variant 1 was fused to GST using recombinant techniques and the pGEX expression vector, expressed, purified and used to immunize a rabbit. Such fusion proteins are purified from induced bacteria using the appropriate affinity matrix.

Other recombinant bacterial fusion proteins that may be employed include maltose binding protein, LacZ, thioredoxin, NusA, or an immunoglobulin constant region (see the section entitled "Production of 191P4D12(b) in Prokaryotic Systems" and Current Protocols In Molecular Biology, Volume 2, Unit 16, Frederick M. Ausubul et al. eds., 1995; Linsley, P.S., Brady, W., Urnes, M., Grosmaire, L., Damle, N., and Ledbetter, L.(1991) J.Exp. Med. 174, 561-566).

In addition to bacterial derived fusion proteins, mammalian expressed protein antigens are also used. These antigens are expressed from mammalian expression vectors such as the Tag5 and Fc-fusion vectors (see the section entitled "Production of Recombinant 191P4D12(b) in Eukaryotic Systems"), and retain post-translational modifications such as glycosylations found in native protein. In one embodiment, amino acids 31-347 of variant 1, encoding the extracellular domain, was cloned into the Tag5 mammalian secretion vector, and expressed in 293T cells resulting in a soluble secreted protein (Figure 22). The recombinant protein is purified by metal chelate chromatography from tissue culture supernatants of 293T cells stably expressing the recombinant vector. The purified Tag5 191P4D12(b) protein is then used as immunogen.

During the immunization protocol, it is useful to mix or emulsify the antigen in adjuvants that enhance the immune response of the host animal. Examples of adjuvants include, but are not limited to, complete Freund's adjuvant (CFA) and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).

In a typical protocol, rabbits are initially immunized subcutaneously with up to 200 μg, typically 100-200 μg, of fusion protein or peptide conjugated to KLH mixed in complete Freund's adjuvant (CFA). Rabbits are then injected subcutaneously every two weeks with up to 200 μg, typically 100-200 μg, of the immunogen in incomplete Freund's adjuvant (IFA). Test bleeds are taken approximately 7-10 days following each immunization and used to monitor the titer of the antiserum by ELISA.

To test reactivity and specificity of immune serum, such as the rabbit serum derived from immunization with the Tag5 -191P4D12(b) variant 1 protein, the full-length 191P4D12(b) variant 1 cDNA is cloned into pCDNA 3.1 myc-his expression vector (Invitrogen, see the Example entitled "Production of Recombinant 191P4D12(b) in Eukaryotic Systems"). After transfection of the constructs into 293T cells, cell lysates are probed with the anti-191P4D12(b) serum and with anti-His antibody (Santa Cruz Biotechnologies, Santa Cruz, CA) to determine specific reactivity to denatured 191P4D12(b) protein using the Western blot technique. In addition, the immune serum is tested by fluorescence microscopy, flow cytometry and immunoprecipitation against 293T (Figure 22) and other recombinant 191P4D12(b)-expressing cells to determine specific recognition of native protein. Western blot, immunoprecipitation, fluorescent microscopy, and flow cytometric techniques using cells that endogenously express 191P4D12(b) are also carried out to test reactivity and specificity.

Anti-serum from rabbits immunized with 191P4D12(b) variant fusion proteins, such as GST and MBP fusion proteins, are purified by depletion of antibodies reactive to the fusion partner sequence by passage over an affinity column containing the fusion partner either alone or in the context of an irrelevant fusion protein. For example, antiserum derived from a GST-191P4D12(b) variant 1 fusion protein is first purified by passage over a column of GST protein covalently coupled to AffiGel

matrix (BioRad, Hercules, Calif.). The antiserum is then affinity purified by passage over a column composed of a MBP-191P4D12(b) fusion protein covalently coupled to Affigel matrix. The serum is then further purified by protein G affinity chromatography to isolate the IgG fraction. Sera from other His-tagged antigens and peptide immunized rabbits as well as fusion partner depleted sera are affinity purified by passage over a column matrix composed of the original protein immunogen or free peptide.

Example 11: Generation of 191P4D12(b) Monoclonal Antibodies (mAbs)

In one embodiment, therapeutic mAbs to 191P4D12(b) variants comprise those that react with epitopes specific for each variant protein or specific to sequences in common between the variants that would disrupt or modulate the biological function of the 191P4D12(b) variants, for example those that would disrupt the interaction with ligands and binding partners. Immunogens for generation of such mAbs include those designed to encode or contain the entire 191P4D12(b) protein variant sequence, regions of the 191P4D12(b) protein variants predicted to be antigenic from computer analysis of the amino acid sequence (see, e.g., Figure 5(A-C), Figure 6(A-C), Figure 7(A-C), Figure 8(A-C), or Figure 9(A-C), and the Example entitled "Antigenicity Profiles"). Immunogens include peptides, recombinant bacterial proteins, and mammalian expressed Tag 5 proteins and human and murine IgG FC fusion proteins. In addition, cells engineered to express high levels of a respective 191P4D12(b) variant, such as 293T-191P4D12(b) variant 1 or 300.19-191P4D12(b) variant 1murine Pre-B cells, are used to immunize mice.

To generate mAbs to a 191P4D12(b) variant, mice are first immunized intraperitoneally (IP) with, typically, 10-50 μg of protein immunogen or 10^7 191P4D12(b)-expressing cells mixed in complete Freund's adjuvant. Mice are then subsequently immunized IP every 2-4 weeks with, typically, 10-50 μg of protein immunogen or 10^7 cells mixed in incomplete Freund's adjuvant. Alternatively, MPL-TDM adjuvant is used in immunizations. In addition to the above protein and cell-based immunization strategies, a DNA-based immunization protocol is employed in which a mammalian expression vector encoding a 191P4D12(b) variant sequence is used to immunize mice by direct injection of the plasmid DNA. For example, amino acids 31-347 was cloned into the Tag5 mammalian secretion vector and the recombinant vector will then be used as immunogen. In another example the same amino acids are cloned into an Fc-fusion secretion vector in which the 191P4D12(b) variant 1 sequence is fused at the amino-terminus to an IgK leader sequence and at the carboxyl-terminus to the coding sequence of the human or murine IgG Fc region. This recombinant vector is then used as immunogen. The plasmid immunization protocols are used in combination with purified proteins expressed from the same vector and with cells expressing the respective 191P4D12(b) variant.

During the immunization protocol, test bleeds are taken 7-10 days following an injection to monitor titer and specificity of the immune response. Once appropriate reactivity and specificity is obtained as determined by ELISA, Western blotting, immunoprecipitation, fluorescence microscopy, and flow cytometric analyses, fusion and hybridoma generation is then carried out with established procedures well known in the art (see, e.g., Harlow and Lane, 1988).

In one embodiment for generating 191P4D12(b) monoclonal antibodies, a Tag5-191P4D12(b) variant 1 antigen encoding amino acids 31-347, was expressed (Figure 22) and then purified from stably transfected 293T cells. Balb C mice are initially immunized intraperitoneally with 25 μg of the Tag5-191P4D12(b) variant 1 protein mixed in complete Freund's adjuvant. Mice are subsequently immunized every two weeks with 25 μg of the antigen mixed in incomplete Freund's adjuvant for a total of three immunizations. ELISA using the Tag5 antigen determines the titer of serum from immunized mice. Reactivity and specificity of serum to full length 191P4D12(b) variant 1 protein is monitored by Western blotting, immunoprecipitation and flow cytometry using 293T cells transfected with an expression vector encoding the 191P4D12(b) variant 1 cDNA (see e.g., the Example entitled "Production of Recombinant 191P4D12(b) (a) & (b) in Eukaryotic Systems" and Figure 22). Other recombinant 191P4D12(b) variant 1-expressing cells or cells endogenously expressing 191P4D12(b)

variant 1 are also used. Mice showing the strongest reactivity are rested and given a final injection of Tag5 antigen in PBS and then sacrificed four days later. The spleens of the sacrificed mice are harvested and fused to SPO/2 myeloma cells using standard procedures (Harlow and Lane, 1988). Supernatants from HAT selected growth wells are screened by ELISA, Western blot, immunoprecipitation, fluorescent microscopy, and flow cytometry to identify 191P4D12(b) specific antibody-producing clones.

To generate monoclonal antibodies that are specific for each 191P4D12(b) variant protein, immunogens are designed to encode sequences unique for each variant. In one embodiment, a GST-fusion antigen encoding the full sequence of 191P4D12(b) variant 9 (AA 1-137) is produced, purified, and used as immunogen to derive monoclonal antibodies specific to 191P4D12(b) variant 2. In another embodiment, an antigenic peptide composed of amino acids 400-420 of 191P4D12(b) variant 7 is coupled to KLH and used as immunogen. Hybridoma supernatants are then screened on the respective antigen and then further screened on cells expressing the specific variant and cross-screened on cells expressing the other variants to derive variant-specific monoclonal antibodies.

The binding affinity of a 191P4D12(b) variant monoclonal antibody is determined using standard technologies. Affinity measurements quantify the strength of antibody to epitope binding and are used to help define which 191P4D12(b) variant monoclonal antibodies preferred for diagnostic or therapeutic use, as appreciated by one of skill in the art. The BIAcore™ system (Uppsala, Sweden) is a preferred method for determining binding affinity. The BIAcore™ system uses surface plasmon resonance (SPR, Welford K. 1991, Opt. Quant. Elect. 23:1; Morton and Myszka, 1998, Methods in Enzymology 295: 268) to monitor biomolecular interactions in real time. BIAcore™ analysis conveniently generates association rate constants, dissociation rate constants, equilibrium dissociation constants, and affinity constants.

Example 12: HLA Class I and Class II Binding Assays

HLA class I and class II binding assays using purified HLA molecules are performed in accordance with disclosed protocols (*e.g.*, PCT publications WO 94/20127 and WO 94/03205; Sidney *et al.*, *Current Protocols in Immunology* 18.3.1 (1998); Sidney, *et al.*, *J. Immunol.* 154:247 (1995); Sette, *et al.*, *Mol. Immunol.* 31:813 (1994)). Briefly, purified MHC molecules (5 to 500 nM) are incubated with various unlabeled peptide inhibitors and 1-10 nM ^{125}I-radiolabeled probe peptides as described. Following incubation, MHC-peptide complexes are separated from free peptide by gel filtration and the fraction of peptide bound is determined. Typically, in preliminary experiments, each MHC preparation is titered in the presence of fixed amounts of radiolabeled peptides to determine the concentration of HLA molecules necessary to bind 10-20% of the total radioactivity. All subsequent inhibition and direct binding assays are performed using these HLA concentrations.

Since under these conditions [label]<[HLA] and $IC_{50} \geq$[HLA], the measured IC_{50} values are reasonable approximations of the true K_D values. Peptide inhibitors are typically tested at concentrations ranging from 120 μg/ml to 1.2 ng/ml, and are tested in two to four completely independent experiments. To allow comparison of the data obtained in different experiments, a relative binding figure is calculated for each peptide by dividing the IC_{50} of a positive control for inhibition by the IC_{50} for each tested peptide (typically unlabeled versions of the radiolabeled probe peptide). For database purposes, and inter-experiment comparisons, relative binding values are compiled. These values can subsequently be converted back into IC_{50} nM values by dividing the IC_{50} nM of the positive controls for inhibition by the relative binding of the peptide of interest. This method of data compilation is accurate and consistent for comparing peptides that have been tested on different days, or with different lots of purified MHC.

Binding assays as outlined above may be used to analyze HLA supermotif and/or HLA motif-bearing peptides (see Table IV).

Example 13: Identification of HLA Supermotif- and Motif-Bearing CTL Candidate Epitopes

HLA vaccine compositions of the invention can include multiple epitopes. The multiple epitopes can comprise multiple HLA supermotifs or motifs to achieve broad population coverage. This example illustrates the identification and confirmation of supermotif- and motif-bearing epitopes for the inclusion in such a vaccine composition. Calculation of population coverage is performed using the strategy described below.

Computer searches and algorithms for identification of supermotif and/or motif-bearing epitopes

The searches performed to identify the motif-bearing peptide sequences in the Example entitled "Antigenicity Profiles" and Tables VIII-XXI and XXII-XLIX employ the protein sequence data from the gene product of 191P4D12(b) set forth in Figures 2 and 3, the specific search peptides used to generate the tables are listed in Table VII.

Computer searches for epitopes bearing HLA Class I or Class II supermotifs or motifs are performed as follows. All translated 191P4D12(b) protein sequences are analyzed using a text string search software program to identify potential peptide sequences containing appropriate HLA binding motifs; such programs are readily produced in accordance with information in the art in view of known motif/supermotif disclosures. Furthermore, such calculations can be made mentally.

Identified A2-, A3-, and DR-supermotif sequences are scored using polynomial algorithms to predict their capacity to bind to specific HLA-Class I or Class II molecules. These polynomial algorithms account for the impact of different amino acids at different positions, and are essentially based on the premise that the overall affinity (or ΔG) of peptide-HLA molecule interactions can be approximated as a linear polynomial function of the type:

$$"\Delta G" = a_{1i} \times a_{2i} \times a_{3i} \ldots\ldots \times a_{ni}$$

where a_{ji} is a coefficient which represents the effect of the presence of a given amino acid (j) at a given position (i) along the sequence of a peptide of n amino acids. The crucial assumption of this method is that the effects at each position are essentially independent of each other (i.e., independent binding of individual side-chains). When residue j occurs at position i in the peptide, it is assumed to contribute a constant amount j_i to the free energy of binding of the peptide irrespective of the sequence of the rest of the peptide.

The method of derivation of specific algorithm coefficients has been described in Gulukota *et al.*, *J. Mol. Biol.* 267:1258-126, 1997; (see also Sidney *et al.*, *Human Immunol.* 45:79-93, 1996; and Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). Briefly, for all i positions, anchor and non-anchor alike, the geometric mean of the average relative binding (ARB) of all peptides carrying j is calculated relative to the remainder of the group, and used as the estimate of j_i. For Class II peptides, if multiple alignments are possible, only the highest scoring alignment is utilized, following an iterative procedure. To calculate an algorithm score of a given peptide in a test set, the ARB values corresponding to the sequence of the peptide are multiplied. If this product exceeds a chosen threshold, the peptide is predicted to bind. Appropriate thresholds are chosen as a function of the degree of stringency of prediction desired.

Selection of HLA-A2 supertype cross-reactive peptides

Protein sequences from 191P4D12(b) are scanned utilizing motif identification software, to identify 8-, 9- 10- and 11-mer sequences containing the HLA-A2-supermotif main anchor specificity. Typically, these sequences are then scored using the protocol described above and the peptides corresponding to the positive-scoring sequences are synthesized and tested for their capacity to bind purified HLA-A*0201 molecules *in vitro* (HLA-A*0201 is considered a prototype A2 supertype molecule).

These peptides are then tested for the capacity to bind to additional A2-supertype molecules (A*0202, A*0203, A*0206, and A*6802). Peptides that bind to at least three of the five A2-supertype alleles tested are typically deemed A2-supertype cross-reactive binders. Preferred peptides bind at an affinity equal to or less than 500 nM to three or more HLA-A2 supertype molecules.

Selection of HLA-A3 supermotif-bearing epitopes

The 191P4D12(b) protein sequence(s) scanned above is also examined for the presence of peptides with the HLA-A3-supermotif primary anchors. Peptides corresponding to the HLA A3 supermotif-bearing sequences are then synthesized and tested for binding to HLA-A*0301 and HLA-A*1101 molecules, the molecules encoded by the two most prevalent A3-supertype alleles. The peptides that bind at least one of the two alleles with binding affinities of ≤500 nM, often ≤ 200 nM, are then tested for binding cross-reactivity to the other common A3-supertype alleles (e.g., A*3101, A*3301, and A*6801) to identify those that can bind at least three of the five HLA-A3-supertype molecules tested.

Selection of HLA-B7 supermotif bearing epitopes

The 191P4D12(b) protein(s) scanned above is also analyzed for the presence of 8-, 9- 10-, or 11-mer peptides with the HLA-B7-supermotif. Corresponding peptides are synthesized and tested for binding to HLA-B*0702, the molecule encoded by the most common B7-supertype allele (*i.e.*, the prototype B7 supertype allele). Peptides binding B*0702 with IC_{50} of ≤500 nM are identified using standard methods. These peptides are then tested for binding to other common B7-supertype molecules (e.g., B*3501, B*5101, B*5301, and B*5401). Peptides capable of binding to three or more of the five B7-supertype alleles tested are thereby identified.

Selection of A1 and A24 motif-bearing epitopes

To further increase population coverage, HLA-A1 and -A24 epitopes can also be incorporated into vaccine compositions. An analysis of the 191P4D12(b) protein can also be performed to identify HLA-A1- and A24-motif-containing sequences.

High affinity and/or cross-reactive binding epitopes that bear other motif and/or supermotifs are identified using analogous methodology.

Example 14: Confirmation of Immunogenicity

Cross-reactive candidate CTL A2-supermotif-bearing peptides that are identified as described herein are selected to confirm *in vitro* immunogenicity. Confirmation is performed using the following methodology:

Target Cell Lines for Cellular Screening:

The .221A2.1 cell line, produced by transferring the HLA-A2.1 gene into the HLA-A, -B, -C null mutant human B-lymphoblastoid cell line 721.221, is used as the peptide-loaded target to measure activity of HLA-A2.1-restricted CTL. This cell line is grown in RPMI-1640 medium supplemented with antibiotics, sodium pyruvate, nonessential amino acids and 10% (v/v) heat inactivated FCS. Cells that express an antigen of interest, or transfectants comprising the gene encoding the antigen of interest, can be used as target cells to confirm the ability of peptide-specific CTLs to recognize endogenous antigen.

Primary CTL Induction Cultures:

Generation of Dendritic Cells (DC): PBMCs are thawed in RPMI with 30 μg/ml DNAse, washed twice and resuspended in complete medium (RPMI-1640 plus 5% AB human serum, non-essential amino acids, sodium pyruvate, L-glutamine and penicillin/streptomycin). The monocytes are purified by plating 10 x 10^6 PBMC/well in a 6-well plate. After 2 hours at 37°C, the non-adherent cells are removed by gently shaking the plates and aspirating the supernatants. The wells are washed a total of three times with 3 ml RPMI to remove most of the non-adherent and loosely adherent cells. Three ml of complete medium containing 50 ng/ml of GM-CSF and 1,000 U/ml of IL-4 are then added to each well. TNFα is added to the DCs on day 6 at 75 ng/ml and the cells are used for CTL induction cultures on day 7.

Induction of CTL with DC and Peptide: CD8+ T-cells are isolated by positive selection with Dynal immunomagnetic beads (Dynabeads® M-450) and the detacha-bead® reagent. Typically about 200-250x10^6 PBMC are processed to obtain 24x10^6 $CD8^+$ T-cells (enough for a 48-well plate culture). Briefly, the PBMCs are thawed in RPMI with 30µg/ml DNAse, washed once with PBS containing 1% human AB serum and resuspended in PBS/1% AB serum at a concentration of 20x10^6cells/ml. The magnetic beads are washed 3 times with PBS/AB serum, added to the cells (140µl beads/20x10^6 cells) and incubated for 1 hour at 4°C with continuous mixing. The beads and cells are washed 4x with PBS/AB serum to remove the nonadherent cells and resuspended at 100x10^6 cells/ml (based on the original cell number) in PBS/AB serum containing 100µl/ml detacha-bead® reagent and 30 µg/ml DNAse. The mixture is incubated for 1 hour at room temperature with continuous mixing. The beads are washed again with PBS/AB/DNAse to collect the CD8+ T-cells. The DC are collected and centrifuged at 1300 rpm for 5-7 minutes, washed once with PBS with 1% BSA, counted and pulsed with 40µg/ml of peptide at a cell concentration of 1-2x10^6/ml in the presence of 3µg/ml $ß_2$- microglobulin for 4 hours at 20°C. The DC are then irradiated (4,200 rads), washed 1 time with medium and counted again.

Setting up induction cultures: 0.25 ml cytokine-generated DC (at 1x10^5 cells/ml) are co-cultured with 0.25ml of CD8+ T-cells (at 2x10^6 cell/ml) in each well of a 48-well plate in the presence of 10 ng/ml of IL-7. Recombinant human IL-10 is added the next day at a final concentration of 10 ng/ml and rhuman IL-2 is added 48 hours later at 10 IU/ml.

Restimulation of the induction cultures with peptide-pulsed adherent cells: Seven and fourteen days after the primary induction, the cells are restimulated with peptide-pulsed adherent cells. The PBMCs are thawed and washed twice with RPMI and DNAse. The cells are resuspended at 5x10^6 cells/ml and irradiated at ~4200 rads. The PBMCs are plated at 2x10^6 in 0.5 ml complete medium per well and incubated for 2 hours at 37°C. The plates are washed twice with RPMI by tapping the plate gently to remove the nonadherent cells and the adherent cells pulsed with 10µg/ml of peptide in the presence of 3 µg/ml $ß_2$ microglobulin in 0.25ml RPMI/5%AB per well for 2 hours at 37°C. Peptide solution from each well is aspirated and the wells are washed once with RPMI. Most of the media is aspirated from the induction cultures (CD8+ cells) and brought to 0.5 ml with fresh media. The cells are then transferred to the wells containing the peptide-pulsed adherent cells. Twenty four hours later recombinant human IL-10 is added at a final concentration of 10 ng/ml and recombinant human IL2 is added the next day and again 2-3 days later at 50IU/ml (Tsai *et al., Critical Reviews in Immunology* 18(1-2):65-75, 1998). Seven days later, the cultures are assayed for CTL activity in a ^{51}Cr release assay. In some experiments the cultures are assayed for peptide-specific recognition in the *in situ* IFNγ ELISA at the time of the second restimulation followed by assay of endogenous recognition 7 days later. After expansion, activity is measured in both assays for a side-by-side comparison.

Measurement of CTL lytic activity by ^{51}Cr release.

Seven days after the second restimulation, cytotoxicity is determined in a standard (5 hr) ^{51}Cr release assay by assaying individual wells at a single E:T. Peptide-pulsed targets are prepared by incubating the cells with 10µg/ml peptide overnight at 37°C.

Adherent target cells are removed from culture flasks with trypsin-EDTA. Target cells are labeled with 200µCi of ^{51}Cr sodium chromate (Dupont, Wilmington, DE) for 1 hour at 37°C. Labeled target cells are resuspended at 10^6 per ml and diluted 1:10 with K562 cells at a concentration of 3.3x10^6/ml (an NK-sensitive erythroblastoma cell line used to reduce non-specific lysis). Target cells (100 µl) and effectors (100µl) are plated in 96 well round-bottom plates and incubated for 5 hours at 37°C. At that time, 100 µl of supernatant are collected from each well and percent lysis is determined according to the formula:

[(cpm of the test sample- cpm of the spontaneous ^{51}Cr release sample)/(cpm of the maximal ^{51}Cr release sample-cpm of the spontaneous ^{51}Cr release sample)] x 100.

Maximum and spontaneous release are determined by incubating the labeled targets with 1% Triton™ X-100 and media alone, respectively. A positive culture is defined as one in which the specific lysis (sample- background) is 10% or higher in the case of individual wells and is 15% or more at the two highest E:T ratios when expanded cultures are assayed.

In situ Measurement of Human IFNγ Production as an Indicator of Peptide-specific and Endogenous Recognition

Immulon 2 plates are coated with mouse anti-human IFNγ monoclonal antibody (4 µg/ml 0.1M $NaHCO_3$, pH8.2) overnight at 4°C. The plates are washed with Ca^{2+}, Mg^{2+}-free PBS/0.05% Tween™ 20 and blocked with PBS/10% FCS for two hours, after which the CTLs (100 µl/well) and targets (100 µl/well) are added to each well, leaving empty wells for the standards and blanks (which received media only). The target cells, either peptide-pulsed or endogenous targets, are used at a concentration of $1x10^6$ cells/ml. The plates are incubated for 48 hours at 37°C with 5% CO_2.

Recombinant human IFN-gamma is added to the standard wells starting at 400 pg or 1200pg/100 microliter/well and the plate incubated for two hours at 37°C. The plates are washed and 100 µl of biotinylated mouse anti-human IFN-gamma monoclonal antibody (2 microgram/ml in PBS/3%FCS/0.05% Tween™ 20) are added and incubated for 2 hours at room temperature. After washing again, 100 microliter HRP-streptavidin (1:4000) are added and the plates incubated for one hour at room temperature. The plates are then washed 6x with wash buffer, 100 microliter/well developing solution (TMB 1:1) are added, and the plates allowed to develop for 5-15 minutes. The reaction is stopped with 50 microliter/well 1M H_3PO_4 and read at OD450. A culture is considered positive if it measured at least 50 pg of IFN-gamma/well above background and is twice the background level of expression.

CTL Expansion.

Those cultures that demonstrate specific lytic activity against peptide-pulsed targets and/or tumor targets are expanded over a two week period with anti-CD3. Briefly, $5x10^4$ CD8+ cells are added to a T25 flask containing the following: $1x10^6$ irradiated (4,200 rad) PBMC (autologous or allogeneic) per ml, $2x10^5$ irradiated (8,000 rad) EBV- transformed cells per ml, and OKT3 (anti-CD3) at 30ng per ml in RPMI-1640 containing 10% (v/v) human AB serum, non-essential amino acids, sodium pyruvate, 25µM 2-mercaptoethanol, L-glutamine and penicillin/streptomycin. Recombinant human IL2 is added 24 hours later at a final concentration of 200IU/ml and every three days thereafter with fresh media at 50IU/ml. The cells are split if the cell concentration exceeds $1x10^6$/ml and the cultures are assayed between days 13 and 15 at E:T ratios of 30, 10, 3 and 1:1 in the ^{51}Cr release assay or at $1x10^6$/ml in the *in situ* IFNγ assay using the same targets as before the expansion.

Cultures are expanded in the absence of anti-$CD3^+$ as follows. Those cultures that demonstrate specific lytic activity against peptide and endogenous targets are selected and $5x10^4$ $CD8^+$ cells are added to a T25 flask containing the following: $1x10^6$ autologous PBMC per ml which have been peptide-pulsed with 10 µg/ml peptide for two hours at 37°C and irradiated (4,200 rad); $2x10^5$ irradiated (8,000 rad) EBV-transformed cells per ml RPMI-1640 containing 10%(v/v) human AB serum, non-essential AA, sodium pyruvate, 25mM 2-ME, L-glutamine and gentamicin.

Immunogenicity of A2 supermotif-bearing peptides

A2-supermotif cross-reactive binding peptides are tested in the cellular assay for the ability to induce peptide-specific CTL in normal individuals. In this analysis, a peptide is typically considered to be an epitope if it induces peptide-specific CTLs in at least individuals, and preferably, also recognizes the endogenously expressed peptide.

Immunogenicity can also be confirmed using PBMCs isolated from patients bearing a tumor that expresses 191P4D12(b). Briefly, PBMCs are isolated from patients, re-stimulated with peptide-pulsed monocytes and assayed for the ability to recognize peptide-pulsed target cells as well as transfected cells endogenously expressing the antigen.

Evaluation of A*03/A11 immunogenicity

HLA-A3 supermotif-bearing cross-reactive binding peptides are also evaluated for immunogenicity using methodology analogous for that used to evaluate the immunogenicity of the HLA-A2 supermotif peptides.

Evaluation of B7 immunogenicity

Immunogenicity screening of the B7-supertype cross-reactive binding peptides identified as set forth herein are confirmed in a manner analogous to the confirmation of A2-and A3-supermotif-bearing peptides.

Peptides bearing other supermotifs/motifs, *e.g.*, HLA-A1, HLA-A24 *etc.* are also confirmed using similar methodology

Example 15: Implementation of the Extended Supermotif to Improve the Binding Capacity of Native Epitopes by Creating Analogs

HLA motifs and supermotifs (comprising primary and/or secondary residues) are useful in the identification and preparation of highly cross-reactive native peptides, as demonstrated herein. Moreover, the definition of HLA motifs and supermotifs also allows one to engineer highly cross-reactive epitopes by identifying residues within a native peptide sequence which can be analoged to confer upon the peptide certain characteristics, *e.g.* greater cross-reactivity within the group of HLA molecules that comprise a supertype, and/or greater binding affinity for some or all of those HLA molecules. Examples of analoging peptides to exhibit modulated binding affinity are set forth in this example.

Analoging at Primary Anchor Residues

Peptide engineering strategies are implemented to further increase the cross-reactivity of the epitopes. For example, the main anchors of A2-supermotif-bearing peptides are altered, for example, to introduce a preferred L, I, V, or M at position 2, and I or V at the C-terminus.

To analyze the cross-reactivity of the analog peptides, each engineered analog is initially tested for binding to the prototype A2 supertype allele A*0201, then, if A*0201 binding capacity is maintained, for A2-supertype cross-reactivity.

Alternatively, a peptide is confirmed as binding one or all supertype members and then analoged to modulate binding affinity to any one (or more) of the supertype members to add population coverage.

The selection of analogs for immunogenicity in a cellular screening analysis is typically further restricted by the capacity of the parent wild type (WT) peptide to bind at least weakly, *i.e.*, bind at an IC_{50} of 5000nM or less, to three of more A2 supertype alleles. The rationale for this requirement is that the WT peptides must be present endogenously in sufficient quantity to be biologically relevant. Analoged peptides have been shown to have increased immunogenicity and cross-reactivity by T cells specific for the parent epitope (*see*, *e.g.*, Parkhurst *et al.*, *J. Immunol.* 157:2539, 1996; and Pogue *et al.*, *Proc. Natl. Acad. Sci. USA* 92:8166, 1995).

In the cellular screening of these peptide analogs, it is important to confirm that analog-specific CTLs are also able to recognize the wild-type peptide and, when possible, target cells that endogenously express the epitope.

Analoging of HLA-A3 and B7-supermotif-bearing peptides

Analogs of HLA-A3 supermotif-bearing epitopes are generated using strategies similar to those employed in analoging HLA-A2 supermotif-bearing peptides. For example, peptides binding to 3/5 of the A3-supertype molecules are engineered at primary anchor residues to possess a preferred residue (V, S, M, or A) at position 2.

The analog peptides are then tested for the ability to bind A*03 and A*11 (prototype A3 supertype alleles). Those peptides that demonstrate ≤ 500 nM binding capacity are then confirmed as having A3-supertype cross-reactivity.

Similarly to the A2- and A3- motif bearing peptides, peptides binding 3 or more B7-supertype alleles can be improved, where possible, to achieve increased cross-reactive binding or greater binding affinity or binding half life. B7 supermotif-bearing peptides are, for example, engineered to possess a preferred residue (V, I, L, or F) at the C-terminal primary anchor position, as demonstrated by Sidney *et al.* (*J. Immunol.* 157:3480-3490, 1996).

Analoging at primary anchor residues of other motif and/or supermotif-bearing epitopes is performed in a like manner.

The analog peptides are then be confirmed for immunogenicity, typically in a cellular screening assay. Again, it is generally important to demonstrate that analog-specific CTLs are also able to recognize the wild-type peptide and, when possible, targets that endogenously express the epitope.

Analoging at Secondary Anchor Residues

Moreover, HLA supermotifs are of value in engineering highly cross-reactive peptides and/or peptides that bind HLA molecules with increased affinity by identifying particular residues at secondary anchor positions that are associated with such properties. For example, the binding capacity of a B7 supermotif-bearing peptide with an F residue at position 1 is analyzed. The peptide is then analoged to, for example, substitute L for F at position 1. The analoged peptide is evaluated for increased binding affinity, binding half life and/or increased cross-reactivity. Such a procedure identifies analoged peptides with enhanced properties.

Engineered analogs with sufficiently improved binding capacity or cross-reactivity can also be tested for immunogenicity in HLA-B7-transgenic mice, following for example, IFA immunization or lipopeptide immunization. Analoged peptides are additionally tested for the ability to stimulate a recall response using PBMC from patients with 191P4D12(b)-expressing tumors.

Other analoging strategies

Another form of peptide analoging, unrelated to anchor positions, involves the substitution of a cysteine with α-amino butyric acid. Due to its chemical nature, cysteine has the propensity to form disulfide bridges and sufficiently alter the peptide structurally so as to reduce binding capacity. Substitution of α-amino butyric acid for cysteine not only alleviates this problem, but has been shown to improve binding and crossbinding capabilities in some instances (*see, e.g.*, the review by Sette *et al.*, In: Persistent Viral Infections, Eds. R. Ahmed and I. Chen, John Wiley & Sons, England, 1999).

Thus, by the use of single amino acid substitutions, the binding properties and/or cross-reactivity of peptide ligands for HLA supertype molecules can be modulated.

Example 16: Identification and confirmation of 191P4D12(b)-derived sequences with HLA-DR binding motifs

Peptide epitopes bearing an HLA class II supermotif or motif are identified and confirmed as outlined below using methodology similar to that described for HLA Class I peptides.

Selection of HLA-DR-supermotif-bearing epitopes.

To identify 191P4D12(b)-derived, HLA class II HTL epitopes, a 191P4D12(b) antigen is analyzed for the presence of sequences bearing an HLA-DR-motif or supermotif. Specifically, 15-mer sequences are selected comprising a DR-supermotif, comprising a 9-mer core, and three-residue N- and C-terminal flanking regions (15 amino acids total).

Protocols for predicting peptide binding to DR molecules have been developed (Southwood *et al.*, *J. Immunol.* 160:3363-3373, 1998). These protocols, specific for individual DR molecules, allow the scoring, and ranking, of 9-mer core regions. Each protocol not only scores peptide sequences for the presence of DR-supermotif primary anchors (i.e., at position 1 and position 6) within a 9-mer core, but additionally evaluates sequences for the presence of secondary anchors. Using allele-specific selection tables (see, *e.g.*, Southwood *et al.*, *ibid.*), it has been found that these protocols efficiently select peptide sequences with a high probability of binding a particular DR molecule. Additionally, it has been found that performing these protocols in tandem, specifically those for DR1, DR4w4, and DR7, can efficiently select DR cross-reactive peptides.

The 191P4D12(b)-derived peptides identified above are tested for their binding capacity for various common HLA-DR molecules. All peptides are initially tested for binding to the DR molecules in the primary panel: DR1, DR4w4, and DR7. Peptides binding at least two of these three DR molecules are then tested for binding to DR2w2 β1, DR2w2 β2, DR6w19,

and DR9 molecules in secondary assays. Finally, peptides binding at least two of the four secondary panel DR molecules, and thus cumulatively at least four of seven different DR molecules, are screened for binding to DR4w15, DR5w11, and DR8w2 molecules in tertiary assays. Peptides binding at least seven of the ten DR molecules comprising the primary, secondary, and tertiary screening assays are considered cross-reactive DR binders. 191P4D12(b)-derived peptides found to bind common HLA-DR alleles are of particular interest.

Selection of DR3 motif peptides

Because HLA-DR3 is an allele that is prevalent in Caucasian, Black, and Hispanic populations, DR3 binding capacity is a relevant criterion in the selection of HTL epitopes. Thus, peptides shown to be candidates may also be assayed for their DR3 binding capacity. However, in view of the binding specificity of the DR3 motif, peptides binding only to DR3 can also be considered as candidates for inclusion in a vaccine formulation.

To efficiently identify peptides that bind DR3, target 191P4D12(b) antigens are analyzed for sequences carrying one of the two DR3-specific binding motifs reported by Geluk *et al.* (*J. Immunol.* 152:5742-5748, 1994). The corresponding peptides are then synthesized and confirmed as having the ability to bind DR3 with an affinity of 1μM or better, i.e., less than 1 μM. Peptides are found that meet this binding criterion and qualify as HLA class II high affinity binders.

DR3 binding epitopes identified in this manner are included in vaccine compositions with DR supermotif-bearing peptide epitopes.

Similarly to the case of HLA class I motif-bearing peptides, the class II motif-bearing peptides are analoged to improve affinity or cross-reactivity. For example, aspartic acid at position 4 of the 9-mer core sequence is an optimal residue for DR3 binding, and substitution for that residue often improves DR 3 binding.

Example 17: Immunogenicity of 191P4D12(b)-derived HTL epitopes

This example determines immunogenic DR supermotif- and DR3 motif-bearing epitopes among those identified using the methodology set forth herein.

Immunogenicity of HTL epitopes are confirmed in a manner analogous to the determination of immunogenicity of CTL epitopes, by assessing the ability to stimulate HTL responses and/or by using appropriate transgenic mouse models. Immunogenicity is determined by screening for: 1.) *in vitro* primary induction using normal PBMC or 2.) recall responses from patients who have 191P4D12(b)-expressing tumors.

Example 18: Calculation of phenotypic frequencies of HLA-supertypes in various ethnic backgrounds to determine breadth of population coverage

This example illustrates the assessment of the breadth of population coverage of a vaccine composition comprised of multiple epitopes comprising multiple supermotifs and/or motifs.

In order to analyze population coverage, gene frequencies of HLA alleles are determined. Gene frequencies for each HLA allele are calculated from antigen or allele frequencies utilizing the binomial distribution formulae gf=1-(SQRT(1-af)) (see, *e.g.*, Sidney *et al.*, *Human Immunol.* 45:79-93, 1996). To obtain overall phenotypic frequencies, cumulative gene frequencies are calculated, and the cumulative antigen frequencies derived by the use of the inverse formula $[af=1-(1-Cgf)^2]$.

Where frequency data is not available at the level of DNA typing, correspondence to the serologically defined antigen frequencies is assumed. To obtain total potential supertype population coverage no linkage disequilibrium is assumed, and only alleles confirmed to belong to each of the supertypes are included (minimal estimates). Estimates of total potential coverage achieved by inter-loci combinations are made by adding to the A coverage the proportion of the non-A covered population that could be expected to be covered by the B alleles considered (e.g., total=A+B*(1-A)). Confirmed members of the A3-like supertype are A3, A11, A31, A*3301, and A*6801. Although the A3-like supertype may also include

A34, A66, and A*7401, these alleles were not included in overall frequency calculations. Likewise, confirmed members of the A2-like supertype family are A*0201, A*0202, A*0203, A*0204, A*0205, A*0206, A*0207, A*6802, and A*6901. Finally, the B7-like supertype-confirmed alleles are: B7, B*3501-03, B51, B*5301, B*5401, B*5501-2, B*5601, B*6701, and B*7801 (potentially also B*1401, B*3504-06, B*4201, and B*5602).

Population coverage achieved by combining the A2-, A3- and B7-supertypes is approximately 86% in five major ethnic groups. Coverage may be extended by including peptides bearing the A1 and A24 motifs. On average, A1 is present in 12% and A24 in 29% of the population across five different major ethnic groups (Caucasian, North American Black, Chinese, Japanese, and Hispanic). Together, these alleles are represented with an average frequency of 39% in these same ethnic populations. The total coverage across the major ethnicities when A1 and A24 are combined with the coverage of the A2-, A3- and B7-supertype alleles is >95%, see, e.g., Table IV (G). An analogous approach can be used to estimate population coverage achieved with combinations of class II motif-bearing epitopes.

Immunogenicity studies in humans (*e.g.*, Bertoni *et al.*, *J. Clin. Invest.* 100:503, 1997; Doolan *et al.*, *Immunity* 7:97, 1997; and Threlkeld *et al.*, *J. Immunol.* 159:1648, 1997) have shown that highly cross-reactive binding peptides are almost always recognized as epitopes. The use of highly cross-reactive binding peptides is an important selection criterion in identifying candidate epitopes for inclusion in a vaccine that is immunogenic in a diverse population.

With a sufficient number of epitopes (as disclosed herein and from the art), an average population coverage is predicted to be greater than 95% in each of five major ethnic populations. The game theory Monte Carlo simulation analysis, which is known in the art (see *e.g.*, Osborne, M.J. and Rubinstein, A. "A course in game theory" MIT Press, 1994), can be used to estimate what percentage of the individuals in a population comprised of the Caucasian, North American Black, Japanese, Chinese, and Hispanic ethnic groups would recognize the vaccine epitopes described herein. A preferred percentage is 90%. A more preferred percentage is 95%.

Example 19: CTL Recognition Of Endogenously Processed Antigens After Priming

This example confirms that CTL induced by native or analoged peptide epitopes identified and selected as described herein recognize endogenously synthesized, *i.e.*, native antigens.

Effector cells isolated from transgenic mice that are immunized with peptide epitopes, for example HLA-A2 supermotif-bearing epitopes, are re-stimulated *in vitro* using peptide-coated stimulator cells. Six days later, effector cells are assayed for cytotoxicity and the cell lines that contain peptide-specific cytotoxic activity are further re-stimulated. An additional six days later, these cell lines are tested for cytotoxic activity on ^{51}Cr labeled Jurkat-A2.1/K^b target cells in the absence or presence of peptide, and also tested on ^{51}Cr labeled target cells bearing the endogenously synthesized antigen, *i.e.* cells that are stably transfected with 191P4D12(b) expression vectors.

The results demonstrate that CTL lines obtained from animals primed with peptide epitope recognize endogenously synthesized 191P4D12(b) antigen. The choice of transgenic mouse model to be used for such an analysis depends upon the epitope(s) that are being evaluated. In addition to HLA-A*0201/K^b transgenic mice, several other transgenic mouse models including mice with human A11, which may also be used to evaluate A3 epitopes, and B7 alleles have been characterized and others (*e.g.*, transgenic mice for HLA-A1 and A24) are being developed. HLA-DR1 and HLA-DR3 mouse models have also been developed, which may be used to evaluate HTL epitopes.

Example 20: Activity Of CTL-HTL Conjugated Epitopes In Transgenic Mice

This example illustrates the induction of CTLs and HTLs in transgenic mice, by use of a 191P4D12(b)-derived CTL and HTL peptide vaccine compositions. The vaccine composition used herein comprise peptides to be administered to a patient with a 191P4D12(b)-expressing tumor. The peptide composition can comprise multiple CTL and/or HTL epitopes.

The epitopes are identified using methodology as described herein. This example also illustrates that enhanced immunogenicity can be achieved by inclusion of one or more HTL epitopes in a CTL vaccine composition; such a peptide composition can comprise an HTL epitope conjugated to a CTL epitope. The CTL epitope can be one that binds to multiple HLA family members at an affinity of 500 nM or less, or analogs of that epitope. The peptides may be lipidated, if desired.

Immunization procedures: Immunization of transgenic mice is performed as described (Alexander *et al.*, *J. Immunol.* 159:4753-4761, 1997). For example, A2/K^b mice, which are transgenic for the human HLA A2.1 allele and are used to confirm the immunogenicity of HLA-A*0201 motif- or HLA-A2 supermotif-bearing epitopes, and are primed subcutaneously (base of the tail) with a 0.1 ml of peptide in Incomplete Freund's Adjuvant, or if the peptide composition is a lipidated CTL/HTL conjugate, in DMSO/saline, or if the peptide composition is a polypeptide, in PBS or Incomplete Freund's Adjuvant. Seven days after priming, splenocytes obtained from these animals are restimulated with syngenic irradiated LPS-activated lymphoblasts coated with peptide.

Cell lines: Target cells for peptide-specific cytotoxicity assays are Jurkat cells transfected with the HLA-A2.1/K^b chimeric gene (*e.g.*, Vitiello *et al.*, *J. Exp. Med.* 173:1007, 1991)

In vitro CTL activation: One week after priming, spleen cells ($30x10^6$ cells/flask) are co-cultured at 37°C with syngeneic, irradiated (3000 rads), peptide coated lymphoblasts ($10x10^6$ cells/flask) in 10 ml of culture medium/T25 flask. After six days, effector cells are harvested and assayed for cytotoxic activity.

Assay for cytotoxic activity: Target cells (1.0 to $1.5x10^6$) are incubated at 37°C in the presence of 200 µl of ^{51}Cr. After 60 minutes, cells are washed three times and resuspended in R10 medium. Peptide is added where required at a concentration of 1 µg/ml. For the assay, 10^4 ^{51}Cr-labeled target cells are added to different concentrations of effector cells (final volume of 200 µl) in U-bottom 96-well plates. After a six hour incubation period at 37°C, a 0.1 ml aliquot of supernatant is removed from each well and radioactivity is determined in a Micromedic automatic gamma counter. The percent specific lysis is determined by the formula: percent specific release = 100 x (experimental release - spontaneous release)/(maximum release - spontaneous release). To facilitate comparison between separate CTL assays run under the same conditions, % ^{51}Cr release data is expressed as lytic units/10^6 cells. One lytic unit is arbitrarily defined as the number of effector cells required to achieve 30% lysis of 10,000 target cells in a six hour ^{51}Cr release assay. To obtain specific lytic units/10^6, the lytic units/10^6 obtained in the absence of peptide is subtracted from the lytic units/10^6 obtained in the presence of peptide. For example, if 30% ^{51}Cr release is obtained at the effector (E): target (T) ratio of 50:1 (i.e., $5x10^5$ effector cells for 10,000 targets) in the absence of peptide and 5:1 (i.e., $5x10^4$ effector cells for 10,000 targets) in the presence of peptide, the specific lytic units would be: $[(1/50,000)-(1/500,000)] \times 10^6 = 18$ LU.

The results are analyzed to assess the magnitude of the CTL responses of animals injected with the immunogenic CTL/HTL conjugate vaccine preparation and are compared to the magnitude of the CTL response achieved using, for example, CTL epitopes as outlined above in the Example entitled "Confirmation of Immunogenicity." Analyses similar to this may be performed to confirm the immunogenicity of peptide conjugates containing multiple CTL epitopes and/or multiple HTL epitopes. In accordance with these procedures, it is found that a CTL response is induced, and concomitantly that an HTL response is induced upon administration of such compositions.

Example 21: Selection of CTL and HTL epitopes for inclusion in a 191P4D12(b)-specific vaccine.

This example illustrates a procedure for selecting peptide epitopes for vaccine compositions of the invention. The peptides in the composition can be in the form of a nucleic acid sequence, either single or one or more sequences (*i.e.*, minigene) that encodes peptide(s), or can be single and/or polyepitopic peptides.

The following principles are utilized when selecting a plurality of epitopes for inclusion in a vaccine composition. Each of the following principles is balanced in order to make the selection.

Epitopes are selected which, upon administration, mimic immune responses that are correlated with 191P4D12(b) clearance. The number of epitopes used depends on observations of patients who spontaneously clear 191P4D12(b). For example, if it has been observed that patients who spontaneously clear 191P4D12(b)-expressing cells generate an immune response to at least three (3) epitopes from 191P4D12(b) antigen, then at least three epitopes should be included for HLA class I. A similar rationale is used to determine HLA class II epitopes.

Epitopes are often selected that have a binding affinity of an IC_{50} of 500 nM or less for an HLA class I molecule, or for class II, an IC_{50} of 1000 nM or less; or HLA Class I peptides with high binding scores from the BIMAS web site.

In order to achieve broad coverage of the vaccine through out a diverse population, sufficient supermotif bearing peptides, or a sufficient array of allele-specific motif bearing peptides, are selected to give broad population coverage. In one embodiment, epitopes are selected to provide at least 80% population coverage. A Monte Carlo analysis, a statistical evaluation known in the art, can be employed to assess breadth, or redundancy, of population coverage.

When creating polyepitopic compositions, or a minigene that encodes same, it is typically desirable to generate the smallest peptide possible that encompasses the epitopes of interest. The principles employed are similar, if not the same, as those employed when selecting a peptide comprising nested epitopes. For example, a protein sequence for the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. Epitopes may be nested or overlapping (*i.e.*, frame shifted relative to one another). For example, with overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Each epitope can be exposed and bound by an HLA molecule upon administration of such a peptide. A multi-epitopic, peptide can be generated synthetically, recombinantly, or via cleavage from the native source. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes. This embodiment provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup that is presently unknown. Furthermore, this embodiment (absent the creating of any analogs) directs the immune response to multiple peptide sequences that are actually present in 191P4D12(b), thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing nucleic acid vaccine compositions. Related to this embodiment, computer programs can be derived in accordance with principles in the art, which identify in a target sequence, the greatest number of epitopes per sequence length.

A vaccine composition comprised of selected peptides, when administered, is safe, efficacious, and elicits an immune response similar in magnitude to an immune response that controls or clears cells that bear or overexpress 191P4D12(b).

Example 22: Construction of "Minigene" Multi-Epitope DNA Plasmids

This example discusses the construction of a minigene expression plasmid. Minigene plasmids may, of course, contain various configurations of B cell, CTL and/or HTL epitopes or epitope analogs as described herein.

A minigene expression plasmid typically includes multiple CTL and HTL peptide epitopes. In the present example, HLA-A2, -A3, -B7 supermotif-bearing peptide epitopes and HLA-A1 and -A24 motif-bearing peptide epitopes are used in conjunction with DR supermotif-bearing epitopes and/or DR3 epitopes. HLA class I supermotif or motif-bearing peptide epitopes derived 191P4D12(b), are selected such that multiple supermotifs/motifs are represented to ensure broad population coverage. Similarly, HLA class II epitopes are selected from 191P4D12(b) to provide broad population coverage,

i.e. both HLA DR-1-4-7 supermotif-bearing epitopes and HLA DR-3 motif-bearing epitopes are selected for inclusion in the minigene construct. The selected CTL and HTL epitopes are then incorporated into a minigene for expression in an expression vector.

Such a construct may additionally include sequences that direct the HTL epitopes to the endoplasmic reticulum. For example, the Ii protein may be fused to one or more HTL epitopes as described in the art, wherein the CLIP sequence of the Ii protein is removed and replaced with an HLA class II epitope sequence so that HLA class II epitope is directed to the endoplasmic reticulum, where the epitope binds to an HLA class II molecules.

This example illustrates the methods to be used for construction of a minigene-bearing expression plasmid. Other expression vectors that may be used for minigene compositions are available and known to those of skill in the art.

The minigene DNA plasmid of this example contains a consensus Kozak sequence and a consensus murine kappa Ig-light chain signal sequence followed by CTL and/or HTL epitopes selected in accordance with principles disclosed herein. The sequence encodes an open reading frame fused to the Myc and His antibody epitope tag coded for by the pcDNA 3.1 Myc-His vector.

Overlapping oligonucleotides that can, for example, average about 70 nucleotides in length with 15 nucleotide overlaps, are synthesized and HPLC-purified. The oligonucleotides encode the selected peptide epitopes as well as appropriate linker nucleotides, Kozak sequence, and signal sequence. The final multiepitope minigene is assembled by extending the overlapping oligonucleotides in three sets of reactions using PCR. A Perkin/Elmer 9600 PCR machine is used and a total of 30 cycles are performed using the following conditions: 95°C for 15 sec, annealing temperature (5° below the lowest calculated Tm of each primer pair) for 30 sec, and 72°C for 1 min.

For example, a minigene is prepared as follows. For a first PCR reaction, 5 µg of each of two oligonucleotides are annealed and extended: in an example using eight oligonucleotides, i.e., four pairs of primers, oligonucleotides 1+2, 3+4, 5+6, and 7+8 are combined in 100 µl reactions containing *Pfu* polymerase buffer (1x= 10 mM KCL, 10 mM $(NH4)_2SO_4$, 20 mM Tris-chloride, pH 8.75, 2 mM $MgSO_4$, 0.1% Triton™ X-100, 100 µg/ml BSA), 0.25mM each dNTP, and 2.5 U of *Pfu* polymerase. The full-length dimer products are gel-purified, and two reactions containing the product of 1+2 and 3+4, and the product of 5+6 and 7+8 are mixed, annealed, and extended for 10 cycles. Half of the two reactions are then mixed, and 5 cycles of annealing and extension carried out before flanking primers are added to amplify the full length product. The full-length product is gel-purified and cloned into pCR-blunt (Invitrogen) and individual clones are screened by sequencing.

Example 23: The Plasmid Construct and the Degree to Which It Induces Immunogenicity.

The degree to which a plasmid construct, for example a plasmid constructed in accordance with the previous Example, is able to induce immunogenicity is confirmed *in vitro* by determining epitope presentation by APC following transduction or transfection of the APC with an epitope-expressing nucleic acid construct. Such a study determines "antigenicity" and allows the use of human APC. The assay determines the ability of the epitope to be presented by the APC in a context that is recognized by a T cell by quantifying the density of epitope-HLA class I complexes on the cell surface. Quantitation can be performed by directly measuring the amount of peptide eluted from the APC (*see, e.g.*, Sijts *et al.*, *J. Immunol.* 156:683-692, 1996; Demotz *et al.*, *Nature* 342:682-684, 1989); or the number of peptide-HLA class I complexes can be estimated by measuring the amount of lysis or lymphokine release induced by diseased or transfected target cells, and then determining the concentration of peptide necessary to obtain equivalent levels of lysis or lymphokine release (*see, e.g.*, Kageyama *et al.*, *J. Immunol.* 154:567-576, 1995).

Alternatively, immunogenicity is confirmed through *in vivo* injections into mice and subsequent *in vitro* assessment of CTL and HTL activity, which are analyzed using cytotoxicity and proliferation assays, respectively, as detailed *e.g.*, in Alexander *et al.*, *Immunity* 1:751-761, 1994.

For example, to confirm the capacity of a DNA minigene construct containing at least one HLA-A2 supermotif peptide to induce CTLs *in vivo*, HLA-A2.1/K^b transgenic mice, for example, are immunized intramuscularly with 100 μg of naked cDNA. As a means of comparing the level of CTLs induced by cDNA immunization, a control group of animals is also immunized with an actual peptide composition that comprises multiple epitopes synthesized as a single polypeptide as they would be encoded by the minigene.

Splenocytes from immunized animals are stimulated twice with each of the respective compositions (peptide epitopes encoded in the minigene or the polyepitopic peptide), then assayed for peptide-specific cytotoxic activity in a ^{51}Cr release assay. The results indicate the magnitude of the CTL response directed against the A2-restricted epitope, thus indicating the *in vivo* immunogenicity of the minigene vaccine and polyepitopic vaccine.

It is, therefore, found that the minigene elicits immune responses directed toward the HLA-A2 supermotif peptide epitopes as does the polyepitopic peptide vaccine. A similar analysis is also performed using other HLA-A3 and HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 and HLA-B7 motif or supermotif epitopes, whereby it is also found that the minigene elicits appropriate immune responses directed toward the provided epitopes.

To confirm the capacity of a class II epitope-encoding minigene to induce HTLs *in vivo*, DR transgenic mice, or for those epitopes that cross react with the appropriate mouse MHC molecule, I-A^b-restricted mice, for example, are immunized intramuscularly with 100 μg of plasmid DNA. As a means of comparing the level of HTLs induced by DNA immunization, a group of control animals is also immunized with an actual peptide composition emulsified in complete Freund's adjuvant. CD4+ T cells, *i.e.* HTLs, are purified from splenocytes of immunized animals and stimulated with each of the respective compositions (peptides encoded in the minigene). The HTL response is measured using a ^3H-thymidine incorporation proliferation assay, (*see, e.g.*, Alexander *et al.* Immunity 1:751-761, 1994). The results indicate the magnitude of the HTL response, thus demonstrating the *in vivo* immunogenicity of the minigene.

DNA minigenes, constructed as described in the previous Example, can also be confirmed as a vaccine in combination with a boosting agent using a prime boost protocol. The boosting agent can consist of recombinant protein (*e.g.*, Barnett *et al.*, *Aids Res. and Human Retroviruses* 14, Supplement 3:S299-S309, 1998) or recombinant vaccinia, for example, expressing a minigene or DNA encoding the complete protein of interest (*see, e.g.*, Hanke *et al.*, *Vaccine* 16:439-445, 1998; Sedegah *et al.*, *Proc. Natl. Acad. Sci USA* 95:7648-53, 1998; Hanke and McMichael, *Immunol. Letters* 66:177-181, 1999; and Robinson *et al.*, *Nature Med.* 5:526-34, 1999).

For example, the efficacy of the DNA minigene used in a prime boost protocol is initially evaluated in transgenic mice. In this example, A2.1/K^b transgenic mice are immunized IM with 100 μg of a DNA minigene encoding the immunogenic peptides including at least one HLA-A2 supermotif-bearing peptide. After an incubation period (ranging from 3-9 weeks), the mice are boosted IP with 10^7 pfu/mouse of a recombinant vaccinia virus expressing the same sequence encoded by the DNA minigene. Control mice are immunized with 100 μg of DNA or recombinant vaccinia without the minigene sequence, or with DNA encoding the minigene, but without the vaccinia boost. After an additional incubation period of two weeks, splenocytes from the mice are immediately assayed for peptide-specific activity in an ELISPOT assay. Additionally, splenocytes are stimulated *in vitro* with the A2-restricted peptide epitopes encoded in the minigene and recombinant vaccinia, then assayed for peptide-specific activity in an alpha, beta and/or gamma IFN ELISA.

It is found that the minigene utilized in a prime-boost protocol elicits greater immune responses toward the HLA-A2 supermotif peptides than with DNA alone. Such an analysis can also be performed using HLA-A11 or HLA-B7 transgenic mouse models to assess CTL induction by HLA-A3 or HLA-B7 motif or supermotif epitopes. The use of prime boost protocols in humans is described below in the Example entitled "Induction of CTL Responses Using a Prime Boost Protocol."

Example 24: Peptide Compositions for Prophylactic Uses

Vaccine compositions of the present invention can be used to prevent 191P4D12(b) expression in persons who are at risk for tumors that bear this antigen. For example, a polyepitopic peptide epitope composition (or a nucleic acid comprising the same) containing multiple CTL and HTL epitopes such as those selected in the above Examples, which are also selected to target greater than 80% of the population, is administered to individuals at risk for a 191P4D12(b)-associated tumor.

For example, a peptide-based composition is provided as a single polypeptide that encompasses multiple epitopes. The vaccine is typically administered in a physiological solution that comprises an adjuvant, such as Incomplete Freunds Adjuvant. The dose of peptide for the initial immunization is from about 1 to about 50,000 μg, generally 100-5,000 μg, for a 70 kg patient. The initial administration of vaccine is followed by booster dosages at 4 weeks followed by evaluation of the magnitude of the immune response in the patient, by techniques that determine the presence of epitope-specific CTL populations in a PBMC sample. Additional booster doses are administered as required. The composition is found to be both safe and efficacious as a prophylaxis against 191P4D12(b)-associated disease.

Alternatively, a composition typically comprising transfecting agents is used for the administration of a nucleic acid-based vaccine in accordance with methodologies known in the art and disclosed herein.

Example 25: Polyepitopic Vaccine Compositions Derived from Native 191P4D12(b) Sequences

A native 191P4D12(b) polyprotein sequence is analyzed, preferably using computer algorithms defined for each class I and/or class II supermotif or motif, to identify "relatively short" regions of the polyprotein that comprise multiple epitopes. The "relatively short" regions are preferably less in length than an entire native antigen. This relatively short sequence that contains multiple distinct or overlapping, "nested" epitopes can be used to generate a minigene construct. The construct is engineered to express the peptide, which corresponds to the native protein sequence. The "relatively short" peptide is generally less than 250 amino acids in length, often less than 100 amino acids in length, preferably less than 75 amino acids in length, and more preferably less than 50 amino acids in length. The protein sequence of the vaccine composition is selected because it has maximal number of epitopes contained within the sequence, *i.e.*, it has a high concentration of epitopes. As noted herein, epitope motifs may be nested or overlapping (*i.e.*, frame shifted relative to one another). For example, with overlapping epitopes, two 9-mer epitopes and one 10-mer epitope can be present in a 10 amino acid peptide. Such a vaccine composition is administered for therapeutic or prophylactic purposes.

The vaccine composition will include, for example, multiple CTL epitopes from 191P4D12(b) antigen and at least one HTL epitope. This polyepitopic native sequence is administered either as a peptide or as a nucleic acid sequence which encodes the peptide. Alternatively, an analog can be made of this native sequence, whereby one or more of the epitopes comprise substitutions that alter the cross-reactivity and/or binding affinity properties of the polyepitopic peptide.

The embodiment of this example provides for the possibility that an as yet undiscovered aspect of immune system processing will apply to the native nested sequence and thereby facilitate the production of therapeutic or prophylactic immune response-inducing vaccine compositions. Additionally, such an embodiment provides for the possibility of motif-bearing epitopes for an HLA makeup(s) that is presently unknown. Furthermore, this embodiment (excluding an analoged embodiment) directs the immune response to multiple peptide sequences that are actually present in native 191P4D12(b), thus avoiding the need to evaluate any junctional epitopes. Lastly, the embodiment provides an economy of scale when producing peptide or nucleic acid vaccine compositions.

Related to this embodiment, computer programs are available in the art which can be used to identify in a target sequence, the greatest number of epitopes per sequence length.

Example 26: Polyepitopic Vaccine Compositions from Multiple Antigens

The 191P4D12(b) peptide epitopes of the present invention are used in conjunction with epitopes from other target tumor-associated antigens, to create a vaccine composition that is useful for the prevention or treatment of cancer that expresses 191P4D12(b) and such other antigens. For example, a vaccine composition can be provided as a single polypeptide that incorporates multiple epitopes from 191P4D12(b) as well as tumor-associated antigens that are often expressed with a target cancer associated with 191P4D12(b) expression, or can be administered as a composition comprising a cocktail of one or more discrete epitopes. Alternatively, the vaccine can be administered as a minigene construct or as dendritic cells which have been loaded with the peptide epitopes *in vitro*.

Example 27: Use of peptides to evaluate an immune response

Peptides of the invention may be used to analyze an immune response for the presence of specific antibodies, CTL or HTL directed to 191P4D12(b). Such an analysis can be performed in a manner described by Ogg *et al., Science* 279:2103-2106, 1998. In this Example, peptides in accordance with the invention are used as a reagent for diagnostic or prognostic purposes, not as an immunogen.

In this example highly sensitive human leukocyte antigen tetrameric complexes ("tetramers") are used for a cross-sectional analysis of, for example, 191P4D12(b) HLA-A*0201-specific CTL frequencies from HLA A*0201-positive individuals at different stages of disease or following immunization comprising a 191P4D12(b) peptide containing an A*0201 motif. Tetrameric complexes are synthesized as described (Musey *et al., N. Engl. J. Med.* 337:1267, 1997). Briefly, purified HLA heavy chain (A*0201 in this example) and β2-microglobulin are synthesized by means of a prokaryotic expression system. The heavy chain is modified by deletion of the transmembrane-cytosolic tail and COOH-terminal addition of a sequence containing a BirA enzymatic biotinylation site. The heavy chain, β2-microglobulin, and peptide are refolded by dilution. The 45-kD refolded product is isolated by fast protein liquid chromatography and then biotinylated by BirA in the presence of biotin (Sigma, St. Louis, Missouri), adenosine 5' triphosphate and magnesium. Streptavidin-phycoerythrin conjugate is added in a 1:4 molar ratio, and the tetrameric product is concentrated to 1 mg/ml. The resulting product is referred to as tetramer-phycoerythrin.

For the analysis of patient blood samples, approximately one million PBMCs are centrifuged at 300g for 5 minutes and resuspended in 50 μl of cold phosphate-buffered saline. Tri-color analysis is performed with the tetramer-phycoerythrin, along with anti-CD8-Tricolor, and anti-CD38. The PBMCs are incubated with tetramer and antibodies on ice for 30 to 60 min and then washed twice before formaldehyde fixation. Gates are applied to contain >99.98% of control samples. Controls for the tetramers include both A*0201-negative individuals and A*0201-positive non-diseased donors. The percentage of cells stained with the tetramer is then determined by flow cytometry. The results indicate the number of cells in the PBMC sample that contain epitope-restricted CTLs, thereby readily indicating the extent of immune response to the 191P4D12(b) epitope, and thus the status of exposure to 191P4D12(b), or exposure to a vaccine that elicits a protective or therapeutic response.

Example 28: Use of Peptide Epitopes to Evaluate Recall Responses

The peptide epitopes of the invention are used as reagents to evaluate T cell responses, such as acute or recall responses, in patients. Such an analysis may be performed on patients who have recovered from 191P4D12(b)-associated disease or who have been vaccinated with a 191P4D12(b) vaccine.

For example, the class I restricted CTL response of persons who have been vaccinated may be analyzed. The vaccine may be any 191P4D12(b) vaccine. PBMC are collected from vaccinated individuals and HLA typed. Appropriate peptide epitopes of the invention that, optimally, bear supermotifs to provide cross-reactivity with multiple HLA supertype family members, are then used for analysis of samples derived from individuals who bear that HLA type.

PBMC from vaccinated individuals are separated on Ficoll-Histopaque density gradients (Sigma Chemical Co., St. Louis, MO), washed three times in HBSS (GIBCO Laboratories), resuspended in RPMI-1640 (GIBCO Laboratories) supplemented with L-glutamine (2mM), penicillin (50U/ml), streptomycin (50 μg/ml), and Hepes (10mM) containing 10% heat-inactivated human AB serum (complete RPMI) and plated using microculture formats. A synthetic peptide comprising an epitope of the invention is added at 10 μg/ml to each well and HBV core 128-140 epitope is added at 1 μg/ml to each well as a source of T cell help during the first week of stimulation.

In the microculture format, 4 x 10^5 PBMC are stimulated with peptide in 8 replicate cultures in 96-well round bottom plate in 100 μl/well of complete RPMI. On days 3 and 10, 100 μl of complete RPMI and 20 U/ml final concentration of rIL-2 are added to each well. On day 7 the cultures are transferred into a 96-well flat-bottom plate and restimulated with peptide, rIL-2 and 10^5 irradiated (3,000 rad) autologous feeder cells. The cultures are tested for cytotoxic activity on day 14. A positive CTL response requires two or more of the eight replicate cultures to display greater than 10% specific ^{51}Cr release, based on comparison with non-diseased control subjects as previously described (Rehermann, *et al., Nature Med.* 2:1104,1108, 1996; Rehermann *et al., J. Clin. Invest.* 97:1655-1665, 1996; and Rehermann *et al. J. Clin. Invest.* 98:1432-1440, 1996).

Target cell lines are autologous and allogeneic EBV-transformed B-LCL that are either purchased from the American Society for Histocompatibility and Immunogenetics (ASHI, Boston, MA) or established from the pool of patients as described (Guilhot, *et al. J. Virol.* 66:2670-2678, 1992).

Cytotoxicity assays are performed in the following manner. Target cells consist of either allogeneic HLA-matched or autologous EBV-transformed B lymphoblastoid cell line that are incubated overnight with the synthetic peptide epitope of the invention at 10 μM, and labeled with 100 μCi of ^{51}Cr (Amersham Corp., Arlington Heights, IL) for 1 hour after which they are washed four times with HBSS.

Cytolytic activity is determined in a standard 4-h, split well ^{51}Cr release assay using U-bottomed 96 well plates containing 3,000 targets/well. Stimulated PBMC are tested at effector/target (E/T) ratios of 20-50:1 on day 14. Percent cytotoxicity is determined from the formula: 100 x [(experimental release-spontaneous release)/maximum release-spontaneous release)]. Maximum release is determined by lysis of targets by detergent (2% Triton X-100; Sigma Chemical Co., St. Louis, MO). Spontaneous release is <25% of maximum release for all experiments.

The results of such an analysis indicate the extent to which HLA-restricted CTL populations have been stimulated by previous exposure to 191P4D12(b) or a 191P4D12(b) vaccine.

Similarly, Class II restricted HTL responses may also be analyzed. Purified PBMC are cultured in a 96-well flat bottom plate at a density of 1.5x10^5 cells/well and are stimulated with 10 μg/ml synthetic peptide of the invention, whole 191P4D12(b) antigen, or PHA. Cells are routinely plated in replicates of 4-6 wells for each condition. After seven days of culture, the medium is removed and replaced with fresh medium containing 10U/ml IL-2. Two days later, 1 μCi ^3H-thymidine is added to each well and incubation is continued for an additional 18 hours. Cellular DNA is then harvested on glass fiber mats and analyzed for ^3H-thymidine incorporation. Antigen-specific T cell proliferation is calculated as the ratio of ^3H-thymidine incorporation in the presence of antigen divided by the ^3H-thymidine incorporation in the absence of antigen.

Example 29: Induction Of Specific CTL Response In Humans

A human clinical trial for an immunogenic composition comprising CTL and HTL epitopes of the invention is set up as an IND Phase I, dose escalation study and carried out as a randomized, double-blind, placebo-controlled trial. Such a trial is designed, for example, as follows:

A total of about 27 individuals are enrolled and divided into 3 groups:

Group I: 3 subjects are injected with placebo and 6 subjects are injected with 5 μg of peptide composition;

Group II: 3 subjects are injected with placebo and 6 subjects are injected with 50 μg peptide composition;

Group III: 3 subjects are injected with placebo and 6 subjects are injected with 500 μg of peptide composition.

After 4 weeks following the first injection, all subjects receive a booster inoculation at the same dosage.

The endpoints measured in this study relate to the safety and tolerability of the peptide composition as well as its immunogenicity. Cellular immune responses to the peptide composition are an index of the intrinsic activity of this the peptide composition, and can therefore be viewed as a measure of biological efficacy. The following summarize the clinical and laboratory data that relate to safety and efficacy endpoints.

Safety: The incidence of adverse events is monitored in the placebo and drug treatment group and assessed in terms of degree and reversibility.

Evaluation of Vaccine Efficacy: For evaluation of vaccine efficacy, subjects are bled before and after injection. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

The vaccine is found to be both safe and efficacious.

Example 30: Phase II Trials In Patients Expressing 191P4D12(b)

Phase II trials are performed to study the effect of administering the CTL-HTL peptide compositions to patients having cancer that expresses 191P4D12(b). The main objectives of the trial are to determine an effective dose and regimen for inducing CTLs in cancer patients that express 191P4D12(b), to establish the safety of inducing a CTL and HTL response in these patients, and to see to what extent activation of CTLs improves the clinical picture of these patients, as manifested, e.g., by the reduction and/or shrinking of lesions. Such a study is designed, for example, as follows:

The studies are performed in multiple centers. The trial design is an open-label, uncontrolled, dose escalation protocol wherein the peptide composition is administered as a single dose followed six weeks later by a single booster shot of the same dose. The dosages are 50, 500 and 5,000 micrograms per injection. Drug-associated adverse effects (severity and reversibility) are recorded.

There are three patient groupings. The first group is injected with 50 micrograms of the peptide composition and the second and third groups with 500 and 5,000 micrograms of peptide composition, respectively. The patients within each group range in age from 21-65 and represent diverse ethnic backgrounds. All of them have a tumor that expresses 191P4D12(b).

Clinical manifestations or antigen-specific T-cell responses are monitored to assess the effects of administering the peptide compositions. The vaccine composition is found to be both safe and efficacious in the treatment of 191P4D12(b)-associated disease.

Example 31: Induction of CTL Responses Using a Prime Boost Protocol

A prime boost protocol similar in its underlying principle to that used to confirm the efficacy of a DNA vaccine in transgenic mice, such as described above in the Example entitled "The Plasmid Construct and the Degree to Which It Induces Immunogenicity," can also be used for the administration of the vaccine to humans. Such a vaccine regimen can include an initial administration of, for example, naked DNA followed by a boost using recombinant virus encoding the vaccine, or recombinant protein/polypeptide or a peptide mixture administered in an adjuvant.

For example, the initial immunization may be performed using an expression vector, such as that constructed in the Example entitled "Construction of "Minigene" Multi-Epitope DNA Plasmids" in the form of naked nucleic acid administered IM (or SC or ID) in the amounts of 0.5-5 mg at multiple sites. The nucleic acid (0.1 to 1000 μg) can also be administered using a gene gun. Following an incubation period of 3-4 weeks, a booster dose is then administered. The booster can be

recombinant fowlpox virus administered at a dose of 5-10^7 to 5x10^9 pfu. An alternative recombinant virus, such as an MVA, canarypox, adenovirus, or adeno-associated virus, can also be used for the booster, or the polyepitopic protein or a mixture of the peptides can be administered. For evaluation of vaccine efficacy, patient blood samples are obtained before immunization as well as at intervals following administration of the initial vaccine and booster doses of the vaccine. Peripheral blood mononuclear cells are isolated from fresh heparinized blood by Ficoll-Hypaque density gradient centrifugation, aliquoted in freezing media and stored frozen. Samples are assayed for CTL and HTL activity.

Analysis of the results indicates that a magnitude of response sufficient to achieve a therapeutic or protective immunity against 191P4D12(b) is generated.

Example 32: Administration of Vaccine Compositions Using Dendritic Cells (DC)

Vaccines comprising peptide epitopes of the invention can be administered using APCs, or "professional" APCs such as DC. In this example, peptide-pulsed DC are administered to a patient to stimulate a CTL response *in vivo*. In this method, dendritic cells are isolated, expanded, and pulsed with a vaccine comprising peptide CTL and HTL epitopes of the invention. The dendritic cells are infused back into the patient to elicit CTL and HTL responses *in vivo*. The induced CTL and HTL then destroy or facilitate destruction, respectively, of the target cells that bear the 191P4D12(b) protein from which the epitopes in the vaccine are derived.

For example, a cocktail of epitope-comprising peptides is administered *ex vivo* to PBMC, or isolated DC therefrom. A pharmaceutical to facilitate harvesting of DC can be used, such as Progenipoietin™ (Monsanto, St. Louis, MO) or GM-CSF/IL-4. After pulsing the DC with peptides, and prior to reinfusion into patients, the DC are washed to remove unbound peptides.

As appreciated clinically, and readily determined by one of skill based on clinical outcomes, the number of DC reinfused into the patient can vary (*see, e.g., Nature Med.* 4:328, 1998; *Nature Med.* 2:52, 1996 and *Prostate* 32:272, 1997). Although 2-50 x 10^6 DC per patient are typically administered, larger number of DC, such as 10^7 or 10^8 can also be provided. Such cell populations typically contain between 50-90% DC.

In some embodiments, peptide-loaded PBMC are injected into patients without purification of the DC. For example, PBMC generated after treatment with an agent such as Progenipoietin™ are injected into patients without purification of the DC. The total number of PBMC that are administered often ranges from 10^8 to 10^{10}. Generally, the cell doses injected into patients is based on the percentage of DC in the blood of each patient, as determined, for example, by immunofluorescence analysis with specific anti-DC antibodies. Thus, for example, if Progenipoietin™ mobilizes 2% DC in the peripheral blood of a given patient, and that patient is to receive 5 x 10^6 DC, then the patient will be injected with a total of 2.5 x 10^8 peptide-loaded PBMC. The percent DC mobilized by an agent such as Progenipoietin™ is typically estimated to be between 2-10%, but can vary as appreciated by one of skill in the art.

Ex vivo activation of CTL/HTL responses

Alternatively, *ex vivo* CTL or HTL responses to 191P4D12(b) antigens can be induced by incubating, in tissue culture, the patient's, or genetically compatible, CTL or HTL precursor cells together with a source of APC, such as DC, and immunogenic peptides. After an appropriate incubation time (typically about 7-28 days), in which the precursor cells are activated and expanded into effector cells, the cells are infused into the patient, where they will destroy (CTL) or facilitate destruction (HTL) of their specific target cells, *i.e.*, tumor cells.

Example 33: An Alternative Method of Identifying and Confirming Motif-Bearing Peptides

Another method of identifying and confirming motif-bearing peptides is to elute them from cells bearing defined MHC molecules. For example, EBV transformed B cell lines used for tissue typing have been extensively characterized to

determine which HLA molecules they express. In certain cases these cells express only a single type of HLA molecule. These cells can be transfected with nucleic acids that express the antigen of interest, e.g. 191P4D12(b). Peptides produced by endogenous antigen processing of peptides produced as a result of transfection will then bind to HLA molecules within the cell and be transported and displayed on the cell's surface. Peptides are then eluted from the HLA molecules by exposure to mild acid conditions and their amino acid sequence determined, e.g., by mass spectral analysis (e.g., Kubo *et al., J. Immunol.* 152:3913, 1994). Because the majority of peptides that bind a particular HLA molecule are motif-bearing, this is an alternative modality for obtaining the motif-bearing peptides correlated with the particular HLA molecule expressed on the cell.

Alternatively, cell lines that do not express endogenous HLA molecules can be transfected with an expression construct encoding a single HLA allele. These cells can then be used as described, *i.e.*, they can then be transfected with nucleic acids that encode 191P4D12(b) to isolate peptides corresponding to 191P4D12(b) that have been presented on the cell surface. Peptides obtained from such an analysis will bear motif(s) that correspond to binding to the single HLA allele that is expressed in the cell.

As appreciated by one in the art, one can perform a similar analysis on a cell bearing more than one HLA allele and subsequently determine peptides specific for each HLA allele expressed. Moreover, one of skill would also recognize that means other than transfection, such as loading with a protein antigen, can be used to provide a source of antigen to the cell.

Example 34: Complementary Polynucleotides

Sequences complementary to the 191P4D12(b)-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring 191P4D12(b). Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using, e.g., OLIGO 4.06 software (National Biosciences) and the coding sequence of 191P4D12(b). To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to a 191P4D12(b)-encoding transcript.

Example 35: Purification of Naturally-occurring or Recombinant 191P4D12(b) Using 191P4D12(b)-Specific Antibodies

Naturally occurring or recombinant 191P4D12(b) is substantially purified by immunoaffinity chromatography using antibodies specific for 191P4D12(b). An immunoaffinity column is constructed by covalently coupling anti-191P4D12(b) antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE™ (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing 191P4D12(b) are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of 191P4D12(b) (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/191P4D12(b) binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and GCR.P is collected.

Example 36: Identification of Molecules Which Interact with 191P4D12(b)

191P4D12(b), or biologically active fragments thereof, are labeled with 121 1 Bolton-Hunter reagent. (See, e.g., Bolton *et al.* (1973) Biochem. J. 133:529.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled 191P4D12(b), washed, and any wells with labeled 191P4D12(b) complex are assayed. Data

obtained using different concentrations of 191P4D12(b) are used to calculate values for the number, affinity, and association of 191P4D12(b) with the candidate molecules.

Example 37: *In Vivo* Assay for 191P4D12(b) Tumor Growth Promotion

The effect of the 191P4D12(b) protein on tumor cell growth is evaluated *in vivo* by evaluating tumor development and growth of cells expressing or lacking 191P4D12(b). For example, SCID mice are injected subcutaneously on each flank with 1 x 10^6 of either 3T3, prostate (e.g. PC3 cells), bladder (e.g. UM-UC3 cells), kidney (e.g. CaKi cells), or lung (e.g. A427 cells) cancer cell lines containing tkNeo empty vector or 191P4D12(b). At least two strategies may be used: (1) Constitutive 191P4D12(b) expression under regulation of a promoter such as a constitutive promoter obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), or from heterologous mammalian promoters, *e.g.*, the actin promoter or an immunoglobulin promoter, provided such promoters are compatible with the host cell systems, and (2) Regulated expression under control of an inducible vector system, such as ecdysone, tetracycline, etc., provided such promoters are compatible with the host cell systems. Tumor volume is then monitored by caliper measurement at the appearance of palpable tumors and followed over time to determine if 191P4D12(b)-expressing cells grow at a faster rate and whether tumors produced by 191P4D12(b)-expressing cells demonstrate characteristics of altered aggressiveness (e.g. enhanced metastasis, vascularization, reduced responsiveness to chemotherapeutic drugs).

Additionally, mice can be implanted with 1 x 10^5 of the same cells orthotopically to determine if 191P4D12(b) has an effect on local growth in the prostate, and whether 191P4D12(b) affects the ability of the cells to metastasize, specifically to lymph nodes, and bone (Miki T et al, Oncol Res. 2001;12:209; Fu X et al, Int J Cancer. 1991, 49:938). The effect of 191P4D12(b) on bone tumor formation and growth may be assessed by injecting tumor cells intratibially.

The assay is also useful to determine the 191P4D12(b) inhibitory effect of candidate therapeutic compositions, such as for example, 191P4D12(b) intrabodies, 191P4D12(b) antisense molecules and ribozymes.

Example 38: 191P4D12(b) Monoclonal Antibody-mediated Inhibition of Tumors *In Vivo*

The significant expression of 191P4D12(b) in cancer tissues and surface localization, together with its restrictive expression in normal tissues makes 191P4D12(b) a good target for antibody therapy. Similarly, 191P4D12(b) is a target for T cell-based immunotherapy. Thus, the therapeutic efficacy of anti-191P4D12(b) mAbs in human cancer xenograft mouse models, including prostate, lung, bladder, kidney and other -191P4D12(b)cancers listed in table 1, is evaluated by using recombinant cell lines such as PC3-191P4D12(b), UM-UC3-191P4D12(b), CaKi--191P4D12(b), A427-191P4D12(b) and 3T3-191P4D12(b) (see, e.g., Kaighn, M.E., *et al.*, Invest Urol, 1979. 17(1): 16-23), as well as human prostate, kidney and bladder xenograft models such as LAPC 9AD, AGS-K3 and AGS-B1 (Saffran et al PNAS 1999, 10:1073-1078).

Antibody efficacy on tumor growth and metastasis formation is studied, e.g., in a mouse orthotopic prostate, kidney, bladder, and lung cancer xenograft models. The antibodies can be unconjugated, as discussed in this Example, or can be conjugated to a therapeutic modality, as appreciated in the art. Anti-191P4D12(b) mAbs inhibit formation of tumors in prostate kidney, bladder and lung xenografts. Anti-191P4D12(b) mAbs also retard the growth of established orthotopic tumors and prolonged survival of tumor-bearing mice. These results indicate the utility of anti-191P4D12(b) mAbs in the treatment of local and advanced stages several solid tumors. (See, e.g., Saffran, D., et al., PNAS 10:1073-1078).

Administration of the anti-191P4D12(b) mAbs led to retardation of established orthotopic tumor growth and inhibition of metastasis to distant sites, resulting in a significant prolongation in the survival of tumor-bearing mice. These

studies indicate that 191P4D12(b) as an attractive target for immunotherapy and demonstrate the therapeutic potential of anti-191P4D12(b) mAbs for the treatment of local and metastatic prostate cancer. This example indicates that unconjugated 191P4D12(b) monoclonal antibodies are effective to inhibit the growth of human prostate, kidney, bladder and lung tumor xenografts grown in SCID mice; accordingly a combination of such efficacious monoclonal antibodies is also effective.

Tumor inhibition using multiple unconjugated 191P4D12(b) mAbs

Materials and Methods

191P4D12(b) Monoclonal Antibodies:

Monoclonal antibodies are raised against 191P4D12(b) as described in the Example entitled "Generation of 191P4D12(b) Monoclonal Antibodies (mAbs)." The antibodies are characterized by ELISA, Western blot, FACS, and immunoprecipitation for their capacity to bind 191P4D12(b). Epitope mapping data for the anti-191P4D12(b) mAbs, as determined by ELISA and Western analysis, recognize epitopes on the 191P4D12(b) protein. Immunohistochemical analysis of prostate, kidney, bladder and lung cancer tissues and cells with these antibodies is performed.

The monoclonal antibodies are purified from ascites or hybridoma tissue culture supernatants by Protein-G Sepharose chromatography, dialyzed against PBS, filter sterilized, and stored at -20°C. Protein determinations are performed by a Bradford assay (Bio-Rad, Hercules, CA). A therapeutic monoclonal antibody or a cocktail comprising a mixture of individual monoclonal antibodies is prepared and used for the treatment of mice receiving subcutaneous or orthotopic injections of PC3, UM-UC3, CaKi and A427 tumor xenografts.

Cell Lines and Xenografts

The cancer cell lines, PC3, UM-UC3, CaKi, and A427 cell line as well as the fibroblast line NIH 3T3 (American Type Culture Collection) are maintained in RPMI (PC3) and DMEM (UM-UC3, CaKi, and A427, 3T3) respectively, supplemented with L-glutamine and 10% FBS.

PC3-191P4D12(b), UM-UC3-191P4D12(b), CaKi-191P4D12(b), A427-191P4D12(b) and 3T3-191P4D12(b) cell populations are generated by retroviral gene transfer as described in Hubert, R.S., et al., Proc Natl Acad Sci U S A, 1999. 96(25): 14523. The LAPC-9 xenograft, which expresses a wild-type androgen receptor and produces prostate-specific antigen (PSA), is passaged in 6- to 8-week-old male ICR-severe combined immunodeficient (SCID) mice (Taconic Farms) by s.c. trocar implant (Craft, N., et al., Nat Med. 1999, 5:280). Single-cell suspensions of LAPC-9 tumor cells are prepared as described in Craft, et al. Similarly, kidney (AGS-K3) and bladder (AGS-B1) patient-derived xenografts are passaged in 6- to 8-week-old male ICR-SCID mice.

Xenograft Mouse Models.

Subcutaneous (s.c.) tumors are generated by injection of 2×10^6 cancer cells mixed at a 1:1 dilution with Matrigel (Collaborative Research) in the right flank of male SCID mice. To test antibody efficacy on tumor formation, i.e. antibody injections are started on the same day as tumor-cell injections. As a control, mice are injected with either purified mouse IgG (ICN) or PBS; or a purified monoclonal antibody that recognizes an irrelevant antigen not expressed in human cells. In preliminary studies, no difference is found between mouse IgG or PBS on tumor growth. Tumor sizes are determined by caliper measurements, and the tumor volume is calculated as length x width x height. Mice with Subcutaneous tumors greater than 1.5 cm in diameter are sacrificed.

Orthotopic injections are performed under anesthesia by using ketamine/xylazine. For prostate orthotopic studies, an incision is made through the abdomen to expose the prostate and LAPC or PC3 tumor cells (5×10^5) mixed with Matrigel are injected into the prostate capsule in a 10-µl volume. To monitor tumor growth, mice are palpated and blood is collected on a weekly basis to measure PSA levels. For kidney orthotopic models, an incision is made through the abdominal muscles to

expose the kidney. AGS-K3 cells mixed with Matrigel are injected under the kidney capsule. The mice are segregated into groups for the appropriate treatments, with anti-191P4D12(b) or control mAbs being injected i.p.

Anti-191P4D12(b) mAbs Inhibit Growth of 191P4D12(b)-Expressing Xenograft-Cancer Tumors

The effect of anti-191P4D12(b) mAbs on tumor formation is tested by using cell line (e.g. PC3, UM-UC3, CaKi, A427, and 3T3) and patient-derived tumor (e.g. LAPC9, AGS-K3, AGS-B1) orthotopic models. As compared with the s.c. tumor model, the orthotopic model, which requires injection of tumor cells directly in the mouse organ, such as prostate, bladder, kidney or lung, results in a local tumor growth, development of metastasis in distal sites, deterioration of mouse health, and subsequent death (Saffran, D., et al., PNAS supra). The features make the orthotopic model more representative of human disease progression and allowed us to follow the therapeutic effect of mAbs on clinically relevant end points.
For example, tumor cells are injected into the mouse prostate, and 2 days later, the mice are segregated into two groups and treated with either: a) 200-500μg, of anti-191P4D12(b) Ab, or b) PBS three times per week for two to five weeks.

A major advantage of the orthotopic cancer models is the ability to study the development of metastases. Formation of metastasis in mice bearing established orthotopic tumors is studies by IHC analysis on lung sections using an antibody against a tumor-specific cell-surface protein such as anti-CK20 for prostate cancer (Lin S et al, Cancer Detect Prev. 2001;25:202).

Another advantage of xenograft cancer models is the ability to study neovascularization and angiogenesis. Tumor growth is partly dependent on new blood vessel development. Although the capillary system and developing blood network is of host origin, the initiation and architecture of the neovascular is regulated by the xenograft tumor (Davidoff AM et al, Clin Cancer Res. 2001;7:2870; Solesvik O et al,, Eur J Cancer Clin Oncol. 1984, 20:1295). The effect of antibody and small molecule on neovascularization is studied in accordance with procedures known in the art, such as by IHC analysis of tumor tissues and their surrounding microenvironment.

Mice bearing established orthotopic tumors are administered 1000μg injections of either anti-191P4D12(b) mAb or PBS over a 4-week period. Mice in both groups are allowed to establish a high tumor burden, to ensure a high frequency of metastasis formation in mouse lungs. Mice then are killed and their bladders, livers, bone and lungs are analyzed for the presence of tumor cells by IHC analysis. These studies demonstrate a broad anti-tumor efficacy of anti-191P4D12(b) antibodies on initiation and progression of prostate cancer in xenograft mouse models. Anti-191P4D12(b) antibodies inhibit tumor formation of tumors as well as retarding the growth of already established tumors and prolong the survival of treated mice. Moreover, anti-191P4D12(b) mAbs demonstrate a dramatic inhibitory effect on the spread of local prostate tumor to distal sites, even in the presence of a large tumor burden. Thus, anti-191P4D12(b) mAbs are efficacious on major clinically relevant end points (tumor growth), prolongation of survival, and health.

Example 39: Therapeutic and Diagnostic use of Anti-191P4D12(b) Antibodies in Humans.

Anti-191P4D12(b) monoclonal antibodies are safely and effectively used for diagnostic, prophylactic, prognostic and/or therapeutic purposes in humans. Western blot and immunohistochemical analysis of cancer tissues and cancer xenografts with anti-191P4D12(b) mAb show strong extensive staining in carcinoma but significantly lower or undetectable levels in normal tissues. Detection of 191P4D12(b) in carcinoma and in metastatic disease demonstrates the usefulness of the mAb as a diagnostic and/or prognostic indicator. Anti-191P4D12(b) antibodies are therefore used in diagnostic applications such as immunohistochemistry of kidney biopsy specimens to detect cancer from suspect patients.

As determined by flow cytometry, anti-191P4D12(b) mAb specifically binds to carcinoma cells. Thus, anti-191P4D12(b) antibodies are used in diagnostic whole body imaging applications, such as radioimmunoscintigraphy and radioimmunotherapy, (see, e.g., Potamianos S., et. al. Anticancer Res 20(2A):925-948 (2000)) for the detection of localized

and metastatic cancers that exhibit expression of 191P4D12(b). Shedding or release of an extracellular domain of 191P4D12(b) into the extracellular milieu, such as that seen for alkaline phosphodiesterase B10 (Meerson, N. R., Hepatology 27:563-568 (1998)), allows diagnostic detection of 191P4D12(b) by anti-191P4D12(b) antibodies in serum and/or urine samples from suspect patients.

Anti-191P4D12(b) antibodies that specifically bind 191P4D12(b) are used in therapeutic applications for the treatment of cancers that express 191P4D12(b). Anti-191P4D12(b) antibodies are used as an unconjugated modality and as conjugated form in which the antibodies are attached to one of various therapeutic or imaging modalities well known in the art, such as a prodrugs, enzymes or radioisotopes. In preclinical studies, unconjugated and conjugated anti-191P4D12(b) antibodies are tested for efficacy of tumor prevention and growth inhibition in the SCID mouse cancer xenograft models, e.g., kidney cancer models AGS-K3 and AGS-K6, (see, e.g., the Example entitled "191P4D12(b) Monoclonal Antibody-mediated Inhibition of Bladder and Lung Tumors *In Vivo*"). Either conjugated and unconjugated anti-191P4D12(b) antibodies are used as a therapeutic modality in human clinical trials either alone or in combination with other treatments as described in following Examples.

Example 40: Human Clinical Trials for the Treatment and Diagnosis of Human Carcinomas through use of Human Anti-191P4D12(b) Antibodies *In vivo*

Antibodies are used in accordance with the present invention which recognize an epitope on 191P4D12(b), and are used in the treatment of certain tumors such as those listed in Table I. Based upon a number of factors, including 191P4D12(b) expression levels, tumors such as those listed in Table I are presently preferred indications. In connection with each of these indications, three clinical approaches are successfully pursued.

I.) Adjunctive therapy: In adjunctive therapy, patients are treated with anti-191P4D12(b) antibodies in combination with a chemotherapeutic or antineoplastic agent and/or radiation therapy. Primary cancer targets, such as those listed in Table I, are treated under standard protocols by the addition anti-191P4D12(b) antibodies to standard first and second line therapy. Protocol designs address effectiveness as assessed by reduction in tumor mass as well as the ability to reduce usual doses of standard chemotherapy. These dosage reductions allow additional and/or prolonged therapy by reducing dose-related toxicity of the chemotherapeutic agent. Anti-191P4D12(b) antibodies are utilized in several adjunctive clinical trials in combination with the chemotherapeutic or antineoplastic agents adriamycin (advanced prostrate carcinoma), cisplatin (advanced head and neck and lung carcinomas), taxol (breast cancer), and doxorubicin (preclinical).

II.) Monotherapy: In connection with the use of the anti-191P4D12(b) antibodies in monotherapy of tumors, the antibodies are administered to patients without a chemotherapeutic or antineoplastic agent. In one embodiment, monotherapy is conducted clinically in end stage cancer patients with extensive metastatic disease. Patients show some disease stabilization. Trials demonstrate an effect in refractory patients with cancerous tumors.

III.) Imaging Agent: Through binding a radionuclide (e.g., iodine or yttrium (I^{131}, Y^{90}) to anti-191P4D12(b) antibodies, the radiolabeled antibodies are utilized as a diagnostic and/or imaging agent. In such a role, the labeled antibodies localize to both solid tumors, as well as, metastatic lesions of cells expressing 191P4D12(b). In connection with the use of the anti-191P4D12(b) antibodies as imaging agents, the antibodies are used as an adjunct to surgical treatment of solid tumors, as both a pre-surgical screen as well as a post-operative follow-up to determine what tumor remains and/or returns. In one embodiment, a (^{111}In)-191P4D12(b) antibody is used as an imaging agent in a Phase I human clinical trial in patients having a carcinoma that expresses 191P4D12(b) (by analogy see, e.g., Divgi *et al. J. Natl. Cancer Inst.* 83:97-104 (1991)). Patients are followed with standard anterior and posterior gamma camera. The results indicate that primary lesions and metastatic lesions are identified.

Dose and Route of Administration

As appreciated by those of ordinary skill in the art, dosing considerations can be determined through comparison with the analogous products that are in the clinic. Thus, anti-191P4D12(b) antibodies can be administered with doses in the range of 5 to 400 mg/m ^{2}, with the lower doses used, e.g., in connection with safety studies. The affinity of anti-191P4D12(b) antibodies relative to the affinity of a known antibody for its target is one parameter used by those of skill in the art for determining analogous dose regimens. Further, anti-191P4D12(b) antibodies that are fully human antibodies, as compared to the chimeric antibody, have slower clearance; accordingly, dosing in patients with such fully human anti-191P4D12(b) antibodies can be lower, perhaps in the range of 50 to 300 mg/m^2, and still remain efficacious. Dosing in mg/m^2, as opposed to the conventional measurement of dose in mg/kg, is a measurement based on surface area and is a convenient dosing measurement that is designed to include patients of all sizes from infants to adults.

Three distinct delivery approaches are useful for delivery of anti-191P4D12(b) antibodies. Conventional intravenous delivery is one standard delivery technique for many tumors. However, in connection with tumors in the peritoneal cavity, such as tumors of the ovaries, biliary duct, other ducts, and the like, intraperitoneal administration may prove favorable for obtaining high dose of antibody at the tumor and to also minimize antibody clearance. In a similar manner, certain solid tumors possess vasculature that is appropriate for regional perfusion. Regional perfusion allows for a high dose of antibody at the site of a tumor and minimizes short term clearance of the antibody.

Clinical Development Plan (CDP)

Overview: The CDP follows and develops treatments of anti-191P4D12(b) antibodies in connection with adjunctive therapy, monotherapy, and as an imaging agent. Trials initially demonstrate safety and thereafter confirm efficacy in repeat doses. Trails are open label comparing standard chemotherapy with standard therapy plus anti-191P4D12(b) antibodies. As will be appreciated, one criteria that can be utilized in connection with enrollment of patients is 191P4D12(b) expression levels in their tumors as determined by biopsy.

As with any protein or antibody infusion-based therapeutic, safety concerns are related primarily to (i) cytokine release syndrome, i.e., hypotension, fever, shaking, chills; (ii) the development of an immunogenic response to the material (i.e., development of human antibodies by the patient to the antibody therapeutic, or HAHA response); and, (iii) toxicity to normal cells that express 191P4D12(b). Standard tests and follow-up are utilized to monitor each of these safety concerns. Anti-191P4D12(b) antibodies are found to be safe upon human administration.

Example 41: Human Clinical Trial Adjunctive Therapy with Human Anti-191P4D12(b) Antibody and Chemotherapeutic Agent

A phase I human clinical trial is initiated to assess the safety of six intravenous doses of a human anti-191P4D12(b) antibody in connection with the treatment of a solid tumor, e.g., a cancer of a tissue listed in Table I. In the study, the safety of single doses of anti-191P4D12(b) antibodies when utilized as an adjunctive therapy to an antineoplastic or chemotherapeutic agent as defined herein, such as, without limitation: cisplatin, topotecan, doxorubicin, adriamycin, taxol, or the like, is assessed. The trial design includes delivery of six single doses of an anti-191P4D12(b) antibody with dosage of antibody escalating from approximately about 25 mg/m ^{2} to about 275 mg/m ^{2} over the course of the treatment in accordance with the following schedule:

	Day 0	Day 7	Day 14	Day 21	Day 28	Day 35
mAb Dose	25 mg/m^2	75 mg/m^2	125 mg/m^2	175 mg/m^2	225 mg/m^2	275 mg/m^2
Chemotherapy (standard dose)	+	+	+	+	+	+

Patients are closely followed for one-week following each administration of antibody and chemotherapy. In particular, patients are assessed for the safety concerns mentioned above: (i) cytokine release syndrome, i.e., hypotension, fever, shaking, chills; (ii) the development of an immunogenic response to the material (i.e., development of human antibodies by the patient to the human antibody therapeutic, or HAHA response); and, (iii) toxicity to normal cells that express 191P4D12(b). Standard tests and follow-up are utilized to monitor each of these safety concerns. Patients are also assessed for clinical outcome, and particularly reduction in tumor mass as evidenced by MRI or other imaging.

The anti-191P4D12(b) antibodies are demonstrated to be safe and efficacious, Phase II trials confirm the efficacy and refine optimum dosing.

Example 42: Human Clinical Trial: Monotherapy with Human Anti-191P4D12(b) Antibody

Anti-191P4D12(b) antibodies are safe in connection with the above-discussed adjunctive trial, a Phase II human clinical trial confirms the efficacy and optimum dosing for monotherapy. Such trial is accomplished, and entails the same safety and outcome analyses, to the above-described adjunctive trial with the exception being that patients do not receive chemotherapy concurrently with the receipt of doses of anti-191P4D12(b) antibodies.

Example 43: Human Clinical Trial: Diagnostic Imaging with Anti-191P4D12(b) Antibody

Once again, as the adjunctive therapy discussed above is safe within the safety criteria discussed above, a human clinical trial is conducted concerning the use of anti-191P4D12(b) antibodies as a diagnostic imaging agent. The protocol is designed in a substantially similar manner to those described in the art, such as in Divgi *et al. J. Natl. Cancer Inst.* 83:97-104 (1991). The antibodies are found to be both safe and efficacious when used as a diagnostic modality.

Example 44: Homology Comparison of 191P4D12(b) to Known Sequences

The human 191P4D12(b) protein exhibit a high degree of homology to a known human protein, namely Ig superfamily receptor LNIR (gi 14714574), also known as human nectin 4 (gi 16506807). Human LNIR shows 100% identity to 191P4D12(b) at the protein level. The mouse homolog of 191P4D12(b) has been identified as murine nectin 4 (gi 18874521). It shows strong homolcgy to 191P4D12(b), exhibiting 92% identity and 95% homology to 191P4D12(b). (See, Figure 4).

The prototype member of the 191P4D12(b) family, 191P4D12(b)v.1, is a 510 amino acids protein, with the N-terminus located extracellulary and intracellular C-terminus. Initial bioinformatics analysis using topology prediction programs suggested that 191P2D14 may contain 2 transmembranes based on hydrophobicity profile. However, the first hydrophobic domain was identified as a signal sequence, rendering 191P2D12 a type I membrane protein, with an extracellular N-terminus.

The 191P4D12(b) gene has several variants, including one SNP represented in 191P4D12(b) v.2, an N-terminal deletion variant represented in 191P4D12(b) v.6 and 191P4D12(b) v.7 which lacks 25 amino acids between amino acids 411 and 412 of 191P4D12(b) v.1.

Motif analysis revealed the presence of several protein functional motifs in the 191P4D12(b) protein (Table L). Two immunoglobulin domains have been identified at positions 45-129 and 263-317. In addition, 191P4D12(b) contains a cadherin signature which includes and RGD sequence. Immunoglobulin domains are found in numerous proteins and participate in protein-protein such including protein-ligand interactions (Weismann et al, J Mol Med 2000, 78:247). In addition, Ig-domains function in cell adhesion, allowing the interaction of leukocytes and blood-born cells with the endothelium (Wang and Springer, Immunol Rev 1998, 163:197). Cadherins are single transmembrane proteins containing immunoglobulin like domains, and are involved in cell adhesion and sorting (Shan et al, Biophys Chem 1999, 82:157). They mediate tissue-specific cell adhesion, such as adhesion of lymphocytes to the surface of epithelial cells. Finally, the closest homolog to 191P4D12(b) is Nectin4, a known adhesion molecule that regulates epithelial and endothelial junctions, strongly suggesting that 191P4D12(b) participates in cell adhesion (Reymond N et al, J Biol Chem 2001, 276:43205).

The motifs found in 191P4D12(b) can participate in tumor growth and progression by enhancing the initial stages of tumorigenesis, such as tumor take or establishment of a tumor, by allowing adhesion to basement membranes and surrounding cells, by mediating cell communication and survival.

Accordingly, when 191P4D12(b) functions as a regulator of tumor establishment, tumor formation, tumor growth, cell signaling or as a modulator of transcription involved in activating genes associated with survival, invasion, tumorigenesis or proliferation, 191P4D12(b) is used for therapeutic, diagnostic, prognostic and/or preventative purposes. In addition, when a molecule, such as a variant or SNP of 191P4D12(b) is expressed in cancerous tissues, such as those listed in Table I, they are used for therapeutic, diagnostic, prognostic and/or preventative purposes.

Example 45: Regulation of Transcription

The cell surface localization of 191P4D12(b) coupled to the presence of Ig-domains within its sequence indicate that 191P4D12(b) modulates signal transduction and the transcriptional regulation of eukaryotic genes. Regulation of gene expression is confirmed, e.g., by studying gene expression in cells expressing or lacking 191P4D12(b). For this purpose, two types of experiments are performed.

In the first set of experiments, RNA from parental and 191P4D12(b)-expressing cells are extracted and hybridized to commercially available gene arrays (Clontech) (Smid-Koopman E et al. Br J Cancer. 2000. 83:246). Resting cells as well as cells treated with FBS, androgen or growth factors are compared. Differentially expressed genes are identified in accordance with procedures known in the art. The differentially expressed genes are then mapped to biological pathways (Chen K et al. Thyroid. 2001. 11:41.).

In the second set of experiments, specific transcriptional pathway activation is evaluated using commercially available (Stratagene) luciferase reporter constructs including: NFkB-luc, SRE-luc, ELK1-luc, ARE-luc, p53-luc, and CRE-luc. These transcriptional reporters contain consensus binding sites for known transcription factors that lie downstream of well-characterized signal transduction pathways, and represent a good tool to ascertain pathway activation and screen for positive and negative modulators of pathway activation.

Thus, 191P4D12(b) plays a role in gene regulation, and it is used as a target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 46: Identification and Confirmation of Potential Signal Transduction Pathways

Many mammalian proteins have been reported to interact with signaling molecules and to participate in regulating signaling pathways. (J Neurochem. 2001; 76:217-223). Immunoglobulin-like molecules in particular has been associated with several tyrpsine kinases including Lyc, Blk, syk (), the MAPK signaling cascade that control cell mitogenesis and calcium flux (Vilen J et al, J Immunol 1997, 159:231; Jiang F, Jia Y, Cohen I. Blood. 2002, 99:3579). In addition, the 191P4D12(b)

protein contains several phosphorylation sites (see Table VI) indicating an association with specific signaling cascades. Using immunoprecipitation and Western blotting techniques, proteins are identified that associate with 191P4D12(b) and mediate signaling events. Several pathways known to play a role in cancer biology can be regulated by 191P4D12(b), including phospholipid pathways such as PI3K, AKT, etc, adhesion and migration pathways, including FAK, Rho, Rac-1, catenin, etc, as well as mitogenic/survival cascades such as ERK, p38, etc (Cell Growth Differ. 2000,11:279; J Biol Chem. 1999, 274:801; Oncogene. 2000, 19:3003, J. Cell Biol. 1997, 138:913.).). In order to determine whether expression of 191P4D12(b) is sufficient to regulate specific signaling pathways not otherwise active in resting PC3 cells, the effect of these genes on the activation of the p38 MAPK cascade was investigated in the prostate cancer cell line PC3 (Figure 21A-B). Activation of the p38 kinase is dependent on its phosphorylation on tyrosine and serine residues. Phosphorylated p38 can be distinguished from the non-phosphorylated state by a Phospho-p38 mAb. This phospho-specific Ab was used to study the phosphorylation state of p38 in engineered PC3 cell lines.

PC3 cells stably expressing 191P4D12(b) neo were grown overnight in either 1% or 10% FBS. Whole cell lysates were analyzed by western blotting. PC3 cells treated with the known p38 activators, NaSal or TNF, were used as a positive control. The results show that while expression of the control neo gene has no effect on p38 phosphorylation, expression of 191P4D12(b) in PC3 cells is sufficient to induce the activation of the p38 pathway (Figure 21A). The results were verified using western blotting with an anti-p38 Ab, which shows equal protein loading on the gels (Figure 21B).

In another set of experiments, the sufficiency of expression of 191P4D12(b) in the prostate cancer cell line PC3 to activate the mitogenic MAPK pathway, namely the ERK cascade, was examined (Figure 22A-B). Activation of ERK is dependent on its phosphorylation on tyrosine and serine residues. Phosphorylated ERK can be distinguished from the non-phosphorylated state by a Phospho-ERK mAb. This phospho-specific Ab was used to study the phosphorylation state of ERK in engineered PC3 cell lines. PC3 cells, expressing an activated form of Ras, were used as a positive control.

The results show that while expression of the control neo gene has no effect on ERK phosphorylation, expression of 191P4D12(b) in PC3 cells is sufficient to induce an increase in ERK phosphorylation (Figure 22A). These results were verified using anti-ERK western blotting (Figure 22B) and confirm the activation of the ERK pathway by 191P4D12(b) and STEAP-2.

Since FBS contains several components that may contribute to receptor-mediated ERK activation, we examined the effect of 191P4D12(b) in low and optimal levels of FBS. PC3 cells expressing neo or 191P4D12(b) were grown in either 0.1% or 10% FBS overnight. The cells were analyzed by anti-Phospho-ERK western blotting. This experiment shows that 191P4D12(b) induces the phosphorylation of ERK in 0.1% FBS, and confirms that expression of 191P4D12(b) is sufficient to induce activation of the ERK signaling cascade in the absence of additional stimuli.

To confirm that 191P4D12(b) directly or indirectly activates known signal transduction pathways in cells, luciferase (luc) based transcriptional reporter assays are carried out in cells expressing individual genes. These transcriptional reporters contain consensus-binding sites for known transcription factors that lie downstream of well-characterized signal transduction pathways. The reporters and examples of these associated transcription factors, signal transduction pathways, and activation stimuli are listed below.

1. NFkB-luc, NFkB/Rel; Ik-kinase/SAPK; growth/apoptosis/stress
2. SRE-luc, SRF/TCF/ELK1; MAPK/SAPK; growth/differentiation
3. AP-1-luc, FOS/JUN; MAPK/SAPK/PKC; growth/apoptosis/stress
4. ARE-luc, androgen receptor; steroids/MAPK; growth/differentiation/apoptosis
5. p53-luc, p53; SAPK; growth/differentiation/apoptosis
6. CRE-luc, CREB/ATF2; PKA/p38; growth/apoptosis/stress

7. TCF-luc, TCF/Lef; ß-catenin, Adhesion/invasion

Gene-mediated effects can be assayed in cells showing mRNA expression. Luciferase reporter plasmids can be introduced by lipid-mediated transfection (TFX-50, Promega). Luciferase activity, an indicator of relative transcriptional activity, is measured by incubation of cell extracts with luciferin substrate and luminescence of the reaction is monitored in a luminometer.

Signaling pathways activated by 191P4D12(b) are mapped and used for the identification and validation of therapeutic targets. When 191P4D12(b) is involved in cell signaling, it is used as target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 47: Involvement in Tumor Progression

Based on the role of Ig-domains and cadherin motifs in cell growth and signal transduction, the 191P4D12(b) gene can contribute to the growth, invasion and transformation of cancer cells. The role of 191P4D12(b) in tumor growth is confirmed in a variety of primary and transfected cell lines including prostate cell lines, as well as NIH 3T3 cells engineered to stably express 191P4D12(b). Parental cells lacking 191P4D12(b) and cells expressing 191P4D12(b) are evaluated for cell growth using a well-documented proliferation assay (Fraser SP, Grimes JA, Djamgoz MB. Prostate. 2000;44:61, Johnson DE, Ochieng J, Evans SL. Anticancer Drugs. 1996, 7:288).

To confirm the role of 191P4D12(b) in the transformation process, its effect in colony forming assays is investigated. Parental NIH-3T3 cells lacking 191P4D12(b) are compared to NIH-3T3 cells expressing 191P4D12(b), using a soft agar assay under stringent and more permissive conditions (Song Z. et al. Cancer Res. 2000;60:6730).

To confirm the role of 191P4D12(b) in invasion and metastasis of cancer cells, a well-established assay is used, e.g., a Transwell Insert System assay (Becton Dickinson) (Cancer Res. 1999; 59:6010). Control cells, including prostate, breast and kidney cell lines lacking 191P4D12(b) are compared to cells expressing 191P4D12(b). Cells are loaded with the fluorescent dye, calcein, and plated in the top well of the Transwell insert coated with a basement membrane analog. Invasion is determined by fluorescence of cells in the lower chamber relative to the fluorescence of the entire cell population.

191P4D12(b) can also play a role in cell cycle and apoptosis. Parental cells and cells expressing 191P4D12(b) are compared for differences in cell cycle regulation using a well-established BrdU assay (Abdel-Malek ZA. J Cell Physiol. 1988, 136:247). In short, cells are grown under both optimal (full serum) and limiting (low serum) conditions are labeled with BrdU and stained with anti-BrdU Ab and propidium iodide. Cells are analyzed for entry into the G1, S, and G2M phases of the cell cycle. Alternatively, the effect of stress on apoptosis is evaluated in control parental cells and cells expressing 191P4D12(b), including normal and tumor prostate cells. Engineered and parental cells are treated with various chemotherapeutic agents, such as etoposide, taxol, etc, and protein synthesis inhibitors, such as cycloheximide. Cells are stained with annexin V-FITC and cell death is measured by FACS analysis. The modulation of cell death by 191P4D12(b) can play a critical role in regulating tumor progression and tumor load.

When 191P4D12(b) plays a role in cell growth, transformation, invasion or apoptosis, it is used as a target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 48: Involvement in Angiogenesis

Angiogenesis or new capillary blood vessel formation is necessary for tumor growth (Hanahan D, Folkman J. Cell. 1996, 86:353; Folkman J. Endocrinology. 1998 139:441). Based on the effect of cadherins on tumor cell adhesion and their interaction with endothelial cells, 191P4D12(b) plays a role in angiogenesis (Mareel and Leroy: Physiol Rev, 83:337; DeFouw L et al, Microvasc Res 2001, 62:263). Several assays have been developed to measure angiogenesis *in vitro* and

in vivo, such as the tissue culture assays endothelial cell tube formation and endothelial cell proliferation. Using these assays as well as *in vitro* neo-vascularization, the role of 191P4D12(b) in angiogenesis, enhancement or inhibition, is confirmed.

For example, endothelial cells engineered to express 191P4D12(b) are evaluated using tube formation and proliferation assays. The effect of 191P4D12(b) is also confirmed in animal models *in vivo*. For example, cells either expressing or lacking 191P4D12(b) are implanted subcutaneously in immunocompromised mice. Endothelial cell migration and angiogenesis are evaluated 5-15 days later using immunohistochemistry techniques. 191P4D12(b) affects angiogenesis, and it is used as a target for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 49: Involvement in Protein-Protein Interactions

Ig-domains and cadherin motifs have been shown to mediate interaction with other proteins, including cell surface protein. Using immunoprecipitation techniques as well as two yeast hybrid systems, proteins are identified that associate with 191P4D12(b). Immunoprecipitates from cells expressing 191P4D12(b) and cells lacking 191P4D12(b) are compared for specific protein-protein associations.

Studies are performed to confirm the extent of association of 191P4D12(b) with effector molecules, such as nuclear proteins, transcription factors, kinases, phosphates etc. Studies comparing 191P4D12(b) positive and 191P4D12(b) negative cells as well as studies comparing unstimulated/resting cells and cells treated with epithelial cell activators, such as cytokines, growth factors, androgen and anti-integrin Ab reveal unique interactions.

In addition, protein-protein interactions are confirmed using two yeast hybrid methodology (Curr. Opin. Chem Biol. 1999, 3:64). A vector carrying a library of proteins fused to the activation domain of a transcription factor is introduced into yeast expressing a 191P4D12(b)-DNA-binding domain fusion protein and a reporter construct. Protein-protein interaction is detected by colorimetric reporter activity. Specific association with effector molecules and transcription factors directs one of skill to the mode of action of 191P4D12(b), and thus identifies therapeutic, prognostic, preventative and/or diagnostic targets for cancer. This and similar assays are also used to identify and screen for small molecules that interact with 191P4D12(b). Thus it is found that 191P4D12(b) associates with proteins and small molecules. Accordingly, 191P4D12(b) and these proteins and small molecules are used for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 50: Involvement of 191P4D12(b) in cell-cell communication.

Cell-cell communication is essential in maintaining organ integrity and homeostasis, both of which become deregulated during tumor formation and progression. Based on the presence of a cadherin motif in 191P4D12(b), a motif known to be involved in cell interaction and cell-cell adhesion, 191P4D12(b) can regulate cell communication. Intercellular communications can be measured using two types of assays (J. Biol. Chem. 2000, 275:25207). In the first assay, cells loaded with a fluorescent dye are incubated in the presence of unlabeled recipient cells and the cell populations are examined under fluorescent microscopy. This qualitative assay measures the exchange of dye between adjacent cells. In the second assay system, donor and recipient cell populations are treated as above and quantitative measurements of the recipient cell population are performed by FACS analysis. Using these two assay systems, cells expressing 191P4D12(b) are compared to controls that do not express 191P4D12(b), and it is found that 191P4D12(b) enhances cell communications. Figure 19 and Figure 20 demonstrate that 191P4D12(b) mediates the transfer of the small molecule calcein between adjacent cells, and thereby regulates cell-cell communication in prostate cancer cells. In this experiment, recipient PC3 cells were labeled with dextran-Texas Red and donor PC3 cells were labeled with calcein AM (green). The donor (green) and recipient (red) cells were co-cultured at 37°C and analyzed by microscopy for the co-localization of Texas red and calcein. The results demonstrated that while PC3 control cells (no detectable 191P4D12(b) protein expression) exhibit little calcein

transfer, the expression of 191P4D12(b) allows the transfer of small molecules between cells (Figure 19), whereby the initially red recipient cells take on a brownish color, and co-localize the red and green molecules. Small molecules and/or antibodies that modulate cell-cell communication mediated by 191P4D12(b) are used as therapeutics for cancers that express 191P4D12(b). When 191P4D12(b) functions in cell-cell communication and small molecule transport, it is used as a target or marker for diagnostic, prognostic, preventative and/or therapeutic purposes.

Example 51: Modulation of 191P4D12(b) function.

Knock down of 191P4D12(b) expression

Several techniques can be used to knock down or knock out 191P4D12(b) expression in vitro and in-vivo, including RNA interference (RNAi) and other anti-sense technologies. RNAi makes use of sequence specific double stranded RNA to prevent gene expression. Small interfering RNA (siRNA) are transfected into mammalian cells and thereby mediate sequence specific mRNA degradation. (Elbashir, *et al*, Nature, 2001; vol. 411: 494-498). Using this approach, 191P4D12(b)-specific RNAi is introduced in 191P4D12(b)-expressing cells by transfection. The effect of knocking down the expression of 191P4D12(b) protein is evaluated using the biological assays mentioned in examples 44 to 50 above.

Reduction of 191P4D12(b) Protein expression is detected 24-48 hours after transfection by immunostaining and flow cytometry. The introduction of 191P4D12(b) specific RNAi reduced the expression of 191P4D12(b) positive cells and reduce the biological effect of 191P4D12(b) on tumor growth and progression.

Accordingly, the RNA oligonucleotide sequences are used in therapeutic and prophylactic applications. Moreover, the RNA oligonucleotide sequences are used to assess how modulating the expression of a 191P4D12(b) gene affects function of cancer cells and/or tissues.

Inhibition using small molecule and antibodies

Using control cell lines and cell lines expressing 191P4D12(b), inhibitors of 191P4D12(b) function are identified. For example, PC3 and PC3-191P4D12(b) cells can be incubated in the presence and absence of mAb or small molecule inhibitors. The effect of these mAb or small molecule inhibitors are investigated using the cell communication, proliferation and signaling assays described above.

Signal transduction and biological output mediated by cadherins can be modulated through various mechanisms, including inhibition of receptor binding, prevention of protein interactions, or affecting the expression of co-receptors and binding partners (Kamei et al, Oncogene 1999, 18:6776). Using control cell lines and cell lines expressing 191P4D12(b), modulators (inhibitors or enhancers) of 191P4D12(b) function are identified. For example, PC3 and PC3-191P4D12(b) cells are incubated in the presence and absence of mAb or small molecule modulators. When mAb and small molecules modulate, e.g., inhibit, the transport and tumorigenic function of 191P4D12(b), they are used for preventative, prognostic, diagnostic and/or therapeutic purposes.

Throughout this application, various website data content, publications, patent applications and patents are referenced. (Websites are referenced by their Uniform Resource Locator, or URL, addresses on the World Wide Web.)

The present invention is not to be limited in scope by the embodiments disclosed herein, which are intended as single illustrations of individual aspects of the invention, and any that are functionally equivalent are within the scope of the invention. Various modifications to the models and methods of the invention, in addition to those described herein, will become apparent to those skilled in the art from the foregoing description and teachings, and are similarly intended to fall within the scope of the invention. Such modifications or other embodiments can be practiced without departing from the true scope and spirit of the invention.

TABLES:

TABLE I: Tissues that Express 191P4D12(b):

a. Malignant Tissues

Prostate
Bladder
Kidney
Colon
Lung
Pancreas
Ovary
Breast
Uterus
Cervix

TABLE II: Amino Acid Abbreviations

SINGLE LETTER	THREE LETTER	FULL NAME
F	Phe	phenylalanine
L	Leu	leucine
S	Ser	serine
Y	Tyr	tyrosine
C	Cys	cysteine
W	Trp	tryptophan
P	Pro	proline
H	His	histidine
Q	Gln	glutamine
R	Arg	arginine
I	Ile	isoleucine
M	Met	methionine
T	Thr	threonine
N	Asn	asparagine
K	Lys	lysine
V	Val	valine
A	Ala	alanine
D	Asp	aspartic acid
E	Glu	glutamic acid
G	Gly	glycine

TABLE III: Amino Acid Substitution Matrix

Adapted from the GCG Software 9.0 BLOSUM62 amino acid substitution matrix (block substitution matrix). The higher the value, the more likely a substitution is found in related, natural proteins.

A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	.
4	0	-2	-1	-2	0	-2	-1	-1	-1	-1	-2	-1	-1	-1	1	0	0	-3	-2	A
	9	-3	-4	-2	-3	-3	-1	-3	-1	-1	-3	-3	-3	-3	-1	-1	-1	-2	-2	C
		6	2	-3	-1	-1	-3	-1	-4	-3	1	-1	0	-2	0	-1	-3	-4	-3	D
			5	-3	-2	0	-3	1	-3	-2	0	-1	2	0	0	-1	-2	-3	-2	E
				6	-3	-1	0	-3	0	0	-3	-4	-3	-3	-2	-2	-1	1	3	F
					6	-2	-4	-2	-4	-3	0	-2	-2	-2	0	-2	-3	-2	-3	G
						8	-3	-1	-3	-2	1	-2	0	0	-1	-2	-3	-2	2	H
							4	-3	2	1	-3	-3	-3	-3	-2	-1	3	-3	-1	I
								5	-2	-1	0	-1	1	2	0	-1	-2	-3	-2	K
									4	2	-3	-3	-2	-2	-2	-1	1	-2	-1	L
										5	-2	-2	0	-1	-1	-1	1	-1	-1	M
											6	-2	0	0	1	0	-3	-4	-2	N
												7	-1	-2	-1	-1	-2	-4	-3	P
													5	1	0	-1	-2	-2	-1	Q
														5	-1	-1	-3	-3	-2	R
															4	1	-2	-3	-2	S
																5	0	-2	-2	T
																	4	-3	-1	V
																		11	2	W
																			7	Y

TABLE IV:
HLA Class I/II Motifs/Supermotifs

TABLE IV (A): HLA Class I Supermotifs/Motifs

SUPERMOTIF	POSITION 2 (Primary Anchor)	POSITION 3 (Primary Anchor)	POSITION C Terminus (Primary Anchor)
A1	**TI***LVMS*		**FWY**
A2	**LIVM***ATQ*		**IV***MATL*
A3	**VSMA***TLI*		**RK**
A24	**YF***WIVLMT*		**FI***YWLM*
B7	**P**		**VILF***MWYA*
B27	**RHK**		**FYL***WMIVA*
B44	**E***D*		**FWYLIMVA**
B58	**ATS**		**FWY***LIVMA*
B62	**QL***IVMP*		**FWY***MIVLA*
MOTIFS			
A1	**TSM**		**Y**
A1		**DE***AS*	**Y**
A2.1	**LM***VQIAT*		**V***LIMAT*
A3	**LMVISATF***CGD*		**KYR***HFA*
A11	**VTMLISAGN***CDF*		**K***RYH*
A24	**YF***WM*		**FLIW**
A*3101	**MVT***ALIS*		**R***K*
A*3301	**MVALF***IST*		**RK**
A*6801	**AVT***MSLI*		**RK**
B*0702	**P**		**LMF***WYAIV*
B*3501	**P**		**LMFWY***IVA*
B51	**P**		**LIVF***WYAM*
B*5301	**P**		**IMFWY***ALV*
B*5401	**P**		**ATIV***LMFWY*

Bolded residues are preferred, italicized residues are less preferred: A peptide is considered motif-bearing if it has primary anchors at each primary anchor position for a motif or supermotif as specified in the above table.

TABLE IV (B): HLA Class II Supermotif

1	6	9
W, F, Y, V, .I, L	A, V, I, L, P, C, S, T	A, V, I, L, C, S, T, M, Y

TABLE IV (C): HLA Class II Motifs

MOTIFS		1° anchor 1	2	3	4	5	1° anchor 6	7	8	9
DR4	preferred	FMY*LIVW*	M	T		I	VST*CPALIM*	MH		MH
	deleterious				W			R		WDE
DR1	preferred	MF*LIVWY*			PAMQ		VMAT*SPLIC*	M		AVM
	deleterious		C	CH	FD	CWD		GDE	D	
DR7	preferred	MF*LIVWY*	M	W	A		IVMSA*CTPL*	M		IV
	deleterious		C		G			GRD	N	G
DR3	MOTIFS	1° anchor 1	2	3	1° anchor 4	5	1° anchor 6			
Motif a preferred		LIVMFY			D					
Motif b preferred		LIVMFAY			DNQEST		KRH			
DR Supermotif		MF*LIVWY*					VMSTA*CPLI*			

Italicized residues indicate less preferred or "tolerated" residues

TABLE IV (D): HLA Class I Supermotifs

SUPER-MOTIFS	POSITION:	1	2	3	4	5	6	7	8	C-terminus
A1			1° Anchor TI*LVMS*							1° Anchor FWY
A2			1° Anchor LIVM*ATQ*							1° Anchor LIVMAT
A3	Preferred		1° Anchor VSMA*TLI*	YFW (4/5)			YFW (3/5)	YFW (4/5)	P (4/5)	1° Anchor RK
	deleterious	DE (3/5); P (5/5)		DE (4/5)						
A24			1° Anchor YF*WIVLMT*							1° Anchor FIY*WLM*
B7	Preferred	FWY (5/5) LIVM (3/5)	1° Anchor P	FWY (4/5)					FWY (3/5)	1°Anchor VILF*MWYA*
	deleterious	DE (3/5); P(5/5); G(4/5); A(3/5); QN(3/5)				DE (3/5)	G (4/5)	QN (4/5)	DE (4/5)	
B27			1° Anchor RHK							1°Anchor FYL*WMIVA*
B44			1° Anchor *ED*							1° Anchor FWYLIMVA
B58			1° Anchor ATS							1° Anchor FWY*LIVMA*
B62			1° Anchor QL*IVMP*							1° Anchor FWY*MIVLA*

Italicized residues indicate less preferred or "tolerated" residues

TABLE IV (E): HLA Class I Motifs

	POSITION 1		2	3	4	5	6	7	8	9 or C-terminus	C-terminus
A1 9-mer	preferred	GFYW	1°Anchor STM	DEA	YFW		P	DEQN	YFW	1°Anchor Y	
	deleterious	DE		RHKLIVMP	A	G	A				
A1 9-mer	preferred	GRHK	ASTCLIVM	1°Anchor DEAS	GSTC		ASTC	LIVM	DE	1°Anchor Y	
	deleterious	A	RHKDEPYFW		DE	PQN	RHK	PG	GP		
A1 10-mer	preferred	YFW	1°Anchor STM	DEAQN	A	YFWQN		PASTC	GDE	P	1°Anchor Y
	deleterious	GP		RHKGLIVM	DE	RHK	QNA	RHKYFW	RHK	A	
A1 10-mer	preferred	YFW	STCLIVM	1°Anchor DEAS	A	YFW		PG	G	YFW	1°Anchor Y
	deleterious	RHK	RHKDEPYFW			P	G		PRHK	QN	
A2.1 9-mer	preferred	YFW	1°Anchor LM*IVQAT*	YFW	STC	YFW		A	P	1°Anchor *VLIMAT*	
	deleterious	DEP		DERKH			RKH	DERKH			
	POSITION:	1	2	3	4	5	6	7	8	9	C-Terminus
A2.1 10-mer	preferred	AYFW	1°Anchor LM*IVQAT*	LVIM	G		*G*		FYWL VIM		1°Anchor *VLIMAT*
	deleterious	DEP		DE	RKHA	P		RKH	DERKH	RKH	
A3	preferred	RHK	1°Anchor LMVISATFCGD	YFW	PRHKYFW	A	YFW		P	1°Anchor KYR*HFA*	
	deleterious	DEP		DE							
A11	preferred	A	1°Anchor VTLMISAGN*CDF*	YFW	YFW	A	YFW	YFW	P	1°Anchor *KRYH*	
	deleterious	DEP						A	G		
A24 9-mer	preferred	YFWRHK	1°Anchor YFW*M*		STC			YFW	YFW	1°Anchor FLIW	
	deleterious	DEG		DE	G	QNP	DERHKG		AQN		
A24 10-mer	Preferred		1°Anchor YFW*M*		P	YFWP		P			1°Anchor FLIW
	Deleterious			GDE	QN	RHK	DE	A	QN	DEA	
A3101	Preferred	RHK	1°Anchor MVT*ALIS*	YFW	P		YFW	YFW	AP	1°Anchor *RK*	
	Deleterious	DEP		DE		ADE	DE	DE	DE		
A3301	Preferred		1°Anchor MVALF*IST*	YFW				AYFW		1°Anchor RK	
	Deleterious	GP		DE							
A6801	Preferred	YFWSTC	1°Anchor AVT*MSLI*			YFWLIVM		YFW	P	1°Anchor RK	
	deleterious	GP		DEG		RHK			A		
B0702	Preferred	RHKFWY	1°Anchor P	RHK		RHK	RHK	RHK	PA	1°Anchor LMF*WYAIV*	
	deleterious	DEQNP		DEP	DE	DE	GDE	QN	DE		
B3501	Preferred	FWYLIVM	1°Anchor P	FWY				FWY		1°Anchor LMFWY*IVA*	

	POSITION	1	2	3	4	5	6	7	8	9	C-terminus
										or C-terminus	
A1 9-mer	preferred	GFYW	1°Anchor STM	DEA	YFW		P	DEQN	YFW	1°Anchor Y	
	deleterious	DE		RHKLIVMP	A	G	A				
A1 9-mer	preferred	GRHK	ASTCLIVM	1°Anchor DEAS	GSTC		ASTC	LIVM	DE	1°Anchor Y	
	deleterious	A	RHKDEPYFW		DE	PQN	RHK	PG	GP		
	deleterious	AGP				G	G				
B51	Preferred	LIVMFWY	1°Anchor P	FWY	STC	FWY		G	FWY	1°Anchor LIVF*WYA M*	
	deleterious	AGPDER HKSTC				DE	G	DEQN	GDE		
B5301	preferred	LIVMFWY	1°Anchor P	FWY	STC	FWY		LIVMFWY	FWY	1°Anchor IMFWY*AL V*	
	deleterious	AGPQN					G	RHKQN	DE		
B5401	preferred	FWY	1°Anchor P	FWYLIVM		LIVM		ALIVM	FWYA P	1°Anchor ATIV*LMF WY*	
	deleterious	GPQNDE		GDESTC		RHKDE	DE	QNDGE	DE		

TABLE IV (F):

Summary of HLA-supertypes								
Overall phenotypic frequencies of HLA-supertypes in different ethnic populations								
	Specificity		Phenotypic frequency					
Supertype	Position 2	C-Terminus	Caucasian	N.A. Black	Japanese	Chinese	Hispanic	Average
B7	P	AILMVFWY	43.2	55.1	57.1	43.0	49.3	49.5
A3	AILMVST	RK	37.5	42.1	45.8	52.7	43.1	44.2
A2	AILMVT	AILMVT	45.8	39.0	42.4	45.9	43.0	42.2
A24	YF (WIVLMT)	FI (YWLM)	23.9	38.9	58.6	40.1	38.3	40.0
B44	E (D)	FWYLIMVA	43.0	21.2	42.9	39.1	39.0	37.0
A1	TI (LVMS)	FWY	47.1	16.1	21.8	14.7	26.3	25.2
B27	RHK	FYL (WMI)	28.4	26.1	13.3	13.9	35.3	23.4
B62	QL (IVMP)	FWY (MIV)	12.6	4.8	36.5	25.4	11.1	18.1
B58	ATS	FWY (LIV)	10.0	25.1	1.6	9.0	5.9	10.3

TABLE IV (G):

Calculated population coverage afforded by different HLA-supertype combinations						
HLA-supertypes	Phenotypic frequency					
	Caucasian	N.A Blacks	Japanese	Chinese	Hispanic	Average
	83.0	86.1	87.5	88.4	86.3	86.2
A2, A3 and B7	99.5	98.1	100.0	99.5	99.4	99.3
A2, A3, B7, A24, B44 and A1	99.9	99.6	100.0	99.8	99.9	99.8
A2, A3, B7, A24, B44, A1, B27, B62, and B 58						
Motifs indicate the residues defining supertype specificites. The motifs incorporate residues determined on the basis of published data to be recognized by multiple alleles within the supertype. Residues within brackets are additional residues also predicted to be tolerated by multiple alleles within the supertype.						

Table V: Frequently Occurring Motifs			
Name	avrg. % identity	Description	Potential Function
zf-C2H2	34%	Zinc finger, C2H2 type	Nucleic acid-binding protein functions as transcription factor, nuclear location probable
cytochrome_b_N	68%	Cytochrome b(N-terminal)/b6/petB	membrane bound oxidase, generate superoxide
Ig	19%	Immunoglobulin domain	domains are one hundred amino acids long and include a conserved intradomain disulfide bond.
WD40	18%	WD domain, G-beta repeat	tandem repeats of about 40 residues, each containing a Trp-Asp motif. Function in signal transduction and protein interaction
PDZ	23%	PDZ domain	may function in targeting signaling molecules to sub-membranous sites
LRR	28%	Leucine Rich Repeat	short sequence motifs involved in protein-protein interactions
Pkinase	23%	Protein kinase domain	conserved catalytic core common to both serine/threonine and tyrosine protein kinases containing an ATP binding site and a catalytic site

PH	16%	PH domain	pleckstrin homology involved in intracellular signaling or as constituents of the cytoskeleton
EGF	34%	EGF-like domain	30-40 amino-acid long found in the extracellular domain of membrane-bound proteins or in secreted proteins
Rvt	49%	Reverse transcriptase (RNA-dependent DNA polymerase)	
Ank	25%	Ank repeat	Cytoplasmic protein, associates integral membrane proteins to the cytoskeleton
Oxidored_q1	32%	NADH-Ubiquinone/plastoquinone (complex I), various chains	membrane associated. Involved in proton translocation across the membrane
Efhand	24%	EF hand	calcium-binding domain, consists of a12 residue loop flanked on both sides by a 12 residue alpha-helical domain
Rvp	79%	Retroviral aspartyl protease	Aspartyl or acid proteases, centered on a catalytic aspartyl residue
Collagen	42%	Collagen triple helix repeat (20 copies)	extracellular structural proteins involved in formation of connective tissue. The sequence consists of the G-X-Y and the polypeptide chains forms a triple helix.
Fn3	20%	Fibronectin type III domain	Located in the extracellular ligand-binding region of receptors and is about 200 amino acid residues long with two pairs of cysteines involved in disulfide bonds
7tm_1	19%	7 transmembrane receptor (rhodopsin family)	seven hydrophobic transmembrane regions, with the N-terminus located extracellularly while the C-terminus is cytoplasmic. Signal through G proteins

Table VI: Motifs and Post-translational Modifications of 191P4D12(b)

Table VI: Post-translational modifications of 191P4D12(b)

N-glycosylation site
281 - 284 NWTR (SEQ ID NO: 61)
430 - 433 NSSC (SEQ ID NO: 62)
489 - 492 NGTL (SEQ ID NO: 63)

Tyrosine sulfation site
118 - 132 VQADEGEYECRVSTF (SEQ ID NO: 64)

Protein kinase C phosphorylation site
26 - 28 TGR
192 - 194 SSR
195 - 197 SFK
249 - 251 SVR
322 - 324 SSR
339 - 341 SGK
383 - 385 TQK
397 - 399 SIR
426 - 428 SLK
450 - 452 TVR
465 - 467 SGR
491 - 493 TLR

Casein kinase II phosphorylation site

283 - 286 TRLD (SEQ ID NO: 65)
322 - 325 SSRD (SEQ ID NO: 66)
410 - 413 SQPE (SEQ ID NO: 67)
426 - 429 SLKD (SEQ ID NO: 68)
450 - 453 TVRE (SEQ ID NO: 69)
456 - 459 TQTE (SEQ ID NO: 70)

N-myristoylation site .
135 - 140 GSFQAR (SEQ ID NO: 71)
162 - 167 GQGLTL (SEQ ID NO: 72)
164 - 169 GLTLAA (SEQ ID NO: 73)
189 - 194 GTTSSR (SEQ ID NO: 74)
218 - 223 GQPLTC (SEQ ID NO: 75)
311 - 316 GIYVCH (SEQ ID NO: 76)
354 - 359 GVIAAL (SEQ ID NO: 77)
464 - 469 GSGRAE (SEQ ID NO: 78)
477 - 482 GIKQAM (SEQ ID NO: 79)
490 - 495 GTLRAK (SEQ ID NO: 80)
500 - 505 GIYING (SEQ ID NO: 81)

RGD Cell attachment sequence
55 - 57 RGD

Table VII:
Search Peptides

191P4D12(b) v.1 aa1-510
9-mers, 10-mers and 15-mers (SEQ ID NO: 82)
MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE
QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA
DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS
VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL
HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL
GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL
FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA
EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ
AMNHFVQENG TLRAKPTGNG IYINGRGHLV

v.2 aa1-510
9-mers 45-61 GQDAKLPCLYRGDSGEQ (SEQ ID NO: 83)
10-mers 44-62 LGQDAKLPCLYRGDSGEQV (SEQ ID NO: 84)
15-mers 39-67 VVTVVLGQDAKLPCLYRGDSGEQVGQVAW (SEQ ID NO: 85)

v.7 ORF: 264..1721 Frame +3
9-mers 403-418 SHHTDPRSQSEEPEGR (SEQ ID NO: 86)
10-mers 402-419 HSHHTDPRSQSEEPEGRS (SEQ ID NO: 87)
15-mers 397-424 SIRRLHSHHTDPRSQSEEPEGRSYSTLT (SEQ ID NO: 88)

V.9: AA 1-137; 9-mers, 10-mers, 15-mers (SEQ ID NO: 89)
MRRELLAGIL LRITFNFFLF FFLPFPLVVF FIYFYFYFFL EMESHYVAQA GLELLGSSNP
PASASLVAGT LSVHHCACFE SFTKRKKKLK KAFRFIQCLL LGLLKVRPLQ HQGVNSCDCE
RGYFQGIFMQ AAPWEGT

v.10 SNP variant
9-mers 27-43 GRCPAGELGTSDVVTVV (SEQ ID NO: 90)
10-mers 26-44 TGRCPAGELGTSDVVTVVL (SEQ ID NO: 91)
15-mers 21-49 LLASFTGRCPAGELGTSDVVTVVLGQDAK (SEQ ID NO: 92)

v.11 SNP variant
9-mers 138-154 QARLRLRVMVPPLPSLN (SEQ ID NO: 93)
10-mers 137-155 FQARLRLRVMVPPLPSLNP (SEQ ID NO: 94)
15-mers 132-160 FPAGSFQARLRLRVMVPPLPSLNPGPALE (SEQ ID NO: 95)

v.12 SNP variant
9-mers 435-451 VMSEEPEGCSYSTLTTV (SEQ ID NO: 96)
10-mers 434-452 SVMSEEPEGCSYSTLTTVRE (SEQ ID NO: 97)
15-mers 429-457 DNSSCSVMSEEPEGCSYSTLTTVREIETQ (SEQ ID NO: 98)

v.13 insertion of one AA at 333-4
9-mers 426-442 SQVTVDVLADPQEDSGK (SEQ ID NO: 99)
10-mers 425-443 DSQVTVDVLADPQEDSGKQ (SEQ ID NO: 100)
15-mers 420-448 EFSSRDSQVTVDVLADPQEDSGKQVDLVS (SEQ ID NO: 101)

191P4D12(b) v.14: AA56-72; 9-mers
GSSNPPASASLVAGTLS (SEQ ID NO: 102)

191P4D12(b) v.14: AA55-73; 10-mers
LGSSNPPASASLVAGTLSV (SEQ ID NO: 103)

191P4D12(b) v.14: AA50-78; 15-mers
AGLELLGSSNPPASASLVAGTLSVHHCAC (SEQ ID NO: 104)

Tables VIII – XXI:

Table VIII-V1-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
294	RVDGDTLGF	25.000
437	SEEPEGRSY	22.500
97	RVEQPPPPR	18.000
306	TTEHSGIYV	11.250
332	VLDPQEDSG	5.000
252	GLEDQNLWH	4.500
457	QTELLSPGS	4.500
271	LSEGQPPPS	2.700
205	TSEFHLVPS	2.700
107	PLDGSVLLR	2.500
386	YEEELTLTR	2.250
411	QPEESVGLR	2.250
184	DTEVKGTTS	2.250
172	TAEGSPAPS	1.800
6	GAEMWGPEA	1.800
33	ELETSDVVT	1.800
36	TSDVVTVVL	1.500
45	GQDAKLPCF	1.500
436	MSEEPEGRS	1.350
305	LTTEHSGIY	1.250
405	HTDPRSQPE	1.250
11	GPEAWLLLL	1.125
119	QADEGEYEC	1.000
89	HVSPAYEGR	1.000
284	RLDGPLPSG	1.000
342	QVDLVSASV	1.000
158	ALEEGQGLT	0.900
245	LAEASVRGL	0.900
419	RAEGHPDSL	0.900
453	EIETQTELL	0.900
486	VQENGTLRA	0.675
76	AQELALLHS	0.675
117	AVQADEGEY	0.500
471	EEDQDEGIK	0.500
236	ITHILHVSF	0.500

Table VIII-V1-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
365	VVVVVLMSR	0.500
366	VVVVLMSRY	0.500
189	GTTSSRSFK	0.500
78	ELALLHSKY	0.500
69	RVDAGEGAQ	0.500
378	KAQQMTQKY	0.500
124	EYECRVSTF	0.450
120	ADEGEYECR	0.450
439	EPEGRSYST	0.450
130	STFPAGSFQ	0.250
86	YGLHVSPAY	0.250
318	SNEFSSRDS	0.225
72	AGEGAQELA	0.225
122	EGEYECRVS	0.225
159	LEEGQGLTL	0.225
262	GREGAMLKC	0.225
58	SGEQVGQVA	0.225
31	AGELETSDV	0.225
145	VLVPPLPSL	0.200
180	SVTWDTEVK	0.200
368	VVLMSRYHR	0.200
41	TVVLGQDAK	0.200
17	LLLLLLASF	0.200
409	RSQPEESVG	0.150
129	VSTFPAGSF	0.150
200	RSAAVTSEF	0.150
423	HPDSLKDNS	0.125
392	LTRENSIRR	0.125
448	LTTVREIET	0.125
55	RGDSGEQVG	0.125
190	TTSSRSFKH	0.125
353	VGVIAALLF	0.125
146	LVPPLPSLN	0.100
369	VLMSRYHRR	0.100
313	YVCHVSNEF	0.100

Table VIII-V1-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
61	QVGQVAWAR	0.100
459	ELLSPGSGR	0.100
329	TVDVLDPQE	0.100
20	LLLASFTGR	0.100
316	HVSNEFSSR	0.100
209	HLVPSRSMN	0.100
460	LLSPGSGRA	0.100
485	FVQENGTLR	0.100
467	RAEEEEDQD	0.090
3	LSLGAEMWG	0.075
225	VSHPGLLQD	0.075
255	DQNLWHIGR	0.075
135	GSFQARLRL	0.075
231	LQDQRITHI	0.075
473	DQDEGIKQA	0.075
296	DGDTLGFPP	0.062
364	LVVVVVLMS	0.050
354	GVIAALLFC	0.050
224	VVSHPGLLQ	0.050
202	AAVTSEFHL	0.050
210	LVPSRSMNG	0.050
19	LLLLASFTG	0.050
355	VIAALLFCL	0.050
299	TLGFPPLTT	0.050
15	WLLLLLLLA	0.050
298	DTLGFPPLT	0.050
287	GPLPSGVRV	0.050
28	RCPAGELET	0.050
435	VMSEEPEGR	0.050
357	AALLFCLLV	0.050

Table VIII-V2-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	GQDAKLPCL	0.150
3	DAKLPCLYR	0.050
4	AKLPCLYRG	0.010
2	QDAKLPCLY	0.003
6	LPCLYRGDS	0.003
7	PCLYRGDSG	0.001
5	KLPCLYRGD	0.001
8	CLYRGDSGE	0.000
9	LYRGDSGEQ	0.000

Table VIII-V7-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
3	HTDPRSQSE	1.250
7	RSQSEEPEG	0.030
8	SQSEEPEGR	0.015
1	SHHTDPRSQ	0.001
2	HHTDPRSQS	0.001
5	DPRSQSEEP	0.000
4	TDPRSQSEE	0.000
6	PRSQSEEPE	0.000

Table VIII-V9-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
116	SCDCERGYF	5.000
13	ITFNFFLFF	1.250
76	CACFESFTK	1.000
27	LVVFFIYFY	1.000

Table VIII-V9-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
97	QCLLLGLLK	1.000
39	FLEMESHYV	0.900
41	EMESHYVAQ	0.900
78	CFESFTKRK	0.900
51	GLELLGSSN	0.900
115	NSCDCERGY	0.750
25	FPLVVFFIY	0.625
23	LPFPLVVFF	0.500
4	ELLAGILLR	0.500
12	RITFNFFLF	0.500
28	VVFFIYFYF	0.500
118	DCERGYFQG	0.450
71	LSVHHCACF	0.300
80	ESFTKRKKK	0.300
22	FLPFPLVVF	0.200
31	FIYFYFYFF	0.200
57	SSNPPASAS	0.150
7	AGILLRITF	0.125
99	LLLGLLKVR	0.100
113	GVNSCDCER	0.100
77	ACFESFTKR	0.100
95	FIQCLLLGL	0.050
9	ILLRITFNF	0.050
98	CLLLGLLKV	0.050
5	LLAGILLRI	0.050
26	PLVVFFIYF	0.050
46	YVAQAGLEL	0.050
49	QAGLELLGS	0.050
29	VFFIYFYFY	0.050
58	SNPPASASL	0.050
65	SLVAGTLSV	0.050
2	RRELLAGIL	0.045
56	GSSNPPASA	0.030
62	ASASLVAGT	0.030
14	TFNFFLFFF	0.025
69	GTLSVHHCA	0.025
30	FFIYFYFYF	0.025

Table VIII-V9-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
21	FFLPFPLVV	0.025
17	FFLFFFLPF	0.025
38	FFLEMESHY	0.025
67	VAGTLSVHH	0.020
126	GIFMQAAPW	0.020
54	LLGSSNPPA	0.020
43	ESHYVAQAG	0.015
64	ASLVAGTLS	0.015
15	FNFFLFFFL	0.013
121	RGYFQGIFM	0.013
79	FESFTKRKK	0.010
70	TLSVHHCAC	0.010
105	KVRPLQHQG	0.010
66	LVAGTLSVH	0.010
63	SASLVAGTL	0.010
6	LAGILLRIT	0.010
47	VAQAGLELL	0.010
10	LLRITFNFF	0.010
75	HCACFESFT	0.010
8	GILLRITFN	0.010
48	AQAGLELLG	0.007
103	LLKVRPLQH	0.005
128	FMQAAPWEG	0.005
55	LGSSNPPAS	0.005
120	ERGYFQGIF	0.005
74	HHCACFESF	0.005
82	FTKRKKKLK	0.005
87	KKLKKAFRF	0.003
90	KKAFRFIQC	0.003
11	LRITFNFFL	0.003
59	NPPASASLV	0.003
101	LGLLKVRPL	0.003
123	YFQGIFMQA	0.003
36	FYFFLEMES	0.003
34	FYFYFFLEM	0.003
19	LFFFLPFPL	0.003
68	AGTLSVHHC	0.003

Table VIII-V9-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
93	FRFIQCLLL	0.003
114	VNSCDCERG	0.003
122	GYFQGIFMQ	0.003
50	AGLELLGSS	0.003
32	IYFYFYFFL	0.003
3	RELLAGILL	0.003
107	RPLQHQGVN	0.003
73	VHHCACFES	0.003
94	RFIQCLLLG	0.003
18	FLFFFLPFP	0.002
102	GLLKVRPLQ	0.002
100	LLGLLKVRP	0.002
108	PLQHQGVNS	0.002
61	PASASLVAG	0.002
96	IQCLLLGLL	0.002
111	HQGVNSCDC	0.002
109	LQHQGVNSC	0.002
124	FQGIFMQAA	0.002
129	MQAAPWEGT	0.002
60	PPASASLVA	0.001
86	KKKLKKAFR	0.001
20	FFFLPFPLV	0.001

Table VIII-V10-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
5	AGELGTSDV	0.225
2	RCPAGELGT	0.050
9	GTSDVVTVV	0.025
7	ELGTSDVVT	0.020
1	GRCPAGELG	0.005
8	LGTSDVVTV	0.005

Table VIII-V10-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
3	CPAGELGTS	0.003
6	GELGTSDVV	0.001
4	PAGELGTSD	0.000

Table VIII-V11-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
9	MVPPLPSLN	0.100
8	VMVPPLPSL	0.100
7	RVMVPPLPS	0.050
5	RLRVMVPPL	0.002
1	QARLRLRVM	0.001
3	RLRLRVMVP	0.001
6	LRVMVPPLP	0.000
2	ARLRLRVMV	0.000
4	LRLRVMVPP	0.000

Table VIII-V12-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
3	SEEPEGCSY	22.500
2	MSEEPEGCS	1.350
5	EPEGCSYST	0.450
8	GCSYSTLTT	0.050
9	CSYSTLTTV	0.015
1	VMSEEPEGC	0.005

Table VIII-V12-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
7	EGCSYSTLT	0.003
4	EEPEGCSYS	0.001
6	PEGCSYSTL	0.000

Table VIII-V13-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	LADPQEDSG	5.000
4	TVDVLADPQ	0.500
9	ADPQEDSGK	0.010
7	VLADPQEDS	0.010
3	VTVDVLADP	0.005
2	QVTVDVLAD	0.005
1	SQVTVDVLA	0.003
6	DVLADPQED	0.001
5	VDVLADPQE	0.000

Table VIII-V14-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
2	SSNPPASAS	0.150
3	SNPPASASL	0.050
1	GSSNPPASA	0.030
7	ASASLVAGT	0.030
9	ASLVAGTLS	0.015
8	SASLVAGTL	0.010
4	NPPASASLV	0.003

Table VIII-V14-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

6	PASASLVAG	0.002
5	PPASASLVA	0.001

Table IX-V1-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
271	LSEGQPPPSY	135.000
332	VLDPQEDSGK	100.000
436	MSEEPEGRSY	67.500
205	TSEFHLVPSR	27.000
419	RAEGHPDSLK	18.000
119	QADEGEYECR	5.000
453	EIETQTELLS	4.500
306	TTEHSGIYVC	4.500
158	ALEEGQGLTL	4.500
45	GQDAKLPCFY	3.750
486	VQENGTLRAK	2.700
76	AQELALLHSK	2.700
405	HTDPRSQPEE	2.500
385	KYEEELTLTR	2.250
457	QTELLSPGSG	2.250
184	DTEVKGTTSS	2.250
33	ELETSDVVTV	1.800
97	RVEQPPPPRN	1.800
172	TAEGSPAPSV	1.800
36	TSDVVTVVLG	1.500
130	STFPAGSFQA	1.250

Table IX-V1-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
411	QPEESVGLRA	1.125
11	GPEAWLLLLL	1.125
72	AGEGAQELAL	1.125
470	EEEDQDEGIK	0.900
252	GLEDQNLWHI	0.900
6	GAEMWGPEAW	0.900
116	NAVQADEGEY	0.500
40	VTVVLGQDAK	0.500
493	RAKPTGNGIY	0.500
365	VVVVVLMSRY	0.500
352	VVGVIAALLF	0.500
342	QVDLVSASVV	0.500
209	HLVPSRSMNG	0.500
364	LVVVVVLMSR	0.500
284	RLDGPLPSGV	0.500
122	EGEYECRVST	0.450
437	SEEPEGRSYS	0.450
58	SGEQVGQVAW	0.450
409	RSQPEESVGL	0.300
296	DGDTLGFPPL	0.250
107	PLDGSVLLRN	0.250
390	LTLTRENSIR	0.250
275	QPPPSYNWTR	0.250
55	RGDSGEQVGQ	0.250
318	SNEFSSRDSQ	0.225
31	AGELETSDVV	0.225
439	EPEGRSYSTL	0.225
235	RITHILHVSF	0.200
16	LLLLLLLASF	0.200

Table IX-V1-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
367	VVVLMSRYHR	0.200
369	VLMSRYHRRK	0.200
242	VSFLAEASVR	0.150
225	VSHPGLLQDQ	0.150
135	GSFQARLRLR	0.150
443	RSYSTLTTVR	0.150
298	DTLGFPPLTT	0.125
189	GTTSSRSFKH	0.125
423	HPDSLKDNSS	0.125
106	NPLDGSVLLR	0.125
305	LTTEHSGIYV	0.125
471	EEDQDEGIKQ	0.125
400	RLHSHHTDPR	0.100
69	RVDAGEGAQE	0.100
145	VLVPPLPSLN	0.100
434	SVMSEEPEGR	0.100
260	HIGREGAMLK	0.100
89	HVSPAYEGRV	0.100
368	VVLMSRYHRR	0.100
128	RVSTFPAGSF	0.100
19	LLLLASFTGR	0.100
474	QDEGIKQAMN	0.090
467	RAEEEEDQDE	0.090
245	LAEASVRGLE	0.090
473	DQDEGIKQAM	0.075
214	RSMNGQPLTC	0.075
231	LQDQRITHIL	0.075
357	AALLFCLLVV	0.050

Table IX-V1-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
43	VLGQDAKLPC	0.050
188	KGTTSSRSFK	0.050
44	LGQDAKLPCF	0.050
217	NGQPLTCVV S	0.050
201	SAAVTSEFHL	0.050
294	RVDGDTLGF P	0.050
18	LLLLLASFTG	0.050
35	ETSDVVTVVL	0.050
171	CTAEGSPAPS	0.050
447	TLTTVREIET	0.050
221	LTCVVSHPGL	0.050
354	GVIAALLFCL	0.050
81	LLHSKYGLHV	0.050
323	SRDSQVTVD V	0.050
329	TVDVLDPQED	0.050
304	PLTTEHSGIY	0.050
273	EGQPPPSYN W	0.050
15	WLLLLLLLAS	0.050
363	LLVVVVVLMS	0.050
85	KYGLHVSPAY	0.050
146	LVPPLPSLNP	0.050
485	FVQENGTLRA	0.050

Table IX-V2-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
2	GQDAKLPCLY	3.750
6	KLPCLYRGDS	0.010
1	LGQDAKLPCL	0.005

Table IX-V2-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
3	QDAKLPCLYR	0.003
7	LPCLYRGDSG	0.003
4	DAKLPCLYRG	0.002
9	CLYRGDSGEQ	0.001
5	AKLPCLYRGD	0.001
8	PCLYRGDSGE	0.000
10	LYRGDSGEQV	0.000

Table IX-V7-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
4	HTDPRSQSEE	1.250
8	RSQSEEPEGR	0.150
1	HSHHTDPRSQ	0.015
9	SQSEEPEGRS	0.002
2	SHHTDPRSQS	0.001
7	PRSQSEEPEG	0.000
3	HHTDPRSQSE	0.000
6	DPRSQSEEPE	0.000
5	TDPRSQSEEP	0.000

Table IX-V9-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
39	FLEMESHYVA	1.800
13	ITFNFFLFFF	1.250
28	VVFFIYFYFY	1.000

Table IX-V9-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
116	SCDCERGYFQ	1.000
75	HCACFESFTK	1.000
78	CFESFTKRKK	0.900
41	EMESHYVAQA	0.900
12	RITFNFFLFF	0.500
27	LVVFFIYFYF	0.500
8	GILLRITFNF	0.500
6	LAGILLRITF	0.500
57	SSNPPASASL	0.300
2	RRELLAGILL	0.225
22	FLPFPLVVFF	0.200
70	TLSVHHCACF	0.200
77	ACFESFTKRK	0.200
96	IQCLLLGLLK	0.150
115	NSCDCERGYF	0.150
114	VNSCDCERGY	0.125
23	LPFPLVVFFI	0.125
25	FPLVVFFIYF	0.125
76	CACFESFTKR	0.100
26	PLVVFFIYFY	0.100
21	FFLPFPLVVF	0.100
98	CLLLGLLKVR	0.100
118	DCERGYFQGI	0.090
51	GLELLGSSNP	0.090
64	ASLVAGTLSV	0.075
31	FIYFYFYFFL	0.050
47	VAQAGLELLG	0.050
72	SVHHCACFES	0.050
4	ELLAGILLRI	0.050
97	QCLLLGLLKV	0.050
18	FLFFFLPFPL	0.050
43	ESHYVAQAGL	0.030
58	SNPPASASLV	0.025
3	RELLAGILLR	0.025
112	QGVNSCDCER	0.025
69	GTLSVHHCAC	0.025
11	LRITFNFFLF	0.025

Table IX-V9-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
82	FTKRKKKLKK	0.025
29	VFFIYFYFYF	0.025
16	NFFLFFFLPF	0.025
37	YFFLEMESHY	0.025
66	LVAGTLSVHH	0.020
54	LLGSSNPPAS	0.020
53	ELLGSSNPPA	0.020
56	GSSNPPASAS	0.015
62	ASASLVAGTL	0.015
80	ESFTKRKKKL	0.015
24	PFPLVVFFIY	0.013
59	NPPASASLVA	0.013
121	RGYFQGIFMQ	0.013
67	VAGTLSVHHC	0.010
105	KVRPLQHQGV	0.010
9	ILLRITFNFF	0.010
79	FESFTKRKKK	0.010
49	QAGLELLGSS	0.010
46	YVAQAGLELL	0.010
63	SASLVAGTLS	0.010
113	GVNSCDCERG	0.010
95	FIQCLLLGLL	0.010
30	FFIYFYFYFF	0.010
5	LLAGILLRIT	0.010
65	SLVAGTLSVH	0.010
100	LLGLLKVRPL	0.010
48	AQAGLELLGS	0.007
102	GLLKVRPLQH	0.005
55	LGSSNPPASA	0.005
101	LGLLKVRPLQ	0.005
73	VHHCACFESF	0.005
125	QGIFMQAAPW	0.005
10	LLRITFNFFL	0.005
107	RPLQHQGVNS	0.005
128	FMQAAPWEGT	0.005
86	KKKLKKAFRF	0.003
117	CDCERGYFQG	0.003

Table IX-V9-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
93	FRFIQCLLLG	0.003
14	TFNFFLFFFL	0.003
33	YFYFYFFLEM	0.003
120	ERGYFQGIFM	0.003
122	GYFQGIFMQA	0.003
35	YFYFFLEMES	0.003
68	AGTLSVHHCA	0.003
45	HYVAQAGLEL	0.003
50	AGLELLGSSN	0.003
7	AGILLRITFN	0.003
20	FFFLPFPLVV	0.003
94	RFIQCLLLGL	0.003
126	GIFMQAAPWE	0.002
99	LLLGLLKVRP	0.002
61	PASASLVAGT	0.002
71	LSVHHCACFE	0.002
15	FNFFLFFFLP	0.001
81	SFTKRKKKLK	0.001
103	LLKVRPLQHQ	0.001
108	PLQHQGVNSC	0.001
40	LEMESHYVAQ	0.001
91	KAFRFIQCLL	0.001
19	LFFFLPFPLV	0.001

Table IX-V10-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
6	AGELGTSDVV	0.225
10	GTSDVVTVVL	0.050
2	GRCPAGELGT	0.025
8	ELGTSDVVTV	0.020
3	RCPAGELGTS	0.010

Table IX-V10-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	LGTSDVVTVV	0.003
7	GELGTSDVVT	0.001
5	PAGELGTSDV	0.001
4	CPAGELGTSD	0.000
1	TGRCPAGELG	0.000

Table IX-V11-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	VMVPPLPSLN	0.050
10	MVPPLPSLNP	0.050
8	RVMVPPLPSL	0.020
7	LRVMVPPLPS	0.003
2	QARLRLRVMV	0.002
6	RLRVMVPPLP	0.000
4	RLRLRVMVPP	0.000
1	FQARLRLRVM	0.000
5	LRLRVMVPPL	0.000
3	ARLRLRVMVP	0.000

Table IX-V12-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
3	MSEEPEGCSY	67.500
4	SEEPEGCSYS	0.450
6	EPEGCSYSTL	0.225

Table IX-V12-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
10	CSYSTLTTVR	0.150
8	EGCSYSTLTT	0.013
9	GCSYSTLTTV	0.010
1	SVMSEEPEGC	0.010
2	VMSEEPEGCS	0.005
5	EEPEGCSYST	0.001
11	SYSTLTTVRE	0.000
7	PEGCSYSTLT	0.000

Table IX-V13-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	LADPQEDSGK	100.000
5	TVDVLADPQE	0.100
1	DSQVTVDVLA	0.030
4	VTVDVLADPQ	0.025
8	VLADPQEDSG	0.010
7	DVLADPQEDS	0.010
3	QVTVDVLADP	0.002
2	SQVTVDVLAD	0.001
10	ADPQEDSGKQ	0.001
6	VDVLADPQED	0.000

Table IX-V14-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score

Table IX-V14-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
3	SSNPPASASL	0.300
10	ASLVAGTLSV	0.075
4	SNPPASASLV	0.025
8	ASASLVAGTL	0.015
2	GSSNPPASAS	0.015
5	NPPASASLVA	0.013
9	SASLVAGTLS	0.010
1	LGSSNPPASA	0.005
7	PASASLVAGT	0.002
6	PPASASLVAG	0.001

Table X- V1-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
359	LLFCLLVVV	412.546
18	LLLLLASFT	257.802
358	ALLFCLLVV	242.674
15	WLLLLLLLA	194.477
145	VLVPPLPSL	83.527
80	ALLHSKYGL	79.041
362	CLLVVVVVL	74.536
355	VIAALLFCL	66.613
8	EMWGPEAWL	52.823
502	YINGRGHLV	43.992
137	FQARLRLRV	32.438
112	VLLRNAVQA	31.249
363	LLVVVVVLM	19.425
357	AALLFCLLV	13.582
42	VVLGQDAKL	11.757
203	AVTSEFHLV	11.563
345	LVSASVVVV	9.756
410	SQPEESVGL	8.880

Table X- V1-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
299	TLGFPPLTT	7.452
164	GLTLAASCT	7.452
351	VVVGVIAAL	7.309
361	FCLLVVVVV	7.287
354	GVIAALLFC	5.499
34	LETSDVVTV	5.288
10	WGPEAWLLL	4.471
21	LLASFTGRC	4.172
32	GELETSDVV	4.122
142	RLRVLVPPL	3.734
215	SMNGQPLTC	3.588
443	RSYSTLTTV	3.342
352	VVGVIAALL	3.178
242	VSFLAEASV	2.856
19	LLLLASFTG	2.719
342	QVDLVSASV	2.434
253	LEDQNLWHI	2.380
229	GLLQDQRIT	2.261
347	SASVVVVGV	2.222
344	DLVSASVVV	2.139
106	NPLDGSVLL	2.115
123	GEYECRVST	1.901
216	MNGQPLTCV	1.775
202	AAVTSEFHL	1.721
452	REIETQTEL	1.703
350	VVVVGVIAA	1.700
287	GPLPSGVRV	1.680
231	LQDQRITHI	1.654
244	FLAEASVRG	1.405
173	AEGSPAPSV	1.352
62	VGQVAWARV	1.312
495	KPTGNGIYI	1.311
460	LLSPGSGRA	1.098
17	LLLLLLASF	1.078
16	LLLLLLLAS	1.078
356	IAALLFCLL	0.958
263	REGAMLKCL	0.955

Table X- V1-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
390	LTLTRENSI	0.911
478	IKQAMNHFV	0.903
230	LLQDQRITH	0.519
135	GSFQARLRL	0.516
238	HILHVSFLA	0.498
60	EQVGQVAWA	0.478
481	AMNHFVQEN	0.470
266	AMLKCLSEG	0.458
110	GSVLLRNAV	0.454
196	FKHSRSAAV	0.444
64	QVAWARVDA	0.435
165	LTLAASCTA	0.434
13	EAWLLLLLL	0.425
121	DEGEYECRV	0.416
73	GEGAQELAL	0.415
275	QPPPSYNWT	0.401
384	QKYEEELTL	0.389
306	TTEHSGIYV	0.340
35	ETSDVVTVV	0.280
4	SLGAEMWGP	0.257
158	ALEEGQGLT	0.254
341	KQVDLVSAS	0.249
343	VDLVSASVV	0.249
382	MTQKYEEEL	0.247
446	STLTTVREI	0.247
223	CVVSHPGLL	0.243
304	PLTTEHSGI	0.230
44	LGQDAKLPC	0.226
1	MPLSLGAEM	0.204
450	TVREIETQT	0.203
237	THILHVSFL	0.188
217	NGQPLTCVV	0.186
214	RSMNGQPLT	0.180
349	SVVVVGVIA	0.178
20	LLLASFTGR	0.178
448	LTTVREIET	0.176
285	LDGPLPSGV	0.164

Table X- V1-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
473	DQDEGIKQA	0.142
322	SSRDSQVTV	0.141
369	VLMSRYHRR	0.141
100	QPPPPRNPL	0.139
222	TCVVSHPGL	0.139
257	NLWHIGREG	0.124
163	QGLTLAASC	0.120
23	ASFTGRCPA	0.120

Table X- V2-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	GQDAKLPCL	1.993
8	CLYRGDSGE	0.048
5	KLPCLYRGD	0.016
4	AKLPCLYRG	0.001
6	LPCLYRGDS	0.000
2	QDAKLPCLY	0.000
7	PCLYRGDSG	0.000
3	DAKLPCLYR	0.000
9	LYRGDSGEQ	0.000

Table X- V7-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	SQSEEPEGR	0.003
7	RSQSEEPEG	0.000

Table X- V7-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
4	TDPRSQSEE	0.000
2	HHTDPRSQS	0.000
3	HTDPRSQSE	0.000
1	SHHTDPRSQ	0.000
5	DPRSQSEEP	0.000
6	PRSQSEEPE	0.000

Table X- V9-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
98	CLLLGLLKV	591.888
15	FNFFLFFFL	143.853
39	FLEMESHYV	112.619
65	SLVAGTLSV	69.552
5	LLAGILLRI	40.792
91	KAFRFIQCL	33.581
95	FIQCLLLGL	31.077
124	FQGIFMQAA	20.251
18	FLFFFLPFP	12.194
46	YVAQAGLEL	8.598
54	LLGSSNPPA	8.446
70	TLSVHHCAC	4.968
32	IYFYFYFFL	3.393
9	ILLRITFNF	2.719
88	KLKKAFRFI	2.671
109	LQHQGVNSC	1.969
28	VVFFIYFYF	1.963
128	FMQAAPWEG	1.857
31	FIYFYFYFF	1.576
20	FFFLPFPLV	1.562
3	RELLAGILL	1.537
21	FFLPFPLVV	1.281

Table X- V9-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
96	IQCLLLGLL	1.101
129	MQAAPWEGT	1.070
40	LEMESHYVA	1.021
11	LRITFNFFL	0.611
121	RGYFQGIFM	0.571
47	VAQAGLELL	0.568
19	LFFFLPFPL	0.541
27	LVVFFIYFY	0.533
8	GILLRITFN	0.480
59	NPPASASLV	0.454
101	LGLLKVRPL	0.403
42	MESHYVAQA	0.378
22	FLPFPLVVF	0.323
13	ITFNFFLFF	0.259
69	GTLSVHHCA	0.255
58	SNPPASASL	0.139
12	RITFNFFLF	0.113
62	ASASLVAGT	0.112
10	LLRITFNFF	0.101
99	LLLGLLKVR	0.088
34	FYFYFFLEM	0.085
68	AGTLSVHHC	0.075
26	PLVVFFIYF	0.065
102	GLLKVRPLQ	0.055
93	FRFIQCLLL	0.050
44	SHYVAQAGL	0.047
90	KKAFRFIQC	0.046
30	FFIYFYFYF	0.043
23	LPFPLVVFF	0.039
63	SASLVAGTL	0.039
126	GIFMQAAPW	0.038
25	FPLVVFFIY	0.037
75	HCACFESFT	0.035
6	LAGILLRIT	0.033
56	GSSNPPASA	0.032
123	YFQGIFMQA	0.030
119	CERGYFQGI	0.029

Table X- V9-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
100	LLGLLKVRP	0.025
111	HQGVNSCDC	0.017
106	VRPLQHQGV	0.016
81	SFTKRKKKL	0.015
14	TFNFFLFFF	0.014
24	PFPLVVFFI	0.012
66	LVAGTLSVH	0.010
4	ELLAGILLR	0.010
87	KKLKKAFRF	0.008
48	AQAGLELLG	0.008
72	SVHHCACFE	0.007
17	FFLFFFLPF	0.006
51	GLELLGSSN	0.005
103	LLKVRPLQH	0.004
53	ELLGSSNPP	0.004
38	FFLEMESHY	0.004
29	VFFIYFYFY	0.003
77	ACFESFTKR	0.003
49	QAGLELLGS	0.002
50	AGLELLGSS	0.002
52	LELLGSSNP	0.002
64	ASLVAGTLS	0.002
1	MRRELLAGI	0.002
67	VAGTLSVHH	0.002
105	KVRPLQHQG	0.002
33	YFYFYFFLE	0.002
108	PLQHQGVNS	0.002
16	NFFLFFFLP	0.002
113	GVNSCDCER	0.001
76	CACFESFTK	0.001
92	AFRFIQCLL	0.001
37	YFFLEMESH	0.001
71	LSVHHCACF	0.001
55	LGSSNPPAS	0.001
35	YFYFFLEME	0.001
73	VHHCACFES	0.001
7	AGILLRITF	0.000

Table X- V9-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
57	SSNPPASAS	0.000
117	CDCERGYFQ	0.000
114	VNSCDCERG	0.000
115	NSCDCERGY	0.000

Table X- V10-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	VMVPPLPSL	60.325
5	RLRVMVPPL	3.734
2	ARLRLRVMV	0.036
7	RVMVPPLPS	0.024
9	MVPPLPSLN	0.011
3	RLRLRVMVP	0.001
1	QARLRLRVM	0.001
4	LRLRVMVPP	0.000
6	LRVMVPPLP	0.000

Table X-V11-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
9	GTSDVVTVV	3.735
8	LGTSDVVTV	1.775
6	GELGTSDVV	1.005
7	ELGTSDVVT	0.229
2	RCPAGELGT	0.049
5	AGELGTSDV	0.029

Table X-V11-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
3	CPAGELGTS	0.000
4	PAGELGTSD	0.000
1	GRCPAGELG	0.000

Table X-V12-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	VMSEEPEGC	12.254
9	CSYSTLTTV	3.342
8	GCSYSTLTT	0.049
6	PEGCSYSTL	0.014
7	EGCSYSTLT	0.004
4	EEPEGCSYS	0.002
5	EPEGCSYST	0.000
3	SEEPEGCSY	0.000
2	MSEEPEGCS	0.000

Table X-V13-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	SQVTVDVLA	0.504
7	VLADPQEDS	0.255
3	VTVDVLADP	0.003
2	QVTVDVLAD	0.003
6	DVLADPQED	0.000
8	LADPQEDSG	0.000
4	TVDVLADPQ	0.000

Table X-V13-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
5	VDVLADPQE	0.000
9	ADPQEDSGK	0.000

Table X-V14-HLA-A201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
4	NPPASASLV	0.454
3	SNPPASASL	0.139
7	ASASLVAGT	0.112
8	SASLVAGTL	0.039
1	GSSNPPASA	0.032
9	ASLVAGTLS	0.002
2	SSNPPASAS	0.000
5	PPASASLVA	0.000
6	PASASLVAG	0.000

Table XI-V1-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
359	LLFCLLVVVV	412.546
17	LLLLLLASFT	257.802
358	ALLFCLLVVV	242.674
244	FLAEASVRGL	185.332
230	LLQDQRITHI	167.248
81	LLHSKYGLHV	118.238
215	SMNGQPLTCV	115.534

Table XI-V1-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
341	KQVDLVSASV	101.193
239	ILHVSFLAEA	73.815
8	EMWGPEAWLL	72.031
252	GLEDQNLWHI	47.223
362	CLLVVVVVLM	42.278
305	LTTEHSGIYV	37.032
284	RLDGPLPSGV	27.821
354	GVIAALLFCL	24.935
257	NLWHIGREGA	20.205
144	RVLVPPLPSL	15.907
20	LLLASFTGRC	15.437
181	VTWDTEVKGT	13.771
61	QVGQVAWARV	10.346
426	SLKDNSSCSV	9.981
355	VIAALLFCLL	9.488
7	AEMWGPEAWL	8.453
43	VLGQDAKLPC	8.446
485	FVQENGTLRA	8.198
381	QMTQKYEEEL	7.560
447	TLTTVREIET	7.452
350	VVVVGVIAAL	7.309
236	ITHILHVSFL	6.381
356	IAALLFCLLV	6.240
274	GQPPPSYNWT	6.233
10	WGPEAWLLLL	6.049
158	ALEEGQGLTL	5.605
319	NEFSSRDSQV	5.004
164	GLTLAASCTA	4.968

Table XI-V1-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
344	DLVSASVVVV	4.919
118	VQADEGEYEC	3.511
357	AALLFCLLVV	3.370
351	VVVGVIAALL	3.178
15	WLLLLLLLAS	2.917
18	LLLLLASFTG	2.719
125	YECRVSTFPA	2.577
132	FPAGSFQARL	2.438
361	FCLLVVVVVL	2.238
34	LETSDVVTVV	2.168
321	FSSRDSQVTV	2.088
137	FQARLRLRVL	1.879
41	TVVLGQDAKL	1.869
79	LALLHSKYGL	1.866
477	GIKQAMNHFV	1.841
202	AAVTSEFHLV	1.835
346	VSASVVVVGV	1.775
201	SAAVTSEFHL	1.721
111	SVLLRNAVQA	1.608
130	STFPAGSFQA	1.481
59	GEQVGQVAWA	1.222
500	GIYINGRGHL	1.222
370	LMSRYHRRKA	1.220
16	LLLLLLLASF	1.078
349	SVVVVGVIAA	1.000
342	QVDLVSASVV	0.998
73	GEGAQELALL	0.955
32	GELETSDVVT	0.901
452	REIETQTELL	0.834
389	ELTLTRENSI	0.782
33	ELETSDVVTV	0.768
39	VVTVVLGQDA	0.739

Table XI-V1-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
353	VGVIAALLFC	0.697
280	YNWTRLDGPL	0.692
231	LQDQRITHIL	0.604
221	LTCVVSHPGL	0.504
63	GQVAWARVDA	0.504
162	GQGLTLAASC	0.504
178	APSVTWDTEV	0.454
13	EAWLLLLLLL	0.425
176	SPAPSVTWDT	0.365
216	MNGQPLTCVV	0.316
384	QKYEEELTLT	0.312
270	CLSEGQPPPS	0.306
363	LLVVVVVLMS	0.291
229	GLLQDQRITH	0.276
343	VDLVSASVVV	0.249
150	LPSLNPGPAL	0.237
5	LGAEMWGPEA	0.226
112	VLLRNAVQAD	0.216
241	HVSFLAEASV	0.207
163	QGLTLAASCT	0.180
459	ELLSPGSGRA	0.179
19	LLLLASFTGR	0.178
25	FTGRCPAGEL	0.177
336	QEDSGKQVDL	0.166
99	EQPPPPRNPL	0.162
445	YSTLTTVREI	0.144
249	SVRGLEDQNL	0.142
334	DPQEDSGKQ	0.140

Table XI-V1-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
	V	
105	RNPLDGSVLL	0.139
409	RSQPEESVGL	0.139
134	AGSFQARLRL	0.139
156	GPALEEGQGL	0.139
145	VLVPPLPSLN	0.127

Table XI-V2-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
1	LGQDAKLPCL	2.236
6	KLPCLYRGDS	0.034
9	CLYRGDSGEQ	0.006
2	GQDAKLPCLY	0.003
10	LYRGDSGEQV	0.001
7	LPCLYRGDSG	0.000
3	QDAKLPCLYR	0.000
5	AKLPCLYRGD	0.000
8	PCLYRGDSGE	0.000
4	DAKLPCLYRG	0.000

Table XI-V7-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	SQSEEPEGRS	0.004

Table XI-V7-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
2	SHHTDPRSQS	0.000
8	RSQSEEPEGR	0.000
5	TDPRSQSEEP	0.000
4	HTDPRSQSEE	0.000
3	HHTDPRSQSE	0.000
1	HSHHTDPRSQ	0.000
6	DPRSQSEEPE	0.000
7	PRSQSEEPEG	0.000

Table XI-V9-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
31	FIYFYFYFFL	7861.874
18	FLFFFLPFPL	2108.811
10	LLRITFNFFL	334.570
23	LPFPLVVFFI	31.429
128	FMQAAPWEGT	20.623
38	FFLEMESHYV	18.538
100	LLGLLKVRPL	16.705
46	YVAQAGLELL	9.690
4	ELLAGILLRI	6.659
9	ILLRITFNFF	4.898
22	FLPFPLVVFF	4.336
95	FIQCLLLGLL	4.040
97	QCLLLGLLKV	3.864
91	KAFRFIQCLL	3.842
5	LLAGILLRIT	2.389
13	ITFNFFLFFF	1.815
64	ASLVAGTLSV	1.680
105	KVRPLQHQG	1.619

Table XI-V9-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
	V	
53	ELLGSSNPPA	1.379
20	FFFLPFPLVV	1.281
90	KKAFRFIQCL	0.908
14	TFNFFLFFFL	0.899
39	FLEMESHYVA	0.600
19	LFFFLPFPLV	0.577
27	LVVFFIYFYF	0.530
58	SNPPASASLV	0.454
28	VVFFIYFYFY	0.429
12	RITFNFFLFF	0.407
87	KKLKKAFRFI	0.392
33	YFYFYFFLEM	0.367
25	FPLVVFFIYF	0.329
102	GLLKVRPLQH	0.276
67	VAGTLSVHHC	0.270
69	GTLSVHHCAC	0.255
108	PLQHQGVNSC	0.251
8	GILLRITFNF	0.220
57	SSNPPASASL	0.139
123	YFQGIFMQAA	0.139
54	LLGSSNPPAS	0.127
99	LLLGLLKVRP	0.094
26	PLVVFFIYFY	0.079
70	TLSVHHCACF	0.075
65	SLVAGTLSVH	0.070
15	FNFFLFFFLP	0.069
29	VFFIYFYFYF	0.059
55	LGSSNPPASA	0.055
98	CLLLGLLKVR	0.052
126	GIFMQAAPWE	0.042
41	EMESHYVAQA	0.040
80	ESFTKRKKKL	0.039

Table XI-V9-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
72	SVHHCACFES	0.038
94	RFIQCLLLGL	0.034
68	AGTLSVHHCA	0.032
62	ASASLVAGTL	0.018
48	AQAGLELLGS	0.017
88	KLKKAFRFIQ	0.016
59	NPPASASLVA	0.013
40	LEMESHYVAQ	0.011
66	LVAGTLSVHH	0.011
43	ESHYVAQAGL	0.010
17	FFLFFFLPFP	0.008
50	AGLELLGSSN	0.007
124	FQGIFMQAAP	0.007
7	AGILLRITFN	0.006
77	ACFESFTKRK	0.006
61	PASASLVAGT	0.005
122	GYFQGIFMQA	0.005
121	RGYFQGIFMQ	0.004
117	CDCERGYFQG	0.004
74	HHCACFESFT	0.004
110	QHQGVNSCDC	0.003
113	GVNSCDCERG	0.003
96	IQCLLLGLLK	0.003
109	LQHQGVNSCD	0.003
30	FFIYFYFYFF	0.002
3	RELLAGILLR	0.002
42	MESHYVAQAG	0.002
127	IFMQAAPWEG	0.002

Table XI-V9-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
103	LLKVRPLQHQ	0.002
52	LELLGSSNPP	0.002
107	RPLQHQGVNS	0.002
6	LAGILLRITF	0.002
47	VAQAGLELLG	0.002
115	NSCDCERGYF	0.001
16	NFFLFFFLPF	0.001
79	FESFTKRKKK	0.001
83	TKRKKKLKKA	0.001
92	AFRFIQCLLL	0.001
63	SASLVAGTLS	0.001
51	GLELLGSSNP	0.001
71	LSVHHCACFE	0.001
37	YFFLEMESHY	0.001
21	FFLPFPLVVF	0.001
89	LKKAFRFIQC	0.001
35	YFYFFLEMES	0.001
118	DCERGYFQGI	0.001
101	LGLLKVRPLQ	0.001
125	QGIFMQAAPW	0.000
56	GSSNPPASAS	0.000
93	FRFIQCLLLG	0.000

Table XI-V10-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	ELGTSDVVTV	11.998
9	LGTSDVVTVV	0.728
10	GTSDVVTVVL	0.499

Table XI-V10-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
7	GELGTSDVVT	0.220
5	PAGELGTSDV	0.087
6	AGELGTSDVV	0.006
2	GRCPAGELGT	0.001
3	RCPAGELGTS	0.000
4	CPAGELGTSD	0.000
1	TGRCPAGELG	0.000

Table XI-V11-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	RVMVPPLPSL	15.907
1	FQARLRLRVM	0.437
9	VMVPPLPSLN	0.091
2	QARLRLRVMV	0.073
5	LRLRVMVPPL	0.043
4	RLRLRVMVPP	0.003
10	MVPPLPSLNP	0.002
6	RLRVMVPPLP	0.001
7	LRVMVPPLPS	0.000
3	ARLRLRVMVP	0.000

Table XI-V12-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	GCSYSTLTTV	1.044
1	SVMSEEPEGC	0.788

Table XI-V12-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
2	VMSEEPEGCS	0.049
5	EEPEGCSYST	0.045
8	EGCSYSTLTT	0.004
7	PEGCSYSTLT	0.003
6	EPEGCSYSTL	0.001
4	SEEPEGCSYS	0.001
3	MSEEPEGCSY	0.000
10	CSYSTLTTVR	0.000
11	SYSTLTTVRE	0.000

Table XI-V13-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	VLADPQEDSG	0.255
2	SQVTVDVLAD	0.003
3	QVTVDVLADP	0.003
1	DSQVTVDVLA	0.002
7	DVLADPQEDS	0.001
4	VTVDVLADPQ	0.001
5	TVDVLADPQE	0.001
9	LADPQEDSGK	0.000
6	VDVLADPQED	0.000
10	ADPQEDSGKQ	0.000

Table XI-V14-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score

Table XI-V14-HLA-A201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
10	ASLVAGTLSV	1.680
4	SNPPASASLV	0.454
3	SSNPPASASL	0.139
1	LGSSNPPASA	0.055
8	ASASLVAGTL	0.018
5	NPPASASLVA	0.013
7	PASASLVAGT	0.005
9	SASLVAGTLS	0.001
2	GSSNPPASAS	0.000
6	PPASASLVAG	0.000

Table XII-V1-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
20	LLLASFTGR	18.000
435	VMSEEPEGR	6.000
369	VLMSRYHRR	6.000
370	LMSRYHRRK	6.000
17	LLLLLLASF	4.500
362	CLLVVVVVL	4.050
391	TLTRENSIR	4.000
107	PLDGSVLLR	3.600
145	VLVPPLPSL	3.038
189	GTTSSRSFK	3.000
41	TVVLGQDAK	3.000
80	ALLHSKYGL	2.700
365	VVVVVLMSR	2.700
459	ELLSPGSGR	2.700
8	EMWGPEAWL	2.025
180	SVTWDTEVK	2.000
61	QVGQVAWAR	1.800
368	VVLMSRYHR	1.800

Table XII-V1-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
142	RLRVLVPPL	1.800
359	LLFCLLVVV	1.500
363	LLVVVVVLM	1.350
316	HVSNEFSSR	1.200
252	GLEDQNLWH	1.200
78	ELALLHSKY	1.200
366	VVVVLMSRY	0.900
358	ALLFCLLVV	0.900
477	GIKQAMNHF	0.900
15	WLLLLLLLA	0.900
89	HVSPAYEGR	0.600
294	RVDGDTLGF	0.600
485	FVQENGTLR	0.600
97	RVEQPPPPR	0.600
215	SMNGQPLTC	0.600
392	LTRENSIRR	0.600
230	LLQDQRITH	0.400
351	VVVGVIAAL	0.304
313	YVCHVSNEF	0.300
112	VLLRNAVQA	0.300
299	TLGFPPLTT	0.300
164	GLTLAASCT	0.300
354	GVIAALLFC	0.270
45	GQDAKLPCF	0.270
355	VIAALLFCL	0.270
255	DQNLWHIGR	0.216
132	FPAGSFQAR	0.180
350	VVVVGVIAA	0.180
16	LLLLLLLAS	0.180
186	EVKGTTSSR	0.180
292	GVRVDGDTL	0.180
206	SEFHLVPSR	0.180
481	AMNHFVQEN	0.180
21	LLASFTGRC	0.180
11	GPEAWLLLL	0.162
18	LLLLLASFT	0.150
77	QELALLHSK	0.135

Table XII-V1-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
42	VVLGQDAKL	0.135
238	HILHVSFLA	0.135
274	GQPPPSYNW	0.121
378	KAQQMTQKY	0.120
239	ILHVSFLAE	0.120
117	AVQADEGEY	0.120
140	RLRLRVLVP	0.120
498	GNGIYINGR	0.108
236	ITHILHVSF	0.100
352	VVGVIAALL	0.090
19	LLLLASFTG	0.090
135	GSFQARLRL	0.090
4	SLGAEMWGP	0.090
344	DLVSASVVV	0.090
305	LTTEHSGIY	0.090
460	LLSPGSGRA	0.090
382	MTQKYEEEL	0.090
420	AEGHPDSLK	0.090
284	RLDGPLPSG	0.068
261	IGREGAMLK	0.060
417	GLRAEGHPD	0.060
81	LLHSKYGLH	0.060
203	AVTSEFHLV	0.060
192	SSRSFKHSR	0.060
260	HIGREGAML	0.060
304	PLTTEHSGI	0.060
113	LLRNAVQAD	0.060
87	GLHVSPAYE	0.060
345	LVSASVVVV	0.060
364	LVVVVVLMS	0.054
495	KPTGNGIYI	0.054
47	DAKLPCFYR	0.054
411	QPEESVGLR	0.054
209	HLVPSRSMN	0.045
229	GLLQDQRIT	0.045
349	SVVVVGVIA	0.045
390	LTLTRENSI	0.045

Table XII-V1-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
158	ALEEGQGLT	0.045
266	AMLKCLSEG	0.045
227	HPGLLQDQR	0.040
426	SLKDNSSCS	0.040
276	PPPSYNWTR	0.036
386	YEEELTLTR	0.036
377	RKAQQMTQK	0.030
244	FLAEASVRG	0.030

Table XII-V2-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	CLYRGDSGE	0.100
1	GQDAKLPCL	0.081
3	DAKLPCLYR	0.036
5	KLPCLYRGD	0.006
2	QDAKLPCLY	0.004
6	LPCLYRGDS	0.000
4	AKLPCLYRG	0.000
7	PCLYRGDSG	0.000
9	LYRGDSGEQ	0.000

Table XII-V7-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	SQSEEPEGR	0.180
3	HTDPRSQSE	0.002

Table XII-V7-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
7	RSQSEEPEG	0.000
2	HHTDPRSQS	0.000
5	DPRSQSEEP	0.000
4	TDPRSQSEE	0.000
6	PRSQSEEPE	0.000
1	SHHTDPRSQ	0.000

Table XII-V9-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
31	FIYFYFYFF	27.000
9	ILLRITFNF	13.500
13	ITFNFFLFF	9.000
27	LVVFFIYFY	8.100
99	LLLGLLKVR	6.750
10	LLRITFNFF	6.000
26	PLVVFFIYF	5.400
4	ELLAGILLR	5.400
28	VVFFIYFYF	4.500
22	FLPFPLVVF	4.500
5	LLAGILLRI	4.050
12	RITFNFFLF	1.800
113	GVNSCDCER	1.200
98	CLLLGLLKV	0.900
77	ACFESFTKR	0.900
25	FPLVVFFIY	0.810
76	CACFESFTK	0.600
65	SLVAGTLSV	0.600
97	QCLLLGLLK	0.600
88	KLKKAFRFI	0.540
29	VFFIYFYFY	0.540
82	FTKRKKKLK	0.500

Table XII-V9-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
23	LPFPLVVFF	0.450
18	FLFFFLPFP	0.450
91	KAFRFIQCL	0.405
103	LLKVRPLQH	0.400
126	GIFMQAAPW	0.300
70	TLSVHHCAC	0.200
54	LLGSSNPPA	0.200
39	FLEMESHYV	0.200
95	FIQCLLLGL	0.180
102	GLLKVRPLQ	0.135
46	YVAQAGLEL	0.120
80	ESFTKRKKK	0.075
69	GTLSVHHCA	0.068
128	FMQAAPWEG	0.060
51	GLELLGSSN	0.060
15	FNFFLFFFL	0.054
17	FFLFFFLPF	0.054
66	LVAGTLSVH	0.045
83	TKRKKKLKK	0.040
78	CFESFTKRK	0.030
30	FFIYFYFYF	0.027
14	TFNFFLFFF	0.027
32	IYFYFYFFL	0.027
124	FQGIFMQAA	0.027
87	KKLKKAFRF	0.027
119	CERGYFQGI	0.024
100	LLGLLKVRP	0.020
109	LQHQGVNSC	0.018
34	FYFYFFLEM	0.018
71	LSVHHCACF	0.015
53	ELLGSSNPP	0.013
8	GILLRITFN	0.013
86	KKKLKKAFR	0.012
38	FFLEMESHY	0.009
47	VAQAGLELL	0.009
105	KVRPLQHQG	0.009
19	LFFFLPFPL	0.009

Table XII-V9-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
11	LRITFNFFL	0.008
96	IQCLLLGLL	0.008
74	HHCACFESF	0.006
7	AGILLRITF	0.006
41	EMESHYVAQ	0.006
116	SCDCERGYF	0.006
111	HQGVNSCDC	0.006
93	FRFIQCLLL	0.006
79	FESFTKRKK	0.006
3	RELLAGILL	0.005
42	MESHYVAQA	0.005
56	GSSNPPASA	0.005
20	FFFLPFPLV	0.005
129	MQAAPWEGT	0.005
40	LEMESHYVA	0.004
108	PLQHQGVNS	0.004
90	KKAFRFIQC	0.004
44	SHYVAQAGL	0.003
75	HCACFESFT	0.003
123	YFQGIFMQA	0.003
16	NFFLFFFLP	0.003
21	FFLPFPLVV	0.003
33	YFYFYFFLE	0.003
63	SASLVAGTL	0.003
72	SVHHCACFE	0.002
115	NSCDCERGY	0.002
67	VAGTLSVHH	0.002
121	RGYFQGIFM	0.002
59	NPPASASLV	0.002
58	SNPPASASL	0.002
48	AQAGLELLG	0.002
37	YFFLEMESH	0.002
62	ASASLVAGT	0.002
122	GYFQGIFMQ	0.001
1	MRRELLAGI	0.001
49	QAGLELLGS	0.001
85	RKKKLKKAF	0.001

Table XII-V9-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
92	AFRFIQCLL	0.001
24	PFPLVVFFI	0.001
68	AGTLSVHHC	0.001
120	ERGYFQGIF	0.001

Table XII-V10-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
9	GTSDVVTVV	0.135
7	ELGTSDVVT	0.030
6	GELGTSDVV	0.004
2	RCPAGELGT	0.002
8	LGTSDVVTV	0.001
3	CPAGELGTS	0.000
5	AGELGTSDV	0.000
1	GRCPAGELG	0.000
4	PAGELGTSD	0.000

Table XII-V11-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	VMVPPLPSL	3.038
5	RLRVMVPPL	1.800
3	RLRLRVMVP	0.120
7	RVMVPPLPS	0.018
9	MVPPLPSLN	0.003
1	QARLRLRVM	0.000

Table XII-V11-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
2	ARLRLRVMV	0.000
4	LRLRVMVPP	0.000
6	LRVMVPPLP	0.000

Table XII-V13-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
7	VLADPQEDS	0.060
9	ADPQEDSGK	0.020
1	SQVTVDVLA	0.013
2	QVTVDVLAD	0.012
3	VTVDVLADP	0.003
4	TVDVLADPQ	0.002
6	DVLADPQED	0.001
8	LADPQEDSG	0.000
5	VDVLADPQE	0.000

Table XII-V14-HLA-A3-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	GSSNPPASA	0.005
8	SASLVAGTL	0.003
4	NPPASASLV	0.002
3	SNPPASASL	0.002
7	ASASLVAGT	0.002
2	SSNPPASAS	0.000

5	PPASASLVA	0.000
9	ASLVAGTLS	0.000
6	PASASLVAG	0.000

Table XIII-V1-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
332	VLDPQEDSGK	30.000
19	LLLLASFTGR	18.000
369	VLMSRYHRRK	9.000
252	GLEDQNLWHI	8.100
391	TLTRENSIRR	8.000
16	LLLLLLLASF	4.500
8	EMWGPEAWLL	4.050
400	RLHSHHTDPR	4.000
260	HIGREGAMLK	4.000
359	LLFCLLVVVV	3.000
364	LVVVVVLMSR	2.700
381	QMTQKYEEEL	1.800
158	ALEEGQGLTL	1.800
229	GLLQDQRITH	1.800
367	VVVLMSRYHR	1.800
40	VTVVLGQDAK	1.500
362	CLLVVVVVLM	1.350
354	GVIAALLFCL	1.215
81	LLHSKYGLHV	1.200
257	NLWHIGREGA	1.000
76	AQELALLHSK	0.900
365	VVVVVLMSRY	0.900
239	ILHVSFLAEA	0.900
230	LLQDQRITHI	0.900
215	SMNGQPLTCV	0.675
434	SVMSEEPEGR	0.600
164	GLTLAASCTA	0.600
368	VVLMSRYHRR	0.600
363	LLVVVVVLMS	0.540
275	QPPPSYNWTR	0.540
419	RAEGHPDSLK	0.450
358	ALLFCLLVVV	0.450
123	GEYECRVSTF	0.405

Table XIII-V1-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
43	VLGQDAKLPC	0.400
352	VVGVIAALLF	0.400
60	EQVGQVAWAR	0.364
106	NPLDGSVLLR	0.360
45	GQDAKLPCFY	0.360
390	LTLTRENSIR	0.300
284	RLDGPLPSGV	0.300
244	FLAEASVRGL	0.270
500	GIYINGRGHL	0.270
87	GLHVSPAYEG	0.270
344	DLVSASVVVV	0.270
20	LLLASFTGRC	0.270
130	STFPAGSFQA	0.225
144	RVLVPPLPSL	0.203
351	VVVGVIAALL	0.203
350	VVVVGVIAAL	0.203
426	SLKDNSSCSV	0.200
447	TLTTVREIET	0.200
235	RITHILHVSF	0.200
15	WLLLLLLLAS	0.180
33	ELETSDVVTV	0.180
355	VIAALLFCLL	0.180
349	SVVVVGVIAA	0.180
389	ELTLTRENSI	0.180
410	SQPEESVGLR	0.162
17	LLLLLLASFT	0.150
304	PLTTEHSGIY	0.120
417	GLRAEGHPDS	0.120
49	KLPCFYRGDS	0.108
443	RSYSTLTTVR	0.100
242	VSFLAEASVR	0.100
18	LLLLLASFTG	0.090
249	SVRGLEDQNL	0.090
209	HLVPSRSMNG	0.090
41	TVVLGQDAKL	0.090
80	ALLHSKYGLH	0.090
189	GTTSSRSFKH	0.090

Table XIII-V1-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
486	VQENGTLRAK	0.090
152	SLNPGPALEE	0.090
112	VLLRNAVQAD	0.090
311	GIYVCHVSNE	0.090
236	ITHILHVSFL	0.090
128	RVSTFPAGSF	0.090
188	KGTTSSRSFK	0.060
270	CLSEGQPPPS	0.060
477	GIKQAMNHFV	0.060
485	FVQENGTLRA	0.060
191	TSSRSFKHSR	0.060
205	TSEFHLVPSR	0.060
119	QADEGEYECR	0.060
11	GPEAWLLLLL	0.054
218	GQPLTCVVSH	0.054
140	RLRLRVLVPP	0.045
299	TLGFPPLTTE	0.045
271	LSEGQPPPSY	0.045
135	GSFQARLRLR	0.045
145	VLVPPLPSLN	0.045
306	TTEHSGIYVC	0.045
96	GRVEQPPPPR	0.041
361	FCLLVVVVVL	0.041
341	KQVDLVSASV	0.041
181	VTWDTEVKGT	0.037
385	KYEEELTLTR	0.036
383	TQKYEEELTL	0.036
376	RRKAQQMTQK	0.030
305	LTTEHSGIYV	0.030
221	LTCVVSHPGL	0.030

Table XIII-V2-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
2	GQDAKLPCLY	0.360
6	KLPCLYRGDS	0.108
9	CLYRGDSGEQ	0.030
3	QDAKLPCLYR	0.012
1	LGQDAKLPCL	0.001
10	LYRGDSGEQV	0.000
4	DAKLPCLYRG	0.000
7	LPCLYRGDSG	0.000
8	PCLYRGDSGE	0.000
5	AKLPCLYRGD	0.000

Table XIII-V7-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	RSQSEEPEGR	0.020
4	HTDPRSQSEE	0.002
9	SQSEEPEGRS	0.001
2	SHHTDPRSQS	0.000
6	DPRSQSEEPE	0.000
5	TDPRSQSEEP	0.000
3	HHTDPRSQSE	0.000
1	HSHHTDPRSQ	0.000
7	PRSQSEEPEG	0.000

Table XIII-V9-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
28	VVFFIYFYFY	54.000
18	FLFFFLPFPL	9.000

Table XIII-V9-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	ILLRITFNFF	9.000
26	PLVVFFIYFY	8.100
13	ITFNFFLFFF	6.750
22	FLPFPLVVFF	6.000
10	LLRITFNFFL	5.400
98	CLLLGLLKVR	4.500
8	GILLRITFNF	4.050
12	RITFNFFLFF	3.600
31	FIYFYFYFFL	2.700
77	ACFESFTKRK	2.250
82	FTKRKKKLKK	2.000
70	TLSVHHCACF	2.000
102	GLLKVRPLQH	1.800
27	LVVFFIYFYF	1.350
4	ELLAGILLRI	1.215
96	IQCLLLGLLK	1.200
23	LPFPLVVFFI	0.608
75	HCACFESFTK	0.600
39	FLEMESHYVA	0.600
25	FPLVVFFIYF	0.540
88	KLKKAFRFIQ	0.540
41	EMESHYVAQA	0.540
65	SLVAGTLSVH	0.450
100	LLGLLKVRPL	0.180
16	NFFLFFFLPF	0.180
128	FMQAAPWEGT	0.150
53	ELLGSSNPPA	0.135
91	KAFRFIQCLL	0.135
76	CACFESFTKR	0.120
105	KVRPLQHQGV	0.090
46	YVAQAGLELL	0.090
29	VFFIYFYFYF	0.090
30	FFIYFYFYFF	0.081
51	GLELLGSSNP	0.060
108	PLQHQGVNSC	0.060
3	RELLAGILLR	0.054
69	GTLSVHHCAC	0.045

Table XIII-V9-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
99	LLLGLLKVRP	0.045
103	LLKVRPLQHQ	0.045
54	LLGSSNPPAS	0.040
6	LAGILLRITF	0.040
66	LVAGTLSVHH	0.030
79	FESFTKRKKK	0.030
126	GIFMQAAPWE	0.030
122	GYFQGIFMQA	0.027
11	LRITFNFFLF	0.027
95	FIQCLLLGLL	0.027
5	LLAGILLRIT	0.022
37	YFFLEMESHY	0.020
86	KKKLKKAFRF	0.018
33	YFYFYFFLEM	0.018
118	DCERGYFQGI	0.016
72	SVHHCACFES	0.012
21	FFLPFPLVVF	0.010
81	SFTKRKKKLK	0.010
97	QCLLLGLLKV	0.009
90	KKAFRFIQCL	0.008
119	CERGYFQGIF	0.008
112	QGVNSCDCER	0.006
73	VHHCACFESF	0.006
67	VAGTLSVHHC	0.006
113	GVNSCDCERG	0.006
20	FFFLPFPLVV	0.006
24	PFPLVVFFIY	0.005
15	FNFFLFFFLP	0.005
48	AQAGLELLGS	0.005
14	TFNFFLFFFL	0.005
19	LFFFLPFPLV	0.005
57	SSNPPASASL	0.005
85	RKKKLKKAFR	0.004
59	NPPASASLVA	0.004
84	KRKKKLKKAF	0.003
64	ASLVAGTLSV	0.003
115	NSCDCERGYF	0.003

Table XIII-V9-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
94	RFIQCLLLGL	0.003
32	IYFYFYFFLE	0.003
80	ESFTKRKKKL	0.002
78	CFESFTKRKK	0.002
45	HYVAQAGLEL	0.002
36	FYFFLEMESH	0.002
123	YFQGIFMQAA	0.001
62	ASASLVAGTL	0.001
2	RRELLAGILL	0.001
89	LKKAFRFIQC	0.001
92	AFRFIQCLLL	0.001
109	LQHQGVNSCD	0.001
56	GSSNPPASAS	0.001
43	ESHYVAQAGL	0.001
87	KKLKKAFRFI	0.001
114	VNSCDCERGY	0.001
116	SCDCERGYFQ	0.001
111	HQGVNSCDCE	0.001
58	SNPPASASLV	0.001
107	RPLQHQGVNS	0.001
124	FQGIFMQAAP	0.001
38	FFLEMESHYV	0.000
34	FYFYFFLEME	0.000
121	RGYFQGIFMQ	0.000

Table XIII-V10-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	ELGTSDVVTV	0.180
10	GTSDVVTVVL	0.135
7	GELGTSDVVT	0.002
2	GRCPAGELGT	0.001

Table XIII-V10-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	LGTSDVVTVV	0.001
5	PAGELGTSDV	0.000
4	CPAGELGTSD	0.000
6	AGELGTSDVV	0.000
3	RCPAGELGTS	0.000
1	TGRCPAGELG	0.000

Table XIII-V11-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	RVMVPPLPSL	0.203
9	VMVPPLPSLN	0.045
4	RLRLRVMVPP	0.045
6	RLRVMVPPLP	0.030
10	MVPPLPSLNP	0.009
5	LRLRVMVPPL	0.003
2	QARLRLRVMV	0.002
1	FQARLRLRVM	0.001
7	LRVMVPPLPS	0.000
3	ARLRLRVMVP	0.000

Table XIII-V12-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
10	CSYSTLTTVR	0.100
1	SVMSEEPEGC	0.030
3	MSEEPEGCSY	0.030
2	VMSEEPEGCS	0.027
9	GCSYSTLTTV	0.009
6	EPEGCSYSTL	0.003
5	EEPEGCSYST	0.000
4	SEEPEGCSYS	0.000
7	PEGCSYSTLT	0.000
8	EGCSYSTLTT	0.000
11	SYSTLTTVRE	0.000

Table XIII-V13-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	LADPQEDSGK	0.300
8	VLADPQEDSG	0.020
2	SQVTVDVLAD	0.005
3	QVTVDVLADP	0.005
7	DVLADPQEDS	0.003
5	TVDVLADPQE	0.002
4	VTVDVLADPQ	0.002
1	DSQVTVDVLA	0.000
6	VDVLADPQED	0.000
10	ADPQEDSGKQ	0.000

Table XIII-V14-HLA-A3-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
3	SSNPPASASL	0.005
5	NPPASASLVA	0.004
10	ASLVAGTLSV	0.003
8	ASASLVAGTL	0.001
2	GSSNPPASAS	0.001
4	SNPPASASLV	0.001
9	SASLVAGTLS	0.000
1	LGSSNPPASA	0.000
7	PASASLVAGT	0.000
6	PPASASLVAG	0.000

Table XIV-V1-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
41	TVVLGQDAK	3.000
189	GTTSSRSFK	3.000
180	SVTWDTEVK	2.000
365	VVVVVLMSR	1.200
97	RVEQPPPPR	1.200
368	VVLMSRYHR	1.200
61	QVGQVAWAR	0.800
485	FVQENGTLR	0.400
392	LTRENSIRR	0.400
89	HVSPAYEGR	0.400
316	HVSNEFSSR	0.400
369	VLMSRYHRR	0.160
186	EVKGTTSSR	0.120
294	RVDGDTLGF	0.120
20	LLLASFTGR	0.120
77	QELALLHSK	0.090
391	TLTRENSIR	0.080

Table XIV-V1-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
444	SYSTLTTVR	0.080
435	VMSEEPEGR	0.080
255	DQNLWHIGR	0.072
377	RKAQQMTQK	0.060
292	GVRVDGDTL	0.060
350	VVVVGVIAA	0.060
420	AEGHPDSLK	0.060
243	SFLAEASVR	0.060
370	LMSRYHRRK	0.040
411	QPEESVGLR	0.040
261	IGREGAMLK	0.040
227	HPGLLQDQR	0.040
132	FPAGSFQAR	0.040
459	ELLSPGSGR	0.036
47	DAKLPCFYR	0.036
274	GQPPPSYNW	0.036
42	VVLGQDAKL	0.030
349	SVVVVGVIA	0.030
190	TTSSRSFKH	0.030
366	VVVVLMSRY	0.030
351	VVVGVIAAL	0.030
223	CVVSHPGLL	0.030
498	GNGIYINGR	0.024
386	YEEELTLTR	0.024
206	SEFHLVPSR	0.024
252	GLEDQNLWH	0.024
117	AVQADEGEY	0.020
342	QVDLVSASV	0.020
352	VVGVIAALL	0.020
333	LDPQEDSGK	0.020
306	TTEHSGIYV	0.020
345	LVSASVVVV	0.020
313	YVCHVSNEF	0.020
203	AVTSEFHLV	0.020
415	SVGLRAEGH	0.020
64	QVAWARVDA	0.020
238	HILHVSFLA	0.018

Table XIV-V1-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
144	RVLVPPLPS	0.018
354	GVIAALLFC	0.018
471	EEDQDEGIK	0.018
45	GQDAKLPCF	0.018
107	PLDGSVLLR	0.016
40	VTVVLGQDA	0.015
390	LTLTRENSI	0.015
165	LTLAASCTA	0.015
75	GAQELALLH	0.012
85	KYGLHVSPA	0.012
358	ALLFCLLVV	0.012
11	GPEAWLLLL	0.012
495	KPTGNGIYI	0.012
486	VQENGTLRA	0.012
15	WLLLLLLLA	0.012
142	RLRVLVPPL	0.012
80	ALLHSKYGL	0.012
477	GIKQAMNHF	0.012
137	FQARLRLRV	0.012
355	VIAALLFCL	0.012
236	ITHILHVSF	0.010
382	MTQKYEEEL	0.010
305	LTTEHSGIY	0.010
287	GPLPSGVRV	0.009
202	AAVTSEFHL	0.009
230	LLQDQRITH	0.008
359	LLFCLLVVV	0.008
276	PPPSYNWTR	0.008
363	LLVVVVVLM	0.006
231	LQDQRITHI	0.006
112	VLLRNAVQA	0.006
410	SQPEESVGL	0.006
419	RAEGHPDSL	0.006
128	RVSTFPAGS	0.006
364	LVVVVVLMS	0.006
378	KAQQMTQKY	0.006
501	IYINGRGHL	0.006

Table XIV-V1-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
69	RVDAGEGAQ	0.006
362	CLLVVVVVL	0.006
6	GAEMWGPEA	0.006
131	TFPAGSFQA	0.006
357	AALLFCLLV	0.006
17	LLLLLLASF	0.006
493	RAKPTGNGI	0.006
487	QENGTLRAK	0.006
301	GFPPLTTEH	0.006

Table XIV-V2-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
3	DAKLPCLYR	0.024
1	GQDAKLPCL	0.018
8	CLYRGDSGE	0.001
9	LYRGDSGEQ	0.000
6	LPCLYRGDS	0.000
2	QDAKLPCLY	0.000
5	KLPCLYRGD	0.000
4	AKLPCLYRG	0.000
7	PCLYRGDSG	0.000

Table XIV-V7-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	SQSEEPEGR	0.120

Table XIV-V7-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
3	HTDPRSQSE	0.001
7	RSQSEEPEG	0.000
5	DPRSQSEEP	0.000
4	TDPRSQSEE	0.000
2	HHTDPRSQS	0.000
6	PRSQSEEPE	0.000
1	SHHTDPRSQ	0.000

Table XIV-V9-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
113	GVNSCDCER	1.200
76	CACFESFTK	0.600
97	QCLLLGLLK	0.600
82	FTKRKKKLK	0.500
28	VVFFIYFYF	0.120
78	CFESFTKRK	0.100
77	ACFESFTKR	0.080
4	ELLAGILLR	0.072
27	LVVFFIYFY	0.060
99	LLLGLLKVR	0.060
69	GTLSVHHCA	0.045
83	TKRKKKLKK	0.040
13	ITFNFFLFF	0.040
46	YVAQAGLEL	0.040
12	RITFNFFLF	0.036
126	GIFMQAAPW	0.024
32	IYFYFYFFL	0.024
66	LVAGTLSVH	0.020
9	ILLRITFNF	0.018
34	FYFYFFLEM	0.016
31	FIYFYFYFF	0.016

Table XIV-V9-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
86	KKKLKKAFR	0.012
19	LFFFLPFPL	0.012
98	CLLLGLLKV	0.012
91	KAFRFIQCL	0.012
65	SLVAGTLSV	0.012
30	FFIYFYFYF	0.009
25	FPLVVFFIY	0.009
103	LLKVRPLQH	0.008
5	LLAGILLRI	0.008
95	FIQCLLLGL	0.008
29	VFFIYFYFY	0.008
122	GYFQGIFMQ	0.007
21	FFLPFPLVV	0.006
14	TFNFFLFFF	0.006
96	IQCLLLGLL	0.006
80	ESFTKRKKK	0.006
17	FFLFFFLPF	0.006
124	FQGIFMQAA	0.006
79	FESFTKRKK	0.006
105	KVRPLQHQG	0.006
3	RELLAGILL	0.005
37	YFFLEMESH	0.004
123	YFQGIFMQA	0.004
39	FLEMESHYV	0.004
10	LLRITFNFF	0.004
23	LPFPLVVFF	0.004
20	FFFLPFPLV	0.004
54	LLGSSNPPA	0.004
22	FLPFPLVVF	0.004
38	FFLEMESHY	0.003
87	KKLKKAFRF	0.003
15	FNFFLFFFL	0.002
121	RGYFQGIFM	0.002
40	LEMESHYVA	0.002
47	VAQAGLELL	0.002
92	AFRFIQCLL	0.002
116	SCDCERGYF	0.002

Table XIV-V9-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
67	VAGTLSVHH	0.002
72	SVHHCACFE	0.002
59	NPPASASLV	0.002
63	SASLVAGTL	0.002
102	GLLKVRPLQ	0.002
94	RFIQCLLLG	0.002
8	GILLRITFN	0.002
36	FYFFLEMES	0.002
26	PLVVFFIYF	0.001
33	YFYFYFFLE	0.001
48	AQAGLELLG	0.001
88	KLKKAFRFI	0.001
16	NFFLFFFLP	0.001
51	GLELLGSSN	0.001
81	SFTKRKKKL	0.001
11	LRITFNFFL	0.001
107	RPLQHQGVN	0.001
128	FMQAAPWEG	0.001
18	FLFFFLPFP	0.001
93	FRFIQCLLL	0.001
2	RRELLAGIL	0.001
24	PFPLVVFFI	0.001
109	LQHQGVNSC	0.001
129	MQAAPWEGT	0.001
111	HQGVNSCDC	0.001
7	AGILLRITF	0.001
56	GSSNPPASA	0.001
45	HYVAQAGLE	0.001
119	CERGYFQGI	0.001
42	MESHYVAQA	0.001
44	SHYVAQAGL	0.000
100	LLGLLKVRP	0.000
70	TLSVHHCAC	0.000
35	YFYFFLEME	0.000
49	QAGLELLGS	0.000
127	IFMQAAPWE	0.000
58	SNPPASASL	0.000

Table XIV-V9-HLA-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
60	PPASASLVA	0.000
71	LSVHHCACF	0.000
85	RKKKLKKAF	0.000
84	KRKKKLKKA	0.000
1	MRRELLAGI	0.000

Table XIV-V10-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
9	GTSDVVTVV	0.030
6	GELGTSDVV	0.003
2	RCPAGELGT	0.001
8	LGTSDVVTV	0.000
5	AGELGTSDV	0.000
3	CPAGELGTS	0.000
7	ELGTSDVVT	0.000
1	GRCPAGELG	0.000
4	PAGELGTSD	0.000

Table XIV-V11-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
7	RVMVPPLPS	0.024
5	RLRVMVPPL	0.012
8	VMVPPLPSL	0.006
3	RLRLRVMVP	0.002
9	MVPPLPSLN	0.002

Table XIV-V11-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
2	ARLRLRVMV	0.000
1	QARLRLRVM	0.000
4	LRLRVMVPP	0.000
6	LRVMVPPLP	0.000

Table XIV-V12-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	GCSYSTLTT	0.001
3	SEEPEGCSY	0.001
9	CSYSTLTTV	0.000
1	VMSEEPEGC	0.000
5	EPEGCSYST	0.000
6	PEGCSYSTL	0.000
2	MSEEPEGCS	0.000
4	EEPEGCSYS	0.000
7	EGCSYSTLT	0.000

Table XIV-V13-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
9	ADPQEDSGK	0.020
1	SQVTVDVLA	0.009
2	QVTVDVLAD	0.004
4	TVDVLADPQ	0.002
3	VTVDVLADP	0.002
6	DVLADPQED	0.001

7	VLADPQEDS	0.000
8	LADPQEDSG	0.000
5	VDVLADPQE	0.000

Table XIV-V14-A1101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	SASLVAGTL	0.002
4	NPPASASLV	0.002
1	GSSNPPASA	0.001
5	PPASASLVA	0.000
3	SNPPASASL	0.000
9	ASLVAGTLS	0.000
7	ASASLVAGT	0.000
2	SSNPPASAS	0.000
6	PASASLVAG	0.000

Table XV-V1-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
40	VTVVLGQDAK	1.500
364	LVVVVVLMSR	1.200
367	VVVLMSRYHR	1.200
260	HIGREGAMLK	0.800
434	SVMSEEPEGR	0.800
76	AQELALLHSK	0.600
419	RAEGHPDSLK	0.600
368	VVLMSRYHRR	0.600
385	KYEEELTLTR	0.480
332	VLDPQEDSGK	0.400
390	LTLTRENSIR	0.300
354	GVIAALLFCL	0.270
400	RLHSHHTDPR	0.240
391	TLTRENSIRR	0.160
19	LLLLASFTGR	0.120

Table XV-V1-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
106	NPLDGSVLLR	0.120
410	SQPEESVGLR	0.120
60	EQVGQVAWAR	0.108
189	GTTSSRSFKH	0.090
144	RVLVPPLPSL	0.090
369	VLMSRYHRRK	0.080
275	QPPPSYNWTR	0.080
486	VQENGTLRAK	0.060
188	KGTTSSRSFK	0.060
376	RRKAQQMTQK	0.060
349	SVVVVGVIAA	0.060
128	RVSTFPAGSF	0.060
484	HFVQENGTLR	0.060
130	STFPAGSFQA	0.060
119	QADEGEYECR	0.040
352	VVGVIAALLF	0.040
485	FVQENGTLRA	0.040
131	TFPAGSFQAR	0.040
229	GLLQDQRITH	0.036
41	TVVLGQDAKL	0.030
365	VVVVVLMSRY	0.030
350	VVVVGVIAAL	0.030
111	SVLLRNAVQA	0.030
351	VVVGVIAALL	0.030
63	GQVAWARVDA	0.027
341	KQVDLVSASV	0.027
443	RSYSTLTTVR	0.024
500	GIYINGRGHL	0.024
252	GLEDQNLWHI	0.024
342	QVDLVSASVV	0.020
61	QVGQVAWARV	0.020
249	SVRGLEDQNL	0.020
305	LTTEHSGIYV	0.020
241	HVSFLAEASV	0.020
89	HVSPAYEGRV	0.020
39	VVTVVLGQDA	0.020
96	GRVEQPPPPR	0.018

Table XV-V1-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
470	EEEDQDEGIK	0.018
185	TEVKGTTSSR	0.018
218	GQPLTCVVSH	0.018
458	TELLSPGSGR	0.018
45	GQDAKLPCFY	0.018
46	QDAKLPCFYR	0.012
11	GPEAWLLLLL	0.012
477	GIKQAMNHFV	0.012
235	RITHILHVSF	0.012
164	GLTLAASCTA	0.012
85	KYGLHVSPAY	0.012
383	TQKYEEELTL	0.012
284	RLDGPLPSGV	0.012
373	RYHRRKAQQM	0.012
25	FTGRCPAGEL	0.010
221	LTCVVSHPGL	0.010
236	ITHILHVSFL	0.010
359	LLFCLLVVVV	0.008
242	VSFLAEASVR	0.008
158	ALEEGQGLTL	0.008
257	NLWHIGREGA	0.008
81	LLHSKYGLHV	0.008
315	CHVSNEFSSR	0.006
88	LHVSPAYEGR	0.006
156	GPALEEGQGL	0.006
358	ALLFCLLVVV	0.006
501	IYINGRGHLV	0.006
201	SAAVTSEFHL	0.006
79	LALLHSKYGL	0.006
80	ALLHSKYGLH	0.006
231	LQDQRITHIL	0.006
493	RAKPTGNGIY	0.006
357	AALLFCLLVV	0.006
97	RVEQPPPPRN	0.006
362	CLLVVVVVLM	0.006
294	RVDGDTLGFP	0.006
16	LLLLLLLASF	0.006

Table XV-V1-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
312	IYVCHVSNEF	0.006
69	RVDAGEGAQE	0.006
6	GAEMWGPEAW	0.006
292	GVRVDGDTLG	0.006
223	CVVSHPGLLQ	0.006
8	EMWGPEAWLL	0.005
490	GTLRAKPTGN	0.005
239	ILHVSFLAEA	0.004
426	SLKDNSSCSV	0.004
411	QPEESVGLRA	0.004
146	LVPPLPSLNP	0.004

Table XV-V2-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
2	GQDAKLPCLY	0.018
3	QDAKLPCLYR	0.008
10	LYRGDSGEQV	0.004
6	KLPCLYRGDS	0.001
9	CLYRGDSGEQ	0.001
7	LPCLYRGDSG	0.000
1	LGQDAKLPCL	0.000
4	DAKLPCLYRG	0.000
8	PCLYRGDSGE	0.000
5	AKLPCLYRGD	0.000

Table XV-V7-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	RSQSEEPEGR	0.012
4	HTDPRSQSEE	0.001
9	SQSEEPEGRS	0.001
6	DPRSQSEEPE	0.000
5	TDPRSQSEEP	0.000
3	HHTDPRSQSE	0.000
2	SHHTDPRSQS	0.000
7	PRSQSEEPEG	0.000
1	HSHHTDPRSQ	0.000

Table XV-V9-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
82	FTKRKKKLKK	2.000
96	IQCLLLGLLK	1.200
75	HCACFESFTK	0.600
77	ACFESFTKRK	0.200
3	RELLAGILLR	0.108
81	SFTKRKKKLK	0.100
27	LVVFFIYFYF	0.090
28	VVFFIYFYFY	0.080
98	CLLLGLLKVR	0.060
105	KVRPLQHQGV	0.060
13	ITFNFFLFFF	0.060
8	GILLRITFNF	0.054
122	GYFQGIFMQA	0.048
76	CACFESFTKR	0.040
102	GLLKVRPLQH	0.036
79	FESFTKRKKK	0.030
12	RITFNFFLFF	0.024
31	FIYFYFYFFL	0.024
18	FLFFFLPFPL	0.024
46	YVAQAGLELL	0.020
78	CFESFTKRKK	0.020

Table XV-V9-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
66	LVAGTLSVHH	0.020
94	RFIQCLLLGL	0.018
85	RKKKLKKAFR	0.012
91	KAFRFIQCLL	0.012
29	VFFIYFYFYF	0.012
10	LLRITFNFFL	0.012
45	HYVAQAGLEL	0.012
23	LPFPLVVFFI	0.012
20	FFFLPFPLVV	0.008
16	NFFLFFFLPF	0.008
33	YFYFYFFLEM	0.008
36	FYFFLEMESH	0.008
39	FLEMESHYVA	0.008
112	QGVNSCDCER	0.006
9	ILLRITFNFF	0.006
72	SVHHCACFES	0.006
65	SLVAGTLSVH	0.006
25	FPLVVFFIYF	0.006
113	GVNSCDCERG	0.006
30	FFIYFYFYFF	0.006
97	QCLLLGLLKV	0.006
14	TFNFFLFFFL	0.006
69	GTLSVHHCAC	0.005
6	LAGILLRITF	0.004
37	YFFLEMESHY	0.004
59	NPPASASLVA	0.004
22	FLPFPLVVFF	0.004
19	LFFFLPFPLV	0.004
70	TLSVHHCACF	0.004
92	AFRFIQCLLL	0.004
95	FIQCLLLGLL	0.004
88	KLKKAFRFIQ	0.004
4	ELLAGILLRI	0.004
21	FFLPFPLVVF	0.003
38	FFLEMESHYV	0.003

Table XV-V9-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
32	IYFYFYFFLE	0.002
126	GIFMQAAPWE	0.002
123	YFQGIFMQAA	0.002
86	KKKLKKAFRF	0.002
53	ELLGSSNPPA	0.002
51	GLELLGSSNP	0.001
2	RRELLAGILL	0.001
48	AQAGLELLGS	0.001
26	PLVVFFIYFY	0.001
41	EMESHYVAQA	0.001
11	LRITFNFFLF	0.001
107	RPLQHQGVNS	0.001
34	FYFYFFLEME	0.001
127	IFMQAAPWEG	0.001
35	YFYFFLEMES	0.001
24	PFPLVVFFIY	0.001
64	ASLVAGTLSV	0.001
99	LLLGLLKVRP	0.001
90	KKAFRFIQCL	0.001
111	HQGVNSCDCE	0.001
124	FQGIFMQAAP	0.001
109	LQHQGVNSCD	0.001
119	CERGYFQGIF	0.001
118	DCERGYFQGI	0.001
128	FMQAAPWEGT	0.000
116	SCDCERGYFQ	0.000
47	VAQAGLELLG	0.000
54	LLGSSNPPAS	0.000
100	LLGLLKVRPL	0.000
58	SNPPASASLV	0.000
103	LLKVRPLQHQ	0.000
121	RGYFQGIFMQ	0.000
125	QGIFMQAAPW	0.000
84	KRKKKLKKAF	0.000
17	FFLFFFLPFP	0.000

Table XV-V9-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
15	FNFFLFFFLP	0.000
115	NSCDCERGYF	0.000
63	SASLVAGTLS	0.000
68	AGTLSVHHCA	0.000
73	VHHCACFESF	0.000
49	QAGLELLGSS	0.000
1	MRRELLAGIL	0.000
67	VAGTLSVHHC	0.000
62	ASASLVAGTL	0.000

Table XV-V10-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length *of peptide is 10 amino acids*, and the end position for each peptide is the start position *plus nine.*

Start	Subsequence	Score
10	GTSDVVTVVL	0.030
8	ELGTSDVVTV	0.001
3	RCPAGELGTS	0.001
7	GELGTSDVVT	0.000
9	LGTSDVVTVV	0.000
6	AGELGTSDVV	0.000
4	CPAGELGTSD	0.000
5	PAGELGTSDV	0.000
2	GRCPAGELGT	0.000
1	TGRCPAGELG	0.000

Table XV-V11-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	RVMVPPLPSL	0.120
10	MVPPLPSLNP	0.004
2	QARLRLRVMV	0.002
6	RLRVMVPPLP	0.001
4	RLRLRVMVPP	0.001
9	VMVPPLPSLN	0.001
1	FQARLRLRVM	0.001
5	LRLRVMVPPL	0.000
3	ARLRLRVMVP	0.000
7	LRVMVPPLPS	0.000

Table XV-V12-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
10	CSYSTLTTVR	0.008
9	GCSYSTLTTV	0.006
1	SVMSEEPEGC	0.004
6	EPEGCSYSTL	0.001
11	SYSTLTTVRE	0.000
2	VMSEEPEGCS	0.000
3	MSEEPEGCSY	0.000
4	SEEPEGCSYS	0.000
5	EEPEGCSYST	0.000
8	EGCSYSTLTT	0.000
7	PEGCSYSTLT	0.000

Table XV-V13-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	LADPQEDSGK	0.200
5	TVDVLADPQE	0.002
3	QVTVDVLADP	0.002
2	SQVTVDVLAD	0.002

Table XV-V13-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
4	VTVDVLADPQ	0.002
7	DVLADPQEDS	0.001
8	VLADPQEDSG	0.000
1	DSQVTVDVLA	0.000
6	VDVLADPQED	0.000
10	ADPQEDSGKQ	0.000

Table XV-V14-HLA-A1101-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
5	NPPASASLVA	0.004
10	ASLVAGTLSV	0.001
4	SNPPASASLV	0.000
8	ASASLVAGTL	0.000
9	SASLVAGTLS	0.000
1	LGSSNPPASA	0.000
3	SSNPPASASL	0.000
2	GSSNPPASAS	0.000
6	PPASASLVAG	0.000
7	PASASLVAGT	0.000

Table XVI-V1-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
501	IYINGRGHL	300.000
124	EYECRVSTF	150.000

Table XVI-V1-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
484	HFVQENGTL	30.000
385	KYEEELTLT	18.000
105	RNPLDGSVL	12.000
419	RAEGHPDSL	12.000
85	KYGLHVSPA	10.000
142	RLRVLVPPL	9.600
100	QPPPPRNPL	8.640
362	CLLVVVVVL	8.400
351	VVVGVIAAL	8.400
14	AWLLLLLLL	7.200
410	SQPEESVGL	7.200
145	VLVPPLPSL	7.200
106	NPLDGSVLL	7.200
10	WGPEAWLLL	7.200
42	VVLGQDAKL	6.600
382	MTQKYEEEL	6.600
71	DAGEGAQEL	6.336
200	RSAAVTSEF	6.160
222	TCVVSHPGL	6.000
223	CVVSHPGLL	6.000
325	DSQVTVDVL	6.000
453	EIETQTELL	6.000
80	ALLHSKYGL	6.000
202	AAVTSEFHL	6.000
11	GPEAWLLLL	6.000
245	LAEASVRGL	6.000
356	IAALLFCLL	5.760
352	VVGVIAALL	5.600
36	TSDVVTVVL	5.600
281	NWTRLDGPL	4.800
13	EAWLLLLLL	4.800
355	VIAALLFCL	4.800
9	MWGPEAWLL	4.800
26	TGRCPAGEL	4.400
8	EMWGPEAWL	4.000
294	RVDGDTLGF	4.000

Table XVI-V1-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
135	GSFQARLRL	4.000
138	QARLRLRVL	4.000
292	GVRVDGDTL	4.000
260	HIGREGAML	4.000
74	EGAQELALL	4.000
188	KGTTSSRSF	4.000
313	YVCHVSNEF	3.696
17	LLLLLLASF	3.600
353	VGVIAALLF	3.000
493	RAKPTGNGI	2.880
236	ITHILHVSF	2.400
477	GIKQAMNHF	2.400
348	ASVVVVGVI	2.100
45	GQDAKLPCF	2.000
129	VSTFPAGSF	2.000
495	KPTGNGIYI	2.000
390	LTLTRENSI	1.800
446	STLTTVREI	1.650
452	REIETQTEL	1.584
363	LLVVVVVLM	1.050
231	LQDQRITHI	1.000
373	RYHRRKAQQ	1.000
1	MPLSLGAEM	0.990
157	PALEEGQGL	0.864
232	QDQRITHIL	0.840
263	REGAMLKCL	0.800
93	AYEGRVEQP	0.750
312	IYVCHVSNE	0.750
279	SYNWTRLDG	0.750
131	TFPAGSFQA	0.750
207	EFHLVPSRS	0.700
360	LFCLLVVVV	0.600
151	PSLNPGPAL	0.600
444	SYSTLTTVR	0.600
393	TRENSIRRL	0.600
159	LEEGQGLTL	0.600

Table XVI-V1-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
237	THILHVSFL	0.600
53	FYRGDSGEQ	0.550
320	EFSSRDSQV	0.500
195	SFKHSRSAA	0.500
213	SRSMNGQPL	0.480
297	GDTLGFPPL	0.480
250	VRGLEDQNL	0.480
384	QKYEEELTL	0.480
251	RGLEDQNLW	0.432
341	KQVDLVSAS	0.432
73	GEGAQELAL	0.400
277	PPSYNWTRL	0.400
337	EDSGKQVDL	0.400
133	PAGSFQARL	0.400
378	KAQQMTQKY	0.396
28	RCPAGELET	0.330
144	RVLVPPLPS	0.300
214	RSMNGQPLT	0.300
235	RITHILHVS	0.280
58	SGEQVGQVA	0.252
146	LVPPLPSLN	0.216
110	GSVLLRNAV	0.216
217	NGQPLTCVV	0.216
275	QPPPSYNWT	0.216
40	VTVVLGQDA	0.216
349	SVVVVGVIA	0.210

Table XVI-V2-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	GQDAKLPCL	4.000

Table XVI-V2-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
9	LYRGDSGEQ	0.550
6	LPCLYRGDS	0.100
5	KLPCLYRGD	0.036
2	QDAKLPCLY	0.012
8	CLYRGDSGE	0.010
3	DAKLPCLYR	0.010
4	AKLPCLYRG	0.002
7	PCLYRGDSG	0.002

Table XVI-V7-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
7	RSQSEEPEG	0.033
3	HTDPRSQSE	0.014
8	SQSEEPEGR	0.012
2	HHTDPRSQS	0.012
5	DPRSQSEEP	0.011
4	TDPRSQSEE	0.002
1	SHHTDPRSQ	0.001
6	PRSQSEEPE	0.000

Table XVI-V9-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
32	IYFYFYFFL	200.000
34	FYFYFFLEM	33.000

Table XVI-V9-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
92	AFRFIQCLL	28.000
19	LFFFLPFPL	24.000
81	SFTKRKKKL	22.000
17	FFLFFFLPF	18.000
30	FFIYFYFYF	15.000
14	TFNFFLFFF	15.000
91	KAFRFIQCL	9.600
95	FIQCLLLGL	7.200
58	SNPPASASL	7.200
36	FYFFLEMES	6.600
47	VAQAGLELL	6.000
101	LGLLKVRPL	6.000
15	FNFFLFFFL	5.760
63	SASLVAGTL	5.600
96	IQCLLLGLL	4.800
12	RITFNFFLF	4.800
46	YVAQAGLEL	4.400
9	ILLRITFNF	4.200
7	AGILLRITF	3.600
22	FLPFPLVVF	3.000
71	LSVHHCACF	3.000
10	LLRITFNFF	2.880
23	LPFPLVVFF	2.880
28	VVFFIYFYF	2.800
31	FIYFYFYFF	2.400
13	ITFNFFLFF	2.400
88	KLKKAFRFI	2.400
116	SCDCERGYF	2.000
2	RRELLAGIL	1.440
5	LLAGILLRI	1.400
123	YFQGIFMQA	1.260
3	RELLAGILL	1.200
24	PFPLVVFFI	1.050
121	RGYFQGIFM	1.000
38	FFLEMESHY	0.900
21	FFLPFPLVV	0.900
45	HYVAQAGLE	0.750

Table XVI-V9-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
11	LRITFNFFL	0.600
20	FFFLPFPLV	0.600
29	VFFIYFYFY	0.600
87	KKLKKAFRF	0.600
122	GYFQGIFMQ	0.500
85	RKKKLKKAF	0.480
44	SHYVAQAGL	0.400
93	FRFIQCLLL	0.400
26	PLVVFFIYF	0.360
107	RPLQHQGVN	0.300
25	FPLVVFFIY	0.252
74	HHCACFESF	0.240
50	AGLELLGSS	0.216
69	GTLSVHHCA	0.210
120	ERGYFQGIF	0.200
51	GLELLGSSN	0.180
57	SSNPPASAS	0.180
98	CLLLGLLKV	0.165
94	RFIQCLLLG	0.150
39	FLEMESHYV	0.150
59	NPPASASLV	0.150
64	ASLVAGTLS	0.150
65	SLVAGTLSV	0.150
27	LVVFFIYFY	0.150
8	GILLRITFN	0.150
119	CERGYFQGI	0.144
1	MRRELLAGI	0.144
62	ASASLVAGT	0.120
124	FQGIFMQAA	0.120
6	LAGILLRIT	0.120
109	LQHQGVNSC	0.120
115	NSCDCERGY	0.120
56	GSSNPPASA	0.100
55	LGSSNPPAS	0.100
49	QAGLELLGS	0.100
129	MQAAPWEGT	0.100
111	HQGVNSCDC	0.100

Table XVI-V9-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
126	GIFMQAAPW	0.100
68	AGTLSVHHC	0.100
75	HCACFESFT	0.100
70	TLSVHHCAC	0.100
54	LLGSSNPPA	0.100
127	IFMQAAPWE	0.075
78	CFESFTKRK	0.075
33	YFYFYFFLE	0.060
16	NFFLFFFLP	0.060
37	YFFLEMESH	0.050
35	YFYFFLEME	0.050
105	KVRPLQHQG	0.029
90	KKAFRFIQC	0.024
84	KRKKKLKKA	0.022
102	GLLKVRPLQ	0.021
106	VRPLQHQGV	0.018
40	LEMESHYVA	0.018
99	LLLGLLKVR	0.018
97	QCLLLGLLK	0.018
53	ELLGSSNPP	0.018
43	ESHYVAQAG	0.017
128	FMQAAPWEG	0.017
113	GVNSCDCER	0.017
77	ACFESFTKR	0.016

Table XVI-V10-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
2	RCPAGELGT	0.300
9	GTSDVVTVV	0.168
5	AGELGTSDV	0.150
7	ELGTSDVVT	0.100

Table XVI-V10-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	LGTSDVVTV	0.100
3	CPAGELGTS	0.100
6	GELGTSDVV	0.015
4	PAGELGTSD	0.001
1	GRCPAGELG	0.001

Table XVI-V11-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
5	RLRVMVPPL	8.000
8	VMVPPLPSL	7.200
1	QARLRLRVM	0.500
7	RVMVPPLPS	0.300
9	MVPPLPSLN	0.216
3	RLRLRVMVP	0.020
2	ARLRLRVMV	0.018
6	LRVMVPPLP	0.002
4	LRLRVMVPP	0.002

Table XVI-V12-HLA-A24-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
2	MSEEPEGCS	0.180
5	EPEGCSYST	0.150
1	VMSEEPEGC	0.120
9	CSYSTLTTV	0.100
7	EGCSYSTLT	0.100

Table XVI-V12-HLA-A24-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Start	Subsequence	Score
8	GCSYSTLTT	0.100
6	PEGCSYSTL	0.040
3	SEEPEGCSY	0.018
4	EEPEGCSYS	0.018

Table XVI-V13-HLA-A24-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Start	Subsequence	Score
1	SQVTVDVLA	0.210
7	VLADPQEDS	0.120
3	VTVDVLADP	0.025
6	DVLADPQED	0.020
8	LADPQEDSG	0.012
4	TVDVLADPQ	0.012
2	QVTVDVLAD	0.010
9	ADPQEDSGK	0.002
5	VDVLADPQE	0.002

Table XVI-V14-HLA-A24-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Start	Subsequence	Score
3	SNPPASASL	7.200
8	SASLVAGTL	5.600
2	SSNPPASAS	0.180
9	ASLVAGTLS	0.150
4	NPPASASLV	0.150
7	ASASLVAGT	0.120
1	GSSNPPASA	0.100
5	PPASASLVA	0.010
6	PASASLVAG	0.001

Table XVII-V1-HLA-A24-10mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Start	Subsequence	Score
312	IYVCHVSNEF	277.200
373	RYHRRKAQQM	60.000
409	RSQPEESVGL	14.400
85	KYGLHVSPAY	14.000
144	RVLVPPLPSL	12.000
105	RNPLDGSVLL	12.000
99	EQPPPPRNPL	8.640
351	VVVGVIAALL	8.400
361	FCLLVVVVVL	8.400
350	VVVVGVIAAL	8.400
501	IYINGRGHLV	7.500
158	ALEEGQGLTL	7.200
11	GPEAWLLLLL	7.200
10	WGPEAWLLLL	7.200
354	GVIAALLFCL	7.200
35	ETSDVVTVVL	6.720
41	TVVLGQDAKL	6.600
291	SGVRVDGDTL	6.000
79	LALLHSKYGL	6.000
439	EPEGRSYSTL	6.000
72	AGEGAQELAL	6.000
222	TCVVSHPGLL	6.000
355	VIAALLFCLL	5.760
231	LQDQRITHIL	5.600
53	FYRGDSGEQV	5.000
249	SVRGLEDQNL	4.800
244	FLAEASVRGL	4.800
13	EAWLLLLLLL	4.800
392	LTRENSIRRL	4.800
280	YNWTRLDGPL	4.800
235	RITHILHVSF	4.800

Table XVII-V1-HLA-A24-10mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Start	Subsequence	Score
9	MWGPEAWLL	4.800
296	DGDTLGFPPL	4.800
156	GPALEEGQGL	4.800
25	FTGRCPAGEL	4.400
381	QMTQKYEEEL	4.400
132	FPAGSFQARL	4.000
236	ITHILHVSFL	4.000
221	LTCVVSHPGL	4.000
128	RVSTFPAGSF	4.000
137	FQARLRLRVL	4.000
201	SAAVTSEFHL	4.000
134	AGSFQARLRL	4.000
500	GIYINGRGHL	4.000
8	EMWGPEAWL	4.000
383	TQKYEEELTL	4.000
150	LPSLNPGPAL	4.000
16	LLLLLLASF	3.600
44	LGQDAKLPCF	3.600
476	EGIKQAMNHF	3.600
207	EFHLVPSRSM	2.500
385	KYEEELTLTR	2.160
352	VVGVIAALLF	2.000
252	GLEDQNLWHI	1.800
230	LLQDQRITHI	1.800
452	REIETQTELL	1.440
347	SASVVVVGVI	1.400
93	AYEGRVEQPP	1.260
389	ELTLTRENSI	1.200
227	HPGLLQDQRI	1.200
445	YSTLTTVREI	1.100
124	EYECRVSTFP	1.050
362	CLLVVVVVLM	1.050
473	DQDEGIKQAM	1.008
301	GFPPLTTEHS	0.900
136	SFQARLRLRV	0.900

Table XVII-V1-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
324	RDSQVTVDVL	0.800
279	SYNWTRLDGP	0.750
141	LRLRVLVPPL	0.720
360	LFCLLVVVVV	0.700
451	VREIETQTEL	0.660
262	GREGAMLKCL	0.600
259	WHIGREGAML	0.600
320	EFSSRDSQVT	0.600
276	PPPSYNWTRL	0.600
7	AEMWGPEAWL	0.600
70	VDAGEGAQEL	0.528
341	KQVDLVSASV	0.504
258	LWHIGREGAM	0.500
195	SFKHSRSAAV	0.500
444	SYSTLTTVRE	0.500
418	LRAEGHPDSL	0.480
212	PSRSMNGQPL	0.480
336	QEDSGKQVDL	0.400
483	NHFVQENGTL	0.400
73	GEGAQELALL	0.400
293	VRVDGDTLGF	0.360
199	SRSAAVTSEF	0.308
97	RVEQPPPPRN	0.300
214	RSMNGQPLTC	0.300
28	RCPAGELETS	0.300
49	KLPCFYRGDS	0.300
411	QPEESVGLRA	0.252
284	RLDGPLPSGV	0.240
493	RAKPTGNGIY	0.240
123	GEYECRVSTF	0.240

Table XVII-V1-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
145	VLVPPLPSLN	0.216
274	GQPPPSYNWT	0.216
363	LLVVVVVLMS	0.210
348	ASVVVVGVIA	0.210

Table XVII-V2-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
1	LGQDAKLPCL	7.200
10	LYRGDSGEQV	5.000
6	KLPCLYRGDS	0.300
2	GQDAKLPCLY	0.120
9	CLYRGDSGEQ	0.011
7	LPCLYRGDSG	0.010
4	DAKLPCLYRG	0.010
5	AKLPCLYRGD	0.002
8	PCLYRGDSGE	0.002
3	QDAKLPCLYR	0.001

Table XVII-V7-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	SQSEEPEGRS	0.120
8	RSQSEEPEGR	0.030
4	HTDPRSQSEE	0.013

Table XVII-V7-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
6	DPRSQSEEPE	0.010
1	HSHHTDPRSQ	0.010
2	SHHTDPRSQS	0.010
5	TDPRSQSEEP	0.002
3	HHTDPRSQSE	0.001
7	PRSQSEEPEG	0.000

Table XVII-V9-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
45	HYVAQAGLEL	330.000
94	RFIQCLLLGL	72.000
14	TFNFFLFFFL	43.200
92	AFRFIQCLLL	20.000
30	FFIYFYFYFF	18.000
21	FFLPFPLVVF	18.000
16	NFFLFFFLPF	12.000
91	KAFRFIQCLL	11.200
29	VFFIYFYFYF	10.000
122	GYFQGIFMQA	8.400
57	SSNPPASASL	7.200
95	FIQCLLLGLL	7.200
62	ASASLVAGTL	5.600
12	RITFNFFLFF	4.800
18	FLFFFLPFPL	4.800
80	ESFTKRKKKL	4.400
9	ILLRITFNFF	4.320
8	GILLRITFNF	4.200
27	LVVFFIYFYF	4.200
31	FIYFYFYFFL	4.000
10	LLRITFNFFL	4.000

Table XVII-V9-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
46	YVAQAGLELL	4.000
100	LLGLLKVRPL	4.000
43	ESHYVAQAGL	4.000
25	FPLVVFFIYF	3.600
22	FLPFPLVVFF	3.600
33	YFYFYFFLEM	3.300
115	NSCDCERGYF	2.400
6	LAGILLRITF	2.400
118	DCERGYFQGI	2.160
4	ELLAGILLRI	2.100
13	ITFNFFLFFF	2.000
70	TLSVHHCACF	2.000
23	LPFPLVVFFI	1.680
2	RRELLAGILL	1.200
90	KKAFRFIQCL	0.960
123	YFQGIFMQAA	0.900
38	FFLEMESHYV	0.900
35	YFYFFLEMES	0.660
32	IYFYFYFFLE	0.600
19	LFFFLPFPLV	0.600
1	MRRELLAGIL	0.576
34	FYFYFFLEME	0.500
37	YFFLEMESHY	0.500
20	FFFLPFPLVV	0.500
36	FYFFLEMESH	0.500
84	KRKKKLKKAF	0.480
86	KKKLKKAFRF	0.400
11	LRITFNFFLF	0.360
87	KKLKKAFRFI	0.360
107	RPLQHQGVNS	0.300
105	KVRPLQHQGV	0.288
73	VHHCACFESF	0.240
50	AGLELLGSSN	0.216
119	CERGYFQGIF	0.200
58	SNPPASASLV	0.180
97	QCLLLGLLKV	0.165
53	ELLGSSNPPA	0.150

Table XVII-V9-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
64	ASLVAGTLSV	0.150
39	FLEMESHYVA	0.150
128	FMQAAPWEGT	0.150
125	QGIFMQAAPW	0.150
59	NPPASASLVA	0.150
69	GTLSVHHCAC	0.150
7	AGILLRITFN	0.150
41	EMESHYVAQA	0.150
68	AGTLSVHHCA	0.140
24	PFPLVVFFIY	0.126
28	VVFFIYFYFY	0.120
49	QAGLELLGSS	0.120
5	LLAGILLRIT	0.120
72	SVHHCACFES	0.110
55	LGSSNPPASA	0.100
114	VNSCDCERGY	0.100
54	LLGSSNPPAS	0.100
48	AQAGLELLGS	0.100
56	GSSNPPASAS	0.100
63	SASLVAGTLS	0.100
67	VAGTLSVHHC	0.100
78	CFESFTKRKK	0.083
127	IFMQAAPWEG	0.083
17	FFLFFFLPFP	0.075
120	ERGYFQGIFM	0.050
81	SFTKRKKKLK	0.050
101	LGLLKVRPLQ	0.021
121	RGYFQGIFMQ	0.020
88	KLKKAFRFIQ	0.020
108	PLQHQGVNSC	0.018
99	LLLGLLKVRP	0.018
98	CLLLGLLKVR	0.018
47	VAQAGLELLG	0.018
112	QGVNSCDCER	0.017
51	GLELLGSSNP	0.015
110	QHQGVNSCDC	0.015
26	PLVVFFIYFY	0.015

Table XVII-V9-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
102	GLLKVRPLQH	0.015
71	LSVHHCACFE	0.015
106	VRPLQHQGVN	0.015
65	SLVAGTLSVH	0.015
113	GVNSCDCERG	0.015

Table XVII-V10-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
10	GTSDVVTVVL	6.720
3	RCPAGELGTS	0.300
6	AGELGTSDVV	0.150
9	LGTSDVVTVV	0.140
8	ELGTSDVVTV	0.100
7	GELGTSDVVT	0.015
4	CPAGELGTSD	0.012
5	PAGELGTSDV	0.012
2	GRCPAGELGT	0.012
1	TGRCPAGELG	0.010

Table XVII-V11-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	RVMVPPLPSL	12.000
5	LRLRVMVPPL	0.600
1	FQARLRLRVM	0.500

Table XVII-V11-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	VMVPPLPSLN	0.216
2	QARLRLRVMV	0.120
6	RLRVMVPPLP	0.028
4	RLRLRVMVPP	0.028
10	MVPPLPSLNP	0.018
7	LRVMVPPLPS	0.015
3	ARLRLRVMVP	0.002

Table XVII-V12-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
6	EPEGCSYSTL	6.000
11	SYSTLTTVRE	0.500
3	MSEEPEGCSY	0.180
1	SVMSEEPEGC	0.150
2	VMSEEPEGCS	0.120
8	EGCSYSTLTT	0.100
9	GCSYSTLTTV	0.100
5	EEPEGCSYST	0.018
4	SEEPEGCSYS	0.018
10	CSYSTLTTVR	0.012
7	PEGCSYSTLT	0.001

Table XVII-V13-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score

Table XVII-V13-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
1	DSQVTVDVLA	0.210
7	DVLADPQEDS	0.150
4	VTVDVLADPQ	0.022
2	SQVTVDVLAD	0.015
3	QVTVDVLADP	0.014
8	VLADPQEDSG	0.012
9	LADPQEDSGK	0.012
5	TVDVLADPQE	0.010
6	VDVLADPQED	0.002
10	ADPQEDSGKQ	0.002

Table XVII-V14-HLA-A24-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
3	SSNPPASASL	7.200
8	ASASLVAGTL	5.600
4	SNPPASASLV	0.180
10	ASLVAGTLSV	0.150
5	NPPASASLVA	0.150
9	SASLVAGTLS	0.100
1	LGSSNPPASA	0.100
2	GSSNPPASAS	0.100
7	PASASLVAGT	0.012
6	PPASASLVAG	0.001

Table XVIII-V1-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
292	GVRVDGDTL	200.000
100	QPPPPRNPL	180.000
138	QARLRLRVL	120.000
106	NPLDGSVLL	80.000
26	TGRCPAGEL	60.000
142	RLRVLVPPL	40.000
202	AAVTSEFHL	36.000
11	GPEAWLLLL	24.000
42	VVLGQDAKL	20.000
1	MPLSLGAEM	20.000
351	VVVGVIAAL	20.000
352	VVGVIAALL	20.000
223	CVVSHPGLL	20.000
13	EAWLLLLLL	12.000
71	DAGEGAQEL	12.000
80	ALLHSKYGL	12.000
356	IAALLFCLL	12.000
277	PPSYNWTRL	8.000
495	KPTGNGIYI	8.000
135	GSFQARLRL	6.000
8	EMWGPEAWL	6.000
145	VLVPPLPSL	6.000
450	TVREIETQT	5.000
222	TCVVSHPGL	4.000
325	DSQVTVDVL	4.000
287	GPLPSGVRV	4.000
362	CLLVVVVVL	4.000
10	WGPEAWLLL	4.000
260	HIGREGAML	4.000
410	SQPEESVGL	4.000
355	VIAALLFCL	4.000
105	RNPLDGSVL	4.000
74	EGAQELALL	4.000
382	MTQKYEEEL	4.000
407	DPRSQPEES	4.000
419	RAEGHPDSL	3.600
245	LAEASVRGL	3.600
203	AVTSEFHLV	3.000
275	QPPPSYNWT	2.000
322	SSRDSQVTV	2.000
150	LPSLNPGPA	2.000
357	AALLFCLLV	1.800

Table XVIII-V1-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
371	MSRYHRRKA	1.500
133	PAGSFQARL	1.200
493	RAKPTGNGI	1.200
14	AWLLLLLLL	1.200
36	TSDVVTVVL	1.200
453	EIETQTELL	1.200
157	PALEEGQGL	1.200
348	ASVVVVGVI	1.200
249	SVRGLEDQN	1.000
374	YHRRKAQQM	1.000
441	EGRSYSTLT	1.000
363	LLVVVVVLM	1.000
345	LVSASVVVV	1.000
126	ECRVSTFPA	1.000
64	QVAWARVDA	0.750
103	PPRNPLDGS	0.600
358	ALLFCLLVV	0.600
178	APSVTWDTE	0.600
501	IYINGRGHL	0.600
151	PSLNPGPAL	0.600
50	LPCFYRGDS	0.600
439	EPEGRSYST	0.600
347	SASVVVVGV	0.600
349	SVVVVGVIA	0.500
350	VVVVGVIAA	0.500
354	GVIAALLFC	0.500
23	ASFTGRCPA	0.450
29	CPAGELETS	0.400
446	STLTTVREI	0.400
297	GDTLGFPPL	0.400
232	QDQRITHIL	0.400
263	REGAMLKCL	0.400
281	NWTRLDGPL	0.400
390	LTLTRENSI	0.400
484	HFVQENGTL	0.400
452	REIETQTEL	0.400
384	QKYEEELTL	0.400

Table XVIII-V1-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
302	FPPLTTEHS	0.400
237	THILHVSFL	0.400
250	VRGLEDQNL	0.400
73	GEGAQELAL	0.400
9	MWGPEAWLL	0.400
213	SRSMNGQPL	0.400
337	EDSGKQVDL	0.400
289	LPSGVRVDG	0.300
110	GSVLLRNAV	0.300
117	AVQADEGEY	0.300
216	MNGQPLTCV	0.300
147	VPPLPSLNP	0.300
137	FQARLRLRV	0.300
67	WARVDAGEG	0.300
342	QVDLVSASV	0.300
462	SPGSGRAEE	0.300
214	RSMNGQPLT	0.300
211	VPSRSMNGQ	0.200
217	NGQPLTCVV	0.200
35	ETSDVVTVV	0.200
154	NPGPALEEG	0.200

Table XVIII-V2-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	GQDAKLPCL	1.200
6	LPCLYRGDS	0.600
3	DAKLPCLYR	0.045
8	CLYRGDSGE	0.010
9	LYRGDSGEQ	0.010
5	KLPCLYRGD	0.010
4	AKLPCLYRG	0.003

Table XVIII-V2-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
2	QDAKLPCLY	0.002
7	PCLYRGDSG	0.001

Table XVIII-V7-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
5	DPRSQSEEP	2.000
7	RSQSEEPEG	0.010
8	SQSEEPEGR	0.010
2	HHTDPRSQS	0.005
3	HTDPRSQSE	0.003
4	TDPRSQSEE	0.001
1	SHHTDPRSQ	0.001
6	PRSQSEEPE	0.000

Table XVIII-V9-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
46	YVAQAGLEL	20.000
92	AFRFIQCLL	12.000
91	KAFRFIQCL	12.000
63	SASLVAGTL	12.000
47	VAQAGLELL	12.000
59	NPPASASLV	4.000
95	FIQCLLLGL	4.000
96	IQCLLLGLL	4.000
15	FNFFLFFFL	4.000

Table XVIII-V9-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
101	LGLLKVRPL	4.000
58	SNPPASASL	4.000
121	RGYFQGIFM	1.000
105	KVRPLQHQG	0.500
5	LLAGILLRI	0.400
107	RPLQHQGVN	0.400
23	LPFPLVVFF	0.400
88	KLKKAFRFI	0.400
44	SHYVAQAGL	0.400
19	LFFFLPFPL	0.400
81	SFTKRKKKL	0.400
25	FPLVVFFIY	0.400
32	IYFYFYFFL	0.400
3	RELLAGILL	0.400
119	CERGYFQGI	0.400
93	FRFIQCLLL	0.400
1	MRRELLAGI	0.400
11	LRITFNFFL	0.400
6	LAGILLRIT	0.300
62	ASASLVAGT	0.300
68	AGTLSVHHC	0.300
60	PPASASLVA	0.200
10	LLRITFNFF	0.200
98	CLLLGLLKV	0.200
65	SLVAGTLSV	0.200
56	GSSNPPASA	0.150
129	MQAAPWEGT	0.150
2	RRELLAGIL	0.120
70	TLSVHHCAC	0.100
109	LQHQGVNSC	0.100
69	GTLSVHHCA	0.100
28	VVFFIYFYF	0.100
34	FYFYFFLEM	0.100
54	LLGSSNPPA	0.100
27	LVVFFIYFY	0.100
124	FQGIFMQAA	0.100
75	HCACFESFT	0.100

Table XVIII-V9-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
111	HQGVNSCDC	0.100
7	AGILLRITF	0.090
49	QAGLELLGS	0.060
64	ASLVAGTLS	0.060
50	AGLELLGSS	0.060
39	FLEMESHYV	0.060
66	LVAGTLSVH	0.050
72	SVHHCACFE	0.050
113	GVNSCDCER	0.050
48	AQAGLELLG	0.030
40	LEMESHYVA	0.030
77	ACFESFTKR	0.030
67	VAGTLSVHH	0.030
22	FLPFPLVVF	0.030
76	CACFESFTK	0.030
20	FFFLPFPLV	0.030
57	SSNPPASAS	0.030
71	LSVHHCACF	0.020
55	LGSSNPPAS	0.020
106	VRPLQHQGV	0.020
21	FFLPFPLVV	0.020
12	RITFNFFLF	0.020
9	ILLRITFNF	0.020
115	NSCDCERGY	0.020
13	ITFNFFLFF	0.020
126	GIFMQAAPW	0.020
8	GILLRITFN	0.020
31	FIYFYFYFF	0.020
102	GLLKVRPLQ	0.015
80	ESFTKRKKK	0.015
125	QGIFMQAAP	0.010
128	FMQAAPWEG	0.010
18	FLFFFLPFP	0.010
97	QCLLLGLLK	0.010
100	LLGLLKVRP	0.010
123	YFQGIFMQA	0.010
103	LLKVRPLQH	0.010

Table XVIII-V9-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
83	TKRKKKLKK	0.010
90	KKAFRFIQC	0.010
112	QGVNSCDCE	0.010
42	MESHYVAQA	0.010
4	ELLAGILLR	0.010
82	FTKRKKKLK	0.010
43	ESHYVAQAG	0.010
84	KRKKKLKKA	0.010
99	LLLGLLKVR	0.010
53	ELLGSSNPP	0.010
114	VNSCDCERG	0.010
116	SCDCERGYF	0.009
51	GLELLGSSN	0.006
24	PFPLVVFFI	0.004
127	IFMQAAPWE	0.003
61	PASASLVAG	0.003
118	DCERGYFQG	0.003

Table XVIII-V11-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
5	RLRVMVPPL	40.000
1	QARLRLRVM	30.000
8	VMVPPLPSL	6.000
7	RVMVPPLPS	0.450
9	MVPPLPSLN	0.100
3	RLRLRVMVP	0.100
2	ARLRLRVMV	0.090
6	LRVMVPPLP	0.001
4	LRLRVMVPP	0.001

Table XVIII-V12-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
5	EPEGCSYST	0.600
9	CSYSTLTTV	0.200
7	EGCSYSTLT	0.100
1	VMSEEPEGC	0.100
8	GCSYSTLTT	0.100
6	PEGCSYSTL	0.040
2	MSEEPEGCS	0.009
4	EEPEGCSYS	0.002
3	SEEPEGCSY	0.001

Table XVIII-V13-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	SQVTVDVLA	0.100
6	DVLADPQED	0.050
2	QVTVDVLAD	0.050
7	VLADPQEDS	0.030
4	TVDVLADPQ	0.015
3	VTVDVLADP	0.010
8	LADPQEDSG	0.009
9	ADPQEDSGK	0.003
5	VDVLADPQE	0.001

Table XVIII-V14-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
8	SASLVAGTL	12.000

Table XVIII-V14-HLA-B7-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
4	NPPASASLV	4.000
3	SNPPASASL	4.000
7	ASASLVAGT	0.300
5	PPASASLVA	0.200
1	GSSNPPASA	0.150
9	ASLVAGTLS	0.060
2	SSNPPASAS	0.030
6	PASASLVAG	0.003

Table XIX-V1-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
249	SVRGLEDQNL	200.000
150	LPSLNPGPAL	120.000
156	GPALEEGQGL	80.000
132	FPAGSFQARL	80.000
407	DPRSQPEESV	60.000
392	LTRENSIRRL	40.000
144	RVLVPPLPSL	30.000
11	GPEAWLLLLL	24.000
439	EPEGRSYSTL	24.000
350	VVVVGVIAAL	20.000
351	VVVGVIAALL	20.000
354	GVIAALLFCL	20.000
41	TVVLGQDAKL	20.000
134	AGSFQARLRL	18.000
178	APSVTWDTEV	12.000
13	EAWLLLLLLL	12.000
201	SAAVTSEFHL	12.000
79	LALLHSKYGL	12.000

Table XIX-V1-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
99	EQPPPPRNPL	9.000
138	QARLRLRVLV	9.000
276	PPPSYNWTRL	8.000
227	HPGLLQDQRI	8.000
500	GIYINGRGHL	6.000
25	FTGRCPAGEL	6.000
7	AEMWGPEAWL	5.400
409	RSQPEESVGL	4.000
103	PPRNPLDGSV	4.000
244	FLAEASVRGL	4.000
8	EMWGPEAWLL	4.000
383	TQKYEEELTL	4.000
137	FQARLRLRVL	4.000
236	ITHILHVSFL	4.000
291	SGVRVDGDTL	4.000
334	DPQEDSGKQV	4.000
10	WGPEAWLLLL	4.000
222	TCVVSHPGLL	4.000
212	PSRSMNGQPL	4.000
280	YNWTRLDGPL	4.000
221	LTCVVSHPGL	4.000
355	VIAALLFCLL	4.000
381	QMTQKYEEEL	4.000
35	ETSDVVTVVL	4.000
361	FCLLVVVVVL	4.000
105	RNPLDGSVLL	4.000
158	ALEEGQGLTL	3.600
72	AGEGAQELAL	3.600
67	WARVDAGEGA	3.000
176	SPAPSVTWDT	2.000
233	DQRITHILHV	2.000
202	AAVTSEFHLV	1.800
357	AALLFCLLVV	1.800
231	LQDQRITHIL	1.200
347	SASVVVVGVI	1.200
296	DGDTLGFPPL	1.200
261	IGREGAMLKC	1.000

Table XIX-V1-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
397	SIRRLHSHHT	1.000
61	QVGQVAWARV	1.000
441	EGRSYSTLTT	1.000
89	HVSPAYEGRV	1.000
362	CLLVVVVVLM	1.000
241	HVSFLAEASV	1.000
303	PPLTTEHSGI	0.800
411	QPEESVGLRA	0.600
356	IAALLFCLLV	0.600
358	ALLFCLLVVV	0.600
349	SVVVVGVIAA	0.500
485	FVQENGTLRA	0.500
450	TVREIETQTE	0.500
292	GVRVDGDTLG	0.500
39	VVTVVLGQDA	0.500
111	SVLLRNAVQA	0.500
22	LASFTGRCPA	0.450
452	REIETQTELL	0.400
324	RDSQVTVDVL	0.400
70	VDAGEGAQEL	0.400
1	MPLSLGAEMW	0.400
389	ELTLTRENSI	0.400
259	WHIGREGAML	0.400
73	GEGAQELALL	0.400
495	KPTGNGIYIN	0.400
418	LRAEGHPDSL	0.400
9	MWGPEAWLLL	0.400
483	NHFVQENGTL	0.400
230	LLQDQRITHI	0.400
141	LRLRVLVPPL	0.400
445	YSTLTTVREI	0.400
342	QVDLVSASVV	0.300
215	SMNGQPLTCV	0.300
71	DAGEGAQELA	0.300
214	RSMNGQPLTC	0.300
348	ASVVVVGVIA	0.300
109	DGSVLLRNAV	0.300

Table XIX-V1-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
169	ASCTAEGSPA	0.300
91	SPAYEGRVEQ	0.300
473	DQDEGIKQAM	0.300
172	TAEGSPAPSV	0.270
289	LPSGVRVDGD	0.200
81	LLHSKYGLHV	0.200
417	GLRAEGHPDS	0.200
321	FSSRDSQVTV	0.200

Table XIX-V2-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
1	LGQDAKLPCL	4.000
7	LPCLYRGDSG	0.200
10	LYRGDSGEQV	0.200
4	DAKLPCLYRG	0.030
6	KLPCLYRGDS	0.030
9	CLYRGDSGEQ	0.010
2	GQDAKLPCLY	0.006
5	AKLPCLYRGD	0.003
3	QDAKLPCLYR	0.002
8	PCLYRGDSGE	0.001

Table XIX-V7-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
6	DPRSQSEEPE	2.000

Table XIX-V7-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
9	SQSEEPEGRS	0.030
8	RSQSEEPEGR	0.010
1	HSHHTDPRSQ	0.010
2	SHHTDPRSQS	0.005
4	HTDPRSQSEE	0.003
3	HHTDPRSQSE	0.001
5	TDPRSQSEEP	0.001
7	PRSQSEEPEG	0.000

Table XIX-V9-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
10	LLRITFNFFL	40.000
46	YVAQAGLELL	20.000
92	AFRFIQCLLL	12.000
91	KAFRFIQCLL	12.000
62	ASASLVAGTL	12.000
105	KVRPLQHQGV	10.000
23	LPFPLVVFFI	8.000
100	LLGLLKVRPL	4.000
31	FIYFYFYFFL	4.000
1	MRRELLAGIL	4.000
95	FIQCLLLGLL	4.000
57	SSNPPASASL	4.000
80	ESFTKRKKKL	4.000
18	FLFFFLPFPL	4.000
43	ESHYVAQAGL	4.000
59	NPPASASLVA	2.000
64	ASLVAGTLSV	0.600
4	ELLAGILLRI	0.400
107	RPLQHQGVNS	0.400
14	TFNFFLFFFL	0.400

Table XIX-V9-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
25	FPLVVFFIYF	0.400
94	RFIQCLLLGL	0.400
45	HYVAQAGLEL	0.400
90	KKAFRFIQCL	0.400
67	VAGTLSVHHC	0.300
68	AGTLSVHHCA	0.300
97	QCLLLGLLKV	0.200
58	SNPPASASLV	0.200
128	FMQAAPWEGT	0.150
55	LGSSNPPASA	0.150
2	RRELLAGILL	0.120
118	DCERGYFQGI	0.120
33	YFYFYFFLEM	0.100
28	VVFFIYFYFY	0.100
53	ELLGSSNPPA	0.100
72	SVHHCACFES	0.100
83	TKRKKKLKKA	0.100
5	LLAGILLRIT	0.100
69	GTLSVHHCAC	0.100
27	LVVFFIYFYF	0.100
120	ERGYFQGIFM	0.100
6	LAGILLRITF	0.090
63	SASLVAGTLS	0.060
48	AQAGLELLGS	0.060
7	AGILLRITFN	0.060
50	AGLELLGSSN	0.060
49	QAGLELLGSS	0.060
113	GVNSCDCERG	0.050
66	LVAGTLSVHH	0.050
87	KKLKKAFRFI	0.040
115	NSCDCERGYF	0.030
47	VAQAGLELLG	0.030
61	PASASLVAGT	0.030
76	CACFESFTKR	0.030
56	GSSNPPASAS	0.030
19	LFFFLPFPLV	0.030
77	ACFESFTKRK	0.030

Table XIX-V9-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
39	FLEMESHYVA	0.030
41	EMESHYVAQA	0.030
38	FFLEMESHYV	0.020
22	FLPFPLVVFF	0.020
119	CERGYFQGIF	0.020
9	ILLRITFNFF	0.020
70	TLSVHHCACF	0.020
125	QGIFMQAAPW	0.020
60	PPASASLVAG	0.020
8	GILLRITFNF	0.020
12	RITFNFFLFF	0.020
114	VNSCDCERGY	0.020
54	LLGSSNPPAS	0.020
13	ITFNFFLFFF	0.020
20	FFFLPFPLVV	0.020
101	LGLLKVRPLQ	0.015
103	LLKVRPLQHQ	0.015
88	KLKKAFRFIQ	0.015
108	PLQHQGVNSC	0.010
96	IQCLLLGLLK	0.010
89	LKKAFRFIQC	0.010
75	HCACFESFTK	0.010
82	FTKRKKKLKK	0.010
102	GLLKVRPLQH	0.010
121	RGYFQGIFMQ	0.010
15	FNFFLFFFLP	0.010
65	SLVAGTLSVH	0.010
98	CLLLGLLKVR	0.010
109	LQHQGVNSCD	0.010
110	QHQGVNSCDC	0.010
122	GYFQGIFMQA	0.010
111	HQGVNSCDCE	0.010
71	LSVHHCACFE	0.010
126	GIFMQAAPWE	0.010
99	LLLGLLKVRP	0.010
123	YFQGIFMQAA	0.010
124	FQGIFMQAAP	0.010

Table XIX-V9-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
74	HHCACFESFT	0.010
112	QGVNSCDCER	0.010
21	FFLPFPLVVF	0.003
127	IFMQAAPWEG	0.003
40	LEMESHYVAQ	0.003
116	SCDCERGYFQ	0.003

Table XIX-V10-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
10	GTSDVVTVVL	4.000
9	LGTSDVVTVV	0.200
8	ELGTSDVVTV	0.200
4	CPAGELGTSD	0.200
6	AGELGTSDVV	0.180
1	TGRCPAGELG	0.100
5	PAGELGTSDV	0.060
3	RCPAGELGTS	0.020
2	GRCPAGELGT	0.010
7	GELGTSDVVT	0.010

Table XIX-V11-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	RVMVPPLPSL	90.000
2	QARLRLRVMV	9.000

Table XIX-V11-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
1	FQARLRLRVM	1.000
5	LRLRVMVPPL	0.400
6	RLRVMVPPLP	0.100
4	RLRLRVMVPP	0.100
10	MVPPLPSLNP	0.075
9	VMVPPLPSLN	0.020
7	LRVMVPPLPS	0.003
3	ARLRLRVMVP	0.003

Table XIX-V12-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
6	EPEGCSYSTL	24.000
1	SVMSEEPEGC	1.500
9	GCSYSTLTTV	0.200
8	EGCSYSTLTT	0.100
2	VMSEEPEGCS	0.030
5	EEPEGCSYST	0.010
10	CSYSTLTTVR	0.010
3	MSEEPEGCSY	0.006
11	SYSTLTTVRE	0.001
7	PEGCSYSTLT	0.001
4	SEEPEGCSYS	0.001

Table XIX-V13-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
7	DVLADPQEDS	0.150
1	DSQVTVDVLA	0.100
3	QVTVDVLADP	0.050
5	TVDVLADPQE	0.015
4	VTVDVLADPQ	0.010
2	SQVTVDVLAD	0.010
8	VLADPQEDSG	0.010
9	LADPQEDSGK	0.009
10	ADPQEDSGKQ	0.003
6	VDVLADPQED	0.001

Table XIX-V14-HLA-B7-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	ASASLVAGTL	12.000
3	SSNPPASASL	4.000
5	NPPASASLVA	2.000
10	ASLVAGTLSV	0.600
4	SNPPASASLV	0.200
1	LGSSNPPASA	0.150
9	SASLVAGTLS	0.060
7	PASASLVAGT	0.030
2	GSSNPPASAS	0.030
6	PPASASLVAG	0.020

Table XX-V1-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	MPLSLGAEM	40.000
106	NPLDGSVLL	40.000
100	QPPPPRNPL	20.000
495	KPTGNGIYI	16.000
378	KAQQMTQKY	12.000
200	RSAAVTSEF	10.000

Table XX-V1-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
138	QARLRLRVL	9.000
493	RAKPTGNGI	7.200
322	SSRDSQVTV	6.000
407	DPRSQPEES	6.000
142	RLRVLVPPL	6.000
11	GPEAWLLLL	6.000
71	DAGEGAQEL	6.000
129	VSTFPAGSF	5.000
325	DSQVTVDVL	5.000
135	GSFQARLRL	5.000
292	GVRVDGDTL	4.500
305	LTTEHSGIY	4.000
287	GPLPSGVRV	4.000
117	AVQADEGEY	3.000
26	TGRCPAGEL	3.000
202	AAVTSEFHL	3.000
251	RGLEDQNLW	3.000
29	CPAGELETS	3.000
105	RNPLDGSVL	3.000
13	EAWLLLLLL	3.000
356	IAALLFCLL	3.000
410	SQPEESVGL	3.000
477	GIKQAMNHF	3.000
175	GSPAPSVTW	2.500
366	VVVVLMSRY	2.000
275	QPPPSYNWT	2.000
50	LPCFYRGDS	2.000
150	LPSLNPGPA	2.000
78	ELALLHSKY	2.000
348	ASVVVVGVI	2.000
363	LLVVVVVLM	2.000
57	DSGEQVGQV	2.000
86	YGLHVSPAY	2.000
10	WGPEAWLLL	2.000
188	KGTTSSRSF	2.000
302	FPPLTTEHS	2.000
277	PPSYNWTRL	2.000

Table XX-V1-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
443	RSYSTLTTV	2.000
419	RAEGHPDSL	1.800
74	EGAQELALL	1.500
260	HIGREGAML	1.500
36	TSDVVTVVL	1.500
83	HSKYGLHVS	1.500
198	HSRSAAVTS	1.500
371	MSRYHRRKA	1.500
8	EMWGPEAWL	1.000
222	TCVVSHPGL	1.000
17	LLLLLLASF	1.000
80	ALLHSKYGL	1.000
355	VIAALLFCL	1.000
42	VVLGQDAKL	1.000
242	VSFLAEASV	1.000
214	RSMNGQPLT	1.000
351	VVVGVIAAL	1.000
382	MTQKYEEEL	1.000
313	YVCHVSNEF	1.000
309	HSGIYVCHV	1.000
353	VGVIAALLF	1.000
352	VVGVIAALL	1.000
362	CLLVVVVVL	1.000
90	VSPAYEGRV	1.000
194	RSFKHSRSA	1.000
145	VLVPPLPSL	1.000
223	CVVSHPGLL	1.000
338	DSGKQVDLV	1.000
110	GSVLLRNAV	1.000
236	ITHILHVSF	1.000
157	PALEEGQGL	0.900
294	RVDGDTLGF	0.900
245	LAEASVRGL	0.900
321	FSSRDSQVT	0.750
425	DSLKDNSSC	0.750
347	SASVVVVGV	0.600
357	AALLFCLLV	0.600

Table XX-V1-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
439	EPEGRSYST	0.600
450	TVREIETQT	0.600
334	DPQEDSGKQ	0.600
423	HPDSLKDNS	0.600
103	PPRNPLDGS	0.600
426	SLKDNSSCS	0.600
374	YHRRKAQQM	0.600
23	ASFTGRCPA	0.500
274	GQPPPSYNW	0.500
191	TSSRSFKHS	0.500
151	PSLNPGPAL	0.500
402	HSHHTDPRS	0.500
383	TQKYEEELT	0.450
428	KDNSSCSVM	0.400
446	STLTTVREI	0.400
390	LTLTRENSI	0.400
35	ETSDVVTVV	0.400
341	KQVDLVSAS	0.400
452	REIETQTEL	0.400
491	TLRAKPTGN	0.300

Table XX-V2-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
6	LPCLYRGDS	2.000
1	GQDAKLPCL	0.300
2	QDAKLPCLY	0.200
3	DAKLPCLYR	0.090
5	KLPCLYRGD	0.020
8	CLYRGDSGE	0.010
9	LYRGDSGEQ	0.005
4	AKLPCLYRG	0.001
7	PCLYRGDSG	0.001

Table XX-V7-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
5	DPRSQSEEP	0.600
7	RSQSEEPEG	0.150
8	SQSEEPEGR	0.030
2	HHTDPRSQS	0.020
3	HTDPRSQSE	0.003
1	SHHTDPRSQ	0.002
4	TDPRSQSEE	0.001
6	PRSQSEEPE	0.000

Table XX-V9-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
25	FPLVVFFIY	40.000
23	LPFPLVVFF	20.000
115	NSCDCERGY	20.000
91	KAFRFIQCL	6.000
71	LSVHHCACF	5.000
107	RPLQHQGVN	4.000
59	NPPASASLV	4.000
121	RGYFQGIFM	4.000
10	LLRITFNFF	3.000
47	VAQAGLELL	3.000
63	SASLVAGTL	3.000
88	KLKKAFRFI	2.400
27	LVVFFIYFY	2.000
12	RITFNFFLF	2.000
46	YVAQAGLEL	1.000
15	FNFFLFFFL	1.000
7	AGILLRITF	1.000
22	FLPFPLVVF	1.000
95	FIQCLLLGL	1.000
101	LGLLKVRPL	1.000
31	FIYFYFYFF	1.000

Table XX-V9-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
58	SNPPASASL	1.000
28	VVFFIYFYF	1.000
9	ILLRITFNF	1.000
13	ITFNFFLFF	1.000
96	IQCLLLGLL	1.000
85	RKKKLKKAF	0.600
126	GIFMQAAPW	0.500
57	SSNPPASAS	0.500
62	ASASLVAGT	0.500
64	ASLVAGTLS	0.500
56	GSSNPPASA	0.500
116	SCDCERGYF	0.450
49	QAGLELLGS	0.450
5	LLAGILLRI	0.400
38	FFLEMESHY	0.400
92	AFRFIQCLL	0.300
6	LAGILLRIT	0.300
1	MRRELLAGI	0.240
87	KKLKKAFRF	0.200
60	PPASASLVA	0.200
3	RELLAGILL	0.200
98	CLLLGLLKV	0.200
34	FYFYFFLEM	0.200
65	SLVAGTLSV	0.200
50	AGLELLGSS	0.200
29	VFFIYFYFY	0.200
119	CERGYFQGI	0.120
93	FRFIQCLLL	0.100
70	TLSVHHCAC	0.100
19	LFFFLPFPL	0.100
111	HQGVNSCDC	0.100
30	FFIYFYFYF	0.100
11	LRITFNFFL	0.100
55	LGSSNPPAS	0.100
32	IYFYFYFFL	0.100
54	LLGSSNPPA	0.100
26	PLVVFFIYF	0.100

Table XX-V9-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
14	TFNFFLFFF	0.100
44	SHYVAQAGL	0.100
69	GTLSVHHCA	0.100
109	LQHQGVNSC	0.100
17	FFLFFFLPF	0.100
81	SFTKRKKKL	0.100
124	FQGIFMQAA	0.100
74	HHCACFESF	0.100
75	HCACFESFT	0.100
120	ERGYFQGIF	0.100
68	AGTLSVHHC	0.100
129	MQAAPWEGT	0.100
8	GILLRITFN	0.100
39	FLEMESHYV	0.090
84	KRKKKLKKA	0.060
105	KVRPLQHQG	0.060
2	RRELLAGIL	0.060
80	ESFTKRKKK	0.050
43	ESHYVAQAG	0.050
76	CACFESFTK	0.045
67	VAGTLSVHH	0.030
82	FTKRKKKLK	0.030
103	LLKVRPLQH	0.030
51	GLELLGSSN	0.030
90	KKAFRFIQC	0.020
20	FFFLPFPLV	0.020
40	LEMESHYVA	0.020
77	ACFESFTKR	0.020
106	VRPLQHQGV	0.020
21	FFLPFPLVV	0.020
114	VNSCDCERG	0.015
42	MESHYVAQA	0.010
66	LVAGTLSVH	0.010
72	SVHHCACFE	0.010
100	LLGLLKVRP	0.010
18	FLFFFLPFP	0.010
125	QGIFMQAAP	0.010

Table XX-V9-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
97	QCLLLGLLK	0.010
99	LLLGLLKVR	0.010
48	AQAGLELLG	0.010
102	GLLKVRPLQ	0.010
73	VHHCACFES	0.010

Table XX-V10-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
3	CPAGELGTS	3.000
9	GTSDVVTVV	0.400
8	LGTSDVVTV	0.300
2	RCPAGELGT	0.200
7	ELGTSDVVT	0.100
5	AGELGTSDV	0.060
6	GELGTSDVV	0.020
4	PAGELGTSD	0.006
1	GRCPAGELG	0.001

Table XX-V11-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
1	QARLRLRVM	18.000
5	RLRVMVPPL	6.000
8	VMVPPLPSL	1.000
7	RVMVPPLPS	0.200
9	MVPPLPSLN	0.100
3	RLRLRVMVP	0.060
2	ARLRLRVMV	0.020

Table XX-V11-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
6	LRVMVPPLP	0.001
4	LRLRVMVPP	0.001

Table XX-V12-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
9	CSYSTLTTV	1.000
5	EPEGCSYST	0.600
1	VMSEEPEGC	0.300
2	MSEEPEGCS	0.300
8	GCSYSTLTT	0.100
7	EGCSYSTLT	0.100
3	SEEPEGCSY	0.090
4	EEPEGCSYS	0.020
6	PEGCSYSTL	0.010

Table XX-V13-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
7	VLADPQEDS	0.200
1	SQVTVDVLA	0.100
3	VTVDVLADP	0.020
2	QVTVDVLAD	0.015
6	DVLADPQED	0.015
8	LADPQEDSG	0.009
4	TVDVLADPQ	0.003
9	ADPQEDSGK	0.002
5	VDVLADPQE	0.001

Table XX-V14-HLA-B3501-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Start	Subsequence	Score
4	NPPASASLV	4.000
8	SASLVAGTL	3.000
3	SNPPASASL	1.000
9	ASLVAGTLS	0.500
7	ASASLVAGT	0.500
1	GSSNPPASA	0.500
2	SSNPPASAS	0.500
5	PPASASLVA	0.200
6	PASASLVAG	0.003

Table XXI-V1-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
493	RAKPTGNGIY	36.000
156	GPALEEGQGL	30.000
150	LPSLNPGPAL	20.000
132	FPAGSFQARL	20.000
409	RSQPEESVGL	15.000
407	DPRSQPEESV	12.000
1	MPLSLGAEMW	10.000
116	NAVQADEGEY	9.000
436	MSEEPEGRSY	9.000
334	DPQEDSGKQV	8.000
227	HPGLLQDQRI	8.000
11	GPEAWLLLLL	6.000
392	LTRENSIRRL	6.000
439	EPEGRSYSTL	6.000
383	TQKYEEELTL	4.500
249	SVRGLEDQNL	4.500
178	APSVTWDTEV	4.000
495	KPTGNGIYIN	4.000
271	LSEGQPPPSY	3.000
79	LALLHSKYGL	3.000

Table XXI-V1-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
13	EAWLLLLLLL	3.000
201	SAAVTSEFHL	3.000
365	VVVVVLMSRY	2.000
276	PPPSYNWTRL	2.000
128	RVSTFPAGSF	2.000
35	ETSDVVTVVL	2.000
362	CLLVVVVVLM	2.000
235	RITHILHVSF	2.000
44	LGQDAKLPCF	2.000
144	RVLVPPLPSL	2.000
445	YSTLTTVREI	2.000
10	WGPEAWLLLL	2.000
176	SPAPSVTWDT	2.000
105	RNPLDGSVLL	2.000
244	FLAEASVRGL	2.000
138	QARLRLRVLV	1.800
291	SGVRVDGDTL	1.500
192	SSRSFKHSRS	1.500
212	PSRSMNGQPL	1.500
8	EMWGPEAWLL	1.500
426	SLKDNSSCSV	1.200
411	QPEESVGLRA	1.200
103	PPRNPLDGSV	1.200
303	PPLTTEHSGI	1.200
347	SASVVVVGVI	1.200
473	DQDEGIKQAM	1.200
361	FCLLVVVVVL	1.000
236	ITHILHVSFL	1.000
221	LTCVVSHPGL	1.000
222	TCVVSHPGLL	1.000
25	FTGRCPAGEL	1.000
346	VSASVVVVGV	1.000
354	GVIAALLFCL	1.000
57	DSGEQVGQVA	1.000
194	RSFKHSRSAA	1.000
214	RSMNGQPLTC	1.000
381	QMTQKYEEEL	1.000

Table XXI-V1-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
137	FQARLRLRVL	1.000
355	VIAALLFCLL	1.000
350	VVVVGVIAAL	1.000
352	VVGVIAALLF	1.000
351	VVVGVIAALL	1.000
317	VSNEFSSRDS	1.000
500	GIYINGRGHL	1.000
16	LLLLLLLASF	1.000
99	EQPPPPRNPL	1.000
41	TVVLGQDAKL	1.000
280	YNWTRLDGPL	1.000
134	AGSFQARLRL	1.000
476	EGIKQAMNHF	1.000
321	FSSRDSQVTV	1.000
202	AAVTSEFHLV	0.900
67	WARVDAGEGA	0.900
341	KQVDLVSASV	0.800
230	LLQDQRITHI	0.800
169	ASCTAEGSPA	0.750
71	DAGEGAQELA	0.600
233	DQRITHILHV	0.600
158	ALEEGQGLTL	0.600
45	GQDAKLPCFY	0.600
477	GIKQAMNHFV	0.600
75	GAQELALLHS	0.600
357	AALLFCLLVV	0.600
261	IGREGAMLKC	0.600
356	IAALLFCLLV	0.600
423	HPDSLKDNSS	0.600
309	HSGIYVCHVS	0.500
248	ASVRGLEDQN	0.500
348	ASVVVVGVIA	0.500
174	EGSPAPSVTW	0.500
425	DSLKDNSSCS	0.500
338	DSGKQVDLVS	0.500
273	EGQPPPSYNW	0.500
6	GAEMWGPEAW	0.450

Table XXI-V1-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
339	SGKQVDLVSA	0.450
106	NPLDGSVLLR	0.400
377	RKAQQMTQKY	0.400
452	REIETQTELL	0.400
389	ELTLTRENSI	0.400
305	LTTEHSGIYV	0.400

Table XXI-V2-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
1	LGQDAKLPCL	2.000
2	GQDAKLPCLY	0.600
7	LPCLYRGDSG	0.200
6	KLPCLYRGDS	0.200
4	DAKLPCLYRG	0.090
10	LYRGDSGEQV	0.060
9	CLYRGDSGEQ	0.015
3	QDAKLPCLYR	0.001
8	PCLYRGDSGE	0.001
5	AKLPCLYRGD	0.001

Table XXI-V7-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
6	DPRSQSEEPE	0.600
9	SQSEEPEGRS	0.200
8	RSQSEEPEGR	0.150
1	HSHHTDPRSQ	0.075
2	SHHTDPRSQS	0.010

Table XXI-V7-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
4	HTDPRSQSEE	0.003
3	HHTDPRSQSE	0.002
5	TDPRSQSEEP	0.001
7	PRSQSEEPEG	0.000

Table XXI-V9-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
25	FPLVVFFIYF	20.000
115	NSCDCERGYF	15.000
23	LPFPLVVFFI	8.000
91	KAFRFIQCLL	6.000
57	SSNPPASASL	5.000
80	ESFTKRKKKL	5.000
43	ESHYVAQAGL	5.000
62	ASASLVAGTL	5.000
107	RPLQHQGVNS	4.000
6	LAGILLRITF	3.000
10	LLRITFNFFL	3.000
59	NPPASASLVA	2.000
28	VVFFIYFYFY	2.000
114	VNSCDCERGY	2.000
12	RITFNFFLFF	2.000
105	KVRPLQHQGV	1.200
64	ASLVAGTLSV	1.000
70	TLSVHHCACF	1.000
13	ITFNFFLFFF	1.000
18	FLFFFLPFPL	1.000
100	LLGLLKVRPL	1.000
95	FIQCLLLGLL	1.000
8	GILLRITFNF	1.000
9	ILLRITFNFF	1.000
46	YVAQAGLELL	1.000

Table XXI-V9-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
31	FIYFYFYFFL	1.000
27	LVVFFIYFYF	1.000
22	FLPFPLVVFF	1.000
86	KKKLKKAFRF	0.600
84	KRKKKLKKAF	0.600
1	MRRELLAGIL	0.600
56	GSSNPPASAS	0.500
125	QGIFMQAAPW	0.500
4	ELLAGILLRI	0.400
119	CERGYFQGIF	0.300
63	SASLVAGTLS	0.300
67	VAGTLSVHHC	0.300
92	AFRFIQCLLL	0.300
49	QAGLELLGSS	0.300
120	ERGYFQGIFM	0.200
58	SNPPASASLV	0.200
90	KKAFRFIQCL	0.200
33	YFYFYFFLEM	0.200
50	AGLELLGSSN	0.200
97	QCLLLGLLKV	0.200
26	PLVVFFIYFY	0.200
37	YFFLEMESHY	0.200
94	RFIQCLLLGL	0.200
48	AQAGLELLGS	0.150
118	DCERGYFQGI	0.120
21	FFLPFPLVVF	0.100
14	TFNFFLFFFL	0.100
30	FFIYFYFYFF	0.100
72	SVHHCACFES	0.100
55	LGSSNPPASA	0.100
69	GTLSVHHCAC	0.100
45	HYVAQAGLEL	0.100
53	ELLGSSNPPA	0.100
16	NFFLFFFLPF	0.100
128	FMQAAPWEGT	0.100
11	LRITFNFFLF	0.100
68	AGTLSVHHCA	0.100

Table XXI-V9-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
7	AGILLRITFN	0.100
54	LLGSSNPPAS	0.100
73	VHHCACFESF	0.100
29	VFFIYFYFYF	0.100
5	LLAGILLRIT	0.100
87	KKLKKAFRFI	0.080
38	FFLEMESHYV	0.060
88	KLKKAFRFIQ	0.060
2	RRELLAGILL	0.060
71	LSVHHCACFE	0.050
83	TKRKKKLKKA	0.030
47	VAQAGLELLG	0.030
103	LLKVRPLQHQ	0.030
61	PASASLVAGT	0.030
76	CACFESFTKR	0.030
82	FTKRKKKLKK	0.030
89	LKKAFRFIQC	0.030
41	EMESHYVAQA	0.030
39	FLEMESHYVA	0.030
121	RGYFQGIFMQ	0.020
24	PFPLVVFFIY	0.020
60	PPASASLVAG	0.020
77	ACFESFTKRK	0.020
19	LFFFLPFPLV	0.020
20	FFFLPFPLVV	0.020
75	HCACFESFTK	0.015
113	GVNSCDCERG	0.015
108	PLQHQGVNSC	0.010
98	CLLLGLLKVR	0.010
110	QHQGVNSCDC	0.010
15	FNFFLFFFLP	0.010
99	LLLGLLKVRP	0.010
65	SLVAGTLSVH	0.010
101	LGLLKVRPLQ	0.010
111	HQGVNSCDCE	0.010
126	GIFMQAAPWE	0.010
96	IQCLLLGLLK	0.010

Table XXI-V9-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
102	GLLKVRPLQH	0.010

Table XXI-V10-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
10	GTSDVVTVVL	2.000
8	ELGTSDVVTV	0.300
3	RCPAGELGTS	0.300
4	CPAGELGTSD	0.200
9	LGTSDVVTVV	0.200
5	PAGELGTSDV	0.120
6	AGELGTSDVV	0.060
1	TGRCPAGELG	0.030
2	GRCPAGELGT	0.010
7	GELGTSDVVT	0.010

Table XXI-V11-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	RVMVPPLPSL	2.000
1	FQARLRLRVM	2.000
2	QARLRLRVMV	1.800
9	VMVPPLPSLN	0.100
5	LRLRVMVPPL	0.100
4	RLRLRVMVPP	0.060
6	RLRVMVPPLP	0.060
10	MVPPLPSLNP	0.010
7	LRVMVPPLPS	0.010
3	ARLRLRVMVP	0.001

Table XXI-V12-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
3	MSEEPEGCSY	9.000
6	EPEGCSYSTL	6.000
2	VMSEEPEGCS	0.200
9	GCSYSTLTTV	0.200
1	SVMSEEPEGC	0.150
8	EGCSYSTLTT	0.100
10	CSYSTLTTVR	0.050
5	EEPEGCSYST	0.020
4	SEEPEGCSYS	0.003
7	PEGCSYSTLT	0.001
11	SYSTLTTVRE	0.001

Table XXI-V13-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
1	DSQVTVDVLA	0.500
7	DVLADPQEDS	0.100
8	VLADPQEDSG	0.020
4	VTVDVLADPQ	0.020
2	SQVTVDVLAD	0.015
9	LADPQEDSGK	0.013
3	QVTVDVLADP	0.010
5	TVDVLADPQE	0.003
10	ADPQEDSGKQ	0.002
6	VDVLADPQED	0.002

Table XXI-V14-HLA-B3501-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Start	Subsequence	Score
8	ASASLVAGTL	5.000
3	SSNPPASASL	5.000
5	NPPASASLVA	2.000
10	ASLVAGTLSV	1.000
2	GSSNPPASAS	0.500
9	SASLVAGTLS	0.300
4	SNPPASASLV	0.200
1	LGSSNPPASA	0.100
7	PASASLVAGT	0.030
6	PPASASLVAG	0.020

Tables XXII – XLIX:

TableXXII-V1-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
437	SEEPEGRSY	32
107	PLDGSVLLR	21
305	LTTEHSGIY	21
306	TTEHSGIYV	21
159	LEEGQGLTL	20
252	GLEDQNLWH	20
405	HTDPRSQPE	20
86	YGLHVSPAY	19
262	GREGAMLKC	19
412	PEESVGLRA	19
486	VQENGTLRA	19
494	AKPTGNGIY	19
11	GPEAWLLLL	18
78	ELALLHSKY	18
272	SEGQPPPSY	18
332	VLDPQEDSG	18
386	YEEELTLTR	18
36	TSDVVTVVL	17
76	AQELALLHS	17
184	DTEVKGTTS	17
225	VSHPGLLQD	17
271	LSEGQPPPS	17
294	RVDGDTLGF	17
378	KAQQMTQKY	17
58	SGEQVGQVA	16
117	AVQADEGEY	16
158	ALEEGQGLT	16
323	SRDSQVTVD	16
366	VVVVLMSRY	16
457	QTELLSPGS	16
46	QDAKLPCFY	15
436	MSEEPEGRS	15

TableXXII-V2-HLA-A1-9mers-191P4D12

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	QDAKLPCLY	17
1	GQDAKLPCL	10

TableXXII-V7-HLA-A1-9mers-191P4D12

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	HTDPRSQSE	20

TableXXII-V9-HLA-A1-9mers-191P4D12

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
25	FPLVVFFIY	21
29	VFFIYFYFY	20
115	NSCDCERGY	19
38	FFLEMESHY	16
13	ITFNFFLFF	15
27	LVVFFIYFY	15
116	SCDCERGYF	13
21	FFLPFPLVV	12
39	FLEMESHYV	12
51	GLELLGSSN	12
118	DCERGYFQG	12
4	ELLAGILLR	11
57	SSNPPASAS	11
65	SLVAGTLSV	11
93	FRFIQCLLL	11

TableXXII-V9-HLA-A1-9mers-191P4D12

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
98	CLLLGLLKV	11
2	RRELLAGIL	10
17	FFLFFFLPF	10
34	FYFYFFLEM	10
41	EMESHYVAQ	10
48	AQAGLELLG	10
78	CFESFTKRK	10

TableXXII-V10-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	AGELGTSDV	13
9	GTSDVVTVV	10
2	RCPAGELGT	8
1	GRCPAGELG	7

TableXXII-V11-HLA-A1-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
7	RVMVPPLPS	7
8	VMVPPLPSL	6
9	MVPPLPSLN	6
6	LRVMVPPLP	4
2	ARLRLRVMV	3

TableXXII-V11-HLA-A1-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
3	RLRLRVMVP	3

TableXXII-V12-HLA-A1-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
3	SEEPEGCSY	32

TableXXII-V13-HLA-A1-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
8	LADPQEDSG	16
4	TVDVLADPQ	10
3	VTVDVLADP	9
2	QVTVDVLAD	7

TableXXII-V14-HLA-A1-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
2	SSNPPASAS	11
9	ASLVAGTLS	8
5	PPASASLVA	7
3	SNPPASASL	6
7	ASASLVAGT	6
1	GSSNPPASA	5

TableXXIII-V1-HLA-A0201-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
145	VLVPPLPSL	31
359	LLFCLLVVV	30
358	ALLFCLLVV	28
362	CLLVVVVVL	28
80	ALLHSKYGL	26
142	RLRVLVPPL	26
355	VIAALLFCL	26
351	VVVGVIAAL	24
502	YINGRGHLV	24
17	LLLLLLASF	23
42	VVLGQDAKL	23
347	SASVVVVGV	23
15	WLLLLLLLA	22
345	LVSASVVVV	22
363	LLVVVVVLM	22
446	STLTTVREI	22
8	EMWGPEAWL	21
16	LLLLLLLAS	21
344	DLVSASVVV	21
14	AWLLLLLLL	20
245	LAEASVRGL	20
260	HIGREGAML	20
284	RLDGPLPSG	20
357	AALLFCLLV	20
460	LLSPGSGRA	20
18	LLLLLASFT	19
34	LETSDVVTV	19
71	DAGEGAQEL	19
112	VLLRNAVQA	19
152	SLNPGPALE	19
158	ALEEGQGLT	19
356	IAALLFCLL	19
360	LFCLLVVVV	19

TableXXIII-V1-HLA-A0201-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
361	FCLLVVVVV	19
390	LTLTRENSI	19
13	EAWLLLLLL	18
138	QARLRLRVL	18
266	AMLKCLSEG	18
342	QVDLVSASV	18
481	AMNHFVQEN	18
21	LLASFTGRC	17
106	NPLDGSVLL	17
113	LLRNAVQAD	17
139	ARLRLRVLV	17
229	GLLQDQRIT	17
234	QRITHILHV	17
244	FLAEASVRG	17
287	GPLPSGVRV	17
292	GVRVDGDTL	17
299	TLGFPPLTT	17
322	SSRDSQVTV	17
352	VVGVIAALL	17
382	MTQKYEEEL	17
410	SQPEESVGL	17
419	RAEGHPDSL	17
443	RSYSTLTTV	17
19	LLLLASFTG	16
35	ETSDVVTVV	16
157	PALEEGQGL	16
159	LEEGQGLTL	16
173	AEGSPAPSV	16
202	AAVTSEFHL	16
203	AVTSEFHLV	16
215	SMNGQPLTC	16
237	THILHVSFL	16
242	VSFLAEASV	16
285	LDGPLPSGV	16
350	VVVVGVIAA	16
384	QKYEEELTL	16
452	REIETQTEL	16

TableXXIII-V1-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
453	EIETQTELL	16
501	IYINGRGHL	16
11	GPEAWLLLL	15
12	PEAWLLLLL	15
20	LLLASETGR	15
32	GELETSDVV	15
57	DSGEQVGQV	15
74	EGAQELALL	15
137	FQARLRLRV	15
140	RLRLRVLVP	15
216	MNGQPLTCV	15
217	NGQPLTCVV	15
230	LLQDQRITH	15
240	LHVSFLAEA	15
270	CLSEGQPPP	15
304	PLTTEHSGI	15
309	HSGIYVCHV	15
332	VLDPQEDSG	15
493	RAKPTGNGI	15

TableXXIII-V2-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GQDAKLPCL	17
8	CLYRGDSGE	14
5	KLPCLYRGD	13
4	AKLPCLYRG	11

TableXXIII-V7-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	HTDPRSQSE	8
8	SQSEEPEGR	5
1	SHHTDPRSQ	4
7	RSQSEEPEG	3

TableXXIII-V9-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
98	CLLLGLLKV	31
5	LLAGILLRI	29
65	SLVAGTLSV	29
95	FIQCLLLGL	26
39	FLEMESHYV	21
46	YVAQAGLEL	21
47	VAQAGLELL	21
91	KAFRFIQCL	21
99	LLLGLLKVR	20
101	LGLLKVRPL	19
1	MRRELLAGI	18
58	SNPPASASL	18
63	SASLVAGTL	18
88	KLKKAFRFI	18
18	FLFFFLPFP	17
21	FFLPFPLVV	17
22	FLPFPLVVF	17
54	LLGSSNPPA	17
96	IQCLLLGLL	17
4	ELLAGILLR	16
9	ILLRITFNF	16
44	SHYVAQAGL	16
62	ASASLVAGT	16
6	LAGILLRIT	15
8	GILLRITFN	15

TableXXIII-V9-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
11	LRITFNFFL	15
100	LLGLLKVRP	15

TableXXIII-V10-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	GTSDVVTVV	20
8	LGTSDVVTV	19
5	AGELGTSDV	15
6	GELGTSDVV	15
7	ELGTSDVVT	13
3	CPAGELGTS	10

TableXXIII-V11-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	VMVPPLPSL	29
5	RLRVMVPPL	25
2	ARLRLRVMV	17
3	RLRLRVMVP	14

TableXXIII-V12-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	CSYSTLTTV	17
1	VMSEEPEGC	12
6	PEGCSYSTL	9
8	GCSYSTLTT	9

TableXXIII-V13-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
7	VLADPQEDS	15
3	VTVDVLADP	12
8	LADPQEDSG	10
2	QVTVDVLAD	9
1	SQVTVDVLA	8
6	DVLADPQED	7

TableXXIII-V14-HLA-A0201-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	SNPPASASL	18
8	SASLVAGTL	18
7	ASASLVAGT	16
1	GSSNPPASA	10
4	NPPASASLV	10
6	PASASLVAG	8

TableXXIV-V1-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXIV-V2-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXIV-V7-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXIV-V9-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXIV-V10-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXIV-V11-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXIV-V12-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXIV-V13-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXIV-V14-HLA-A0203-9mers-191P4D12B

Pos	123456789	score

TableXXIV-V14-HLA-A0203-9mers-191P4D12B

Pos	123456789	score
NoResultsFound.		

TableXXV-V1-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
140	RLRLRVLVP	27
112	VLLRNAVQA	25
180	SVTWDTEVK	25
41	TVVLGQDAK	24
111	SVLLRNAVQ	23
294	RVDGDTLGF	23
17	LLLLLLASF	22
117	AVQADEGEY	22
186	EVKGTTSSR	22
261	IGREGAMLK	22
358	ALLFCLLVV	22
397	SIRRLHSHH	22
459	ELLSPGSGR	22
61	QVGQVAWAR	21
78	ELALLHSKY	21
362	CLLVVVVVL	21
415	SVGLRAEGH	21
69	RVDAGEGAQ	20
144	RVLVPPLPS	20
152	SLNPGPALE	20
230	LLQDQRITH	20
292	GVRVDGDTL	20
316	HVSNEFSSR	20
345	LVSASVVVV	20
391	TLTRENSIR	20
500	GIYINGRGH	20
18	LLLLLASFT	19
20	LLLASFTGR	19
97	RVEQPPPPR	19
107	PLDGSVLLR	19
243	SFLAEASVR	19
249	SVRGLEDQN	19

TableXXV-V1-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
252	GLEDQNLWH	19
342	QVDLVSASV	19
349	SVVVVGVIA	19
366	VVVVLMSRY	19
377	RKAQQMTQK	19
485	FVQENGTLR	19
33	ELETSDVVT	18
64	QVAWARVDA	18
77	QELALLHSK	18
128	RVSTFPAGS	18
209	HLVPSRSMN	18
260	HIGREGAML	18
284	RLDGPLPSG	18
299	TLGFPPLTT	18
311	GIYVCHVSN	18
344	DLVSASVVV	18
354	GVIAALLFC	18
359	LLFCLLVVV	18
365	VVVVVLMSR	18
417	GLRAEGHPD	18
450	TVREIETQT	18
491	TLRAKPTGN	18
2	PLSLGAEMW	17
16	LLLLLLLAS	17
19	LLLLASFTG	17
42	VVLGQDAKL	17
89	HVSPAYEGR	17
142	RLRVLVPPL	17
146	LVPPLPSLN	17
158	ALEEGQGLT	17
164	GLTLAASCT	17
351	VVVGVIAAL	17
368	VVLMSRYHR	17
15	WLLLLLLLA	16
81	LLHSKYGLH	16
197	KHSRSAAVT	16
224	VVSHPGLLQ	16

TableXXV-V1-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
235	RITHILHVS	16
239	ILHVSFLAE	16
244	FLAEASVRG	16
288	PLPSGVRVD	16
352	VVGVIAALL	16
369	VLMSRYHRR	16
420	AEGHPDSLK	16
426	SLKDNSSCS	16
460	LLSPGSGRA	16
39	VVTVVLGQD	15
80	ALLHSKYGL	15
105	RNPLDGSVL	15
113	LLRNAVQAD	15
145	VLVPPLPSL	15
166	TLAASCTAE	15
200	RSAAVTSEF	15
313	YVCHVSNEF	15
327	QVTVDVLDP	15
332	VLDPQEDSG	15
363	LLVVVVVLM	15
364	LVVVVVLMS	15
367	VVVLMSRYH	15
373	RYHRRKAQQ	15
400	RLHSHHTDP	15
437	SEEPEGRSY	15
487	QENGTLRAK	15
502	YINGRGHLV	15
38	DVVTVVLGQ	14
87	GLHVSPAYE	14
189	GTTSSRSFK	14
198	HSRSAAVTS	14
219	QPLTCVVSH	14
220	PLTCVVSHP	14
241	HVSFLAEAS	14
384	QKYEEELTL	14
396	NSIRRLHSH	14
409	RSQPEESVG	14

TableXXV-V1-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
4	SLGAEMWGP	13
43	VLGQDAKLP	13
49	KLPCFYRGD	13
84	SKYGLHVSP	13
124	EYECRVSTF	13
139	ARLRLRVLV	13
203	AVTSEFHLV	13
210	LVPSRSMNG	13
236	ITHILHVSF	13
257	NLWHIGREG	13
270	CLSEGQPPP	13
304	PLTTEHSGI	13
322	SSRDSQVTV	13
329	TVDVLDPQE	13
331	DVLDPQEDS	13
333	LDPQEDSGK	13
350	VVVVGVIAA	13
370	LMSRYHRRK	13
374	YHRRKAQQM	13
443	RSYSTLTTV	13
477	GIKQAMNHF	13

TableXXV-V2-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	CLYRGDSGE	22
5	KLPCLYRGD	13
2	QDAKLPCLY	10

TableXXV-V7-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	HHTDPRSQS	8
3	HTDPRSQSE	7
8	SQSEEPEGR	7
4	TDPRSQSEE	6
1	SHHTDPRSQ	4
7	RSQSEEPEG	4
5	DPRSQSEEP	3

TableXXV-V9-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
66	LVAGTLSVH	24
103	LLKVRPLQH	24
4	ELLAGILLR	23
22	FLPFPLVVF	22
99	LLLGLLKVR	22
105	KVRPLQHQG	22
9	ILLRITFNF	21
97	QCLLLGLLK	21
65	SLVAGTLSV	20
51	GLELLGSSN	19
10	LLRITFNFF	18
98	CLLLGLLKV	18
46	YVAQAGLEL	17
83	TKRKKKLKK	17
108	PLQHQGVNS	17
5	LLAGILLRI	16
7	AGILLRITF	16
12	RITFNFFLF	16
27	LVVFFIYFY	16
31	FIYFYFYFF	16
82	FTKRKKKLK	15
100	LLGLLKVRP	15

TableXXV-V9-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	GILLRITFN	14
26	PLVVFFIYF	14
28	VVFFIYFYF	14
53	ELLGSSNPP	14
72	SVHHCACFE	14
76	CACFESFTK	14
88	KLKKAFRFI	14
102	GLLKVRPLQ	14
113	GVNSCDCER	14
126	GIFMQAAPW	14
21	FFLPFPLVV	13
86	KKKLKKAFR	13
87	KKLKKAFRF	13
38	FFLEMESHY	12
80	ESFTKRKKK	12
23	LPFPLVVFF	11
57	SSNPPASAS	11
63	SASLVAGTL	11
70	TLSVHHCAC	11
95	FIQCLLLGL	11
107	RPLQHQGVN	11
121	RGYFQGIFM	11

TableXXV-V10-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
7	ELGTSDVVT	18
2	RCPAGELGT	11
5	AGELGTSDV	9
3	CPAGELGTS	8
6	GELGTSDVV	8
8	LGTSDVVTV	8

TableXXV-V11-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	RLRLRVMVP	25
7	RVMVPPLPS	18
5	RLRVMVPPL	17
9	MVPPLPSLN	17
2	ARLRLRVMV	14
1	QARLRLRVM	12

TableXXV-V12-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	SEEPEGCSY	15
9	CSYSTLTTV	9
6	PEGCSYSTL	7
8	GCSYSTLTT	7

TableXXV-V13-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	QVTVDVLAD	16
9	ADPQEDSGK	16
6	DVLADPQED	15
4	TVDVLADPQ	13
7	VLADPQEDS	12

TableXXV-V14-HLA-A03-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	SSNPPASAS	11
8	SASLVAGTL	11
3	SNPPASASL	9
9	ASLVAGTLS	9
4	NPPASASLV	8
5	PPASASLVA	8
1	GSSNPPASA	7
6	PASASLVAG	7
7	ASASLVAGT	7

TableXXVI-V1-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
38	DVVTVVLGQ	27
351	VVVGVIAAL	27
366	VVVVLMSRY	26
13	EAWLLLLLL	24
124	EYECRVSTF	24
223	CVVSHPGLL	24
455	ETQTELLSP	24
35	ETSDVVTVV	23
78	ELALLHSKY	23
74	EGAQELALL	22
186	EVKGTTSSR	22
305	LTTEHSGIY	22
453	EIETQTELL	22
117	AVQADEGEY	21
292	GVRVDGDTL	20
325	DSQVTVDVL	20
350	VVVVGVIAA	20
352	VVGVIAALL	20
364	LVVVVVLMS	20

TableXXVI-V1-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
42	VVLGQDAKL	19
184	DTEVKGTTS	19
294	RVDGDTLGF	19
331	DVLDPQEDS	19
337	EDSGKQVDL	19
354	GVIAALLFC	19
365	VVVVVLMSR	19
8	EMWGPEAWL	18
60	EQVGQVAWA	18
71	DAGEGAQEL	18
145	VLVPPLPSL	18
236	ITHILHVSF	18
237	THILHVSFL	18
313	YVCHVSNEF	18
449	TTVREIETQ	18
39	VVTVVLGQD	17
328	VTVDVLDPQ	17
355	VIAALLFCL	17
41	TVVLGQDAK	16
57	DSGEQVGQV	16
130	STFPAGSFQ	16
298	DTLGFPPLT	16
327	QVTVDVLDP	16
349	SVVVVGVIA	16
382	MTQKYEEEL	16
450	TVREIETQT	16
413	EESVGLRAE	15
414	ESVGLRAEG	15
473	DQDEGIKQA	15
12	PEAWLLLLL	14
14	AWLLLLLLL	14
17	LLLLLLASF	14
40	VTVVLGQDA	14
160	EEGQGLTLA	14
260	HIGREGAML	14
345	LVSASVVVV	14
367	VVVLMSRYH	14

TableXXVI-V1-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
387	EEELTLTRE	14
437	SEEPEGRSY	14
452	REIETQTEL	14
472	EDQDEGIKQ	14
476	EGIKQAMNH	14
484	HFVQENGTL	14
485	FVQENGTLR	14
11	GPEAWLLLL	13
45	GQDAKLPCF	13
109	DGSVLLRNA	13
135	GSFQARLRL	13
142	RLRVLVPPL	13
146	LVPPLPSLN	13
161	EGQGLTLAA	13
222	TCVVSHPGL	13
249	SVRGLEDQN	13
320	EFSSRDSQV	13
329	TVDVLDPQE	13
344	DLVSASVVV	13
353	VGVIAALLF	13
393	TRENSIRRL	13
421	EGHPDSLKD	13
438	EEPEGRSYS	13
446	STLTTVREI	13
459	ELLSPGSGR	13
501	IYINGRGHL	13

TableXXVI-V2-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GQDAKLPCL	13
2	QDAKLPCLY	11

TableXXVI-V2-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	DAKLPCLYR	9

TableXXVI-V7-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	HTDPRSQSE	10
5	DPRSQSEEP	9
2	HHTDPRSQS	4

TableXXVI-V9-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
27	LVVFFIYFY	28
28	VVFFIYFYF	24
13	ITFNFFLFF	21
46	YVAQAGLEL	20
120	ERGYFQGIF	19
23	LPFPLVVFF	18
95	FIQCLLLGL	18
80	ESFTKRKKK	16
91	KAFRFIQCL	16
4	ELLAGILLR	15
7	AGILLRITF	15
66	LVAGTLSVH	15
12	RITFNFFLF	14
29	VFFIYFYFY	14

TableXXVI-V9-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
96	IQCLLLGLL	14
14	TFNFFLFFF	13
15	FNFFLFFFL	13
19	LFFFLPFPL	13
26	PLVVFFIYF	13
38	FFLEMESHY	13
93	FRFIQCLLL	13
101	LGLLKVRPL	13
105	KVRPLQHQG	13

TableXXVI-V10-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	GTSDVVTVV	13
7	ELGTSDVVT	10
8	LGTSDVVTV	7
3	CPAGELGTS	6

TableXXVI-V11-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	VMVPPLPSL	18
9	MVPPLPSLN	13
5	RLRVMVPPL	12
7	RVMVPPLPS	11

TableXXVI-V12-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	SEEPEGCSY	14
4	EEPEGCSYS	13
5	EPEGCSYST	11
7	EGCSYSTLT	11
6	PEGCSYSTL	10
9	CSYSTLTTV	6

TableXXVI-V13-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
6	DVLADPQED	18
2	QVTVDVLAD	17
3	VTVDVLADP	17
4	TVDVLADPQ	12

TableXXVI-V14-HLA-A26-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	SNPPASASL	11
8	SASLVAGTL	11
7	ASASLVAGT	6
6	PASASLVAG	5

TableXXVII-V1-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
100	QPPPPRNPL	26
11	GPEAWLLLL	23
277	PPSYNWTRL	23
106	NPLDGSVLL	22
287	GPLPSGVRV	20
495	KPTGNGIYI	20
150	LPSLNPGPA	19
439	EPEGRSYST	19
1	MPLSLGAEM	18
8	EMWGPEAWL	17
275	QPPPSYNWT	17
289	LPSGVRVDG	17
337	EDSGKQVDL	17
142	RLRVLVPPL	16
151	PSLNPGPAL	16
26	TGRCPAGEL	15
36	TSDVVTVVL	15
73	GEGAQELAL	15
103	PPRNPLDGS	15
132	FPAGSFQAR	15
145	VLVPPLPSL	15
147	VPPLPSLNP	15
159	LEEGQGLTL	15
14	AWLLLLLLL	14
176	SPAPSVTWD	14
178	APSVTWDTE	14
213	SRSMNGQPL	14
351	VVVGVIAAL	14
362	CLLVVVVVL	14
12	PEAWLLLLL	13
13	EAWLLLLLL	13
29	CPAGELETS	13
42	VVLGQDAKL	13
74	EGAQELALL	13
91	SPAYEGRVE	13
105	RNPLDGSVL	13
135	GSFQARLRL	13
138	QARLRLRVL	13
161	EGQGLTLAA	13

TableXXVII-V1-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
173	AEGSPAPSV	13
219	QPLTCVVSH	13
260	HIGREGAML	13
263	REGAMLKCL	13
292	GVRVDGDTL	13
294	RVDGDTLGF	13
297	GDTLGFPPL	13
345	LVSASVVVV	13
356	IAALLFCLL	13
419	RAEGHPDSL	13
462	SPGSGRAEE	13
9	MWGPEAWLL	12
10	WGPEAWLLL	12
35	ETSDVVTVV	12
80	ALLHSKYGL	12
82	LHSKYGLHV	12
101	PPPPRNPLD	12
102	PPPRNPLDG	12
133	PAGSFQARL	12
148	PPLPSLNPG	12
154	NPGPALEEG	12
202	AAVTSEFHL	12
211	VPSRSMNGQ	12
237	THILHVSFL	12
245	LAEASVRGL	12
299	TLGFPPLTT	12
324	RDSQVTVDV	12
325	DSQVTVDVL	12
352	VVGVIAALL	12
355	VIAALLFCL	12
384	QKYEEELTL	12
407	DPRSQPEES	12
410	SQPEESVGL	12
452	REIETQTEL	12
453	EIETQTELL	12
501	IYINGRGHL	12

TableXXVII-V2-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GQDAKLPCL	13
6	LPCLYRGDS	11

TableXXVII-V7-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	DPRSQSEEP	12

TableXXVII-V9-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
23	LPFPLVVFF	21
60	PPASASLVA	20
59	NPPASASLV	17
46	YVAQAGLEL	14
92	AFRFIQCLL	14
3	RELLAGILL	12
15	FNFFLFFFL	12
22	FLPFPLVVF	12
32	IYFYFYFFL	12
56	GSSNPPASA	12
58	SNPPASASL	12
63	SASLVAGTL	12
93	FRFIQCLLL	12

TableXXVII-V9-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
95	FIQCLLLGL	12
101	LGLLKVRPL	12
107	RPLQHQGVN	12
2	RRELLAGIL	11
5	LLAGILLRI	11
11	LRITFNFFL	11
13	ITFNFFLFF	11
19	LFFFLPFPL	11
20	FFFLPFPLV	11
25	FPLVVFFIY	11
44	SHYVAQAGL	11
47	VAQAGLELL	11
62	ASASLVAGT	11
81	SFTKRKKKL	11
91	KAFRFIQCL	11
96	IQCLLLGLL	11
119	CERGYFQGI	11
129	MQAAPWEGT	11
10	LLRITFNFF	10
17	FFLFFFLPF	10
21	FFLPFPLVV	10
42	MESHYVAQA	10
65	SLVAGTLSV	10
88	KLKKAFRFI	10

TableXXVII-V10-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	CPAGELGTS	13
7	ELGTSDVVT	11
9	GTSDVVTVV	11

TableXXVII-V10-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	RCPAGELGT	10
5	AGELGTSDV	9
6	GELGTSDVV	9
8	LGTSDVVTV	9

TableXXVII-V11-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	RLRVMVPPL	16
8	VMVPPLPSL	15
2	ARLRLRVMV	11
1	QARLRLRVM	9
7	RVMVPPLPS	8

TableXXVII-V12-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	EPEGCSYST	19
6	PEGCSYSTL	11
8	GCSYSTLTT	11

TableXXVII-V13-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	SQVTVDVLA	8
2	QVTVDVLAD	4
7	VLADPQEDS	4

TableXXVII-V14-HLA-B0702-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	PPASASLVA	20
4	NPPASASLV	17
1	GSSNPPASA	12
3	SNPPASASL	12
8	SASLVAGTL	12
7	ASASLVAGT	11

TableXXVIII-V1-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
138	QARLRLRVL	29
142	RLRVLVPPL	24
337	EDSGKQVDL	23
140	RLRLRVLVP	22
491	TLRAKPTGN	22
477	GIKQAMNHF	21
493	RAKPTGNGI	20
362	CLLVVVVVL	19
292	GVRVDGDTL	18
426	SLKDNSSCS	18

TableXXVIII-V1-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
11	GPEAWLLLL	17
13	EAWLLLLLL	17
26	TGRCPAGEL	17
45	GQDAKLPCF	17
71	DAGEGAQEL	17
106	NPLDGSVLL	17
124	EYECRVSTF	17
145	VLVPPLPSL	17
277	PPSYNWTRL	17
80	ALLHSKYGL	16
81	LLHSKYGLH	16
100	QPPPPRNPL	16
157	PALEEGQGL	16
247	EASVRGLED	16
265	GAMLKCLSE	16
267	MLKCLSEGQ	16
356	IAALLFCLL	16
374	YHRRKAQQM	16
439	EPEGRSYST	16
453	EIETQTELL	16
47	DAKLPCFYR	15
65	VAWARVDAG	15
101	PPPPRNPLD	15
231	LQDQRITHI	15
245	LAEASVRGL	15
260	HIGREGAML	15
355	VIAALLFCL	15
369	VLMSRYHRR	15
410	SQPEESVGL	15
113	LLRNAVQAD	14
133	PAGSFQARL	14
202	AAVTSEFHL	14
390	LTLTRENSI	14
419	RAEGHPDSL	14

TableXXVIII-V2-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GQDAKLPCL	21
3	DAKLPCLYR	15

TableXXVIII-V7-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	DPRSQSEEP	13
3	HTDPRSQSE	9

TableXXVIII-V9-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
103	LLKVRPLQH	25
82	FTKRKKKLK	22
88	KLKKAFRFI	22
101	LGLLKVRPL	22
81	SFTKRKKKL	21
84	KRKKKLKKA	21
86	KKKLKKAFR	21
10	LLRITFNFF	18
85	RKKKLKKAF	18
63	SASLVAGTL	17
83	TKRKKKLKK	16
87	KKLKKAFRF	16
92	AFRFIQCLL	16
8	GILLRITFN	15
47	VAQAGLELL	15
91	KAFRFIQCL	15

TableXXVIII-V9-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
95	FIQCLLLGL	15
1	MRRELLAGI	14
22	FLPFPLVVF	14
23	LPFPLVVFF	14
9	ILLRITFNF	13
26	PLVVFFIYF	13
44	SHYVAQAGL	13
80	ESFTKRKKK	13
5	LLAGILLRI	12
32	IYFYFYFFL	12
58	SNPPASASL	12
96	IQCLLLGLL	12
119	CERGYFQGI	12

TableXXVIII-V10-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
7	ELGTSDVVT	9
3	CPAGELGTS	6
4	PAGELGTSD	6

TableXXVIII-V11-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	RLRVMVPPL	24
3	RLRLRVMVP	22

TableXXVIII-V11-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	QARLRLRVM	19
8	VMVPPLPSL	11

TableXXVIII-V12-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
6	PEGCSYSTL	10
5	EPEGCSYST	8
4	EEPEGCSYS	4

TableXXVIII-V13-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
7	VLADPQEDS	7
8	LADPQEDSG	4
1	SQVTVDVLA	3
2	QVTVDVLAD	3

TableXXVIII-V14-HLA-B08-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	SASLVAGTL	17
3	SNPPASASL	12

TableXXIX-V1-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
237	THILHVSFL	22
208	FHLVPSRSM	20
259	WHIGREGAM	18
374	YHRRKAQQM	17
393	TRENSIRRL	17
36	TSDVVTVVL	16
362	CLLVVVVVL	16
135	GSFQARLRL	15
308	EHSGIYVCH	15
337	EDSGKQVDL	15
100	QPPPPRNPL	14
106	NPLDGSVLL	14
138	QARLRLRVL	14
145	VLVPPLPSL	14
245	LAEASVRGL	14
277	PPSYNWTRL	14
325	DSQVTVDVL	14
501	IYINGRGHL	14
8	EMWGPEAWL	13
26	TGRCPAGEL	13
71	DAGEGAQEL	13
74	EGAQELALL	13
142	RLRVLVPPL	13
151	PSLNPGPAL	13
159	LEEGQGLTL	13
197	KHSRSAAVT	13
222	TCVVSHPGL	13
292	GVRVDGDTL	13
297	GDTLGFPPL	13
351	VVVGVIAAL	13
356	IAALLFCLL	13
403	SHHTDPRSQ	13
404	HHTDPRSQP	13
410	SQPEESVGL	13

TableXXIX-V1-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
419	RAEGHPDSL	13
9	MWGPEAWLL	12
11	GPEAWLLLL	12
73	GEGAQELAL	12
82	LHSKYGLHV	12
88	LHVSPAYEG	12
105	RNPLDGSVL	12
133	PAGSFQARL	12
213	SRSMNGQPL	12
382	MTQKYEEEL	12
384	QKYEEELTL	12
422	GHPDSLKDN	12
452	REIETQTEL	12
453	EIETQTELL	12
484	HFVQENGTL	12
10	WGPEAWLLL	11
12	PEAWLLLLL	11
13	EAWLLLLLL	11
42	VVLGQDAKL	11
80	ALLHSKYGL	11
157	PALEEGQGL	11
223	CVVSHPGLL	11
226	SHPGLLQDQ	11
240	LHVSFLAEA	11
315	CHVSNEFSS	11
352	VVGVIAALL	11
355	VIAALLFCL	11
401	LHSHHTDPR	11
440	PEGRSYSTL	11
483	NHFVQENGT	11
14	AWLLLLLLL	10
124	EYECRVSTF	10
202	AAVTSEFHL	10
232	QDQRITHIL	10
236	ITHILHVSF	10
250	VRGLEDQNL	10
260	HIGREGAML	10

TableXXIX-V1-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
263	REGAMLKCL	10
281	NWTRLDGPL	10
363	LLVVVVVLM	10
474	QDEGIKQAM	10

TableXXIX-V2-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GQDAKLPCL	12

TableXXIX-V7-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	SHHTDPRSQ	13
2	HHTDPRSQS	13

TableXXIX-V9-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
44	SHYVAQAGL	21
74	HHCACFESF	16
46	YVAQAGLEL	14
101	LGLLKVRPL	13
32	IYFYFYFFL	12
58	SNPPASASL	12
63	SASLVAGTL	12
81	SFTKRKKKL	12
96	IQCLLLGLL	12
2	RRELLAGIL	11
19	LFFFLPFPL	11
22	FLPFPLVVF	11
23	LPFPLVVFF	11
47	VAQAGLELL	11
73	VHHCACFES	11
91	KAFRFIQCL	11
110	QHQGVNSCD	11
3	RELLAGILL	10
11	LRITFNFFL	10
15	FNFFLFFFL	10
92	AFRFIQCLL	10
93	FRFIQCLLL	10
95	FIQCLLLGL	10

TableXXIX-V10-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	GTSDVVTVV	6
7	ELGTSDVVT	5
6	GELGTSDVV	4
8	LGTSDVVTV	4
1	GRCPAGELG	3
3	CPAGELGTS	3
5	AGELGTSDV	2

TableXXIX-V11-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	VMVPPLPSL	14
5	RLRVMVPPL	13
1	QARLRLRVM	10

TableXXIX-V12-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
6	PEGCSYSTL	11

TableXXIX-V13-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	QVTVDVLAD	3
7	VLADPQEDS	3
1	SQVTVDVLA	2
4	TVDVLADPQ	2
6	DVLADPQED	2
8	LADPQEDSG	2
3	VTVDVLADP	1
5	VDVLADPQE	1
9	ADPQEDSGK	1

TableXXIX-V14-HLA-B1510-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each

start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
3	SNPPASASL	12
8	SASLVAGTL	12

TableXXX-V1-HLA-B2705-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
393	TRENSIRRL	26
250	VRGLEDQNL	25
452	REIETQTEL	22
135	GSFQARLRL	21
213	SRSMNGQPL	20
377	RKAQQMTQK	19
42	VVLGQDAKL	18
97	RVEQPPPPR	18
262	GREGAMLKC	18
351	VVVGVIAAL	18
376	RRKAQQMTQ	18
399	RRLHSHHTD	18
14	AWLLLLLLL	17
17	LLLLLLASF	17
105	RNPLDGSVL	17
142	RLRVLVPPL	17
200	RSAAVTSEF	17
206	SEFHLVPSR	17
294	RVDGDTLGF	17
297	GDTLGFPPL	17
419	RAEGHPDSL	17
498	GNGIYINGR	17
41	TVVLGQDAK	16
45	GQDAKLPCF	16
80	ALLHSKYGL	16
96	GRVEQPPPP	16
106	NPLDGSVLL	16
145	VLVPPLPSL	16
234	QRITHILHV	16

TableXXX-V1-HLA-B2705-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
243	SFLAEASVR	16
261	IGREGAMLK	16
293	VRVDGDTLG	16
301	GFPPLTTEH	16
337	EDSGKQVDL	16
362	CLLVVVVVL	16
384	QKYEEELTL	16
442	GRSYSTLTT	16
476	EGIKQAMNH	16
477	GIKQAMNHF	16
484	HFVQENGTL	16
11	GPEAWLLLL	15
20	LLLASFTGR	15
61	QVGQVAWAR	15
71	DAGEGAQEL	15
74	EGAQELALL	15
75	GAQELALLH	15
77	QELALLHSK	15
107	PLDGSVLLR	15
133	PAGSFQARL	15
139	ARLRLRVLV	15
141	LRLRVLVPP	15
188	KGTTSSRSF	15
189	GTTSSRSFK	15
227	HPGLLQDQR	15
237	THILHVSFL	15
263	REGAMLKCL	15
283	TRLDGPLPS	15
333	LDPQEDSGK	15
365	VVVVVLMSR	15
392	LTRENSIRR	15
466	GRAEEEEDQ	15
492	LRAKPTGNG	15
501	IYINGRGHL	15
8	EMWGPEAWL	14
9	MWGPEAWLL	14
13	EAWLLLLLL	14

TableXXX-V1-HLA-B2705-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
27	GRCPAGELE	14
73	GEGAQELAL	14
104	PRNPLDGSV	14
114	LRNAVQADE	14
120	ADEGEYECR	14
143	LRVLVPPLP	14
151	PSLNPGPAL	14
157	PALEEGQGL	14
159	LEEGQGLTL	14
186	EVKGTTSSR	14
193	SRSFKHSRS	14
199	SRSAAVTSE	14
236	ITHILHVSF	14
277	PPSYNWTRL	14
286	DGPLPSGVR	14
292	GVRVDGDTL	14
313	YVCHVSNEF	14
323	SRDSQVTVD	14
368	VVLMSRYHR	14
375	HRRKAQQMT	14
378	KAQQMTQKY	14
386	YEEELTLTR	14
408	PRSQPEESV	14
410	SQPEESVGL	14
418	LRAEGHPDS	14
420	AEGHPDSLK	14
444	SYSTLTTVR	14
459	ELLSPGSGR	14
1	MPLSLGAEM	13
12	PEAWLLLLL	13
26	TGRCPAGEL	13
36	TSDVVTVVL	13
78	ELALLHSKY	13
86	YGLHVSPAY	13
100	QPPPPRNPL	13
124	EYECRVSTF	13
129	VSTFPAGSF	13

TableXXX-V1-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
132	FPAGSFQAR	13
138	QARLRLRVL	13
202	AAVTSEFHL	13
208	FHLVPSRSM	13
219	QPLTCVVSH	13
222	TCVVSHPGL	13
231	LQDQRITHI	13
252	GLEDQNLWH	13
272	SEGQPPPSY	13
276	PPPSYNWTR	13
316	HVSNEFSSR	13
352	VVGVIAALL	13
353	VGVIAALLF	13
356	IAALLFCLL	13
366	VVVVLMSRY	13
382	MTQKYEEEL	13
391	TLTRENSIR	13
394	RENSIRRLH	13
398	IRRLHSHHT	13
411	QPEESVGLR	13
428	KDNSSCSVM	13
440	PEGRSYSTL	13
485	FVQENGTLR	13
487	QENGTLRAK	13
500	GIYINGRGH	13
10	WGPEAWLLL	12
47	DAKLPCFYR	12
54	YRGDSGEQV	12
68	ARVDAGEGA	12
127	CRVSTFPAG	12
134	AGSFQARLR	12
192	SSRSFKHSR	12
228	PGLLQDQRI	12
245	LAEASVRGL	12
255	DQNLWHIGR	12
259	WHIGREGAM	12
260	HIGREGAML	12

TableXXX-V1-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
281	NWTRLDGPL	12
308	EHSGIYVCH	12
325	DSQVTVDVL	12
355	VIAALLFCL	12
363	LLVVVVVLM	12
369	VLMSRYHRR	12
370	LMSRYHRRK	12
372	SRYHRRKAQ	12
396	NSIRRLHSH	12
435	VMSEEPEGR	12
451	VREIETQTE	12
471	EEDQDEGIK	12
474	QDEGIKQAM	12
493	RAKPTGNGI	12
494	AKPTGNGIY	12

TableXXX-V2-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GQDAKLPCL	16
3	DAKLPCLYR	13
2	QDAKLPCLY	11
4	AKLPCLYRG	8

TableXXX-V7-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
6	PRSQSEEPE	13
8	SQSEEPEGR	12
7	RSQSEEPEG	7

TableXXX-V9-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	RRELLAGIL	27
93	FRFIQCLLL	24
11	LRITFNFFL	23
120	ERGYFQGIF	22
1	MRRELLAGI	20
77	ACFESFTKR	20
87	KKLKKAFRF	20
3	RELLAGILL	18
4	ELLAGILLR	18
84	KRKKKLKKA	18
85	RKKKLKKAF	18
91	KAFRFIQCL	18
7	AGILLRITF	17
23	LPFPLVVFF	17
83	TKRKKKLKK	17
99	LLLGLLKVR	17
9	ILLRITFNF	16
80	ESFTKRKKK	16
86	KKKLKKAFR	16
13	ITFNFFLFF	15
44	SHYVAQAGL	15
81	SFTKRKKKL	15
97	QCLLLGLLK	15
101	LGLLKVRPL	15
113	GVNSCDCER	15
121	RGYFQGIFM	15

TableXXX-V9-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
12	RITFNFFLF	14
15	FNFFLFFFL	14
19	LFFFLPFPL	14
22	FLPFPLVVF	14
28	VVFFIYFYF	14
32	IYFYFYFFL	14
37	YFFLEMESH	14
46	YVAQAGLEL	14
58	SNPPASASL	14
63	SASLVAGTL	14
92	AFRFIQCLL	14
96	IQCLLLGLL	14
5	LLAGILLRI	13
17	FFLFFFLPF	13
27	LVVFFIYFY	13
31	FIYFYFYFF	13
34	FYFYFFLEM	13
47	VAQAGLELL	13
66	LVAGTLSVH	13
76	CACFESFTK	13
79	FESFTKRKK	13
95	FIQCLLLGL	13
122	GYFQGIFMQ	13

TableXXX-V10-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GRCPAGELG	14
6	GELGTSDVV	9
9	GTSDVVTVV	8

TableXXX-V10-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	RCPAGELGT	7
3	CPAGELGTS	5
4	PAGELGTSD	5
5	AGELGTSDV	5

TableXXX-V11-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	RLRVMVPPL	16
8	VMVPPLPSL	16
2	ARLRLRVMV	15
4	LRLRVMVPP	14
6	LRVMVPPLP	13
1	QARLRLRVM	11
3	RLRLRVMVP	8

TableXXX-V12-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
6	PEGCSYSTL	13
3	SEEPEGCSY	11
8	GCSYSTLTT	6
9	CSYSTLTTV	6

TableXXX-V13-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	ADPQEDSGK	16

TableXXX-V14-HLA-B2705-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	SNPPASASL	14
8	SASLVAGTL	14
1	GSSNPPASA	6

TableXXXI-V1-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
139	ARLRLRVLV	22
250	VRGLEDQNL	21
393	TRENSIRRL	21
213	SRSMNGQPL	20
234	QRITHILHV	20
54	YRGDSGEQV	19
104	PRNPLDGSV	19
408	PRSQPEESV	18
135	GSFQARLRL	17
142	RLRVLVPPL	16
287	GPLPSGVRV	16
399	RRLHSHHTD	16

TableXXXI-V1-HLA-B2709-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
96	GRVEQPPPP	15
105	RNPLDGSVL	15
297	GDTLGFPPL	15
443	RSYSTLTTV	15
452	REIETQTEL	15
11	GPEAWLLLL	14
14	AWLLLLLLL	14
27	GRCPAGELE	14
73	GEGAQELAL	14
80	ALLHSKYGL	14
262	GREGAMLKC	14
263	REGAMLKCL	14
292	GVRVDGDTL	14
294	RVDGDTLGF	14
362	CLLVVVVVL	14
376	RRKAQQMTQ	14
419	RAEGHPDSL	14
442	GRSYSTLTT	14
32	GELETSDVV	13
34	LETSDVVTV	13
106	NPLDGSVLL	13
127	CRVSTFPAG	13
141	LRLRVLVPP	13
145	VLVPPLPSL	13
151	PSLNPGPAL	13
283	TRLDGPLPS	13
324	RDSQVTVDV	13
384	QKYEEELTL	13
466	GRAEEEEDQ	13
493	RAKPTGNGI	13
9	MWGPEAWLL	12
42	VVLGQDAKL	12
45	GQDAKLPCF	12
68	ARVDAGEGA	12
110	GSVLLRNAV	12
133	PAGSFQARL	12
143	LRVLVPPLP	12

TableXXXI-V1-HLA-B2709-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
157	PALEEGQGL	12
173	AEGSPAPSV	12
200	RSAAVTSEF	12
202	AAVTSEFHL	12
222	TCVVSHPGL	12
223	CVVSHPGLL	12
237	THILHVSFL	12
323	SRDSQVTVD	12
352	VVGVIAALL	12
357	AALLFCLLV	12
358	ALLFCLLVV	12
361	FCLLVVVVV	12
372	SRYHRRKAQ	12
501	IYINGRGHL	12
1	MPLSLGAEM	11
10	WGPEAWLLL	11
12	PEAWLLLLL	11
13	EAWLLLLLL	11
26	TGRCPAGEL	11
36	TSDVVTVVL	11
71	DAGEGAQEL	11
100	QPPPPRNPL	11
159	LEEGQGLTL	11
188	KGTTSSRSF	11
193	SRSFKHSRS	11
199	SRSAAVTSE	11
203	AVTSEFHLV	11
228	PGLLQDQRI	11
232	QDQRITHIL	11
245	LAEASVRGL	11
277	PPSYNWTRL	11
281	NWTRLDGPL	11
293	VRVDGDTLG	11
325	DSQVTVDVL	11
337	EDSGKQVDL	11
343	VDLVSASVV	11
344	DLVSASVVV	11

TableXXXI-V1-HLA-B2709-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
348	ASVVVVGVI	11
351	VVVGVIAAL	11
353	VGVIAALLF	11
356	IAALLFCLL	11
359	LLFCLLVVV	11
363	LLVVVVVLM	11
398	IRRLHSHHT	11
410	SQPEESVGL	11
418	LRAEGHPDS	11
428	KDNSSCSVM	11
446	STLTTVREI	11
477	GIKQAMNHF	11
484	HFVQENGTL	11
492	LRAKPTGNG	11
495	KPTGNGIYI	11
8	EMWGPEAWL	10
17	LLLLLASF	10
57	DSGEQVGQV	10
74	EGAQELALL	10
114	LRNAVQADE	10
129	VSTFPAGSF	10
137	FQARLRLRV	10
138	QARLRLRVL	10
208	FHLVPSRSM	10
236	ITHILHVSF	10
242	VSFLAEASV	10
260	HIGREGAML	10
320	EFSSRDSQV	10
345	LVSASVVVV	10
347	SASVVVVGV	10
355	VIAALLFCL	10
360	LFCLLVVVV	10
374	YHRRKAQQM	10
375	HRRKAQQMT	10
382	MTQKYEEEL	10
390	LTLTRENSI	10
440	PEGRSYSTL	10

TableXXXI-V1-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
451	VREIETQTE	10
453	EIETQTELL	10

TableXXXI-V2-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GQDAKLPCL	14
4	AKLPCLYRG	6

TableXXXI-V7-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
6	PRSQSEEPE	10
7	RSQSEEPEG	6

TableXXXI-V9-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score

TableXXXI-V9-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	RRELLAGIL	25
93	FRFIQCLLL	23
11	LRITFNFFL	21
1	MRRELLAGI	18
106	VRPLQHQGV	18
120	ERGYFQGIF	18
3	RELLAGILL	16
87	KKLKKAFRF	14
91	KAFRFIQCL	14
121	RGYFQGIFM	14
9	ILLRITFNF	13
12	RITFNFFLF	13
23	LPFPLVVFF	13
32	IYFYFYFFL	13
101	LGLLKVRPL	13
13	ITFNFFLFF	12
15	FNFFLFFFL	12
19	LFFFLPFPL	12
21	FFLPFPLVV	12
44	SHYVAQAGL	12
84	KRKKKLKKA	12
85	RKKKLKKAF	12
92	AFRFIQCLL	12

TableXXXI-V10-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GRCPAGELG	14
6	GELGTSDVV	13
8	LGTSDVVTV	13

TableXXXI-V10-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	GTSDVVTVV	12
5	AGELGTSDV	9

TableXXXI-V11-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
2	ARLRLRVMV	22
5	RLRVMVPPL	16
4	LRLRVMVPP	13
8	VMVPPLPSL	13
6	LRVMVPPLP	12

TableXXXI-V12-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	CSYSTLTTV	11
6	PEGCSYSTL	10

TableXXXI-V13-HLA-B2709-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
2	QVTVDVLAD	4
5	VDVLADPQE	3
6	DVLADPQED	3
1	SQVTVDVLA	2
3	VTVDVLADP	1
4	TVDVLADPQ	1
8	LADPQEDSG	1
9	ADPQEDSGK	1

TableXXXI-V14-HLA-B2709-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
3	SNPPASASL	11
8	SASLVAGTL	11
4	NPPASASLV	9

TableXXXII-V1-HLA-B4402-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
7	AEMWGPEAW	27
437	SEEPEGRSY	25
12	PEAWLLLLL	23
59	GEQVGQVAW	23
73	GEGAQELAL	23
159	LEEGQGLTL	23
263	REGAMLKCL	23
452	REIETQTEL	23

TableXXXII-V1-HLA-B4402-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
272	SEGQPPPSY	22
440	PEGRSYSTL	22
253	LEDQNLWHI	21
470	EEEDQDEGI	21
14	AWLLLLLLL	18
413	EESVGLRAE	17
13	EAWLLLLLL	16
100	QPPPPRNPL	16
351	VVVGVIAAL	16
388	EELTLTREN	16
9	MWGPEAWLL	15
106	NPLDGSVLL	15
124	EYECRVSTF	15
138	QARLRLRVL	15
237	THILHVSFL	15
246	AEASVRGLE	15
337	EDSGKQVDL	15
393	TRENSIRRL	15
453	EIETQTELL	15
487	QENGTLRAK	15
494	AKPTGNGIY	15
501	IYINGRGHL	15
36	TSDVVTVVL	14
74	EGAQELALL	14
78	ELALLHSKY	14
80	ALLHSKYGL	14
98	VEQPPPPRN	14
135	GSFQARLRL	14
145	VLVPPLPSL	14
151	PSLNPGPAL	14
160	EEGQGLTLA	14
173	AEGSPAPSV	14
202	AAVTSEFHL	14
206	SEFHLVPSR	14
232	QDQRITHIL	14
274	GQPPPSYNW	14
294	RVDGDTLGF	14

TableXXXII-V1-HLA-B4402-9mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.		
Pos	123456789	score
307	TEHSGIYVC	14
319	NEFSSRDSQ	14
362	CLLVVVVVL	14
387	EEELTLTRE	14
394	RENSIRRLH	14
420	AEGHPDSLK	14
438	EEPEGRSYS	14
2	PLSLGAEMW	13
8	EMWGPEAWL	13
10	WGPEAWLLL	13
11	GPEAWLLLL	13
17	LLLLLLASF	13
34	LETSDVVTV	13
42	VVLGQDAKL	13
77	QELALLHSK	13
86	YGLHVSPAY	13
105	RNPLDGSVL	13
117	AVQADEGEY	13
175	GSPAPSVTW	13
188	KGTTSSRSF	13
213	SRSMNGQPL	13
231	LQDQRITHI	13
251	RGLEDQNLW	13
348	ASVVVVGVI	13
352	VVGVIAALL	13
353	VGVIAALLF	13
356	IAALLFCLL	13
378	KAQQMTQKY	13
386	YEEELTLTR	13
410	SQPEESVGL	13
446	STLTTVREI	13
458	TELLSPGSG	13
468	AEEEEDQDE	13
471	EEDQDEGIK	13

TableXXXII-V2-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	GQDAKLPCL	12
2	QDAKLPCLY	12
4	AKLPCLYRG	8

TableXXXII-V7-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	HTDPRSQSE	5
1	SHHTDPRSQ	4
2	HHTDPRSQS	3
8	SQSEEPEGR	3
4	TDPRSQSEE	2

TableXXXII-V9-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	RELLAGILL	24
7	AGILLRITF	20
119	CERGYFQGI	20
23	LPFPLVVFF	17
91	KAFRFIQCL	17
13	ITFNFFLFF	15
58	SNPPASASL	15
63	SASLVAGTL	15
81	SFTKRKKKL	15
92	AFRFIQCLL	15

TableXXXII-V9-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	ILLRITFNF	14
11	LRITFNFFL	14
22	FLPFPLVVF	14
85	RKKKLKKAF	14
93	FRFIQCLLL	14
101	LGLLKVRPL	14
12	RITFNFFLF	13
15	FNFFLFFFL	13
17	FFLFFFLPF	13
19	LFFFLPFPL	13
27	LVVFFIYFY	13
28	VVFFIYFYF	13
29	VFFIYFYFY	13
30	FFIYFYFYF	13
42	MESHYVAQA	13
79	FESFTKRKK	13
87	KKLKKAFRF	13
96	IQCLLLGLL	13
115	NSCDCERGY	13
116	SCDCERGYF	13
126	GIFMQAAPW	13
2	RRELLAGIL	12
5	LLAGILLRI	12
10	LLRITFNFF	12
25	FPLVVFFIY	12
26	PLVVFFIYF	12
32	IYFYFYFFL	12
40	LEMESHYVA	12
47	VAQAGLELL	12
52	LELLGSSNP	12
95	FIQCLLLGL	12
120	ERGYFQGIF	12
14	TFNFFLFFF	11
24	PFPLVVFFI	11
31	FIYFYFYFF	11
38	FFLEMESHY	11
44	SHYVAQAGL	11

TableXXXII-V9-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
46	YVAQAGLEL	11
74	HHCACFESF	11
88	KLKKAFRFI	11

TableXXXII-V10-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
6	GELGTSDVV	13

TableXXXII-V11-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	VMVPPLPSL	14
5	RLRVMVPPL	11
2	ARLRLRVMV	7
9	MVPPLPSLN	6

TableXXXII-V12-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	SEEPEGCSY	24
6	PEGCSYSTL	21
4	EEPEGCSYS	13

TableXXXII-V13-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	SQVTVDVLA	4
2	QVTVDVLAD	4
8	LADPQEDSG	4
9	ADPQEDSGK	4
3	VTVDVLADP	2
4	TVDVLADPQ	2
5	VDVLADPQE	2
6	DVLADPQED	2
7	VLADPQEDS	1

TableXXXII-V14-HLA-B4402-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	SNPPASASL	15
8	SASLVAGTL	15
2	SSNPPASAS	7

TableXXXIIII-V1-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
71	DAGEGAQEL	23
245	LAEASVRGL	23
287	GPLPSGVRV	23
347	SASVVVVGV	23
493	RAKPTGNGI	22
495	KPTGNGIYI	22
106	NPLDGSVLL	21
138	QARLRLRVL	21
357	AALLFCLLV	21
157	PALEEGQGL	20
11	GPEAWLLLL	19
13	EAWLLLLLL	19
202	AAVTSEFHL	19
228	PGLLQDQRI	19
356	IAALLFCLL	19
361	FCLLVVVVV	19
100	QPPPPRNPL	18
217	NGQPLTCVV	18
277	PPSYNWTRL	18
334	DPQEDSGKQ	18
345	LVSASVVVV	18
419	RAEGHPDSL	18
35	ETSDVVTVV	17
92	PAYEGRVEQ	17
133	PAGSFQARL	17
348	ASVVVVGVI	17
443	RSYSTLTTV	17
446	STLTTVREI	17
10	WGPEAWLLL	16
32	GELETSDVV	16
57	DSGEQVGQV	16
62	VGQVAWARV	16
121	DEGEYECRV	16
219	QPLTCVVSH	16
289	LPSGVRVDG	16
325	DSQVTVDVL	16
343	VDLVSASVV	16
344	DLVSASVVV	16
359	LLFCLLVVV	16

TableXXXIIII-V1-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
360	LFCLLVVVV	16
362	CLLVVVVVL	16
390	LTLTRENSI	16
34	LETSDVVTV	15
65	VAWARVDAG	15
79	LALLHSKYG	15
148	PPLPSLNPG	15
231	LQDQRITHI	15
276	PPPSYNWTR	15
338	DSGKQVDLV	15
358	ALLFCLLVV	15
384	QKYEEELTL	15
407	DPRSQPEES	15
411	QPEESVGLR	15
22	LASFTGRCP	14
26	TGRCPAGEL	14
29	CPAGELETS	14
31	AGELETSDV	14
47	DAKLPCFYR	14
75	GAQELALLH	14
82	LHSKYGLHV	14
91	SPAYEGRVE	14
132	FPAGSFQAR	14
172	TAEGSPAPS	14
176	SPAPSVTWD	14
253	LEDQNLWHI	14
286	DGPLPSGVR	14
302	FPPLTTEHS	14
303	PPLTTEHSG	14
1	MPLSLGAEM	13
30	PAGELETSD	13
36	TSDVVTVVL	13
50	LPCFYRGDS	13
74	EGAQELALL	13
90	VSPAYEGRV	13
102	PPPRNPLDG	13
147	VPPLPSLNP	13

TableXXXIIII-V1-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
150	LPSLNPGPA	13
177	PAPSVTWDT	13
178	APSVTWDTE	13
211	VPSRSMNGQ	13
275	QPPPSYNWT	13
300	LGFPPLTTE	13
322	SSRDSQVTV	13
378	KAQQMTQKY	13
478	IKQAMNHFV	13
42	VVLGQDAKL	12
54	YRGDSGEQV	12
86	YGLHVSPAY	12
101	PPPPRNPLD	12
109	DGSVLLRNA	12
119	QADEGEYEC	12
154	NPGPALEEG	12
159	LEEGQGLTL	12
167	LAASCTAEG	12
168	AASCTAEGS	12
234	QRITHILHV	12
265	GAMLKCLSE	12
309	HSGIYVCHV	12
339	SGKQVDLVS	12
467	RAEEEEDQD	12
480	QAMNHFVQE	12
5	LGAEMWGPE	11
58	SGEQVGQVA	11
67	WARVDAGEG	11
103	PPRNPLDGS	11
116	NAVQADEGE	11
137	FQARLRLRV	11
139	ARLRLRVLV	11
201	SAAVTSEFH	11
216	MNGQPLTCV	11
247	EASVRGLED	11
251	RGLEDQNLW	11
261	IGREGAMLK	11

TableXXXIIII-V1-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
285	LDGPLPSGV	11
296	DGDTLGFPP	11
304	PLTTEHSGI	11
306	TTEHSGIYV	11
310	SGIYVCHVS	11
324	RDSQVTVDV	11
335	PQEDSGKQV	11
351	VVVGVIAAL	11
393	TRENSIRRL	11
427	LKDNSSCSV	11
439	EPEGRSYST	11
470	EEEDQDEGI	11
502	YINGRGHLV	11

TableXXXIIII-V2-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
3	DAKLPCLYR	15
6	LPCLYRGDS	13
1	GQDAKLPCL	9

TableXXXIIII-V7-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score

TableXXXIIII-V7-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
5	DPRSQSEEP	14

TableXXXIIII-V9-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
59	NPPASASLV	23
63	SASLVAGTL	21
101	LGLLKVRPL	20
47	VAQAGLELL	19
91	KAFRFIQCL	18
5	LLAGILLRI	16
21	FFLPFPLVV	16
23	LPFPLVVFF	16
25	FPLVVFFIY	16
24	PFPLVVFFI	15
107	RPLQHQGVN	15
1	MRRELLAGI	14
6	LAGILLRIT	14
60	PPASASLVA	14
61	PASASLVAG	14
67	VAGTLSVHH	14
98	CLLLGLLKV	14
88	KLKKAFRFI	13
119	CERGYFQGI	13
49	QAGLELLGS	12
76	CACFESFTK	12
20	FFFLPFPLV	11
50	AGLELLGSS	11
121	RGYFQGIFM	11

TableXXXIII-V10-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	LGTSDVVTV	21
9	GTSDVVTVV	17
6	GELGTSDVV	15
3	CPAGELGTS	14
5	AGELGTSDV	14
4	PAGELGTSD	13

TableXXXIII-V11-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
1	QARLRLRVM	15
2	ARLRLRVMV	11
5	RLRVMVPPL	9
8	VMVPPLPSL	8
4	LRLRVMVPP	7

TableXXXIII-V12-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
9	CSYSTLTTV	17
5	EPEGCSYST	11
6	PEGCSYSTL	9
7	EGCSYSTLT	8

TableXXXIII-V13-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
8	LADPQEDSG	12
6	DVLADPQED	8
3	VTVDVLADP	5

TableXXXIII-V14-HLA-B5101-9mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 9 amino acids, and the end position for each peptide is the start position plus eight.

Pos	123456789	score
4	NPPASASLV	23
8	SASLVAGTL	21
5	PPASASLVA	14
6	PASASLVAG	14

TableXXXIV-V1-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
271	LSEGQPPPSY	30
436	MSEEPEGRSY	30
45	GQDAKLPCFY	25
405	HTDPRSQPEE	20
493	RAKPTGNGIY	20
158	ALEEGQGLTL	19
11	GPEAWLLLLL	18
72	AGEGAQELAL	18
107	PLDGSVLLRN	18
453	EIETQTELLS	18

TableXXXIV-V1-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
36	TSDVVTVVLG	17
77	QELALLHSKY	17
306	TTEHSGIYVC	17
377	RKAQQMTQKY	17
411	QPEESVGLRA	17
437	SEEPEGRSYS	17
471	EEDQDEGIKQ	17
184	DTEVKGTTSS	16
304	PLTTEHSGIY	16
332	VLDPQEDSGK	16
365	VVVVVLMSRY	16
385	KYEEELTLTR	16
457	QTELLSPGSG	16
85	KYGLHVSPAY	15
116	NAVQADEGEY	15
205	TSEFHLVPSR	15

TableXXXIV-V2-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
2	GQDAKLPCLY	27

TableXXXIV-V7-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
4	HTDPRSQSEE	20

TableXXXIV-V9-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
28	VVFFIYFYFY	19
24	PFPLVVFFIY	18
2	RRELLAGILL	17
37	YFFLEMESHY	17
26	PLVVFFIYFY	16
114	VNSCDCERGY	16
82	FTKRKKKLKK	15
39	FLEMESHYVA	13
116	SCDCERGYFQ	13
118	DCERGYFQGI	13
78	CFESFTKRKK	12
33	YFYFYFFLEM	11
41	EMESHYVAQA	11
51	GLELLGSSNP	11
64	ASLVAGTLSV	11
57	SSNPPASASL	10
12	RITFNFFLFF	9
16	NFFLFFFLPF	9
47	VAQAGLELLG	9
92	AFRFIQCLLL	9
93	FRFIQCLLLG	9
96	IQCLLLGLLK	

TableXXXIV-V10-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
6	AGELGTSDVV	12
2	GRCPAGELGT	10
10	GTSDVVTVVL	7

TableXXXIV-V11-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
10	MVPPLPSLNP	10
9	VMVPPLPSLN	7
7	LRVMVPPLPS	6

TableXXXIV-V12-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
3	MSEEPEGCSY	30
4	SEEPEGCSYS	16

TableXXXIV-V13-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
9	LADPQEDSGK	14
5	TVDVLADPQE	10
2	SQVTVDVLAD	9
4	VTVDVLADPQ	7
1	DSQVTVDVLA	6

TableXXXIV-V14-HLA-A1-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
10	ASLVAGTLSV	11
3	SSNPPASASL	10
4	SNPPASASLV	8
5	NPPASASLVA	7
8	ASASLVAGTL	5

TableXXXV-V1-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
244	FLAEASVRGL	30
358	ALLFCLLVVV	29
359	LLFCLLVVVV	29
215	SMNGQPLTCV	27
158	ALEEGQGLTL	26
230	LLQDQRITHI	25
344	DLVSASVVVV	25
33	ELETSDVVTV	24
239	ILHVSFLAEA	24
426	SLKDNSSCSV	24
81	LLHSKYGLHV	23
144	RVLVPPLPSL	23
252	GLEDQNLWHI	23
284	RLDGPLPSGV	23
357	AALLFCLLVV	23
16	LLLLLLLASF	22
350	VVVVGVIAAL	22
362	CLLVVVVVLM	22
392	LTRENSIRRL	22
354	GVIAALLFCL	21
355	VIAALLFCLL	21
79	LALLHSKYGL	20
236	ITHILHVSFL	20
346	VSASVVVVGV	20
500	GIYINGRGHL	20
141	LRLRVLVPPL	19
351	VVVGVIAALL	19
356	IAALLFCLLV	19
361	FCLLVVVVVL	19
381	QMTQKYEEEL	19
477	GIKQAMNHFV	19
8	EMWGPEAWLL	18
15	WLLLLLLLAS	18

TableXXXV-V1-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
17	LLLLLLASFT	18
41	TVVLGQDAKL	18
112	VLLRNAVQAD	18
152	SLNPGPALEE	18
172	TAEGSPAPSV	18
201	SAAVTSEFHL	18
221	LTCVVSHPGL	18
249	SVRGLEDQNL	18
347	SASVVVVGVI	18
360	LFCLLVVVVV	18
418	LRAEGHPDSL	18
10	WGPEAWLLLL	17
13	EAWLLLLLLL	17
25	FTGRCPAGEL	17
56	GDSGEQVGQV	17
70	VDAGEGAQEL	17
73	GEGAQELALL	17
132	FPAGSFQARL	17
137	FQARLRLRVL	17
202	AAVTSEFHLV	17
241	HVSFLAEASV	17
305	LTTEHSGIYV	17
363	LLVVVVVLMS	17
389	ELTLTRENSI	17
18	LLLLLASFTG	16
61	QVGQVAWARV	16
89	HVSPAYEGRV	16
138	QARLRLRVLV	16
140	RLRLRVLVPP	16
164	GLTLAASCTA	16
166	TLAASCTAEG	16
257	NLWHIGREGA	16
259	WHIGREGAML	16
341	KQVDLVSASV	16
370	LMSRYHRRKA	16
442	GRSYSTLTTV	16
7	AEMWGPEAWL	15
11	GPEAWLLLLL	15

TableXXXV-V1-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
19	LLLLASFTGR	15
34	LETSDVVTVV	15
72	AGEGAQELAL	15
181	VTWDTEVKGT	15
229	GLLQDQRITH	15
262	GREGAMLKCL	15
299	TLGFPPLTTE	15
321	FSSRDSQVTV	15
343	VDLVSASVVV	15
349	SVVVVGVIAA	15
397	SIRRLHSHHT	15
409	RSQPEESVGL	15
445	YSTLTTVREI	15
447	TLTTVREIET	15
460	LLSPGSGRAE	15
501	IYINGRGHLV	15
12	PEAWLLLLLL	14
20	LLLASFTGRC	14
21	LLASFTGRCP	14
35	ETSDVVTVVL	14
80	ALLHSKYGLH	14
87	GLHVSPAYEG	14
107	PLDGSVLLRN	14
111	SVLLRNAVQA	14
113	LLRNAVQADE	14
150	LPSLNPGPAL	14
156	GPALEEGQGL	14
178	APSVTWDTEV	14
195	SFKHSRSAAV	14
233	DQRITHILHV	14
291	SGVRVDGDTL	14
298	DTLGFPPLTT	14
311	GIYVCHVSNE	14
323	SRDSQVTVDV	14
324	RDSQVTVDVL	14
332	VLDPQEDSGK	14
342	QVDLVSASVV	14
452	REIETQTELL	14

TableXXXV-V1-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
492	LRAKPTGNGI	14

TableXXXV-V2-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
1	LGQDAKLPCL	18
10	LYRGDSGEQV	14
9	CLYRGDSGEQ	13
6	KLPCLYRGDS	11

TableXXXV-V7-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
4	HTDPRSQSEE	8
9	SQSEEPEGRS	4

TableXXXV-V9-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
100	LLGLLKVRPL	26
5	LLAGILLRIT	24

TableXXXV-V9-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
95	FIQCLLLGLL	23
4	ELLAGILLRI	22
10	LLRITFNFFL	22
46	YVAQAGLELL	22
18	FLFFFLPFPL	21
31	FIYFYFYFFL	19
57	SSNPPASASL	19
97	QCLLLGLLKV	19
94	RFIQCLLLGL	18
99	LLLGLLKVRP	18
105	KVRPLQHQGV	18
23	LPFPLVVFFI	17
64	ASLVAGTLSV	17
22	FLPFPLVVFF	16
38	FFLEMESHYV	16
53	ELLGSSNPPA	16
62	ASASLVAGTL	16
65	SLVAGTLSVH	16
90	KKAFRFIQCL	16
91	KAFRFIQCLL	16
9	ILLRITFNFF	15
39	FLEMESHYVA	15
98	CLLLGLLKVR	15
103	LLKVRPLQHQ	15
41	EMESHYVAQA	14
54	LLGSSNPPAS	14
58	SNPPASASLV	14
102	GLLKVRPLQH	14
108	PLQHQGVNSC	14
128	FMQAAPWEGT	14
19	LFFFLPFPLV	13
20	FFFLPFPLVV	13
45	HYVAQAGLEL	13
1	MRRELLAGIL	12
26	PLVVFFIYFY	12
48	AQAGLELLGS	12
61	PASASLVAGT	12
66	LVAGTLSVHH	12

TableXXXV-V9-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
70	TLSVHHCACF	12
92	AFRFIQCLLL	12

TableXXXV-V10-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
8	ELGTSDVVTV	25
10	GTSDVVTVVL	18
9	LGTSDVVTVV	15
5	PAGELGTSDV	13

TableXXXV-V11-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
8	RVMVPPLPSL	22
5	LRLRVMVPPL	19
2	QARLRLRVMV	16
4	RLRLRVMVPP	12
1	FQARLRLRVM	11
6	RLRVMVPPLP	11
9	VMVPPLPSLN	11

TableXXXV-V12-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
9	GCSYSTLTTV	16
2	VMSEEPEGCS	11
6	EPEGCSYSTL	10
1	SVMSEEPEGC	8

TableXXXV-V13-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
8	VLADPQEDSG	16
3	QVTVDVLADP	9
9	LADPQEDSGK	9
2	SQVTVDVLAD	8

TableXXXV-V14-HLA-A0201-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
3	SSNPPASASL	19
10	ASLVAGTLSV	17
8	ASASLVAGTL	16
4	SNPPASASLV	14
7	PASASLVAGT	12
1	LGSSNPPASA	10

TableXXXVI-V1-HLA-A0203-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
160	EEGQGLTLAA	19
194	RSFKHSRSAA	19
349	SVVVVGVIAA	19
59	GEQVGQVAWA	18
239	ILHVSFLAEA	18
161	EGQGLTLAAS	17
195	SFKHSRSAAV	17
350	VVVVGVIAAL	17
5	LGAEMWGPEA	10
14	AWLLLLLLLA	10
22	LASFTGRCPA	10
39	VVTVVLGQDA	10
57	DSGEQVGQVA	10
63	GQVAWARVDA	10
67	WARVDAGEGA	10
71	DAGEGAQELA	10
84	SKYGLHVSPA	10
108	LDGSVLLRNA	10
111	SVLLRNAVQA	10
125	YECRVSTFPA	10
130	STFPAGSFQA	10
149	PLPSLNPGPA	10
159	LEEGQGLTLA	10
164	GLTLAASCTA	10
169	ASCTAEGSPA	10
193	SRSFKHSRSA	10
237	THILHVSFLA	10
257	NLWHIGREGA	10
339	SGKQVDLVSA	10
348	ASVVVVGVIA	10
370	LMSRYHRRKA	10
411	QPEESVGLRA	10
459	ELLSPGSGRA	10
472	EDQDEGIKQA	10
485	FVQENGTLRA	10
6	GAEMWGPEAW	9
15	WLLLLLLLAS	9
23	ASFTGRCPAG	9
40	VTVVLGQDAK	9
58	SGEQVGQVAW	9
60	EQVGQVAWAR	9
64	QVAWARVDAG	9
68	ARVDAGEGAQ	9
72	AGEGAQELAL	9
85	KYGLHVSPAY	9

TableXXXVI-V1-HLA-A0203-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
109	DGSVLLRNAV	9
112	VLLRNAVQAD	9
126	ECRVSTFPAG	9
131	TFPAGSFQAR	9
150	LPSLNPGPAL	9
165	LTLAASCTAE	9
170	SCTAEGSPAP	9
238	HILHVSFLAE	9
240	LHVSFLAEAS	9
258	LWHIGREGAM	9
340	GKQVDLVSAS	9
371	MSRYHRRKAQ	9
412	PEESVGLRAE	9
460	LLSPGSGRAE	9
473	DQDEGIKQAM	9
486	VQENGTLRAK	9

TableXXXVI-V2-HLA-A0203-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
160	EEGQGLTLAA	19

TableXXXVI-V7-HLA-A0203-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXXXVI-V9-HLA-A0203-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
123	YFQGIFMQAA	19
41	EMESHYVAQA	18
55	LGSSNPPASA	18
124	FQGIFMQAAP	17
39	FLEMESHYVA	10
53	ELLGSSNPPA	10
59	NPPASASLVA	10
68	AGTLSVHHCA	10
83	TKRKKKLKKA	10
122	GYFQGIFMQA	10
40	LEMESHYVAQ	9
42	MESHYVAQAG	9
54	LLGSSNPPAS	9
56	GSSNPPASAS	9
60	PPASASLVAG	9
69	GTLSVHHCAC	9
84	KRKKKLKKAF	9

TableXXXVI-V10-HLA-A0203-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXXXVI-V11-HLA-A0203-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXXXVI-V12-HLA-A0203-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXXXVI-V13-HLA-A0203-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10

amino acids, and the end position for each peptide is the start position plus nine.		
Pos	1234567890	score
1	DSQVTVDVLA	10
2	SQVTVDVLAD	9
3	QVTVDVLADP	8

TableXXXVI-V14-HLA-A0203-10mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	1234567890	score
1	LGSSNPPASA	18
5	NPPASASLVA	10
2	GSSNPPASAS	9
6	PPASASLVAG	9
3	SSNPPASASL	8
7	PASASLVAGT	8

TableXXXVII-V1-HLA-A03-10mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	1234567890	score
332	VLDPQEDSGK	26
69	RVDAGEGAQE	25
260	HIGREGAMLK	25
111	SVLLRNAVQA	24
128	RVSTFPAGSF	24
158	ALEEGQGLTL	24
342	QVDLVSASVV	23
358	ALLFCLLVVV	23
16	LLLLLLLASF	22
140	RLRLRVLVPP	22
235	RITHILHVSF	22
229	GLLQDQRITH	21
376	RRKAQQMTQK	21
80	ALLHSKYGLH	20

TableXXXVII-V1-HLA-A03-10mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	1234567890	score
152	SLNPGPALEE	20
203	AVTSEFHLVP	20
284	RLDGPLPSGV	20
345	LVSASVVVVG	20
352	VVGVIAALLF	20
369	VLMSRYHRRK	20
17	LLLLLLASFT	19
365	VVVVVLMSRY	19
419	RAEGHPDSLK	19
19	LLLLASFTGR	18
33	ELETSDVVTV	18
117	AVQADEGEYE	18
142	RLRVLVPPLP	18
144	RVLVPPLPSL	18
344	DLVSASVVVV	18
351	VVVGVIAALL	18
359	LLFCLLVVVV	18
400	RLHSHHTDPR	18
450	TVREIETQTE	18
15	WLLLLLLLAS	17
18	LLLLLASFTG	17
42	VVLGQDAKLP	17
113	LLRNAVQADE	17
145	VLVPPLPSLN	17
188	KGTTSSRSFK	17
197	KHSRSAAVTS	17
294	RVDGDTLGFP	17
304	PLTTEHSGIY	17
364	LVVVVVLMSR	17
391	TLTRENSIRR	17
443	RSYSTLTTVR	17
460	LLSPGSGRAE	17
76	AQELALLHSK	16
81	LLHSKYGLHV	16
112	VLLRNAVQAD	16
123	GEYECRVSTF	16
146	LVPPLPSLNP	16
166	TLAASCTAEG	16

TableXXXVII-V1-HLA-A03-10mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	1234567890	score
186	EVKGTTSSRS	16
223	CVVSHPGLLQ	16
224	VVSHPGLLQD	16
249	SVRGLEDQNL	16
362	CLLVVVVVLM	16
367	VVVLMSRYHR	16
368	VVLMSRYHRR	16
434	SVMSEEPEGR	16
491	TLRAKPTGNG	16
20	LLLASFTGRC	15
49	KLPCFYRGDS	15
61	QVGQVAWARV	15
77	QELALLHSKY	15
97	RVEQPPPPRN	15
107	PLDGSVLLRN	15
139	ARLRLRVLVP	15
164	GLTLAASCTA	15
180	SVTWDTEVKG	15
239	ILHVSFLAEA	15
241	HVSFLAEASV	15
242	VSFLAEASVR	15
251	RGLEDQNLWH	15
267	MLKCLSEGQP	15
288	PLPSGVRVDG	15
299	TLGFPPLTTE	15
311	GIYVCHVSNE	15
331	DVLDPQEDSG	15
354	GVIAALLFCL	15
385	KYEEELTLTR	15
397	SIRRLHSHHT	15
417	GLRAEGHPDS	15
426	SLKDNSSCSV	15
493	RAKPTGNGIY	15
500	GIYINGRGHL	15
4	SLGAEMWGPE	14
21	LLASFTGRCP	14
38	DVVTVVLGQD	14
41	TVVLGQDAKL	14

TableXXXVII-V1-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
64	QVAWARVDAG	14
89	HVSPAYEGRV	14
179	PSVTWDTEVK	14
209	HLVPSRSMNG	14
238	HILHVSFLAE	14
292	GVRVDGDTLG	14
316	HVSNEFSSRD	14
350	VVVVGVIAAL	14
363	LLVVVVVLMS	14
366	VVVVLMSRYH	14
485	FVQENGTLRA	14
2	PLSLGAEMWG	13
39	VVTVVLGQDA	13
43	VLGQDAKLPC	13
87	GLHVSPAYEG	13
104	PRNPLDGSVL	13
214	RSMNGQPLTC	13
275	QPPPSYNWTR	13
357	AALLFCLLVV	13
373	RYHRRKAQQM	13
389	ELTLTRENSI	13
396	NSIRRLHSHH	13
415	SVGLRAEGHP	13
458	TELLSPGSGR	13
459	ELLSPGSGRA	13
78	ELALLHSKYG	12
149	PLPSLNPGPA	12
230	LLQDQRITHI	12
244	FLAEASVRGL	12
259	WHIGREGAML	12
270	CLSEGQPPPS	12
285	LDGPLPSGVR	12
298	DTLGFPPLTT	12
327	QVTVDVLDPQ	12
349	SVVVVGVIAA	12
436	MSEEPEGRSY	12
470	EEEDQDEGIK	12
486	VQENGTLRAK	12

TableXXXVII-V2-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
9	CLYRGDSGEQ	18
6	KLPCLYRGDS	15
10	LYRGDSGEQV	11
3	QDAKLPCLYR	10
2	GQDAKLPCLY	9
5	AKLPCLYRGD	8

TableXXXVII-V7-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
8	RSQSEEPEGR	9
2	SHHTDPRSQS	8
4	HTDPRSQSEE	6

TableXXXVII-V9-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
65	SLVAGTLSVH	24
102	GLLKVRPLQH	23
9	ILLRITFNFF	21
66	LVAGTLSVHH	21
98	CLLLGLLKVR	21
12	RITFNFFLFF	19
96	IQCLLLGLLK	19
105	KVRPLQHQGV	19
22	FLPFPLVVFF	18
99	LLLGLLKVRP	18

TableXXXVII-V9-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
4	ELLAGILLRI	17
21	FFLPFPLVVF	17
70	TLSVHHCACF	17
82	FTKRKKKLKK	17
26	PLVVFFIYFY	16
28	VVFFIYFYFY	16
8	GILLRITFNF	15
75	HCACFESFTK	15
88	KLKKAFRFIQ	15
3	RELLAGILLR	14
10	LLRITFNFFL	14
27	LVVFFIYFYF	14
39	FLEMESHYVA	14
50	AGLELLGSSN	14
51	GLELLGSSNP	14
53	ELLGSSNPPA	14
77	ACFESFTKRK	14
5	LLAGILLRIT	13
107	RPLQHQGVNS	13
31	FIYFYFYFFL	12
54	LLGSSNPPAS	12
62	ASASLVAGTL	12
85	RKKKLKKAFR	12
86	KKKLKKAFRF	12
108	PLQHQGVNSC	12
126	GIFMQAAPWE	12
18	FLFFFLPFPL	11
46	YVAQAGLELL	11
72	SVHHCACFES	11
79	FESFTKRKKK	11
81	SFTKRKKKLK	11
100	LLGLLKVRPL	11
103	LLKVRPLQHQ	11
125	QGIFMQAAPW	11

TableXXXVII-V10-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
8	ELGTSDVVTV	18
7	GELGTSDVVT	12
3	RCPAGELGTS	11
4	CPAGELGTSD	9
10	GTSDVVTVVL	9
6	AGELGTSDVV	8

TableXXXVII-V11-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
4	RLRLRVMVPP	22
6	RLRVMVPPLP	18
8	RVMVPPLPSL	16
10	MVPPLPSLNP	16
3	ARLRLRVMVP	13
2	QARLRLRVMV	12

TableXXXVII-V12-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
10	CSYSTLTTVR	13
1	SVMSEEPEGC	12
3	MSEEPEGCSY	12
6	EPEGCSYSTL	9
4	SEEPEGCSYS	7
8	EGCSYSTLTT	7

TableXXXVII-V13-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
9	LADPQEDSGK	16
3	QVTVDVLADP	15
7	DVLADPQEDS	14
8	VLADPQEDSG	14
5	TVDVLADPQE	13

TableXXXVII-V14-HLA-A03-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
8	ASASLVAGTL	12
4	SNPPASASLV	10
10	ASLVAGTLSV	10
3	SSNPPASASL	9
5	NPPASASLVA	9
2	GSSNPPASAS	8
1	LGSSNPPASA	6
6	PPASASLVAG	6
9	SASLVAGTLS	6
7	PASASLVAGT	5

TableXXXVIII-V1-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
38	DVVTVVLGQD	28
35	ETSDVVTVVL	27
350	VVVVGVIAAL	27
354	GVIAALLFCL	26
365	VVVVVLMSRY	25
41	TVVLGQDAKL	24
13	EAWLLLLLLL	23

TableXXXVIII-V1-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
144	RVLVPPLPSL	23
455	ETQTELLSPG	23
351	VVVGVIAALL	22
392	LTRENSIRRL	22
476	EGIKQAMNHF	22
186	EVKGTTSSRS	21
236	ITHILHVSFL	21
349	SVVVVGVIAA	21
128	RVSTFPAGSF	20
331	DVLDPQEDSG	20
439	EPEGRSYSTL	20
99	EQPPPPRNPL	19
249	SVRGLEDQNL	19
352	VVGVIAALLF	19
364	LVVVVVLMSR	19
8	EMWGPEAWLL	18
298	DTLGFPPLTT	18
25	FTGRCPAGEL	17
184	DTEVKGTTSS	17
223	CVVSHPGLLQ	17
344	DLVSASVVVV	17
123	GEYECRVSTF	16
221	LTCVVSHPGL	16
224	VVSHPGLLQD	16
296	DGDTLGFPPL	16
472	EDQDEGIKQA	16
10	WGPEAWLLLL	15
33	ELETSDVVTV	15
60	EQVGQVAWAR	15
64	QVAWARVDAG	15
116	NAVQADEGEY	15
130	STFPAGSFQA	15
161	EGQGLTLAAS	15
291	SGVRVDGDTL	15
294	RVDGDTLGFP	15
327	QVTVDVLDPQ	15
395	ENSIRRLHSH	15
421	EGHPDSLKDN	15

TableXXXVIII-V1-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
453	EIETQTELLS	15
204	VTSEFHLVPS	14
222	TCVVSHPGLL	14
235	RITHILHVSF	14
244	FLAEASVRGL	14
247	EASVRGLEDQ	14
259	WHIGREGAML	14
293	VRVDGDTLGF	14
308	EHSGIYVCHV	14
328	VTVDVLDPQE	14
337	EDSGKQVDLV	14
345	LVSASVVVVG	14
366	VVVVLMSRYH	14
367	VVVLMSRYHR	14
414	ESVGLRAEGH	14
429	DNSSCSVMSE	14
436	MSEEPEGRSY	14
448	LTTVREIETQ	14
449	TTVREIETQT	14
450	TVREIETQTE	14
452	REIETQTELL	14
483	NHFVQENGTL	14
11	GPEAWLLLLL	13
12	PEAWLLLLLL	13
16	LLLLLLLASF	13
40	VTVVLGQDAK	13
44	LGQDAKLPCF	13
158	ALEEGQGLTL	13
180	SVTWDTEVKG	13
181	VTWDTEVKGT	13
203	AVTSEFHLVP	13
233	DQRITHILHV	13
255	DQNLWHIGRE	13
305	LTTEHSGIYV	13
306	TTEHSGIYVC	13
438	EEPEGRSYST	13
441	EGRSYSTLTT	13
471	EEDQDEGIKQ	13

TableXXXVIII-V1-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
485	FVQENGTLRA	13
500	GIYINGRGHL	13

TableXXXVIII-V2-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
1	LGQDAKLPCL	13
4	DAKLPCLYRG	12
2	GQDAKLPCLY	10

TableXXXVIII-V7-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
4	HTDPRSQSEE	10
6	DPRSQSEEPE	9
9	SQSEEPEGRS	4

TableXXXVIII-V9-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
13	ITFNFFLFFF	24
28	VVFFIYFYFY	24
80	ESFTKRKKKL	23

TableXXXVIII-V9-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
27	LVVFFIYFYF	22
46	YVAQAGLELL	22
26	PLVVFFIYFY	18
43	ESHYVAQAGL	18
94	RFIQCLLLGL	17
95	FIQCLLLGLL	17
41	EMESHYVAQA	16
4	ELLAGILLRI	15
37	YFFLEMESHY	15
12	RITFNFFLFF	14
45	HYVAQAGLEL	14
16	NFFLFFFLPF	13
21	FFLPFPLVVF	13
8	GILLRITFNF	12
11	LRITFNFFLF	12
18	FLFFFLPFPL	12
22	FLPFPLVVFF	12
29	VFFIYFYFYF	12
30	FFIYFYFYFF	12
31	FIYFYFYFFL	12
90	KKAFRFIQCL	12
91	KAFRFIQCLL	12
100	LLGLLKVRPL	12
120	ERGYFQGIFM	12
1	MRRELLAGIL	11
57	SSNPPASASL	11
62	ASASLVAGTL	11
72	SVHHCACFES	11
105	KVRPLQHQGV	11
113	GVNSCDCERG	11

TableXXXVIII-V10-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
10	GTSDVVTVVL	17
8	ELGTSDVVTV	15

TableXXXVIII-V11-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
8	RVMVPPLPSL	23
5	LRLRVMVPPL	12
10	MVPPLPSLNP	12

TableXXXVIII-V12-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
6	EPEGCSYSTL	20
3	MSEEPEGCSY	14
5	EEPEGCSYST	13
8	EGCSYSTLTT	13
1	SVMSEEPEGC	12

TableXXXVIII-V13-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
7	DVLADPQEDS	18
3	QVTVDVLADP	15
4	VTVDVLADPQ	13
5	TVDVLADPQE	12
2	SQVTVDVLAD	11
1	DSQVTVDVLA	8

TableXXXVIII-V14-HLA-A26-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
3	SSNPPASASL	11
8	ASASLVAGTL	11
6	PPASASLVAG	6

TableXXXIX-V1-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
132	FPAGSFQARL	24
150	LPSLNPGPAL	24
11	GPEAWLLLLL	23
439	EPEGRSYSTL	23
156	GPALEEGQGL	21
178	APSVTWDTEV	21
276	PPPSYNWTRL	21
176	SPAPSVTWDT	19
103	PPRNPLDGSV	18
407	DPRSQPEESV	18
411	QPEESVGLRA	18
35	ETSDVVTVVL	17
72	AGEGAQELAL	17
134	AGSFQARLRL	17
227	HPGLLQDQRI	17
303	PPLTTEHSGI	16
334	DPQEDSGKQV	16
289	LPSGVRVDGD	15
324	RDSQVTVDVL	15

TableXXXIX-V1-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
7	AEMWGPEAWL	14
9	MWGPEAWLLL	14
29	CPAGELETSD	14
91	SPAYEGRVEQ	14
99	EQPPPPRNPL	14
158	ALEEGQGLTL	14
249	SVRGLEDQNL	14
296	DGDTLGFPPL	14
361	FCLLVVVVVL	14
409	RSQPEESVGL	14
8	EMWGPEAWLL	13
12	PEAWLLLLLL	13
13	EAWLLLLLLL	13
70	VDAGEGAQEL	13
73	GEGAQELALL	13
101	PPPPRNPLDG	13
105	RNPLDGSVLL	13
106	NPLDGSVLLR	13
141	LRLRVLVPPL	13
212	PSRSMNGQPL	13
236	ITHILHVSFL	13
259	WHIGREGAML	13
277	PPSYNWTRLD	13
287	GPLPSGVRVD	13
336	QEDSGKQVDL	13
351	VVVGVIAALL	13
355	VIAALLFCLL	13
495	KPTGNGIYIN	13
10	WGPEAWLLLL	12
100	QPPPPRNPLD	12
104	PRNPLDGSVL	12
137	FQARLRLRVL	12
144	RVLVPPLPSL	12
148	PPLPSLNPGP	12
154	NPGPALEEGQ	12
160	EEGQGLTLAA	12
211	VPSRSMNGQP	12
231	LQDQRITHIL	12

TableXXXIX-V1-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
244	FLAEASVRGL	12
262	GREGAMLKCL	12
308	EHSGIYVCHV	12
337	EDSGKQVDLV	12
350	VVVVGVIAAL	12
383	TQKYEEELTL	12
392	LTRENSIRRL	12
441	EGRSYSTLTT	12
452	REIETQTELL	12
25	FTGRCPAGEL	11
41	TVVLGQDAKL	11
56	GDSGEQVGQV	11
138	QARLRLRVLV	11
147	VPPLPSLNPG	11
201	SAAVTSEFHL	11
219	QPLTCVVSHP	11
221	LTCVVSHPGL	11
275	QPPPSYNWTR	11
280	YNWTRLDGPL	11
354	GVIAALLFCL	11
357	AALLFCLLVV	11
358	ALLFCLLVVV	11
418	LRAEGHPDSL	11
423	HPDSLKDNSS	11
451	VREIETQTEL	11
462	SPGSGRAEEE	11
500	GIYINGRGHL	11

TableXXXIX-V2-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
1	LGQDAKLPCL	11

TableXXXIX-V2-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
7	LPCLYRGDSG	10
10	LYRGDSGEQV	10

TableXXXIX-V7-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
6	DPRSQSEEPE	13

TableXXXIX-V9-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
59	NPPASASLVA	20
23	LPFPLVVFFI	19
25	FPLVVFFIYF	17
92	AFRFIQCLLL	16
60	PPASASLVAG	14
10	LLRITFNFFL	13
45	HYVAQAGLEL	13
62	ASASLVAGTL	13
94	RFIQCLLLGL	13
100	LLGLLKVRPL	13
107	RPLQHQGVNS	13
1	MRRELLAGIL	12
14	TFNFFLFFFL	12
43	ESHYVAQAGL	12
57	SSNPPASASL	12

TableXXXIX-V9-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
90	KKAFRFIQCL	12
2	RRELLAGILL	11
12	RITFNFFLFF	11
18	FLFFFLPFPL	11
31	FIYFYFYFFL	11
46	YVAQAGLELL	11
53	ELLGSSNPPA	11
61	PASASLVAGT	11
64	ASLVAGTLSV	11
80	ESFTKRKKKL	11
91	KAFRFIQCLL	11
4	ELLAGILLRI	10
16	NFFLFFFLPF	10
21	FFLPFPLVVF	10
22	FLPFPLVVFF	10
87	KKLKKAFRFI	10
95	FIQCLLLGLL	10
105	KVRPLQHQGV	10
119	CERGYFQGIF	10
5	LLAGILLRIT	9
9	ILLRITFNFF	9
20	FFFLPFPLVV	9
33	YFYFYFFLEM	9
41	EMESHYVAQA	9
55	LGSSNPPASA	9
70	TLSVHHCACF	9
83	TKRKKKLKKA	9
84	KRKKKLKKAF	9
120	ERGYFQGIFM	9
123	YFQGIFMQAA	9

TableXXXIX-V10-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
10	GTSDVVTVVL	16
4	CPAGELGTSD	14
7	GELGTSDVVT	11
8	ELGTSDVVTV	11
2	GRCPAGELGT	9
6	AGELGTSDVV	9
9	LGTSDVVTVV	9
5	PAGELGTSDV	8

TableXXXIX-V11-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
5	LRLRVMVPPL	13
8	RVMVPPLPSL	13
2	QARLRLRVMV	11
1	FQARLRLRVM	8
4	RLRLRVMVPP	6

TableXXXIX-V12-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
6	EPEGCSYSTL	23

TableXXXIX-V13-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
1	DSQVTVDVLA	8
2	SQVTVDVLAD	4

TableXXXIX-V14-HLA-B0702-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
5	NPPASASLVA	20
6	PPASASLVAG	14
8	ASASLVAGTL	13
3	SSNPPASASL	12
7	PASASLVAGT	11
10	ASLVAGTLSV	11
1	LGSSNPPASA	9

TableXL-V1-HLA-B08-10mers-191P4D12B

Pos	1234567890	score

NoResultsFound.

TableXXIV-V7-HLA-A0203-9mers-191P4D12B

Pos	123456789	score

NoResultsFound.

TableXXIV-V9-HLA-A0203-9mers-191P4D12B

Pos	123456789	score

NoResultsFound.

TableXXIV-V10-HLA-A0203-9mers-191P4D12B

Pos	123456789	score

NoResultsFound.

TableXXIV-V11-HLA-A0203-9mers-191P4D12B

Pos	123456789	score

NoResultsFound.

TableXXIV-V12-HLA-A0203-9mers-191P4D12B

Pos	123456789	score

NoResultsFound.

TableXXIV-V13-HLA-A0203-9mers-191P4D12B

Pos	123456789	score

NoResultsFound.

TableXXIV-V14-HLA-A0203-9mers-191P4D12B

Pos	123456789	score

NoResultsFound.

TableXLI-V1-HLA-B1510-10mers-191P4D12B

Pos	1234567890	score

NoResultsFound.

TableXLI-V2-HLA-B1510-10mers-191P4D12B

Pos	1234567890	score

NoResultsFound.

TableXLI-V7-HLA-B1510-10mers-191P4D12B

Pos	1234567890	score

NoResultsFound.

TableXLI-V9-HLA-B1510-10mers-191P4D12B

Pos	1234567890	score

NoResultsFound.

TableXLI-V10-HLA-B1510-10mers-191P4D12B

Pos	1234567890	score

TableXLI-V10-HLA-B1510-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLI-V11-HLA-B1510-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLI-V12-HLA-B1510-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLI-V13-HLA-B1510-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLI-V14-HLA-B1510-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V1-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V2-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V7-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V9-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V9-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V10-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V11-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V12-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V13-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLII-V14-HLA-B2705-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V1-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V2-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V7-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V7-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V9-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V10-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V11-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V12-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V13-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIII-V14-HLA-B2709-10mers-191P4D12B		
Pos	1234567890	score
NoResultsFound.		

TableXLIV-V1-HLA-B4402-10mers-191P4D12B		
Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.		
Pos	1234567890	score

TableXLIV-V1-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
452	REIETQTELL	25
7	AEMWGPEAWL	24
12	PEAWLLLLLL	23
73	GEGAQELALL	22
77	QELALLHSKY	22
123	GEYECRVSTF	22
336	QEDSGKQVDL	22
469	EEEEDQDEGI	20
99	EQPPPPRNPL	18
174	EGSPAPSVTW	18
35	ETSDVVTVVL	17
72	AGEGAQELAL	17
13	EAWLLLLLLL	16
134	AGSFQARLRL	16
160	EEGQGLTLAA	16
476	EGIKQAMNHF	16
8	EMWGPEAWLL	15
9	MWGPEAWLLL	15
98	VEQPPPPRNP	15
158	ALEEGQGLTL	15
173	AEGSPAPSVT	15
273	EGQPPPSYNW	15
350	VVVVGVIAAL	15
361	FCLLVVVVVL	15
387	EEELTLTREN	15
388	EELTLTRENS	15
420	AEGHPDSLKD	15
437	SEEPEGRSYS	15
471	EEDQDEGIKQ	15
10	WGPEAWLLLL	14
58	SGEQVGQVAW	14
85	KYGLHVSPAY	14
104	PRNPLDGSVL	14
105	RNPLDGSVLL	14
137	FQARLRLRVL	14
150	LPSLNPGPAL	14
206	SEFHLVPSRS	14
246	AEASVRGLED	14

TableXLIV-V1-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
259	WHIGREGAML	14
262	GREGAMLKCL	14
319	NEFSSRDSQV	14
354	GVIAALLFCL	14
392	LTRENSIRRL	14
409	RSQPEESVGL	14
412	PEESVGLRAE	14
413	EESVGLRAEG	14
439	EPEGRSYSTL	14
483	NHFVQENGTL	14
494	AKPTGNGIYI	14
6	GAEMWGPEAW	13
11	GPEAWLLLLL	13
16	LLLLLLLASF	13
32	GELETSDVVT	13
128	RVSTFPAGSF	13
141	LRLRVLVPPL	13
159	LEEGQGLTLA	13
199	SRSAAVTSEF	13
231	LQDQRITHIL	13
250	VRGLEDQNLW	13
291	SGVRVDGDTL	13
293	VRVDGDTLGF	13
296	DGDTLGFPPL	13
324	RDSQVTVDVL	13
351	VVVGVIAALL	13
352	VVGVIAALLF	13
438	EEPEGRSYST	13
468	AEEEEDQDEG	13
470	EEEDQDEGIK	13
487	QENGTLRAKP	13
493	RAKPTGNGIY	13
1	MPLSLGAEMW	12
25	FTGRCPAGEL	12
34	LETSDVVTVV	12
41	TVVLGQDAKL	12
44	LGQDAKLPCF	12
45	GQDAKLPCFY	12

TableXLIV-V1-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
70	VDAGEGAQEL	12
79	LALLHSKYGL	12
121	DEGEYECRVS	12
125	YECRVSTFPA	12
144	RVLVPPLPSL	12
187	VKGTTSSRSF	12
222	TCVVSHPGLL	12
230	LLQDQRITHI	12
244	FLAEASVRGL	12
249	SVRGLEDQNL	12
253	LEDQNLWHIG	12
271	LSEGQPPPSY	12
272	SEGQPPPSYN	12
347	SASVVVVGVI	12
355	VIAALLFCLL	12
377	RKAQQMTQKY	12
383	TQKYEEELTL	12
389	ELTLTRENSI	12
394	RENSIRRLHS	12
440	PEGRSYSTLT	12
454	IETQTELLSP	12
458	TELLSPGSGR	12

TableXLIV-V2-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
2	GQDAKLPCLY	13
1	LGQDAKLPCL	12
5	AKLPCLYRGD	8

TableXLIV-V7-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
2	SHHTDPRSQS	4
4	HTDPRSQSEE	4
1	HSHHTDPRSQ	2
5	TDPRSQSEEP	2
9	SQSEEPEGRS	2
3	HHTDPRSQSE	1
7	PRSQSEEPEG	1
8	RSQSEEPEGR	1

TableXLIV-V9-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
119	CERGYFQGIF	21
80	ESFTKRKKKL	18
3	RELLAGILLR	17
21	FFLPFPLVVF	17
11	LRITFNFFLF	16
16	NFFLFFFLPF	16
62	ASASLVAGTL	15
79	FESFTKRKKK	15
84	KRKKKLKKAF	15
91	KAFRFIQCLL	15
92	AFRFIQCLLL	15
94	RFIQCLLLGL	15
9	ILLRITFNFF	14
13	ITFNFFLFFF	14
23	LPFPLVVFFI	14
30	FFIYFYFYFF	14
40	LEMESHYVAQ	14
42	MESHYVAQAG	14
57	SSNPPASASL	14
90	KKAFRFIQCL	14
125	QGIFMQAAPW	14
2	RRELLAGILL	13
4	ELLAGILLRI	13

TableXLIV-V9-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
6	LAGILLRITF	13
8	GILLRITFNF	13
18	FLFFFLPFPL	13
22	FLPFPLVVFF	13
24	PFPLVVFFIY	13
25	FPLVVFFIYF	13
26	PLVVFFIYFY	13
28	VVFFIYFYFY	13
37	YFFLEMESHY	13
52	LELLGSSNPP	13
86	KKKLKKAFRF	13
100	LLGLLKVRPL	13
115	NSCDCERGYF	13
12	RITFNFFLFF	12
29	VFFIYFYFYF	12
43	ESHYVAQAGL	12
46	YVAQAGLELL	12
87	KKLKKAFRFI	12
95	FIQCLLLGLL	12
114	VNSCDCERGY	12
1	MRRELLAGIL	11
14	TFNFFLFFFL	11
45	HYVAQAGLEL	11
70	TLSVHHCACF	11
73	VHHCACFESF	11
7	AGILLRITFN	10
10	LLRITFNFFL	10
27	LVVFFIYFYF	10
31	FIYFYFYFFL	10
118	DCERGYFQGI	10

TableXLIV-V10-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
10	GTSDVVTVVL	15
7	GELGTSDVVT	14

TableXLIV-V11-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
5	LRLRVMVPPL	13
8	RVMVPPLPSL	12
3	ARLRLRVMVP	7

TableXLIV-V12-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
4	SEEPEGCSYS	14
6	EPEGCSYSTL	14
5	EEPEGCSYST	13
7	PEGCSYSTLT	11
3	MSEEPEGCSY	10

TableXLIV-V13-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
2	SQVTVDVLAD	6
10	ADPQEDSGKQ	5
9	LADPQEDSGK	4
1	DSQVTVDVLA	2

4	VTVDVLADPQ	2
5	TVDVLADPQE	2
6	VDVLADPQED	2

TableXLIV-V14-HLA-B4402-10mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 10 amino acids, and the end position for each peptide is the start position plus nine.

Pos	1234567890	score
8	ASASLVAGTL	15
3	SSNPPASASL	14
4	SNPPASASLV	7

TableXLV-V1-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLV-V2-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLV-V7-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLV-V9-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLV-V10-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLV-V11-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLV-V12-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLV-V13-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLV-V14-HLA-B5101-10mers-191P4D12B

Pos	1234567890	score
NoResultsFound.		

TableXLVI-V1-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
279	SYNWTRLDGPLPSGV	35
140	RLRLRVLVPPLPSLN	32
205	TSEFHLVPSRSMNGQ	32
299	TLGFPPLTTEHSGIY	32
37	SDVVTVVLGQDAKLP	31
40	VTVVLGQDAKLPCFY	31
340	GKQVDLVSASVVVVG	31
349	SVVVVGVIAALLFCL	31
144	RVLVPPLPSLNPGPA	30
147	VPPLPSLNPGPALEE	30
350	VVVVGVIAALLFCLL	30
51	PCFYRGDSGEQVGQV	28
12	PEAWLLLLLLLASFT	27
247	EASVRGLEDQNLWHI	27
358	ALLFCLLVVVVVLMS	27
371	MSRYHRRKAQQMTQK	26
6	GAEMWGPEAWLLLLL	25
13	EAWLLLLLLLASFTG	25
14	AWLLLLLLLASFTGR	25
15	WLLLLLLLASFTGRC	25

TableXLVI-V1-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
19	LLLLASFTGRCPAGE	25
102	PPPRNPLDGSVLLRN	25
109	DGSVLLRNAVQADEG	25
122	EGEYECRVSTFPAGS	25
193	SRSFKHSRSAAVTSE	25
239	ILHVSFLAEASVRGL	25
255	DQNLWHIGREGAMLK	25
265	GAMLKCLSEGQPPPS	25
310	SGIYVCHVSNEFSSR	25
454	IETQTELLSPGSGRA	25
64	QVAWARVDAGEGAQE	24
76	AQELALLHSKYGLHV	24
79	LALLHSKYGLHVSPA	24
126	ECRVSTFPAGSFQAR	24
156	GPALEEGQGLTLAAS	24
162	GQGLTLAASCTAEGS	24
181	VTWDTEVKGTTSSRS	24
210	LVPSRSMNGQPLTCV	24
213	SRSMNGQPLTCVVSH	24
282	WTRLDGPLPSGVRVD	24
347	SASVVVVGVIAALLF	24
353	VGVIAALLFCLLVVV	24
357	AALLFCLLVVVVVLM	24
364	LVVVVVLMSRYHRRK	24
395	ENSIRRLHSHHTDPR	24
442	GRSYSTLTTVREIET	24
16	LLLLLLLASFTGRCP	23
28	RCPAGELETSDVVTV	23
184	DTEVKGTTSSRSFKH	23
228	PGLLQDQRITHILHV	23
233	DQRITHILHVSFLAE	23
289	LPSGVRVDGDTLGFP	23
339	SGKQVDLVSASVVVV	23
346	VSASVVVVGVIAALL	23
361	FCLLVVVVVLMSRYH	23
424	PDSLKDNSSCSVMSE	23
448	LTTVREIETQTELLS	23
457	QTELLSPGSGRAEEE	23
483	NHFVQENGTLRAKPT	23

TableXLVI-V1-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
3	LSLGAEMWGPEAWLL	22
55	RGDSGEQVGQVAWAR	22
59	GEQVGQVAWARVDAG	22
141	LRLRVLVPPLPSLNP	22
204	VTSEFHLVPSRSMNG	22
250	VRGLEDQNLWHIGRE	22
268	LKCLSEGQPPPSYNW	22
311	GIYVCHVSNEFSSRD	22
327	QVTVDVLDPQEDSGK	22
360	LFCLLVVVVVLMSRY	22
451	VREIETQTELLSPGS	22
218	GQPLTCVVSHPGLLQ	21
256	QNLWHIGREGAMLKC	21
277	PPSYNWTRLDGPLPS	21
33	ELETSDVVTVVLGQD	20
65	VAWARVDAGEGAQEL	20
123	GEYECRVSTFPAGSF	20
154	NPGPALEEGQGLTLA	20
321	FSSRDSQVTVDVLDP	20
429	DNSSCSVMSEEPEGR	20
482	MNHFVQENGTLRAKP	20
490	GTLRAKPTGNGIYIN	20
22	LASFTGRCPAGELET	19
39	VVTVVLGQDAKLPCF	19
138	QARLRLRVLVPPLPS	19
234	QRITHILHVSFLAEA	19
242	VSFLAEASVRGLEDQ	19
412	PEESVGLRAEGHPDS	19
415	SVGLRAEGHPDSLKD	19
7	AEMWGPEAWLLLLLL	18
91	SPAYEGRVEQPPPPR	18
134	AGSFQARLRLRVLVP	18
165	LTLAASCTAEGSPAP	18
264	EGAMLKCLSEGQPPP	18
266	AMLKCLSEGQPPPSY	18
280	YNWTRLDGPLPSGVR	18
368	VVLMSRYHRRKAQQM	18
387	EEELTLTRENSIRRL	18
11	GPEAWLLLLLLLASF	17

TableXLVI-V1-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
67	WARVDAGEGAQELAL	17
68	ARVDAGEGAQELALL	17
83	HSKYGLHVSPAYEGR	17
115	RNAVQADEGEYECRV	17
125	YECRVSTFPAGSFQA	17
135	GSFQARLRLRVLVPP	17
148	PPLPSLNPGPALEEG	17
150	LPSLNPGPALEEGQG	17
167	LAASCTAEGSPAPSV	17
201	SAAVTSEFHLVPSRS	17
221	LTCVVSHPGLLQDQR	17
225	VSHPGLLQDQRITHI	17
238	HILHVSFLAEASVRG	17
257	NLWHIGREGAMLKCL	17
258	LWHIGREGAMLKCLS	17
284	RLDGPLPSGVRVDGD	17
291	SGVRVDGDTLGFPPL	17
294	RVDGDTLGFPPLTTE	17
303	PPLTTEHSGIYVCHV	17
330	VDVLDPQEDSGKQVD	17
332	VLDPQEDSGKQVDLV	17
342	QVDLVSASVVVVGVI	17
348	ASVVVVGVIAALLFC	17
354	GVIAALLFCLLVVVV	17
356	IAALLFCLLVVVVVL	17
379	AQQMTQKYEEELTLT	17
407	DPRSQPEESVGLRAE	17
413	EESVGLRAEGHPDSL	17
432	SCSVMSEEPEGRSYS	17
458	TELLSPGSGRAEEEE	17
475	DEGIKQAMNHFVQEN	17
486	VQENGTLRAKPTGNG	17

TableXLVI-V2-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
2	VTVVLGQDAKLPCLY	31
13	PCLYRGDSGEQVGQV	28
9	DAKLPCLYRGDSGEQ	24
1	VVTVVLGQDAKLPCL	19

TableXLVI-V7-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
2	IRRLHSHHTDPRSQS	14
8	HHTDPRSQSEEPEGR	14
13	RSQSEEPEGRSYSTL	10
1	SIRRLHSHHTDPRSQ	9
11	DPRSQSEEPEGRSYS	9
14	SQSEEPEGRSYSTLT	9
3	RRLHSHHTDPRSQSE	8
5	LHSHHTDPRSQSEEP	8
9	HTDPRSQSEEPEGRS	8
12	PRSQSEEPEGRSYST	8
4	RLHSHHTDPRSQSEE	7
6	HSHHTDPRSQSEEPE	7

TableXLVI-V9-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
43	ESHYVAQAGLELLGS	33
49	QAGLELLGSSNPPAS	32
36	FYFFLEMESHYVAQA	31
103	LLKVRPLQHQGVNSC	28
17	FFLFFFLPFPLVVFF	27
90	KKAFRFIQCLLLGLL	27
98	CLLLGLLKVRPLQHQ	26
18	FLFFFLPFPLVVFFI	25
60	PPASASLVAGTLSVH	24
61	PASASLVAGTLSVHH	24
93	FRFIQCLLLGLLKVR	24
97	QCLLLGLLKVRPLQH	24
121	RGYFQGIFMQAAPWE	24

TableXLVI-V9-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
6	LAGILLRITFNFFLF	23
16	NFFLFFFLPFPLVVF	23
7	AGILLRITFNFFLFF	22
52	LELLGSSNPPASASL	22
100	LLGLLKVRPLQHQGV	22
8	GILLRITFNFFLFFF	21
27	LVVFFIYFYFYFFLE	21
12	RITFNFFLFFFLPFP	20
34	FYFYFFLEMESHYVA	20
92	AFRFIQCLLLGLLKV	20
4	ELLAGILLRITFNFF	19
14	TFNFFLFFFLPFPLV	19
15	FNFFLFFFLPFPLVV	19
31	FIYFYFYFFLEMESH	19
33	YFYFYFFLEMESHYV	19
46	YVAQAGLELLGSSNP	19
95	FIQCLLLGLLKVRPL	19
10	LLRITFNFFLFFFLP	18
19	LFFFLPFPLVVFFIY	18
25	FPLVVFFIYFYFYFF	18
28	VVFFIYFYFYFFLEM	18
84	KRKKKLKKAFRFIQC	18
120	ERGYFQGIFMQAAPW	18
13	ITFNFFLFFFLPFPL	17
20	FFFLPFPLVVFFIYF	17
22	FLPFPLVVFFIYFYF	17
29	VFFIYFYFYFFLEME	17
37	YFFLEMESHYVAQAG	17
44	SHYVAQAGLELLGSS	17
94	RFIQCLLLGLLKVRP	17
2	RRELLAGILLRITFN	16
21	FFLPFPLVVFFIYFY	16
39	FLEMESHYVAQAGLE	16
41	EMESHYVAQAGLELL	16
48	AQAGLELLGSSNPPA	16
51	GLELLGSSNPPASAS	16
54	LLGSSNPPASASLVA	16
56	GSSNPPASASLVAGT	16
68	AGTLSVHHCACFESF	16

TableXLVI-V9-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
70	TLSVHHCACFESFTK	16
105	KVRPLQHQGVNSCDC	16
118	DCERGYFQGIFMQAA	16

TableXLVI-V10-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
8	RCPAGELGTSDVVTV	23
13	ELGTSDVVTVVLGQD	20
2	LASFTGRCPAGELGT	19
3	ASFTGRCPAGELGTS	16
11	AGELGTSDVVTVVLG	16
9	CPAGELGTSDVVTVV	15

TableXLVI-V11-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
9	RLRLRVMVPPLPSLN	30
13	RVMVPPLPSLNPGPA	30
10	LRLRVMVPPLPSLNP	22
7	QARLRLRVMVPPLPS	19
3	AGSFQARLRLRVMVP	18
4	GSFQARLRLRVMVPP	17
6	FQARLRLRVMVPPLP	16
11	RLRVMVPPLPSLNPG	16
1	FPAGSFQARLRLRVM	15
12	LRVMVPPLPSLNPGP	15
8	ARLRLRVMVPPLPSL	14

TableXLVI-V12-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
14	GCSYSTLTTVREIET	24
1	DNSSCSVMSEEPEGC	20
4	SCSVMSEEPEGCSYS	17
5	CSVMSEEPEGCSYST	16
15	CSYSTLTTVREIETQ	11

TableXLVI-V13-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
2	FSSRDSQVTVDVLAD	20
6	DSQVTVDVLADPQED	17
14	LADPQEDSGKQVDLV	17
8	QVTVDVLADPQEDSG	16
10	TVDVLADPQEDSGKQ	16
7	SQVTVDVLADPQEDS	15
3	SSRDSQVTVDVLADP	14
12	DVLADPQEDSGKQVD	9

TableXLVI-V14-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
11	PPASASLVAGTLSVH	24
12	PASASLVAGTLSVHH	24
3	LELLGSSNPPASASL	22
2	GLELLGSSNPPASAS	16
5	LLGSSNPPASASLVA	16
7	GSSNPPASASLVAGT	16
1	AGLELLGSSNPPASA	15
6	LGSSNPPASASLVAG	15
13	ASASLVAGTLSVHHC	15
4	ELLGSSNPPASASLV	14
8	SSNPPASASLVAGTL	14

TableXLVI-V14-HLA-DRB1-0101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
15	ASLVAGTLSVHHCAC	14

TableXLVII-V1-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
178	APSVTWDTEVKGTTS	29
227	HPGLLQDQRITHILH	28
41	TVVLGQDAKLPCFYR	27
379	AQQMTQKYEEELTLT	25
14	AWLLLLLLLASFTGR	23
290	PSGVRVDGDTLGFPP	23
39	VVTVVLGQDAKLPCF	22
103	PPRNPLDGSVLLRNA	22
247	EASVRGLEDQNLWHI	22
115	RNAVQADEGEYECRV	21
142	RLRVLVPPLPSLNPG	21
233	DQRITHILHVSFLAE	21
325	DSQVTVDVLDPQEDS	21
348	ASVVVVGVIAALLFC	21
349	SVVVVGVIAALLFCL	21
6	GAEMWGPEAWLLLLL	20
156	GPALEEGQGLTLAAS	20
242	VSFLAEASVRGLEDQ	20
249	SVRGLEDQNLWHIGR	20
292	GVRVDGDTLGFPPLT	20
350	VVVVGVIAALLFCLL	20
352	VVGVIAALLFCLLVV	20
353	VGVIAALLFCLLVVV	20
363	LLVVVVVLMSRYHRR	20
126	ECRVSTFPAGSFQAR	19
302	FPPLTTEHSGIYVCH	19
328	VTVDVLDPQEDSGKQ	19
365	VVVVVLMSRYHRRKA	19
387	EEELTLTRENSIRRL	19
77	QELALLHSKYGLHVS	18

TableXLVII-V1-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
111	SVLLRNAVQADEGEY	18
265	GAMLKCLSEGQPPPS	18
286	DGPLPSGVRVDGDTL	18
319	NEFSSRDSQVTVDVL	18
329	TVDVLDPQEDSGKQV	18
433	CSVMSEEPEGRSYST	18
451	VREIETQTELLSPGS	18
87	GLHVSPAYEGRVEQP	17
97	RVEQPPPPRNPLDGS	17
239	ILHVSFLAEASVRGL	17
255	DQNLWHIGREGAMLK	17
311	GIYVCHVSNEFSSRD	17
334	DPQEDSGKQVDLVSA	17
368	VVLMSRYHRRKAQQM	17
381	QMTQKYEEELTLTRE	17
401	LHSHHTDPRSQPEES	17
413	EESVGLRAEGHPDSL	17
445	YSTLTTVREIETQTE	17
475	DEGIKQAMNHFVQEN	17
479	KQAMNHFVQENGTLR	17
491	TLRAKPTGNGIYING	17
5	LGAEMWGPEAWLLLL	16
13	EAWLLLLLLLASFTG	16
47	DAKLPCFYRGDSGEQ	16
70	VDAGEGAQELALLHS	16
134	AGSFQARLRLRVLVP	16
114	LRNAVQADEGEYECR	15
130	STFPAGSFQARLRLR	15
132	FPAGSFQARLRLRVL	15
199	SRSAAVTSEFHLVPS	15
221	LTCVVSHPGLLQDQR	15
236	ITHILHVSFLAEASV	15
481	AMNHFVQENGTLRAK	15
15	WLLLLLLLASFTGRC	14
17	LLLLLLASFTGRCPA	14
78	ELALLHSKYGLHVSP	14
109	DGSVLLRNAVQADEG	14
110	GSVLLRNAVQADEGE	14
143	LRVLVPPLPSLNPGP	14

TableXLVII-V1-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
144	RVLVPPLPSLNPGPA	14
280	YNWTRLDGPLPSGVR	14
342	QVDLVSASVVVVGVI	14
356	IAALLFCLLVVVVVL	14
360	LFCLLVVVVVLMSRY	14
448	LTTVREIETQTELLS	14
449	TTVREIETQTELLSP	14
457	QTELLSPGSGRAEEE	14

TableXLVII-V2-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
3	TVVLGQDAKLPCLYR	27
1	VVTVVLGQDAKLPCL	22
9	DAKLPCLYRGDSGEQ	16
2	VTVVLGQDAKLPCLY	13

TableXLVII-V7-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
5	LHSHHTDPRSQSEEP	17
2	IRRLHSHHTDPRSQS	11
13	RSQSEEPEGRSYSTL	10
9	HTDPRSQSEEPEGRS	9
7	SHHTDPRSQSEEPEG	8
12	PRSQSEEPEGRSYST	8
14	SQSEEPEGRSYSTLT	8

TableXLVII-V9-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
8	GILLRITFNFFLFFF	25
112	QGVNSCDCERGYFQG	24
35	YFYFFLEMESHYVAQ	23
6	LAGILLRITFNFFLF	22
7	AGILLRITFNFFLFF	21
19	LFFFLPFPLVVFFIY	21
10	LLRITFNFFLFFFLP	20
20	FFFLPFPLVVFFIYF	20
44	SHYVAQAGLELLGSS	20
93	FRFIQCLLLGLLKVR	20
97	QCLLLGLLKVRPLQH	20
98	CLLLGLLKVRPLQHQ	20
16	NFFLFFFLPFPLVVF	19
24	PFPLVVFFIYFYFYF	19
25	FPLVVFFIYFYFYFF	19
51	GLELLGSSNPPASAS	19
68	AGTLSVHHCACFESF	19
90	KKAFRFIQCLLLGLL	19
92	AFRFIQCLLLGLLKV	19
14	TFNFFLFFFLPFPLV	18
26	PLVVFFIYFYFYFFL	18
29	VFFIYFYFYFFLEME	18
12	RITFNFFLFFFLPFP	17
22	FLPFPLVVFFIYFYF	17
28	VVFFIYFYFYFFLEM	17
79	FESFTKRKKKLKKAF	17
82	FTKRKKKLKKAFRFI	17
86	KKKLKKAFRFIQCLL	17
27	LVVFFIYFYFYFFLE	16
76	CACFESFTKRKKKLK	16
4	ELLAGILLRITFNFF	15
33	YFYFYFFLEMESHYV	15
41	EMESHYVAQAGLELL	15
78	CFESFTKRKKKLKKA	15
89	LKKAFRFIQCLLLGL	15
113	GVNSCDCERGYFQGI	15
117	CDCERGYFQGIFMQA	15
96	IQCLLLGLLKVRPLQ	14
2	RRELLAGILLRITFN	13
49	QAGLELLGSSNPPAS	13
100	LLGLLKVRPLQHQGV	13

TableXLVII-V9-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
101	LGLLKVRPLQHQGVN	13
103	LLKVRPLQHQGVNSC	13
36	FYFFLEMESHYVAQA	12
37	YFFLEMESHYVAQAG	12
39	FLEMESHYVAQAGLE	12
52	LELLGSSNPPASASL	12
64	ASLVAGTLSVHHCAC	12
106	VRPLQHQGVNSCDCE	12

TableXLVII-V10-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
12	GELGTSDVVTVVLGQ	12
11	AGELGTSDVVTVVLG	11
2	LASFTGRCPAGELGT	10
3	ASFTGRCPAGELGTS	9
5	FTGRCPAGELGTSDV	9
13	ELGTSDVVTVVLGQD	9

TableXLVII-V11-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
11	RLRVMVPPLPSLNPG	19
3	AGSFQARLRLRVMVP	16
1	FPAGSFQARLRLRVM	15
12	LRVMVPPLPSLNPGP	14
13	RVMVPPLPSLNPGPA	14
7	QARLRLRVMVPPLPS	13
9	RLRLRVMVPPLPSLN	12
5	SFQARLRLRVMVPPL	10
8	ARLRLRVMVPPLPSL	10
15	MVPPLPSLNPGPALE	10

TableXLVII-V12-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
5	CSVMSEEPEGCSYST	18
4	SCSVMSEEPEGCSYS	12
6	SVMSEEPEGCSYSTL	10
3	SSCSVMSEEPEGCSY	9
9	SEEPEGCSYSTLTTV	9

TableXLVII-V13-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
10	TVDVLADPQEDSGKQ	29
6	DSQVTVDVLADPQED	22
11	VDVLADPQEDSGKQV	16

TableXLVII-V14-HLA-DRB1-0301-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
2	GLELLGSSNPPASAS	19
3	LELLGSSNPPASASL	12
15	ASLVAGTLSVHHCAC	12
14	SASLVAGTLSVHHCA	11
6	LGSSNPPASASLVAG	10
11	PPASASLVAGTLSVH	9

TableXLVIII-V1-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
205	TSEFHLVPSRSMNGQ	28
299	TLGFPPLTTEHSGIY	28
47	DAKLPCFYRGDSGEQ	26
162	GQGLTLAASCTAEGS	26
255	DQNLWHIGREGAMLK	26
311	GIYVCHVSNEFSSRD	26
395	ENSIRRLHSHHTDPR	26
415	SVGLRAEGHPDSLKD	26
475	DEGIKQAMNHFVQEN	26
7	AEMWGPEAWLLLLLL	22
12	PEAWLLLLLLLASFT	22
50	LPCFYRGDSGEQVGQ	22
51	PCFYRGDSGEQVGQV	22
180	SVTWDTEVKGTTSSR	22
193	SRSFKHSRSAAVTSE	22
241	HVSFLAEASVRGLED	22
358	ALLFCLLVVVVVLMS	22
383	TQKYEEELTLTRENS	22
442	GRSYSTLTTVREIET	22
13	EAWLLLLLLLASFTG	20
15	WLLLLLLLASFTGRC	20
16	LLLLLLLASFTGRCP	20
37	SDVVTVVLGQDAKLP	20
59	GEQVGQVAWARVDAG	20
76	AQELALLHSKYGLHV	20
87	GLHVSPAYEGRVEQP	20
111	SVLLRNAVQADEGEY	20
144	RVLVPPLPSLNPGPA	20
147	VPPLPSLNPGPALEE	20
184	DTEVKGTTSSRSFKH	20
201	SAAVTSEFHLVPSRS	20
218	GQPLTCVVSHPGLLQ	20
227	HPGLLQDQRITHILH	20
233	DQRITHILHVSFLAE	20
239	ILHVSFLAEASVRGL	20
242	VSFLAEASVRGLEDQ	20
247	EASVRGLEDQNLWHI	20
258	LWHIGREGAMLKCLS	20
264	EGAMLKCLSEGQPPP	20
302	FPPLTTEHSGIYVCH	20
314	VCHVSNEFSSRDSQV	20

TableXLVIII-V1-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
325	DSQVTVDVLDPQEDS	20
340	GKQVDLVSASVVVVG	20
342	QVDLVSASVVVVGVI	20
347	SASVVVVGVIAALLF	20
349	SVVVVGVIAALLFCL	20
352	VVGVIAALLFCLLVV	20
353	VGVIAALLFCLLVVV	20
357	AALLFCLLVVVVVLM	20
360	LFCLLVVVVVLMSRY	20
361	FCLLVVVVVLMSRYH	20
364	LVVVVVLMSRYHRRK	20
368	VVLMSRYHRRKAQQM	20
389	ELTLTRENSIRRLHS	20
424	PDSLKDNSSCSVMSE	20
433	CSVMSEEPEGRSYST	20
445	YSTLTTVREIETQTE	20
448	LTTVREIETQTELLS	20
457	QTELLSPGSGRAEEE	20
479	KQAMNHFVQENGTLR	20
483	NHFVQENGTLRAKPT	20
28	RCPAGELETSDVVTV	18
29	CPAGELETSDVVTVV	18
33	ELETSDVVTVVLGQD	18
38	DVVTVVLGQDAKLPC	18
89	HVSPAYEGRVEQPPP	18
103	PPRNPLDGSVLLRNA	18
107	PLDGSVLLRNAVQAD	18
108	LDGSVLLRNAVQADE	18
120	ADEGEYECRVSTFPA	18
123	GEYECRVSTFPAGSF	18
128	RVSTFPAGSFQARLR	18
155	PGPALEEGQGLTLAA	18
190	TTSSRSFKHSRSAAV	18
219	QPLTCVVSHPGLLQD	18
308	EHSGIYVCHVSNEFS	18
315	CHVSNEFSSRDSQVT	18
319	NEFSSRDSQVTVDVL	18
328	VTVDVLDPQEDSGKQ	18
331	DVLDPQEDSGKQVDL	18

TableXLVIII-V1-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
339	SGKQVDLVSASVVVV	18
373	RYHRRKAQQMTQKYE	18
386	YEEELTLTRENSIRR	18
392	LTRENSIRRLHSHHT	18
407	DPRSQPEESVGLRAE	18
423	HPDSLKDNSSCSVMS	18
435	VMSEEPEGRSYSTLT	18
449	TTVREIETQTELLSP	18
454	IETQTELLSPGSGRA	18
472	EDQDEGIKQAMNHFV	18
134	AGSFQARLRLRVLVP	17
318	SNEFSSRDSQVTVDV	17
64	QVAWARVDAGEGAQE	16
83	HSKYGLHVSPAYEGR	16
256	QNLWHIGREGAMLKC	16
279	SYNWTRLDGPLPSGV	16
310	SGIYVCHVSNEFSSR	16
482	MNHFVQENGTLRAKP	16
367	VVVLMSRYHRRKAQQ	15
2	PLSLGAEMWGPEAWL	14
6	GAEMWGPEAWLLLLL	14
14	AWLLLLLLLASFTGR	14
17	LLLLLLASFTGRCPA	14
18	LLLLLASFTGRCPAG	14
19	LLLLASFTGRCPAGE	14
31	AGELETSDVVTVVLG	14
36	TSDVVTVVLGQDAKL	14
39	VVTVVLGQDAKLPCF	14
41	TVVLGQDAKLPCFYR	14
62	VGQVAWARVDAGEGA	14
95	EGRVEQPPPPRNPLD	14
105	RNPLDGSVLLRNAVQ	14
115	RNAVQADEGEYECRV	14
126	ECRVSTFPAGSFQAR	14
140	RLRLRVLVPPLPSLN	14
142	RLRVLVPPLPSLNPG	14
143	LRVLVPPLPSLNPGP	14
156	GPALEEGQGLTLAAS	14
164	GLTLAASCTAEGSPA	14

TableXLVIII-V1-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
178	APSVTWDTEVKGTTS	14
207	EFHLVPSRSMNGQPL	14
213	SRSMNGQPLTCVVSH	14
221	LTCVVSHPGLLQDQR	14
228	PGLLQDQRITHILHV	14
236	ITHILHVSFLAEASV	14
237	THILHVSFLAEASVR	14
250	VRGLEDQNLWHIGRE	14
265	GAMLKCLSEGQPPPS	14
268	LKCLSEGQPPPSYNW	14
282	WTRLDGPLPSGVRVD	14
286	DGPLPSGVRVDGDTL	14
290	PSGVRVDGDTLGFPP	14
292	GVRVDGDTLGFPPLT	14
327	QVTVDVLDPQEDSGK	14
330	VDVLDPQEDSGKQVD	14
348	ASVVVVGVIAALLFC	14
350	VVVVGVIAALLFCLL	14
356	IAALLFCLLVVVVVL	14
362	CLLVVVVVLMSRYHR	14
363	LLVVVVVLMSRYHRR	14
365	VVVVVLMSRYHRRKA	14
387	EEELTLTRENSIRRL	14
398	IRRLHSHHTDPRSQP	14
432	SCSVMSEEPEGRSYS	14
451	VREIETQTELLSPGS	14

TableXLVIII-V2-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
9	DAKLPCLYRGDSGEQ	26
13	PCLYRGDSGEQVGQV	22
12	LPCLYRGDSGEQVGQ	20
1	VVTVVLGQDAKLPCL	14
3	TVVLGQDAKLPCLYR	14

TableXLVIII-V2-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
4	VVLGQDAKLPCLYRG	12
15	LYRGDSGEQVGQVAW	12

TableXLVIII-V7-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
5	LHSHHTDPRSQSEEP	18
14	SQSEEPEGRSYSTLT	18
2	IRRLHSHHTDPRSQS	14
12	PRSQSEEPEGRSYST	12

TableXLVIII-V9-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
37	YFFLEMESHYVAQAG	26
86	KKKLKKAFRFIQCLL	26
103	LLKVRPLQHQGVNSC	26
12	RITFNFFLFFFLPFP	22
17	FFLFFFLPFPLVVFF	22
33	YFYFYFFLEMESHYV	22
36	FYFFLEMESHYVAQA	22
76	CACFESFTKRKKKLK	22
90	KKAFRFIQCLLLGLL	22
121	RGYFQGIFMQAAPWE	22
3	RELLAGILLRITFNF	20
8	GILLRITFNFFLFFF	20
16	NFFLFFFLPFPLVVF	20
44	SHYVAQAGLELLGSS	20
49	QAGLELLGSSNPPAS	20
51	GLELLGSSNPPASAS	20

TableXLVIII-V9-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
93	FRFIQCLLLGLLKVR	20
98	CLLLGLLKVRPLQHQ	20
41	EMESHYVAQAGLELL	18
62	ASASLVAGTLSVHHC	18
73	VHHCACFESFTKRKK	18
89	LKKAFRFIQCLLLGL	18
14	TFNFFLFFFLPFPLV	16
15	FNFFLFFFLPFPLVV	16
18	FLFFFLPFPLVVFFI	16
19	LFFFLPFPLVVFFIY	16
22	FLPFPLVVFFIYFYF	16
28	VVFFIYFYFYFFLEM	16
30	FFIYFYFYFFLEMES	16
31	FIYFYFYFFLEMESH	16
32	IYFYFYFFLEMESHY	16
34	FYFYFFLEMESHYVA	16
35	YFYFFLEMESHYVAQ	16
43	ESHYVAQAGLELLGS	16
92	AFRFIQCLLLGLLKV	16
120	ERGYFQGIFMQAAPW	16
2	RRELLAGILLRITFN	14
7	AGILLRITFNFFLFF	14
24	PFPLVVFFIYFYFYF	14
25	FPLVVFFIYFYFYFF	14
26	PLVVFFIYFYFYFFL	14
29	VFFIYFYFYFFLEME	14
39	FLEMESHYVAQAGLE	14
52	LELLGSSNPPASASL	14
64	ASLVAGTLSVHHCAC	14
70	TLSVHHCACFESFTK	14
97	QCLLLGLLKVRPLQH	14
100	LLGLLKVRPLQHQGV	14
4	ELLAGILLRITFNFF	12
5	LLAGILLRITFNFFL	12
21	FFLPFPLVVFFIYFY	12
46	YVAQAGLELLGSSNP	12
47	VAQAGLELLGSSNPP	12
48	AQAGLELLGSSNPPA	12
55	LGSSNPPASASLVAG	12

TableXLVIII-V9-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
56	GSSNPPASASLVAGT	12
57	SSNPPASASLVAGTL	12
60	PPASASLVAGTLSVH	12
61	PASASLVAGTLSVHH	12
66	LVAGTLSVHHCACFE	12
67	VAGTLSVHHCACFES	12
75	HCACFESFTKRKKKL	12
77	ACFESFTKRKKKLKK	12
94	RFIQCLLLGLLKVRP	12
95	FIQCLLLGLLKVRPL	12
104	LKVRPLQHQGVNSCD	12
108	PLQHQGVNSCDCERG	12
114	VNSCDCERGYFQGIF	12
118	DCERGYFQGIFMQAA	12
122	GYFQGIFMQAAPWEG	12

TableXLVIII-V10-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
8	RCPAGELGTSDVVTV	18
13	ELGTSDVVTVVLGQD	18
11	AGELGTSDVVTVVLG	14
5	FTGRCPAGELGTSDV	12
9	CPAGELGTSDVVTVV	12
12	GELGTSDVVTVVLGQ	12

TableXLVIII-V11-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
13	RVMVPPLPSLNPGPA	20

TableXLVIII-V11-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
3	AGSFQARLRLRVMVP	17
11	RLRVMVPPLPSLNPG	14
12	LRVMVPPLPSLNPGP	14
1	FPAGSFQARLRLRVM	12
4	GSFQARLRLRVMVPP	12
8	ARLRLRVMVPPLPSL	12
10	LRLRVMVPPLPSLNP	12

TableXLVIII-V12-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
14	GCSYSTLTTVREIET	22
5	CSVMSEEPEGCSYST	20
4	SCSVMSEEPEGCSYS	14
1	DNSSCSVMSEEPEGC	12
7	VMSEEPEGCSYSTLT	12
8	MSEEPEGCSYSTLTT	12
10	EEPEGCSYSTLTTVR	12
11	EPEGCSYSTLTTVRE	12

TableXLVIII-V13-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
10	TVDVLADPQEDSGKQ	26
13	VLADPQEDSGKQVDL	18
6	DSQVTVDVLADPQED	14
8	QVTVDVLADPQEDSG	14
2	FSSRDSQVTVDVLAD	12
3	SSRDSQVTVDVLADP	12
7	SQVTVDVLADPQEDS	12
14	LADPQEDSGKQVDLV	12

TableXLVIII-V14-HLA-DRB1-0401-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 29; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
2	GLELLGSSNPPASAS	20
13	ASASLVAGTLSVHHC	18
3	LELLGSSNPPASASL	14
15	ASLVAGTLSVHHCAC	14
6	LGSSNPPASASLVAG	12
7	GSSNPPASASLVAGT	12
8	SSNPPASASLVAGTL	12
11	PPASASLVAGTLSVH	12
12	PASASLVAGTLSVHH	12

TableXLIX-V1-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
255	DQNLWHIGREGAMLK	26
279	SYNWTRLDGPLPSGV	25
12	PEAWLLLLLLLASFT	23
201	SAAVTSEFHLVPSRS	23
64	QVAWARVDAGEGAQE	22
140	RLRLRVLVPPLPSLN	22
218	GQPLTCVVSHPGLLQ	22
233	DQRITHILHVSFLAE	22
286	DGPLPSGVRVDGDTL	22
299	TLGFPPLTTEHSGIY	22
368	VVLMSRYHRRKAQQM	22
37	SDVVTVVLGQDAKLP	21
261	IGREGAMLKCLSEGQ	21
361	FCLLVVVVVLMSRYH	21
47	DAKLPCFYRGDSGEQ	20
134	AGSFQARLRLRVLVP	20
180	SVTWDTEVKGTTSSR	20
365	VVVVVLMSRYHRRKA	20
386	YEEELTLTRENSIRR	20
392	LTRENSIRRLHSHHT	20

TableXLIX-V1-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
415	SVGLRAEGHPDSLKD	20
347	SASVVVVGVIAALLF	19
358	ALLFCLLVVVVVLMS	19
13	EAWLLLLLLLASFTG	18
16	LLLLLLLASFTGRCP	18
76	AQELALLHSKYGLHV	18
91	SPAYEGRVEQPPPPR	18
122	EGEYECRVSTFPAGS	18
144	RVLVPPLPSLNPGPA	18
147	VPPLPSLNPGPALEE	18
241	HVSFLAEASVRGLED	18
265	GAMLKCLSEGQPPPS	18
311	GIYVCHVSNEFSSRD	18
442	GRSYSTLTTVREIET	18
204	VTSEFHLVPSRSMNG	17
205	TSEFHLVPSRSMNGQ	17
367	VVVLMSRYHRRKAQQ	17
190	TTSSRSFKHSRSAAV	16
277	PPSYNWTRLDGPLPS	16
346	VSASVVVVGVIAALL	16
360	LFCLLVVVVVLMSRY	16
487	QENGTLRAKPTGNGI	16
75	GAQELALLHSKYGLH	15
107	PLDGSVLLRNAVQAD	15
178	APSVTWDTEVKGTTS	15
192	SSRSFKHSRSAAVTS	15
219	QPLTCVVSHPGLLQD	15
230	LLQDQRITHILHVSF	15
343	VDLVSASVVVVGVIA	15
362	CLLVVVVVLMSRYHR	15
363	LLVVVVVLMSRYHRR	15
411	QPEESVGLRAEGHPD	15
476	EGIKQAMNHFVQENG	15
485	FVQENGTLRAKPTGN	15
20	LLLASFTGRCPAGEL	14
34	LETSDVVTVVLGQDA	14
36	TSDVVTVVLGQDAKL	14
41	TVVLGQDAKLPCFYR	14
59	GEQVGQVAWARVDAG	14

TableXLIX-V1-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
61	QVGQVAWARVDAGEG	14
81	LLHSKYGLHVSPAYE	14
138	QARLRLRVLVPPLPS	14
162	GQGLTLAASCTAEGS	14
181	VTWDTEVKGTTSSRS	14
184	DTEVKGTTSSRSFKH	14
227	HPGLLQDQRITHILH	14
252	GLEDQNLWHIGREGA	14
276	PPPSYNWTRLDGPLP	14
290	PSGVRVDGDTLGFPP	14
308	EHSGIYVCHVSNEFS	14
350	VVVVGVIAALLFCLL	14
357	AALLFCLLVVVVVLM	14
364	LVVVVVLMSRYHRRK	14
397	SIRRLHSHHTDPRSQ	14
401	LHSHHTDPRSQPEES	14
420	AEGHPDSLKDNSSCS	14
433	CSVMSEEPEGRSYST	14
435	VMSEEPEGRSYSTLT	14
445	YSTLTTVREIETQTE	14
454	IETQTELLSPGSGRA	14
457	QTELLSPGSGRAEEE	14
479	KQAMNHFVQENGTLR	14
483	NHFVQENGTLRAKPT	14
19	LLLLASFTGRCPAGE	13
40	VTVVLGQDAKLPCFY	13
85	KYGLHVSPAYEGRVE	13
106	NPLDGSVLLRNAVQA	13
137	FQARLRLRVLVPPLP	13
215	SMNGQPLTCVVSHPG	13
237	THILHVSFLAEASVR	13
327	QVTVDVLDPQEDSGK	13
340	GKQVDLVSASVVVVG	13
349	SVVVVGVIAALLFCL	13
353	VGVIAALLFCLLVVV	13
451	VREIETQTELLSPGS	13
3	LSLGAEMWGPEAWLL	12
14	AWLLLLLLLASFTGR	12
15	WLLLLLLLASFTGRC	12

TableXLIX-V1-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
22	LASFTGRCPAGELET	12
62	VGQVAWARVDAGEGA	12
73	GEGAQELALLHSKYG	12
82	LHSKYGLHVSPAYEG	12
83	HSKYGLHVSPAYEGR	12
92	PAYEGRVEQPPPPRN	12
109	DGSVLLRNAVQADEG	12
112	VLLRNAVQADEGEYE	12
123	GEYECRVSTFPAGSF	12
141	LRLRVLVPPLPSLNP	12
153	LNPGPALEEGQGLTL	12
159	LEEGQGLTLAASCTA	12
164	GLTLAASCTAEGSPA	12
207	EFHLVPSRSMNGQPL	12
236	ITHILHVSFLAEASV	12
239	ILHVSFLAEASVRGL	12
247	EASVRGLEDQNLWHI	12
268	LKCLSEGQPPPSYNW	12
292	GVRVDGDTLGFPPLT	12
310	SGIYVCHVSNEFSSR	12
324	RDSQVTVDVLDPQED	12
329	TVDVLDPQEDSGKQV	12
337	EDSGKQVDLVSASVV	12
395	ENSIRRLHSHHTDPR	12
413	EESVGLRAEGHPDSL	12
421	EGHPDSLKDNSSCSV	12
429	DNSSCSVMSEEPEGR	12
448	LTTVREIETQTELLS	12
455	ETQTELLSPGSGRAE	12
489	NGTLRAKPTGNGIYI	12

TableXLIX-V2-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 5; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
9	DAKLPCLYRGDSGEQ	26

3	TVVLGQDAKLPCLYR	14
2	VTVVLGQDAKLPCLY	13

TableXLIX-V7-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 15; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
1	SIRRLHSHHTDPRSQ	14
5	LHSHHTDPRSQSEEP	14
14	SQSEEPEGRSYSTLT	14
3	RRLHSHHTDPRSQSE	8
12	PRSQSEEPEGRSYST	8
2	IRRLHSHHTDPRSQS	6
8	HHTDPRSQSEEPEGR	6
10	TDPRSQSEEPEGRSY	6

TableXLIX-V9-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
97	QCLLLGLLKVRPLQH	28
121	RGYFQGIFMQAAPWE	22
37	YFFLEMESHYVAQAG	21
79	FESFTKRKKKLKKAF	21
76	CACFESFTKRKKKLK	20
103	LLKVRPLQHQGVNSC	20
22	FLPFPLVVFFIYFYF	19
17	FFLFFFLPFPLVVFF	18
49	QAGLELLGSSNPPAS	18
66	LVAGTLSVHHCACFE	18
34	FYFYFFLEMESHYVA	17
90	KKAFRFIQCLLLGLL	17
120	ERGYFQGIFMQAAPW	17
15	FNFFLFFFLPFPLVV	16
33	YFYFYFFLEMESHYV	16
36	FYFFLEMESHYVAQA	16
86	KKKLKKAFRFIQCLL	15
3	RELLAGILLRITFNF	14
4	ELLAGILLRITFNFF	14
13	ITFNFFLFFFLPFPL	14

TableXLIX-V9-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 19; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
67	VAGTLSVHHCACFES	14
83	TKRKKKLKKAFRFIQ	14
111	HQGVNSCDCERGYFQ	14
26	PLVVFFIYFYFYFFL	13
61	PASASLVAGTLSVHH	13
93	FRFIQCLLLGLLKVR	13
98	CLLLGLLKVRPLQHQ	13

TableXLIX-V10-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 21; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
14	LGTSDVVTVVLGQDA	14
2	LASFTGRCPAGELGT	12
13	ELGTSDVVTVVLGQD	9
1	LLASFTGRCPAGELG	7
4	SFTGRCPAGELGTSD	7
6	TGRCPAGELGTSDVV	6
8	RCPAGELGTSDVVTV	6
11	AGELGTSDVVTVVLG	6

TableXLIX-V11-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 23; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
9	RLRLRVMVPPLPSLN	22
3	AGSFQARLRLRVMVP	20
13	RVMVPPLPSLNPGPA	18
7	QARLRLRVMVPPLPS	14
6	FQARLRLRVMVPPLP	13
10	LRLRVMVPPLPSLNP	12
1	FPAGSFQARLRLRVM	10

TableXLIX-V12-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 25; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
14	GCSYSTLTTVREIET	18
1	DNSSCSVMSEEPEGC	12
5	CSVMSEEPEGCSYST	12
2	NSSCSVMSEEPEGCS	7

TableXLIX-V13-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 27; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
6	DSQVTVDVLADPQED	17
8	QVTVDVLADPQEDSG	13
10	TVDVLADPQEDSGKQ	12
11	VDVLADPQEDSGKQV	12
4	SRDSQVTVDVLADPQ	10
15	ADPQEDSGKQVDLVS	9

TableXLIX-V14-HLA-DRB1-1101-15mers-191P4D12B

Each peptide is a portion of SEQ ID NO: 3; each start position is specified, the length of peptide is 15 amino acids, and the end position for each peptide is the start position plus fourteen.

Pos	123456789012345	score
12	PASASLVAGTLSVHH	13
2	GLELLGSSNPPASAS	12
3	LELLGSSNPPASASL	12
11	PPASASLVAGTLSVH	8
8	SSNPPASASLVAGTL	7
14	SASLVAGTLSVHHCA	7
1	AGLELLGSSNPPASA	6
4	ELLGSSNPPASASLV	6
5	LLGSSNPPASASLVA	6
9	SNPPASASLVAGTLS	6
15	ASLVAGTLSVHHCAC	6

Table L: Properties of 191P4D12(b)

191P4D12(b)B v.1	Bioinformatic Program	Outcome
ORF	ORF finder	264-1796
Protein length		510aa
Transmembrane region	TM Pred	2 TM, aa 14-30, 351-370
	HMMTop	1 TM, aa 347-371
	Sosui	2 TM, aa 14-31, 347-369
	TMHMM	1 TM, aa 350-372
Signal Peptide	Signal P	yes, cleaved aa 31-32
pI	pI/MW tool	pI 5.27
Molecular weight	pI/MW tool	55.4 kDa
Localization	PSORT	46% plasma membrane
	PSORT II	39.1% cytoplasmic, 21% nuclear
Motifs	Pfam	Immunoglobulin domain
	Prints	Cadherin signature
	Blocks	Ig domain, Herpesvirus glycoprotein D

v.6	Bioinformatic Program	Outcome
ORF	ORF finder	
Protein length		295 aa
Transmembrane region	TM Pred	1 TM, aa 135-156
	HMMTop	1 TM, aa 132-156
	Sosui	1 TM, aa 132-154
	TMHMM	1 TM, aa 135-157
Signal Peptide	Signal P	none
pI	pI/MW tool	pI 5.28
Molecular weight	pI/MW tool	32.6 kDa
Localization	PSORT	70% plasma membrane, 20% endoplasmic reticulum
	PSORT II	39% cytoplasmic, 21% nuclear
Motifs	Pfam	Immunoglobulin domain
	Prints	none
	Blocks	Herpesvirus glycoprotein D

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Table LI: Exon boundaries of transcript 191P4D12(b) v.1

Exon Number	Start	End	Length
1	2	342	341
2	343	702	360
3	703	993	291
4	994	1114	121
5	1115	1263	149
6	1264	1420	157
7	1421	1496	76
8	1497	1571	75
9	1572	3459	1888

Table LII(a). Nucleotide sequence of transcript variant 191P4D12(b) v.6 (SEQ ID NO: 105)

```
ggccgtcgtt gttggccaca gcgtgggaag cagctctggg ggagctcgga gctcccgatc      60
acggcttctt gggggtagct acggctgggt gtgtagaacg gggccggggc tggggctggg     120
tcccctagtg gagacccaag tgcgagaggc aagaactctg cagcttcctg ccttctgggt     180
cagttcctta ttcaagtctg ctactgctgg catcatttac aggccggtgc cccgcgggtg     240
agctggagac ctcagacgtg gtaactgtgg tgctgggcca ggacgcaaaa ctgccctgct     300
tctaccgagg ggactccggc gagcaagtgg ggcaagtggc atgggctcgg gtggacgcgg     360
gcgaaggcgc ccaggaacta gcgctactgc actccaaata cgggcttcat gtgagcccgg     420
cttacgaggg ccgcgtggag cagccgccgc ccccacgcaa ccccctggac ggctcagtgc     480
tcctgcgcaa cgcagtgcag gcggatgagg gcgagtacga gtgccgggtc agcaccttcc     540
ccgccggcag cttccaggcg cggctgcggc tccgagtgct ggtgcctccc ctgccctcac     600
tgaatcctgg tccagcacta gaagagggcc agggcctgac cctggcagcc tcctgcacag     660
ctgagggcag cccagccccc agcgtgacct gggacacgga ggtcaaaggc acaacgtcca     720
gccgttcctt caagcactcc cgctctgctg ccgtcacctc agagttccac ttggtgccta     780
gccgcagcat gaatgggcag ccactgactt gtgtggtgtc ccatcctggc ctgctccagg     840
accaaaggat cacccacatc ctccacgtgt ccttccttgc tgaggcctct gtgaggggcc     900
ttgaagacca aaatctgtgg cacattggca gagaaggagc tatgctcaag tgcctgagtg     960
aagggcagcc ccctccctca tacaactgga cacggctgga tgggcctctg cccagtgggg    1020
tacgagtgga tggggacact ttgggctttc ccccactgac cactgagcac agcggcatct    1080
acgtctgcca tgtcagcaat gagttctcct caagggattc tcaggtcact gtggatgttc    1140
ttgacccccа ggaagactct gggaagcagg tggacctagt gtcagcctcg gtggtggtgg    1200
tgggtgtgat cgccgcactc ttgttctgcc ttctggtggt ggtggtggtg ctcatgtccc    1260
gataccatcg gcgcaaggcc cagcagatga cccagaaata tgaggaggag ctgaccctga    1320
ccagggagaa ctccatccgg aggctgcatt cccatcacac ggaccccagg agccagccgg    1380
aggagagtgt agggctgaga gccgagggcc accctgatag tctcaaggac aacagtagct    1440
gctctgtgat gagtgaagag cccgagggcc gcagttactc cacgctgacc acggtgaggg    1500
agatagaaac acagactgaa ctgctgtctc caggctctgg gcgggccgag gaggaggaag    1560
atcaggatga aggcatcaaa caggccatga accattttgt tcaggagaat gggaccctac    1620
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Table LIII(a). Nucleotide sequence alignment of 191P4D12(b) v.1 (SEQ ID NO: 106) and 191P4D12(b) v.6 (SEQ ID NO: 107).

```
V.1      1 gGCCGTCGTTGTTGGCCACAGCGTGGGAAGCAGCTCTGGGGGAGCTCGGA   50
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6      1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcgga   50

V.1     51 GCTCCCGATCACGGCTTCTTGGGGGTAGCTACGGCTGGGTGTGTAGAACG   100
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6     51 gctcccgatcacggcttcttgggggtagctacggctgggtgtgtagaacg   100

V.1    101 GGGCCGGGGCTGGGGCTGGGTCCCCTAGTGGAGACCCAAGTGCGAGAGGC   150
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    101 gggccggggctggggctgggtcccctagtggagacccaagtgcgagaggc   150

V.1    151 AAGAACTCTGCAGCTTCCTGCCTTCTGGGTCAGTTCCTTATTCAAGTCTG   200
           |||||||||||||||||||||||||||||||||||||||||||||||||
V.6    151 aagaactctgcagcttcctgccttctgggtcagttccttattcaagt---   197

V.1    201 CAGCCGGCTCCCAGGGAGATCTCGGTGGAACTTCAGAAACGCTGGGCAGT   250

V.6    198 ---------------------------------------------------   197

V.1    251 CTGCCTTTCAACCATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG   300

V.6    198 ---------------------------------------------------   197

V.1    301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGC   350
                               ||||||||||||||||||||||||||||||
V.6    198 -----------------ctgctactgctggcatcatttacaggccggtgc   230

V.1    351 CCCGCGGGTGAGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCA   400
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    231 cccgcgggtgagctggagacctcagacgtggtaactgtggtgctgggcca   280

V.1    401 GGACGCAAAACTGCCCTGCTTCTACCGAGGGGACTCCGGCGAGCAAGTGG   450
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    281 ggacgcaaaactgccctgcttctaccgaggggactccggcgagcaagtgg   330

V.1    451 GGCAAGTGGCATGGGCTCGGGTGGACGCGGGCGAAGGCGCCCAGGAACTA   500
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    331 ggcaagtggcatgggctcgggtggacgcgggcgaaggcgcccaggaacta   380

V.1    501 GCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGGCTTACGAGGG   550
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    381 gcgctactgcactccaaatacgggcttcatgtgagcccggcttacgaggg   430

V.1    551 CCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC   600
           ||||||||||||||||||||||||||||||||||||||||||||||||||
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V.6    431 ccgcgtggagcagccgccgcccccacgcaacccccctggacggctcagtgc    480

V.1    601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTC    650
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    481 tcctgcgcaacgcagtgcaggcggatgagggcgagtacgagtgccgggtc    530

V.1    651 AGCACCTTCCCCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCT    700
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    531 agcaccttccccgccggcagcttccaggcgcggctgcggctccgagtgct    580

V.1    701 GGTGCCTCCCCTGCCCTCACTGAATCCTGGTCCAGCACTAGAAGAGGGCC    750
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    581 ggtgcctcccctgccctcactgaatcctggtccagcactagaagagggcc    630

V.1    751 AGGGCCTGACCCTGGCAGCCTCCTGCACAGCTGAGGGCAGCCCAGCCCCC    800
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    631 agggcctgaccctggcagcctcctgcacagctgagggcagcccagccccc    680

V.1    801 AGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCAGCCGTTCCTT    850
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    681 agcgtgacctgggacacggaggtcaaaggcacaacgtccagccgttcctt    730

V.1    851 CAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA    900
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    731 caagcactcccgctctgctgccgtcacctcagagttccacttggtgccta    780

V.1    901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGC    950
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    781 gccgcagcatgaatgggcagccactgacttgtgtggtgtcccatcctggc    830

V.1    951 CTGCTCCAGGACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGC   1000
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    831 ctgctccaggaccaaaggatcacccacatcctccacgtgtccttccttgc    880

V.1   1001 TGAGGCCTCTGTGAGGGGCCTTGAAGACCAAAATCTGTGGCACATTGGCA   1050
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    881 tgaggcctctgtgaggggccttgaagaccaaaatctgtggcacattggca    930

V.1   1051 GAGAAGGAGCTATGCTCAAGTGCCTGAGTGAAGGGCAGCCCCCTCCCTCA   1100
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    931 gagaaggagctatgctcaagtgcctgagtgaagggcagcccccteccteca    980

V.1   1101 TACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGGTACGAGTGGA   1150
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6    981 tacaactggacacggctggatgggcctctgcccagtggggtacgagtgga   1030

V.1   1151 TGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT   1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6   1031 tggggacactttgggctttccccactgaccactgagcacagcggcatct   1080

V.1   1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACT   1250
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6   1081 acgtctgccatgtcagcaatgagttctcctcaagggattctcaggtcact   1130

V.1   1251 GTGGATGTTCTTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGT   1300
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6   1131 gtggatgttcttgacccccaggaagactctgggaagcaggtggacctagt   1180

V.1   1301 GTCAGCCTCGGTGGTGGTGGTGGGTGTGATCGCCGCACTCTTGTTCTGCC   1350
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6   1181 gtcagcctcggtggtggtggtgggtgtgatcgccgcactcttgttctgcc   1230

V.1   1351 TTCTGGTGGTGGTGGTGGTGCTCATGTCCCGATACCATCGGCGCAAGGCC   1400
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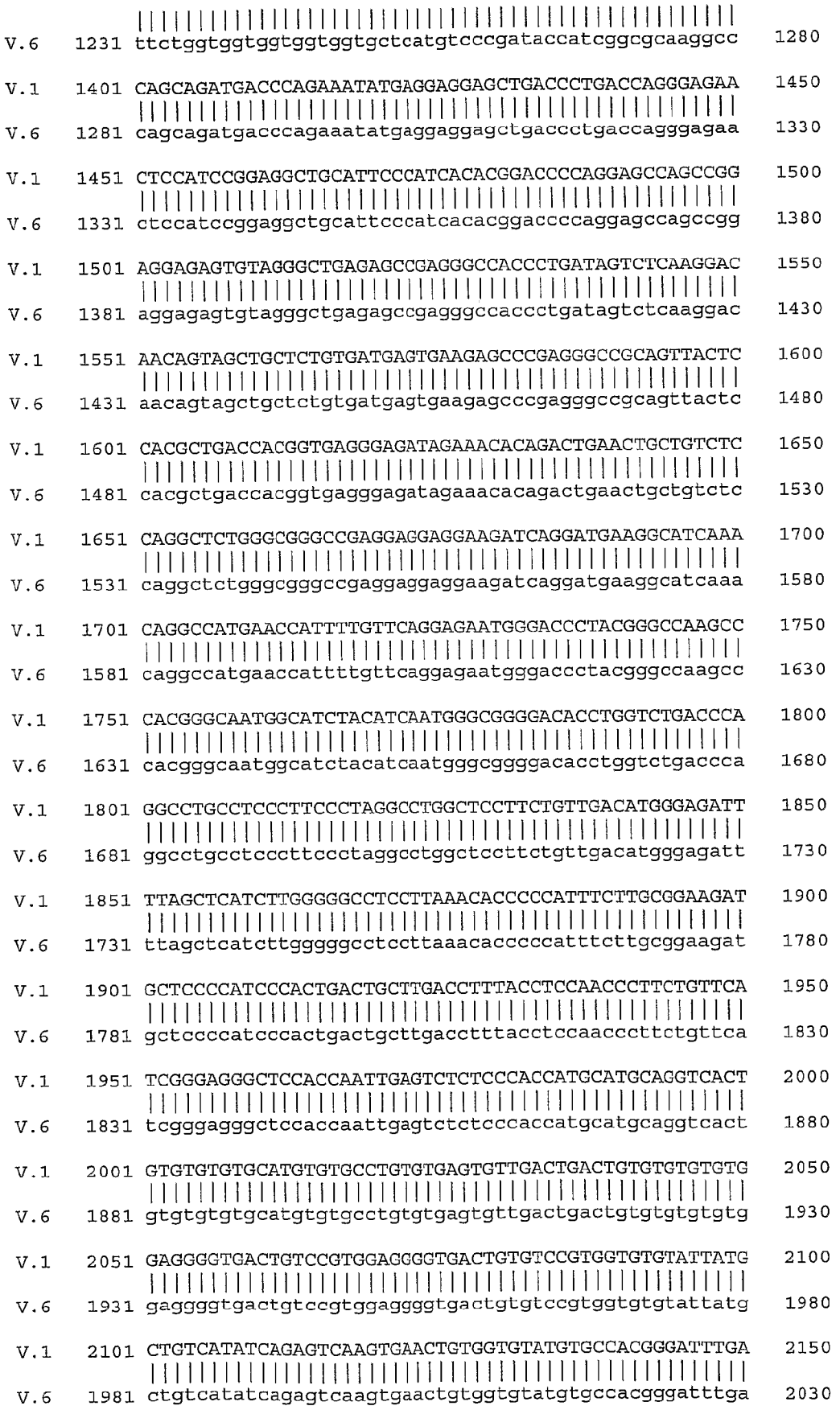
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V.6 1281 cagcagatgacccagaaatatgaggaggagctgaccctgaccagggagaa 1330
V.1 1451 CTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG 1500
V.6 1331 ctccatccggaggctgcattcccatcacacggaccccaggagccagccgg 1380
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V.6 1381 aggagagtgtagggctgagagccgagggccaccctgatagtctcaaggac 1430
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V.6   2031 gtggttgcgtgggcaacactgtcagggtttggcgtgtgtgtcatgtggct 2080

V.1   2201 GTGTGTGACCTCTGCCTGAAAAAGCAGGTATTTTCTCAGACCCCAGAGCA 2250
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6   2081 gtgtgtgacctctgcctgaaaaagcaggtattttctcagaccccagagca 2130

V.1   2251 GTATTAATGATGCAGAGGTTGGAGGAGAGAGGTGGAGACTGTGGCTCAGA 2300
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V.1   2351 AACCTGTCTCCTACCACTTCGGAGCCATGGGGGCAAGTGTGAAGCAGCCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||
V.6   2231 aacctgtctcctaccacttcggagccatggggcaagtgtgaagcagcca 2280

V.1   2401 GTCCCTGGGTCAGCCAGAGGCTTGAACTGTTACAGAAGCCCTCTGCCCTC 2450
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V.6   2281 gtcccctgggtcagccagaggcttgaactgttacagaagccctctgccctc 2330

V.1   2451 TGGTGGCCTCTGGGCCTGCTGCATGTACATATTTTCTGTAAATATACATG 2500
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V.6   2331 tggtggcctctgggcctgctgcatgtacatattttctgtaaatatacatg 2380

V.1   2501 CGCCGGGAGCTTCTTGCAGGAATACTGCTCCGAATCACTTTTAATTTTTT 2550
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V.6   2381 cgccgggagcttcttgcaggaatactgctccgaatcactttttaatttttt 2430

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           ||||||||||||||||||||||||||||||||||||||||||||||||||
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V.6   2631 gaaaaaaaaaattaaagaaagcctttagatttatccaatgtttactactg 2680

V.1   2801 GGATTGCTTAAAGTGAGGCCCCTCCAACACCAGGGGGTTAATTCCTGTGA 2850
           ||||||||||||||||||||||||||||||||||||||||||||||||||
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V.6   2781 agggcacctgagagctggtagagtctgaaattagggatgtgagcctcgtg 2830
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DEMANDES OU BREVETS VOLUMINEUX

LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS COMPREND PLUS D'UN TOME.

CECI EST LE TOME __1___ DE __3___

NOTE: Pour les tomes additionels, veillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE THAN ONE VOLUME.

THIS IS VOLUME __1___ OF __3___

NOTE: For additional volumes please contact the Canadian Patent Office.

CLAIMS:

1. A method for determining if there is dysregulated cellular growth in a human subject, comprising:

(a) contacting a test sample from a human subject suspected of having cancer with a probe that is capable of specifically binding to a 191P4D12(b)-related gene product, wherein the 191P4D12(b)-related gene product is an mRNA comprising the sequence set forth in SEQ ID NO: 2, SEQ ID NO:4, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 or SEQ ID NO:26, or a protein comprising the sequence set forth in SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 or SEQ ID NO:27, respectively;

(b) determining the level of expression of the 191P4D12(b)-related gene product in the test sample; and

(c) comparing the level so determined to the expression level of the 191P4D12(b)-related gene product in a normal tissue sample of the same tissue type as the test sample,

whereby an increase in the 191P4D12(b)-related gene product in the test sample relative to the normal tissue sample indicates dysregulated cellular growth in said test sample from an organ selected from the group consisting of bladder, lung, kidney, pancreas, colon, prostate, cervix, and ovary.

2. The method of claim 1, wherein the probe is an antibody or fragment thereof, either of which specifically binds to the protein.

3. The method of claim 2, wherein the antibody or antigen binding fragment is monoclonal.

4. The method of claim 2 or 3, wherein the antibody or antigen binding fragment thereof is labeled with a detectable marker.

5. The method of claim 1, wherein the gene product is said mRNA and determining the level of expression of the mRNA in the test sample comprises:

producing cDNA from the mRNA by reverse transcription;

amplifying the cDNA obtained; and

detecting the presence of the cDNA.

6. The method of claim 5, wherein the probe is a primer capable of specific binding to the mRNA or cDNA.

7. The method of claim 6, wherein the probe is labeled with a detectable marker.

8. The method of 4 or 7, wherein the detectable marker is a radioactive isotope is selected from the group consisting of ^{211}At, ^{131}I, ^{125}I, ^{90}Y, ^{186}Re, ^{188}Re, ^{153}Sm, ^{212}Bi, ^{32}P and radioactive isotopes of Lu.

9. The method of any one of claims 1 to 8, wherein the dysregulated cellular growth is an indication of the presence of cancer.

10. The method of any one of claims 1 to 8, wherein the dysregulated cellular growth is an indication of the status of cancer.

11. A method for determining susceptibility to developing cancer, comprising:

(a) contacting a test sample from a human subject suspected of having cancer with a probe that is capable of specifically binding to a 191P4D12(b) mRNA or a 191P4D12(b) protein, wherein the 191P4D12(b) mRNA comprising the sequence set forth in SEQ ID NO: 2, SEQ ID NO:4, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24 or SEQ ID NO:26, and the 191P4D12(b) protein comprising the sequence set forth in SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 or SEQ ID NO:27, respectively;

(b) determining the level of expression of the 191P4D12(b) mRNA or the 191P4D12(b) protein in the test sample; and

(c) comparing the level so determined to the expression level of the 191P4D12(b) mRNA or the 191P4D12(b) protein in a normal tissue sample of the same tissue type as the test sample,

whereby an increase in the 191P4D12(b) mRNA or the 191P4D12(b) protein in the test sample relative to the normal tissue sample indicates susceptibility to developing cancer in said test sample from an organ selected from the group consisting of bladder, lung, kidney, pancreas, colon, prostate, cervix, and ovary.

12. Use of an antibody or antigen binding fragment thereof that specifically binds to a protein comprising the amino acid sequence of SEQ ID NO: 3 for inhibiting growth of a tumor cell that expresses the protein, wherein the antibody or antigen binding fragment is conjugated to a cytotoxic agent, and wherein the cell is from a tissue source selected from the group consisting of prostate, bladder, lung, pancreas, and breast cancer.

13. The use of claim 12, wherein the antibody or antigen binding fragment thereof specifically binds to an extracellular domain of the protein comprising the amino acid sequence of SEQ ID NO: 3.

14. The use of claim 12 or 13, wherein the antibody or antigen binding fragment comprises an antigen binding site that specifically binds to an epitope within amino acids of SEQ ID NO: 3.

15. The use of claim 12 or 13, wherein the antibody or antigen binding fragment comprises the variable regions of the heavy chains and light chains of an antibody that binds specifically to the amino acid sequence of SEQ ID NO: 3.

16. The use of any one of claims 12 to 15, wherein the antibody or antigen binding fragment is monoclonal.

17. The use of any one of claims 12 to 16, wherein the antibody or antigen binding fragment is fully human.

18. The use of any one of claims 12 to 17, wherein the antigen binding fragment is an Fab, $F(ab')_2$, Fv or Sfv fragment.

19. The use of claim 12 or 13, wherein the antibody is a recombinant protein.

20. The use of claim 19, wherein the recombinant protein comprises the antigen binding region of the antibody.

21. The use of claim 12, 13 or 14, wherein the antibody is a polyclonal antibody.

22. The use of any one of claims 12 to 21, wherein the cytotoxic agent is a toxin, a therapeutic agent or a radioisotope.

23. The use of claim 22, wherein the radioisotope is selected from the group consisting of ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, ^{186}Re, ^{211}At, ^{125}I, ^{188}Re, ^{153}Sm, ^{213}Bi, ^{32}P, and Lu.

24. The use of claim 21, wherein the cytotoxic agent is selected from the group consisting of auristatins, auromycins, maytansinoids, yttrium, bismuth, ricin, ricin A-chain, combrestatin, duocarmycins, dolostatins, doxorubicin, daunorubicin, taxol, cisplatin, cc1065, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin, diphtheria toxin, *Pseudomonas* exotoxin (PE) A, PE40, abrin, abrin A chain, modeccin A chain, alpha-sarcin, gelonin, mitogellin, retstrictocin, phenomycin, enomycin, curicin, crotin, calicheamicin, and *Sapaonaria officinalis* inhibitor.

25. Use of antibody-agent conjugate comprising: an antibody or antigen binding fragment thereof that binds specifically to a protein comprising the amino acid sequence of SEQ ID NO: 3; and a cytotoxic agent conjugated to the antibody or fragment, for inhibiting growth of a tumor cell that expresses the protein, wherein the cell is from a tissue source selected from the group consisting of prostate, bladder, lung, pancreas, and breast cancer.

26. The use of claim 25, wherein the antibody of the antibody-agent conjugate is a monoclonal antibody or a polyclonal antibody.

27. The use of claim 25, wherein the antigen binding fragment of the antibody of the antibody-agent conjugate is an Fab, $F(ab')_2$, Fv, or Sfv fragment.

28. The use of claim 25, 26 or 27, wherein the cytotoxic agent is a toxin, a therapeutic agent, or a radioisotope.

29. The use of claim 28, wherein the radioisotope is selected from the group consisting of ^{212}Bi, ^{131}I, ^{131}In, ^{90}Y, ^{186}Re, ^{211}At, ^{125}I, ^{188}Re, ^{153}Sm, ^{213}Bi, ^{32}P, and Lu.

30. The use of claim 28, wherein the cytotoxic agent is selected from the group consisting of auristatins, auromycins, maytansinoids, yttrium, bismuth, ricin, ricin A-chain, combrestatin, duocarmycins, dolostatins, doxorubicin, daunorubicin, taxol, cisplatin, cc1065, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin, diphtheria toxin, *Pseudomonas* exotoxin (PE) A, PE40, abrin, abrin A chain, modeccin A chain, alpha-sarcin, gelonin, mitogellin, retstrictocin, phenomycin, enomycin, curicin, crotin, calicheamicin, and *Sapaonaria officinalis* inhibitor.

Figure 1: 191P4D12(b) SSH sequence of 223 nucleotides. (SEQ ID NO: 1)

```
  1 GATCACTAAT TCAAGGCTCT TCTGGATGTT TCTCTGGGTT GGGGCTGGAG TTCAATGAGG
 61 TTTATTTTTA GCTGGCCCAC CCAGATACAC TCAGCCAGAA TACCTAGATT TAGTACCCAA
121 ACTCTTCTTA GTCTGAAATC TGCTGGATTT CTGGCCTAAG GGAGAGGCTC CCATCCTTCG
181 TTCCCCAGCC AGCCTAGGAC TTCGAATGTG GAGCCTGAAG ATC
```

Figure 2:

Figure 2A. The cDNA (SEQ ID. NO.: 2) and amino acid sequence (SEQ ID. NO.: 3) of 191P4D12(b) v.1 clone 1A1. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
 541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
 114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
 601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
 134   A  G  S  F  Q  A  R  L  R  L  R  V  L  V  P  P  L  P  S  L
 661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
 154   N  P  G  P  A  L  E  E  G  Q  G  L  T  L  A  A  S  C  T  A
 721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
 174   E  G  S  P  A  P  S  V  T  W  D  T  E  V  K  G  T  T  S  S
 781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
 194   R  S  F  K  H  S  R  S  A  A  V  T  S  E  F  H  L  V  P  S
 841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
 214   R  S  M  N  G  Q  P  L  T  C  V  V  S  H  P  G  L  L  Q  D
 901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
 234   Q  R  I  T  H  I  L  H  V  S  F  L  A  E  A  S  V  R  G  L
 961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
 254   E  D  Q  N  L  W  H  I  G  R  E  G  A  M  L  K  C  L  S  E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
 274   G  Q  P  P  P  S  Y  N  W  T  R  L  D  G  P  L  P  S  G  V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
 294   R  V  D  G  D  T  L  G  F  P  P  L  T  T  E  H  S  G  I  Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
 314   V  C  H  V  S  N  E  F  S  S  R  D  S  Q  V  T  V  D  V  L
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1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q P E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttatttatttttatttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc

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3181 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3421 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2B. The cDNA (SEQ ID. NO.: 4) and amino acid sequence (SEQ ID. NO.: 5) of 191P4D12(b) v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  L
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCC
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
 541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
 114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
 601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
 134   A  G  S  F  Q  A  R  L  R  L  R  V  L  V  P  P  L  P  S  L
 661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
 154   N  P  G  P  A  L  E  E  G  Q  G  L  T  L  A  A  S  C  T  A
 721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
 174   E  G  S  P  A  P  S  V  T  W  D  T  E  V  K  G  T  T  S  S
 781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
 194   R  S  F  K  H  S  R  S  A  A  V  T  S  E  F  H  L  V  P  S
 841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
 214   R  S  M  N  G  Q  P  L  T  C  V  V  S  H  P  G  L  L  Q  D
 901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
 234   Q  R  I  T  H  I  L  H  V  S  F  L  A  E  A  S  V  R  G  L
 961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
 254   E  D  Q  N  L  W  H  I  G  R  E  G  A  M  L  K  C  L  S  E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
 274   G  Q  P  P  P  S  Y  N  W  T  R  L  D  G  P  L  P  S  G  V
```

1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q P E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttttatttatttttatttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt

2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3421 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa

Figure 2C. The cDNA (SEQ ID. NO. : 6) and amino acid sequence (SEQ ID. NO. : 7) of 191P4D12(b) v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
1 M P L S L G A E M W G P E
241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
14 A W L L L L L L L A S F T G R C P A G E
301 AGGCCTGGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
34 L E T S D V V T V V L G Q D A K L P C F
361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
54 Y R G D S G E Q V G Q V A W A R V D A G
421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
74 E G A Q E L A L L H S K Y G L H V S P A
481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
94 Y E G R V E Q P P P P R N P L D G S V L
541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
114 L R N A V Q A D E G E Y E C R V S T F P
601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
134 A G S F Q A R L R L R V L V P P L P S L
661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
154 N P G P A L E E G Q G L T L A A S C T A
721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
174 E G S P A P S V T W D T E V K G T T S S
781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194 R S F K H S R S A A V T S E F H L V P S
841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L

961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254 E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274 G Q P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q P E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcttgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtatttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttatttatttttattttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc

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2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3421 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2D. The cDNA (SEQ ID. NO. : 8) and amino acid sequence (SEQ ID. NO. : 9) of 191P4D12(b) v.4. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
 541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
 114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
 601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
 134   A  G  S  F  Q  A  R  L  R  L  R  V  L  V  P  P  L  P  S  L
 661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
 154   N  P  G  P  A  L  E  E  G  Q  G  L  T  L  A  A  S  C  T  A
 721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
 174   E  G  S  P  A  P  S  V  T  W  D  T  E  V  K  G  T  T  S  S
 781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
 194   R  S  F  K  H  S  R  S  A  A  V  T  S  E  F  H  L  V  P  S
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841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254 E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274 G Q P P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q P E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaaccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 agtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc

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2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttatttatttttattttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3421 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2E. The cDNA (SEQ ID. NO. : 10) and amino acid sequence (SEQ ID. NO. : 11) of 191P4D12(b) v.5. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                          M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
 541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
 114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
 601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
 134   A  G  S  F  Q  A  R  L  R  L  R  V  L  V  P  P  L  P  S  L
 661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
 154   N  P  G  P  A  L  E  E  G  Q  G  L  T  L  A  A  S  C  T  A
```

721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
174 E G S P A P S V T W D T E V K G T T S S
781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194 R S F K H S R S A A V T S E F H L V P S
841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254 E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274 G Q P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q P E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa

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2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttatttatttttatttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagactccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3421 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2F. The cDNA (SEQ ID. NO. : 12) and amino acid sequence (SEQ ID. NO. : 13) of 191P4D12(b) v.6. The start methionine is underlined. The open reading frame extends from nucleic acid 789-1676 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgctactgctggcatcatttacaggccggtgccccgcgggtg
 241 agctggagacctcagacgtggtaactgtggtgctgggccaggacgcaaaactgccctgct
 301 tctaccgaggggactccggcgagcaagtggggcaagtggcatgggctcgggtggacgcgg
 361 gcgaaggcgcccaggaactagcgctactgcactccaaatacgggcttcatgtgagcccgg
 421 cttacgagggccgcgtggagcagccgccgcccccacgcaacccccctggacggctcagtgc
 481 tcctgcgcaacgcagtgcaggcggatgagggcgagtacgagtgccgggtcagcaccttcc
 541 ccgccggcagcttccaggcgcggctgcggctccgagtgctggtgcctcccctgccctcac
 601 tgaatcctggtccagcactagaagagggccagggcctgaccctggcagcctcctgcacag
 661 ctgagggcagcccagccccagcgtgacctgggacacggaggtcaaaggcacaacgtcca
 721 gccgttccttcaagcactcccgctctgctgccgtcacctcagagttccacttggtgccta
   1         M  N  G  Q  P  L  T  C  V  V  S  H  P  G  L  L  Q  D
 781 gccgcagcATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
  19   Q  R  I  T  H  I  L  H  V  S  F  L  A  E  A  S  V  R  G  L
 841 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
```

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 39   E  D  Q  N  L  W  H  I  G  R  E  G  A  M  L  K  C  L  S  E
901 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
 59   G  Q  P  P  P  S  Y  N  W  T  R  L  D  G  P  L  P  S  G  V
961 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
 79   R  V  D  G  D  T  L  G  F  P  P  L  T  T  E  H  S  G  I  Y
1021 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
 99   V  C  H  V  S  N  E  F  S  S  R  D  S  Q  V  T  V  D  V  L
1081 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
119   D  P  Q  E  D  S  G  K  Q  V  D  L  V  S  A  S  V  V  V  V
1141 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
139   G  V  I  A  A  L  L  F  C  L  L  V  V  V  V  V  L  M  S  R
1201 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
159   Y  H  R  R  K  A  Q  Q  M  T  Q  K  Y  E  E  E  L  T  L  T
1261 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
179   R  E  N  S  I  R  R  L  H  S  H  H  T  D  P  R  S  Q  P  E
1321 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
199   E  S  V  G  L  R  A  E  G  H  P  D  S  L  K  D  N  S  S  C
1381 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
219   S  V  M  S  E  E  P  E  G  R  S  Y  S  T  L  T  T  V  R  E
1441 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
239   I  E  T  Q  T  E  L  L  S  P  G  S  G  R  A  E  E  E  E  D
1501 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
259   Q  D  E  G  I  K  Q  A  M  N  H  F  V  Q  E  N  G  T  L  R
1561 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
279   A  K  P  T  G  N  G  I  Y  I  N  G  R  G  H  L  V  *
1621 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1681 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1741 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1801 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1861 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
1921 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
1981 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2041 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2101 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2161 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2221 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2281 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2341 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2401 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2461 tgtatttttatttatttttatttttatttttttttagagatggagtctcactatgttgc
2521 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
2581 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
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2641 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2701 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2761 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2821 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
2881 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
2941 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3001 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc
3061 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3121 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3181 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3241 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3301 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2G. The cDNA (SEQ ID. NO. : 14) and amino acid sequence (SEQ ID. NO. : 15) of 191P4D12(b) v.7. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1721 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
 541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
 114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
 601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
 134   A  G  S  F  Q  A  R  L  R  L  R  V  L  V  P  P  L  P  S  L
 661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
 154   N  P  G  P  A  L  E  E  G  Q  G  L  T  L  A  A  S  C  T  A
 721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
 174   E  G  S  P  A  P  S  V  T  W  D  T  E  V  K  G  T  T  S  S
 781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
 194   R  S  F  K  H  S  R  S  A  A  V  T  S  E  F  H  L  V  P  S
 841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
```

214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254 E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274 G Q P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q S E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGAGTG
414 E P E G R S Y S T L T T V R E I E T Q T
1501 AAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGGAGATAGAAACACAGA
434 E L L S P G S G R A E E E E D Q D E G I
1561 CTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAGATCAGGATGAAGGCA
454 K Q A M N H F V Q E N G T L R A K P T G
1621 TCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTACGGGCCAAGCCCACGG
474 N G I Y I N G R G H L V *
1681 GCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAcccaggcctgcctcccttc
1741 cctaggcctggctccttctgttgacatgggagattttagctcatcttgggggcctcctta
1801 aacacccccatttcttgcggaagatgctccccatcccactgactgcttgacctttacctc
1861 caacccttctgttcatcgggagggctccaccaattgagtctctcccaccatgcatgcagg
1921 tcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactgtgtgtgtgtggaggg
1981 gtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatgctgtcatatcagagt
2041 caagtgaactgtggtgtatgtgccacgggatttgagtggttgcgtgggcaacactgtcag
2101 ggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaaaaagcaggtattttc
2161 tcagaccccagagcagtattaatgatgcagaggttggaggagagaggtggagactgtggc
2221 tcagacccaggtgtgcgggcatagctggagctggaatctgcctccggtgtgagggaacct
2281 gtctcctaccacttcggagccatgggggcaagtgtgaagcagccagtccctgggtcagcc
2341 agaggcttgaactgttacagaagccctctgccctctggtggcctctgggcctgctgcatg
2401 tacatattttctgtaaatatacatgcgccgggagcttcttgcaggaatactgctccgaat
2461 cacttttaatttttttctttttttttttcttgccctttccattagttgtatttttattta
2521 tttttatttttatttttttttagagatggagtctcactatgttgctcaggctggccttga

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2581 actcctgggctcaagcaatcctcctgcctcagcctccctagtagctgggactttaagtgt
2641 acaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaaattaaagaaagcctt
2701 tagatttatccaatgtttactactgggattgcttaaagtgaggcccctccaacaccaggg
2761 ggttaattcctgtgattgtgaaaggggctacttccaaggcatcttcatgcaggcagcccc
2821 ttgggagggcacctgagagctggtagagtctgaaattagggatgtgagcctcgtggttac
2881 tgagtaaggtaaaattgcatccaccattgtttgtgataccttagggaattgcttggacct
2941 ggtgacaagggctcctgttcaatagtggtgttggggagagagagcagtgattatagac
3001 cgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtgagaatgtcgcctttc
3061 cccctgggttttggatcactaattcaaggctcttctggatgtttctctgggttggggctg
3121 gagttcaatgaggtttatttttagctggcccacccagatacactcagccagaatacctag
3181 atttagtacccaaactcttcttagtctgaaatctgctggatttctggcctaagggagagg
3241 ctcccatccttcgttccccagccagcctaggacttcgaatgtggagcctgaagatctaag
3301 atcctaacatgtacattttatgtaaatatgtgcatatttgtacataaaatgatattctgt
3361 ttttaaataaacagacaaaacttgaaaaa
```

Figure 2H. The cDNA (SEQ ID. NO. : 16) and amino acid sequence (SEQ ID. NO. : 17) of 191P4D12(b) v.8. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
 541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
 114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
 601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
 134   A  G  S  F  Q  A  R  L  R  L  R  V  L  V  P  P  L  P  S  L
 661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
 154   N  P  G  P  A  L  E  E  G  Q  G  L  T  L  A  A  S  C  T  A
 721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
 174   E  G  S  P  A  P  S  V  T  W  D  T  E  V  K  G  T  T  S  S
 781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
```

194 R S F K H S R S A A V T S E F H L V P S
841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254 E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274 G Q P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q P E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca

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2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttatttatttttatttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtgctggtgacaagggctcctgttcaatagtggtgttggggagagagagagca
3001 gtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtgaga
3061 atgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttctct
3121 gggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactcagc
3181 cagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttctggc
3241 ctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtggagcc
3301 tgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacataaa
3361 atgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2i. The cDNA (SEQ ID. NO.: 18) and amino acid sequence (SEQ ID. NO.: 19) of 191P4D12(b) v.9 clone BCP1. The start methionine is underlined. The open reading frame extends from nucleic acid 708-1121 including the stop codon.

```
   1 gtctgacccaggcctgcctcccttccctaggcctggctccttctgttgacatgggagatt
  61 ttagctcatcttgggggcctccttaaacacccccatttcttgcggaagatgctccccatc
 121 ccactgactgcttgacctttacctccaacccttctgttcatcgggagggctccaccaatt
 181 gagtctctcccaccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgt
 241 tgactgactgtgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggt
 301 gtgtattatgctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttga
 361 gtggttgcgtgggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacc
 421 tctgcctgaaaaagcaggtattttctcagaccccagagcagtattaatgatgcagaggtt
 481 ggaggagagaggtggagactgtggctcagacccaggtgtgcgggcatagctggagctgga
 541 atctgcctccggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgt
 601 gaagcagccagtccctgggtcagccagaggcttgaactgttacagaagccctctgccctc
   1                                                 M  R  R  E  L
 661 tggtggcctctgggcctgctgcatgtacatattttctgtaaatatacATGCGCCGGGAGC
   6   L  A  G  I  L  L  R  I  T  F  N  F  F  L  F  F  F  L  P  F
 721 TTCTTGCAGGAATACTGCTCCGAATCACTTTTAATTTTTTTCTTTTTTTTTTTCTTGCCCT
  26   P  L  V  V  F  F  I  Y  F  Y  F  Y  F  F  L  E  M  E  S  H
 781 TTCCATTAGTTGTATTTTTTATTTATTTTTATTTTTATTTTTTTTTTAGAGATGGAGTCTC
  46   Y  V  A  Q  A  G  L  E  L  L  G  S  S  N  P  P  A  S  A  S
 841 ACTATGTTGCTCAGGCTGGCCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTCAGCCT
  66   L  V  A  G  T  L  S  V  H  H  C  A  C  F  E  S  F  T  K  R
 901 CCCTAGTAGCTGGGACTTTAAGTGTACACCACTGTGCCTGCTTTGAATCCTTTACGAAGA
```

```
 86   K  K  K  L  K  K  A  F  R  F  I  Q  C  L  L  L  G  L  L  K
961 GAAAAAAAAAATTAAAGAAAGCCTTTAGATTTATCCAATGTTTACTACTGGGATTGCTTA
106   V  R  P  L  Q  H  Q  G  V  N  S  C  D  C  E  R  G  Y  F  Q
1021 AAGTGAGGCCCCTCCAACACCAGGGGGTTAATTCCTGTGATTGTGAAAGGGGCTACTTCC
126   G  I  F  M  Q  A  A  P  W  E  G  T  *
1081 AAGGCATCTTCATGCAGGCAGCCCCTTGGGAGGGCACCTGAgagctggtagagtctgaaa
1141 ttagggatgtgagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtg
1201 ataccttagggaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggg
1261 gagagagagagcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggt
1321 gctgggggtgagaatgtcgcctttccccctgggttttggatcactaattcaaggctcttc
1381 tggatgtttctctgggttggggctggagttcaatgaggtttatttttagctggcccaccc
1441 agatacactcagccagaatacctagatttagtacccaaactcttcttagtctgaaatctg
1501 ctggatttctggcctaagggagaggctcccatccttcgttccccagccagcctaggactt
1561 cgaatgtggagcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcat
1621 atttgtacataaaatgatattctgtttttaaataaacagacaaaacttg
```

Figure 2J. The cDNA (SEQ ID. NO. : 20) and amino acid sequence (SEQ ID. NO. : 21) of 191P4D12(b) v.10. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  G  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGGGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
 541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
 114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
 601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
 134   A  G  S  F  Q  A  R  L  R  L  R  V  L  V  P  P  L  P  S  L
 661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
 154   N  P  G  P  A  L  E  E  G  Q  G  L  T  L  A  A  S  C  T  A
 721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
 174   E  G  S  P  A  P  S  V  T  W  D  T  E  V  K  G  T  T  S  S
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781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194 R S F K H S R S A A V T S E F H L V P S
841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254 E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274 G Q P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q P E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc

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2341 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttttatttatttttatttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3421 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2K. The cDNA (SEQ ID. NO. : 22) and amino acid sequence (SEQ ID. NO. : 23) of 191P4D12(b) v.11. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
 541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
 114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
 601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
 134   A  G  S  F  Q  A  R  L  R  L  R  V  M  V  P  P  L  P  S  L
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661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGATGGTGCCTCCCCTGCCCTCAC
154 N P G P A L E E G Q G L T L A A S C T A
721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
174 E G S P A P S V T W D T E V K G T T S S
781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194 R S F K H S R S A A V T S E F H L V P S
841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254 E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274 G Q P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 D P Q E D S G K Q V D L V S A S V V V V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354 G V I A A L L F C L L V V V V V L M S R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374 Y H R R K A Q Q M T Q K Y E E E L T L T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394 R E N S I R R L H S H H T D P R S Q P E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414 E S V G L R A E G H P D S L K D N S S C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434 S V M S E E P E G R S Y S T L T T V R E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGAGGG
454 I E T Q T E L L S P G S G R A E E E E D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474 Q D E G I K Q A M N H F V Q E N G T L R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494 A K P T G N G I Y I N G R G H L V *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg

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2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttatttatttttatttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3421 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
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Figure 2L. The cDNA (SEQ ID. NO.: 24) and amino acid sequence (SEQ ID. NO.: 25) of 191P4D12(b) v.12. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1796 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
 421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
  74   E  G  A  Q  E  L  A  L  L  H  S  K  Y  G  L  H  V  S  P  A
 481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
  94   Y  E  G  R  V  E  Q  P  P  P  P  R  N  P  L  D  G  S  V  L
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541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
114   L  R  N  A  V  Q  A  D  E  G  E  Y  E  C  R  V  S  T  F  P
601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
134   A  G  S  F  Q  A  R  L  R  L  R  V  L  V  P  P  L  P  S  L
661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
154   N  P  G  P  A  L  E  E  G  Q  G  L  T  L  A  A  S  C  T  A
721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
174   E  G  S  P  A  P  S  V  T  W  D  T  E  V  K  G  T  T  S  S
781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194   R  S  F  K  H  S  R  S  A  A  V  T  S  E  F  H  L  V  P  S
841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214   R  S  M  N  G  Q  P  L  T  C  V  V  S  H  P  G  L  L  Q  D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234   Q  R  I  T  H  I  L  H  V  S  F  L  A  E  A  S  V  R  G  L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254   E  D  Q  N  L  W  H  I  G  R  E  G  A  M  L  K  C  L  S  E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274   G  Q  P  P  P  S  Y  N  W  T  R  L  D  G  P  L  P  S  G  V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294   R  V  D  G  D  T  L  G  F  P  P  L  T  T  E  H  S  G  I  Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314   V  C  H  V  S  N  E  F  S  S  R  D  S  Q  V  T  V  D  V  L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334   D  P  Q  E  D  S  G  K  Q  V  D  L  V  S  A  S  V  V  V  V
1261 TTGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGGTGG
354   G  V  I  A  A  L  L  F  C  L  L  V  V  V  V  V  L  M  S  R
1321 TGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGTCCC
374   Y  H  R  R  K  A  Q  Q  M  T  Q  K  Y  E  E  E  L  T  L  T
1381 GATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCCTGA
394   R  E  N  S  I  R  R  L  H  S  H  H  T  D  P  R  S  Q  P  E
1441 CCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGCCGG
414   E  S  V  G  L  R  A  E  G  H  P  D  S  L  K  D  N  S  S  C
1501 AGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTAGCT
434   S  V  M  S  E  E  P  E  G  C  S  Y  S  T  L  T  T  V  R  E
1561 GCTCTGTGATGAGTGAAGAGCCCGAGGGCTGCAGTTACTCCACGCTGACCACGGTGAGGG
454   I  E  T  Q  T  E  L  L  S  P  G  S  G  R  A  E  E  E  E  D
1621 AGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGGAAG
474   Q  D  E  G  I  K  Q  A  M  N  H  F  V  Q  E  N  G  T  L  R
1681 ATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCCTAC
494   A  K  P  T  G  N  G  I  Y  I  N  G  R  G  H  L  V  *
1741 GGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAccca
1801 ggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctcatc
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1861 ttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactgactg
1921 cttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctctcc
1981 caccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactgactg
2041 tgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtattatg
2101 ctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttgcgt
2161 gggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcctgaa
2221 aaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggagaga
2281 ggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcctcc
2341 ggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcagcca
2401 gtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggcctc
2461 tgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgcagg
2521 aatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccattagt
2581 tgtatttttttatttatttttatttttatttttttttagagatggagtctcactatgttgc
2641 tcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagtagc
2701 tgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaaaaa
2761 attaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgaggcc
2821 cctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcatctt
2881 catgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattagggatgt
2941 gagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgataccttagg
3001 gaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagagaga
3061 gcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggggtg
3121 agaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgtttc
3181 tctgggttggggctggagttcaatgaggtttatttttagctggcccacccagatacactc
3241 agccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatttct
3301 ggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgtgga
3361 gcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgtacat
3421 aaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2M. The cDNA (SEQ ID. NO. : 26) and amino acid sequence (SEQ ID. NO. : 27) of 191P4D12(b) v.13. The start methionine is underlined. The open reading frame extends from nucleic acid 264-1799 including the stop codon.

```
   1 ggccgtcgttgttggccacagcgtgggaagcagctctgggggagctcggagctcccgatc
  61 acggcttcttgggggtagctacggctgggtgtgtagaacggggccggggctggggctggg
 121 tcccctagtggagacccaagtgcgagaggcaagaactctgcagcttcctgccttctgggt
 181 cagttccttattcaagtctgcagccggctcccagggagatctcggtggaacttcagaaac
   1                         M  P  L  S  L  G  A  E  M  W  G  P  E
 241 gctgggcagtctgcctttcaaccATGCCCCTGTCCCTGGGAGCCGAGATGTGGGGGCCTG
  14   A  W  L  L  L  L  L  L  A  S  F  T  G  R  C  P  A  G  E
 301 AGGCCTGGCTGCTGCTGCTGCTACTGCTGGCATCATTTACAGGCCGGTGCCCCGCGGGTG
  34   L  E  T  S  D  V  V  T  V  V  L  G  Q  D  A  K  L  P  C  F
 361 AGCTGGAGACCTCAGACGTGGTAACTGTGGTGCTGGGCCAGGACGCAAAACTGCCCTGCT
  54   Y  R  G  D  S  G  E  Q  V  G  Q  V  A  W  A  R  V  D  A  G
```

421 TCTACCGAGGGGACTCCGGCGAGCAAGTGGGGCAAGTGGCATGGGCTCGGGTGGACGCGG
74 E G A Q E L A L L H S K Y G L H V S P A
481 GCGAAGGCGCCCAGGAACTAGCGCTACTGCACTCCAAATACGGGCTTCATGTGAGCCCGG
94 Y E G R V E Q P P P P R N P L D G S V L
541 CTTACGAGGGCCGCGTGGAGCAGCCGCCGCCCCCACGCAACCCCCTGGACGGCTCAGTGC
114 L R N A V Q A D E G E Y E C R V S T F P
601 TCCTGCGCAACGCAGTGCAGGCGGATGAGGGCGAGTACGAGTGCCGGGTCAGCACCTTCC
134 A G S F Q A R L R L R V L V P P L P S L
661 CCGCCGGCAGCTTCCAGGCGCGGCTGCGGCTCCGAGTGCTGGTGCCTCCCCTGCCCTCAC
154 N P G P A L E E G Q G L T L A A S C T A
721 TGAATCCTGGTCCAGCACTAGAAGAGGGCCAGGGCCTGACCCTGGCAGCCTCCTGCACAG
174 E G S P A P S V T W D T E V K G T T S S
781 CTGAGGGCAGCCCAGCCCCCAGCGTGACCTGGGACACGGAGGTCAAAGGCACAACGTCCA
194 R S F K H S R S A A V T S E F H L V P S
841 GCCGTTCCTTCAAGCACTCCCGCTCTGCTGCCGTCACCTCAGAGTTCCACTTGGTGCCTA
214 R S M N G Q P L T C V V S H P G L L Q D
901 GCCGCAGCATGAATGGGCAGCCACTGACTTGTGTGGTGTCCCATCCTGGCCTGCTCCAGG
234 Q R I T H I L H V S F L A E A S V R G L
961 ACCAAAGGATCACCCACATCCTCCACGTGTCCTTCCTTGCTGAGGCCTCTGTGAGGGGCC
254 E D Q N L W H I G R E G A M L K C L S E
1021 TTGAAGACCAAAATCTGTGGCACATTGGCAGAGAAGGAGCTATGCTCAAGTGCCTGAGTG
274 G Q P P P S Y N W T R L D G P L P S G V
1081 AAGGGCAGCCCCCTCCCTCATACAACTGGACACGGCTGGATGGGCCTCTGCCCAGTGGGG
294 R V D G D T L G F P P L T T E H S G I Y
1141 TACGAGTGGATGGGGACACTTTGGGCTTTCCCCCACTGACCACTGAGCACAGCGGCATCT
314 V C H V S N E F S S R D S Q V T V D V L
1201 ACGTCTGCCATGTCAGCAATGAGTTCTCCTCAAGGGATTCTCAGGTCACTGTGGATGTTC
334 A D P Q E D S G K Q V D L V S A S V V V
1261 TTGCAGACCCCCAGGAAGACTCTGGGAAGCAGGTGGACCTAGTGTCAGCCTCGGTGGTGG
354 V G V I A A L L F C L L V V V V V L M S
1321 TGGTGGGTGTGATCGCCGCACTCTTGTTCTGCCTTCTGGTGGTGGTGGTGGTGCTCATGT
374 R Y H R R K A Q Q M T Q K Y E E E L T L
1381 CCCGATACCATCGGCGCAAGGCCCAGCAGATGACCCAGAAATATGAGGAGGAGCTGACCC
394 T R E N S I R R L H S H H T D P R S Q P
1441 TGACCAGGGAGAACTCCATCCGGAGGCTGCATTCCCATCACACGGACCCCAGGAGCCAGC
414 E E S V G L R A E G H P D S L K D N S S
1501 CGGAGGAGAGTGTAGGGCTGAGAGCCGAGGGCCACCCTGATAGTCTCAAGGACAACAGTA
434 C S V M S E E P E G R S Y S T L T T V R
1561 GCTGCTCTGTGATGAGTGAAGAGCCCGAGGGCCGCAGTTACTCCACGCTGACCACGGTGA
454 E I E T Q T E L L S P G S G R A E E E E
1621 GGGAGATAGAAACACAGACTGAACTGCTGTCTCCAGGCTCTGGGCGGGCCGAGGAGGAGG
474 D Q D E G I K Q A M N H F V Q E N G T L

```
1681 AAGATCAGGATGAAGGCATCAAACAGGCCATGAACCATTTTGTTCAGGAGAATGGGACCC
 494   R  A  K  P  T  G  N  G  I  Y  I  N  G  R  G  H  L  V  *
1741 TACGGGCCAAGCCCACGGGCAATGGCATCTACATCAATGGGCGGGGACACCTGGTCTGAc
1801 ccaggcctgcctcccttccctaggcctggctccttctgttgacatgggagattttagctc
1861 atcttgggggcctccttaaacacccccatttcttgcggaagatgctccccatcccactga
1921 ctgcttgacctttacctccaacccttctgttcatcgggagggctccaccaattgagtctc
1981 tcccaccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgttgactga
2041 ctgtgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggtgtgtatt
2101 atgctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttgagtggttg
2161 cgtgggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacctctgcct
2221 gaaaaagcaggtattttctcagaccccagagcagtattaatgatgcagaggttggaggag
2281 agaggtggagactgtggctcagacccaggtgtgcgggcatagctggagctggaatctgcc
2341 tccggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgtgaagcag
2401 ccagtccctgggtcagccagaggcttgaactgttacagaagccctctgccctctggtggc
2461 ctctgggcctgctgcatgtacatattttctgtaaatatacatgcgccgggagcttcttgc
2521 aggaatactgctccgaatcacttttaatttttttctttttttttttcttgccctttccatt
2581 agttgtatttttttatttatttttatttttatttttttttagagatggagtctcactatgt
2641 tgctcaggctggccttgaactcctgggctcaagcaatcctcctgcctcagcctccctagt
2701 agctgggactttaagtgtacaccactgtgcctgctttgaatcctttacgaagagaaaaaa
2761 aaaattaaagaaagcctttagatttatccaatgtttactactgggattgcttaaagtgag
2821 gcccctccaacaccaggggttaattcctgtgattgtgaaaggggctacttccaaggcat
2881 cttcatgcaggcagccccttgggagggcacctgagagctggtagagtctgaaattaggga
2941 tgtgagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtgatacctt
3001 agggaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggggagagag
3061 agagcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggtgctgggg
3121 gtgagaatgtcgcctttccccctgggttttggatcactaattcaaggctcttctggatgt
3181 ttctctgggttggggctggagttcaatgaggtttatttttagctggcccacccagataca
3241 ctcagccagaatacctagatttagtacccaaactcttcttagtctgaaatctgctggatt
3301 tctggcctaagggagaggctcccatccttcgttccccagccagcctaggacttcgaatgt
3361 ggagcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcatatttgta
3421 cataaaatgatattctgtttttaaataaacagacaaaacttgaaaaa
```

Figure 2N. The cDNA (SEQ ID. NO.: 28) and amino acid sequence (SEQ ID. NO.: 29) of 191P4D12(b) v.14. The start methionine is underlined. The open reading frame extends from nucleic acid 708-1121 including the stop codon.

```
   1 gtctgacccaggcctgcctcccttccctaggcctggctccttctgttgacatgggagatt
  61 ttagctcatcttgggggcctccttaaacacccccatttcttgcggaagatgctccccatc
 121 ccactgactgcttgacctttacctccaacccttctgttcatcgggagggctccaccaatt
 181 gagtctctcccaccatgcatgcaggtcactgtgtgtgtgcatgtgtgcctgtgtgagtgt
 241 tgactgactgtgtgtgtgtggaggggtgactgtccgtggaggggtgactgtgtccgtggt
 301 gtgtattatgctgtcatatcagagtcaagtgaactgtggtgtatgtgccacgggatttga
 361 gtggttgcgtgggcaacactgtcagggtttggcgtgtgtgtcatgtggctgtgtgtgacc
```

```
421 tctgcctgaaaaagcaggtattttctcagaccccagagcagtattaatgatgcagaggtt
481 ggaggagagaggtggagactgtggctcagacccaggtgtgcgggcatagctggagctgga
541 atctgcctccggtgtgagggaacctgtctcctaccacttcggagccatgggggcaagtgt
601 gaagcagccagtccctgggtcagccagaggcttgaactgttacagaagccctctgccctc
  1                                                   M  R  R  E  L
661 tggtggcctctgggcctgctgcatgtacatattttctgtaaatatacATGCGCCGGGAGC
  6   L  A  G  I  L  L  R  I  T  F  N  F  F  L  F  F  F  L  P  F
721 TTCTTGCAGGAATACTGCTCCGAATCACTTTTAATTTTTTTCTTTTTTTTTTTCTTGCCCT
 26   P  L  V  V  F  F  I  Y  F  Y  F  Y  F  F  L  E  M  E  S  H
781 TTCCATTAGTTGTATTTTTTATTTATTTTTATTTTTATTTTTTTTTAGAGATGGAGTCTC
 46   Y  V  A  Q  A  G  L  E  L  L  G  S  S  N  P  P  A  S  D  S
841 ACTATGTTGCTCAGGCTGGCCTTGAACTCCTGGGCTCAAGCAATCCTCCTGCCTCAGACT
 66   L  V  A  G  T  L  S  V  H  H  C  A  C  F  E  S  F  T  K  R
901 CCCTAGTAGCTGGGACTTTAAGTGTACACCACTGTGCCTGCTTTGAATCCTTTACGAAGA
 86   K  K  K  L  K  K  A  F  R  F  I  Q  C  L  L  L  G  L  L  K
961 GAAAAAAAAAATTAAAGAAAGCCTTTAGATTTATCCAATGTTTACTACTGGGATTGCTTA
106   V  R  P  L  Q  H  Q  G  V  N  S  C  D  C  E  R  G  Y  F  Q
1021 AAGTGAGGCCCCTCCAACACCAGGGGGTTAATTCCTGTGATTGTGAAAGGGGCTACTTCC
126   G  I  F  M  Q  A  A  P  W  E  G  T  *
1081 AAGGCATCTTCATGCAGGCAGCCCCTTGGGAGGGCACCTGAgagctggtagagtctgaaa
1141 ttagggatgtgagcctcgtggttactgagtaaggtaaaattgcatccaccattgtttgtg
1201 ataccttagggaattgcttggacctggtgacaagggctcctgttcaatagtggtgttggg
1261 gagagagagagcagtgattatagaccgagagagtaggagttgaggtgaggtgaaggaggt
1321 gctgggggtgagaatgtcgcctttccccctgggttttggatcactaattcaaggctcttc
1381 tggatgtttctctgggttggggctggagttcaatgaggtttatttttagctggcccaccc
1441 agatacactcagccagaatacctagatttagtacccaaactcttcttagtctgaaatctg
1501 ctggatttctggcctaagggagaggctcccatccttcgttccccagccagcctaggactt
1561 cgaatgtggagcctgaagatctaagatcctaacatgtacattttatgtaaatatgtgcat
1621 atttgtacataaaatgatattctgtttttaaataaacagacaaaacttg
```

Figure 3:

Figure 3A. Amino acid sequence of 191P4D12(b) v.1 (SEQ ID. NO. : 30). The 191P4D12(b) v.1 clone 1A1 protein has 510 amino acids.

```
  1 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE
 61 QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA
121 DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS
181 VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL
241 HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL
301 GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL
361 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA
421 EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ
481 AMNHFVQENG TLRAKPTGNG IYINGRGHLV
```

Figure 3B. Amino acid sequence of 191P4D12(b) v.2 (SEQ ID. NO. : 31). The 191P4D12(b) v.2 protein has 510 amino acids.

```
  1 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCLYRGDSGE
 61 QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA
121 DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS
181 VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL
241 HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL
301 GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL
361 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA
421 EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ
481 AMNHFVQENG TLRAKPTGNG IYINGRGHLV
```

Figure 3C. Amino acid sequence of 191P4D12(b) v.6 (SEQ ID. NO. : 32). The 191P4D12(b) v.6 protein has 295 amino acids.

```
  1 MNGQPLTCVV SHPGLLQDQR ITHILHVSFL AEASVRGLED QNLWHIGREG AMLKCLSEGQ
 61 PPPSYNWTRL DGPLPSGVRV DGDTLGFPPL TTEHSGIYVC HVSNEFSSRD SQVTVDVLDP
121 QEDSGKQVDL VSASVVVVGV IAALLFCLLV VVVVLMSRYH RRKAQQMTQK YEEELTLTRE
181 NSIRRLHSHH TDPRSQPEES VGLRAEGHPD SLKDNSSCSV MSEEPEGRSY STLTTVREIE
241 TQTELLSPGS GRAEEEEDQD EGIKQAMNHF VQENGTLRAK PTGNGIYING RGHLV
```

Figure 3D. Amino acid sequence of 191P4D12(b) v.7 (SEQ ID. NO. : 33). The 191P4D12(b) v.7 protein has 485 amino acids.

```
  1 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE
 61 QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA
121 DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS
```

181 VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL
241 HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL
301 GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL
361 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QSEEPEGRSY
421 STLTTVREIE TQTELLSPGS GRAEEEEDQD EGIKQAMNHF VQENGTLRAK PTGNGIYING
481 RGHLV

Figure 3E. Amino acid sequence of 191P4D12(b) v.10 (SEQ ID. NO. : 34). The 191P4D12(b) v.10 protein has 510 amino acids.

1 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELGTSDVV TVVLGQDAKL PCFYRGDSGE
61 QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA
121 DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS
181 VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL
241 HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL
301 GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL
361 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA
421 EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ
481 AMNHFVQENG TLRAKPTGNG IYINGRGHLV

Figure 3F. Amino acid sequence of 191P4D12(b) v.11 (SEQ ID. NO. : 35). The 191P4D12(b) v.11 protein has 510 amino acids.

1 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE
61 QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA
121 DEGEYECRVS TFPAGSFQAR LRLRVMVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS
181 VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL
241 HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL
301 GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL
361 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA
421 EGHPDSLKDN SSCSVMSEEP EGRSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ
481 AMNHFVQENG TLRAKPTGNG IYINGRGHLV

Figure 3G. Amino acid sequence of 191P4D12(b) v.12 (SEQ ID. NO. : 36). The 191P4D12(b) v.12 protein has 510 amino acids.

1 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE
61 QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA
121 DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS
181 VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL
241 HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL
301 GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLDPQEDSG KQVDLVSASV VVVGVIAALL

```
361 FCLLVVVVVL MSRYHRRKAQ QMTQKYEEEL TLTRENSIRR LHSHHTDPRS QPEESVGLRA
421 EGHPDSLKDN SSCSVMSEEP EGCSYSTLTT VREIETQTEL LSPGSGRAEE EEDQDEGIKQ
481 AMNHFVQENG TLRAKPTGNG IYINGRGHLV
```

Figure 3H. Amino acid sequence of 191P4D12(b) v.13 clone 9C (SEQ ID. NO. : 37). The 191P4D12(b) v.13 protein has 511 amino acids.

```
  1 MPLSLGAEMW GPEAWLLLLL LLASFTGRCP AGELETSDVV TVVLGQDAKL PCFYRGDSGE
 61 QVGQVAWARV DAGEGAQELA LLHSKYGLHV SPAYEGRVEQ PPPPRNPLDG SVLLRNAVQA
121 DEGEYECRVS TFPAGSFQAR LRLRVLVPPL PSLNPGPALE EGQGLTLAAS CTAEGSPAPS
181 VTWDTEVKGT TSSRSFKHSR SAAVTSEFHL VPSRSMNGQP LTCVVSHPGL LQDQRITHIL
241 HVSFLAEASV RGLEDQNLWH IGREGAMLKC LSEGQPPPSY NWTRLDGPLP SGVRVDGDTL
301 GFPPLTTEHS GIYVCHVSNE FSSRDSQVTV DVLADPQEDS GKQVDLVSAS VVVVGVIAAL
361 LFCLLVVVVV LMSRYHRRKA QQMTQKYEEE LTLTRENSIR RLHSHHTDPR SQPEESVGLR
421 AEGHPDSLKD NSSCSVMSEE PEGRSYSTLT TVREIETQTE LLSPGSGRAE EEEDQDEGIK
481 QAMNHFVQEN GTLRAKPTGN GIYINGRGHL V
```

Figure 3I. Amino acid sequence of 191P4D12(b) v.9 clone BCP1 (SEQ ID. NO. : 38). The 191P4D12(b) v.9 protein has 137 amino acids.

```
  1 MRRELLAGIL LRITFNFFLF FFLPFPLVVF FIYFYFYFFL EMESHYVAQA GLELLGSSNP
 61 PASASLVAGT LSVHHCACFE SFTKRKKKLK KAFRFIQCLL LGLLKVRPLQ HQGVNSCDCE
121 RGYFQGIFMQ AAPWEGT
```

Figure 3J. Amino acid sequence of 191P4D12(b) v.14 (SEQ ID. NO. : 39). The 191P4D12(b) v.14 protein has 137 amino acids.

```
  1 MRRELLAGIL LRITFNFFLF FFLPFPLVVF FIYFYFYFFL EMESHYVAQA GLELLGSSNP
 61 PASDSLVAGT LSVHHCACFE SFTKRKKKLK KAFRFIQCLL LGLLKVRPLQ HQGVNSCDCE
121 RGYFQGIFMQ AAPWEGT
```

Figure 4: Alignment of 191P4D12(b) with known homologs.

A) Alignment of 191P4D12(b) (SEQ ID NO: 40) with human Ig superfamily receptor LNIR (gi 14714574) (SEQ ID NO: 41)

```
Score =  927 bits (2397), Expect = 0.0
Identities = 510/510 (100%), Positives = 510/510 (100%)

Query: 1   MPLSLGAEMWGPEAWLLLLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGE 60
           MPLSLGAEMWGPEAWLLLLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGE
Sbjct: 1   MPLSLGAEMWGPEAWLLLLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGE 60

Query: 61  QVGQVAWARVDAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPPRNPLDGSVLLRNAVQA 120
           QVGQVAWARVDAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPPRNPLDGSVLLRNAVQA
Sbjct: 61  QVGQVAWARVDAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPPRNPLDGSVLLRNAVQA 120

Query: 121 DEGEYECRVSTFPAGSFQARLRLRVLVPPLPSLNPGPALEEGQGLTLAASCTAEGSPAPS 180
           DEGEYECRVSTFPAGSFQARLRLRVLVPPLPSLNPGPALEEGQGLTLAASCTAEGSPAPS
Sbjct: 121 DEGEYECRVSTFPAGSFQARLRLRVLVPPLPSLNPGPALEEGQGLTLAASCTAEGSPAPS 180

Query: 181 VTWDTEVKGTTSSRSFKHSRSAAVTSEFHLVPSRSMNGQPLTCVVSHPGLLQDQRITHIL 240
           VTWDTEVKGTTSSRSFKHSRSAAVTSEFHLVPSRSMNGQPLTCVVSHPGLLQDQRITHIL
Sbjct: 181 VTWDTEVKGTTSSRSFKHSRSAAVTSEFHLVPSRSMNGQPLTCVVSHPGLLQDQRITHIL 240

Query: 241 HVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSYNWTRLDGPLPSGVRVDGDTL 300
           HVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSYNWTRLDGPLPSGVRVDGDTL
Sbjct: 241 HVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSYNWTRLDGPLPSGVRVDGDTL 300

Query: 301 GFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLDPQEDSGKQVDLVSASVVVVGVIAALL 360
           GFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLDPQEDSGKQVDLVSASVVVVGVIAALL
Sbjct: 301 GFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLDPQEDSGKQVDLVSASVVVVGVIAALL 360

Query: 361 FCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQPEESVGLRA 420
           FCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQPEESVGLRA
Sbjct: 361 FCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQPEESVGLRA 420

Query: 421 EGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQ 480
           EGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQ
Sbjct: 421 EGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQ 480

Query: 481 AMNHFVQENGTLRAKPTGNGIYINGRGHLV 510
           AMNHFVQENGTLRAKPTGNGIYINGRGHLV
Sbjct: 481 AMNHFVQENGTLRAKPTGNGIYINGRGHLV 510
```

B) Alignment of 191P4D12(b) (SEQ ID NO: 42) with mouse nectin 4 (gi 18874521) (SEQ ID NO: 43).

Score = 893 bits (2308), Expect = 0.0

Identities = 470/510 (92%), Positives = 485/510 (95%), Gaps = 2/510 (0%)

```
Query: 1   MPLSLGAEMWGPEAWLLLLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGE 60
           MPLSLGAEMWGPEAW L LL LASFTG+  AGELETSDVVTVVLGQDAKLPCFYRGD  E
Sbjct: 1   MPLSLGAEMWGPEAW-LRLLFLASFTGQYSAGELETSDVVTVVLGQDAKLPCFYRGDPDE 59

Query: 61  QVGQVAWARVDAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPPRNPLDGSVLLRNAVQA 120
           QVGQVAWARVD  EG +ELALLHSKYGLHV+PAYE RVEQPPPPR+PLDGSVLLRNAVQA
Sbjct: 60  QVGQVAWARVDPNEGIRELALLHSKYGLHVNPAYEDRVEQPPPPRDPLDGSVLLRNAVQA 119

Query: 121 DEGEYECRVSTFPAGSFQARLRLRVLVPPLPSLNPGPALEEGQGLTLAASCTAEGSPAPS 180
           DEGEYECRVSTFPAGSFQAR+RLRVLVPPLPSLNPGP LEEGQGLTLAASCTAEGSPAPS
Sbjct: 120 DEGEYECRVSTFPAGSFQARMRLRVLVPPLPSLNPGPPLEEGQGLTLAASCTAEGSPAPS 179

Query: 181 VTWDTEVKGTTSSRSFKHSRSAAVTSEFHLVPSRSMNGQPLTCVVSHPGLLQDQRITHIL 240
           VTWDTEVKGT SSRSF H RSAAVTSEFHLVPSRSMNGQPLTCVVSHPGLLQD+RITH L
Sbjct: 180 VTWDTEVKGTQSSRSFTHPRSAAVTSEFHLVPSRSMNGQPLTCVVSHPGLLQDRRITHTL 239

Query: 241 HVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSYNWTRLDGPLPSGVRVDGDTL 300
            V+FLAEASVRGLEDQNLW +GREGA LKCLSEGQPPP YNWTRLDGPLPSGVRV GDTL
Sbjct: 240 QVAFLAEASVRGLEDQNLWQVGREGATLKCLSEGQPPPKYNWTRLDGPLPSGVRVKGDTL 299

Query: 301 GFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLDPQEDSGKQVDLVSASVVVVGVIAALL 360
           GFPPLTTEHSG+YVCHVSNE SSRDSQVTV+VLDP ED GKQVDLVSASV++VGVIAALL
Sbjct: 300 GFPPLTTEHSGVYVCHVSNELSSRDSQVTVEVLDP-EDPGKQVDLVSASVIIVGVIAALL 358
```

```
Query: 361 FCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQPEESVGLRA 420
           FCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHH+DPRSQPEESVGLRA
Sbjct: 359 FCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHSDPRSQPEESVGLRA 418

Query: 421 EGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQ 480
           EGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGR EE++DQDEGIKQ
Sbjct: 419 EGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRTEEDDDQDEGIKQ 478

Query: 481 AMNHFVQENGTLRAKPTGNGIYINGRGHLV 510
           AMNHFVQENGTLRAKPTGNGIYINGRGHLV
Sbjct: 479 AMNHFVQENGTLRAKPTGNGIYINGRGHLV 508
```

Figure 5a: 191P4D12B variant 1 Hydrophilicity profile (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

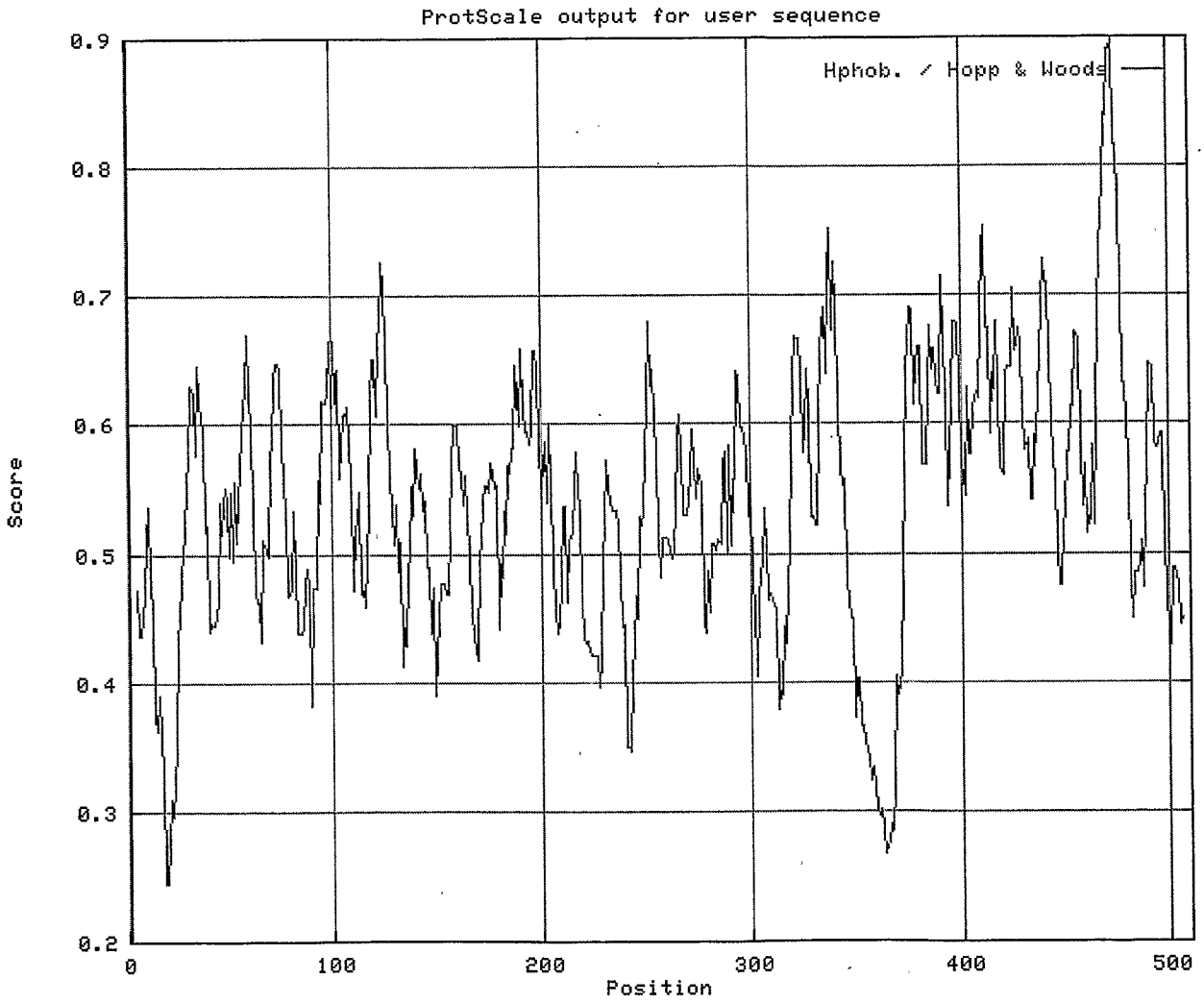

Figure 5b: 191P4D12B variant 7 Hydrophilicity profile (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

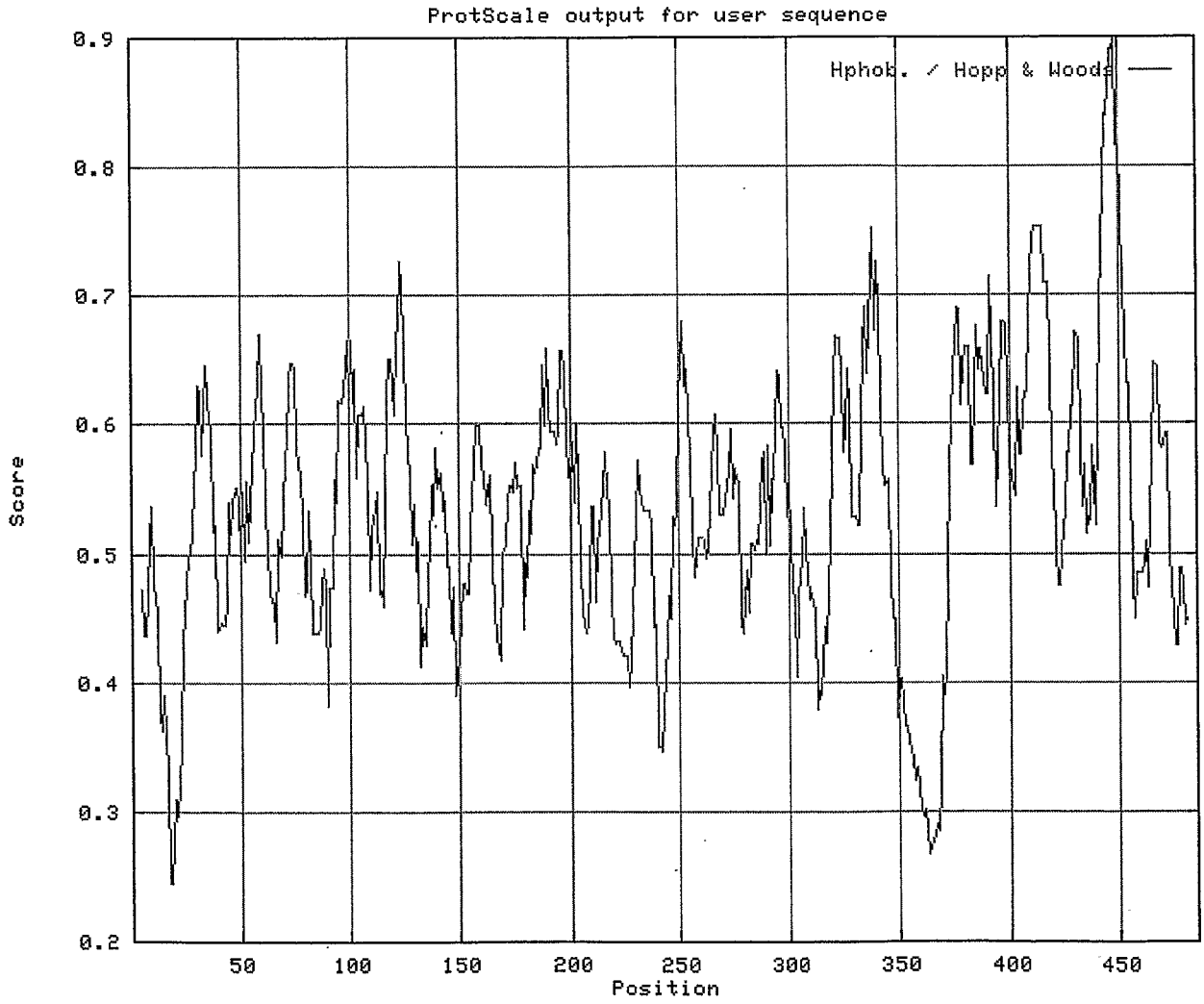

Figure 5c: 191P4D12B variant 9 Hydrophilicity profile (Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

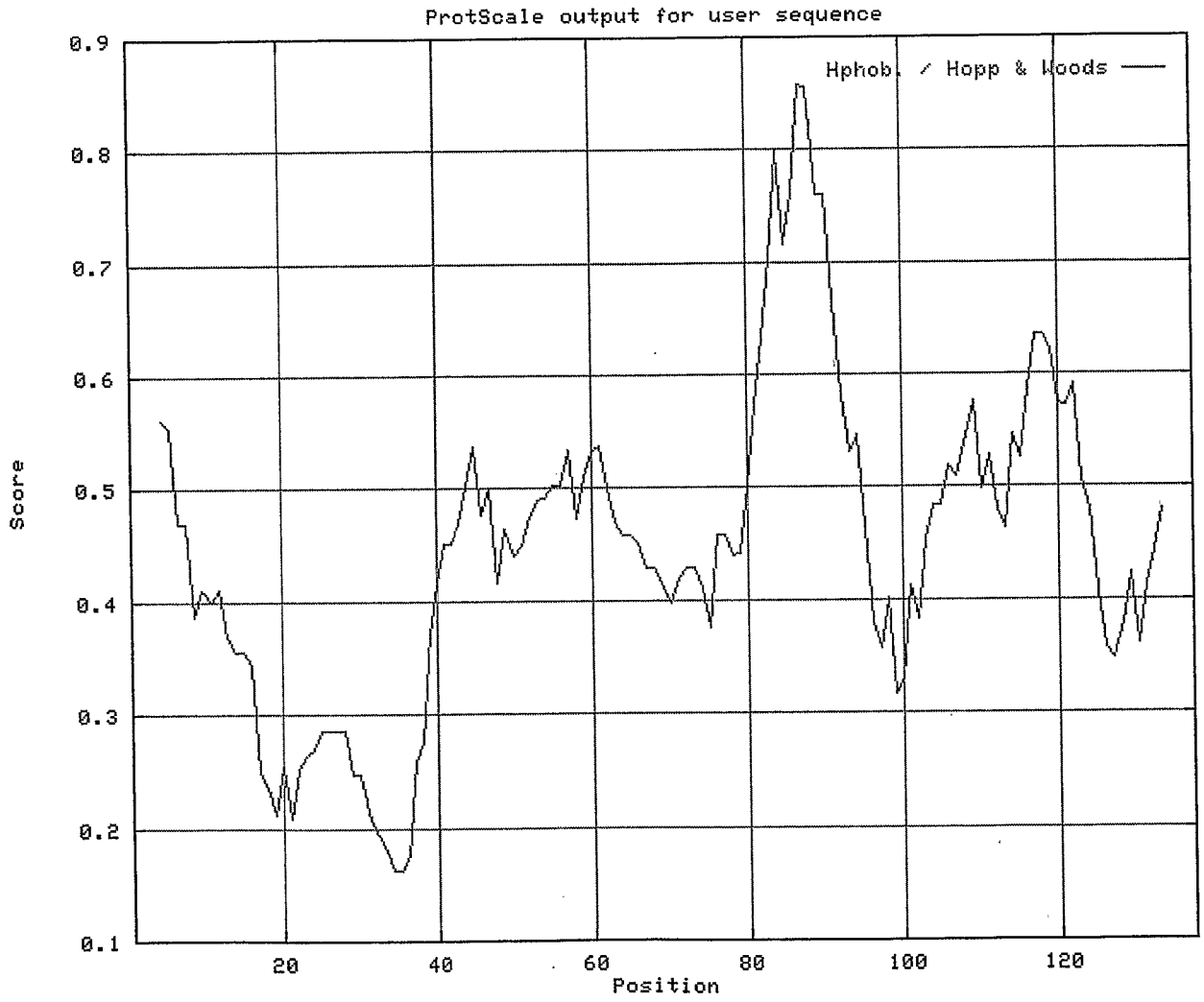

Figure 6a: 191P4D12B variant 1 Hydropathicity Profile (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

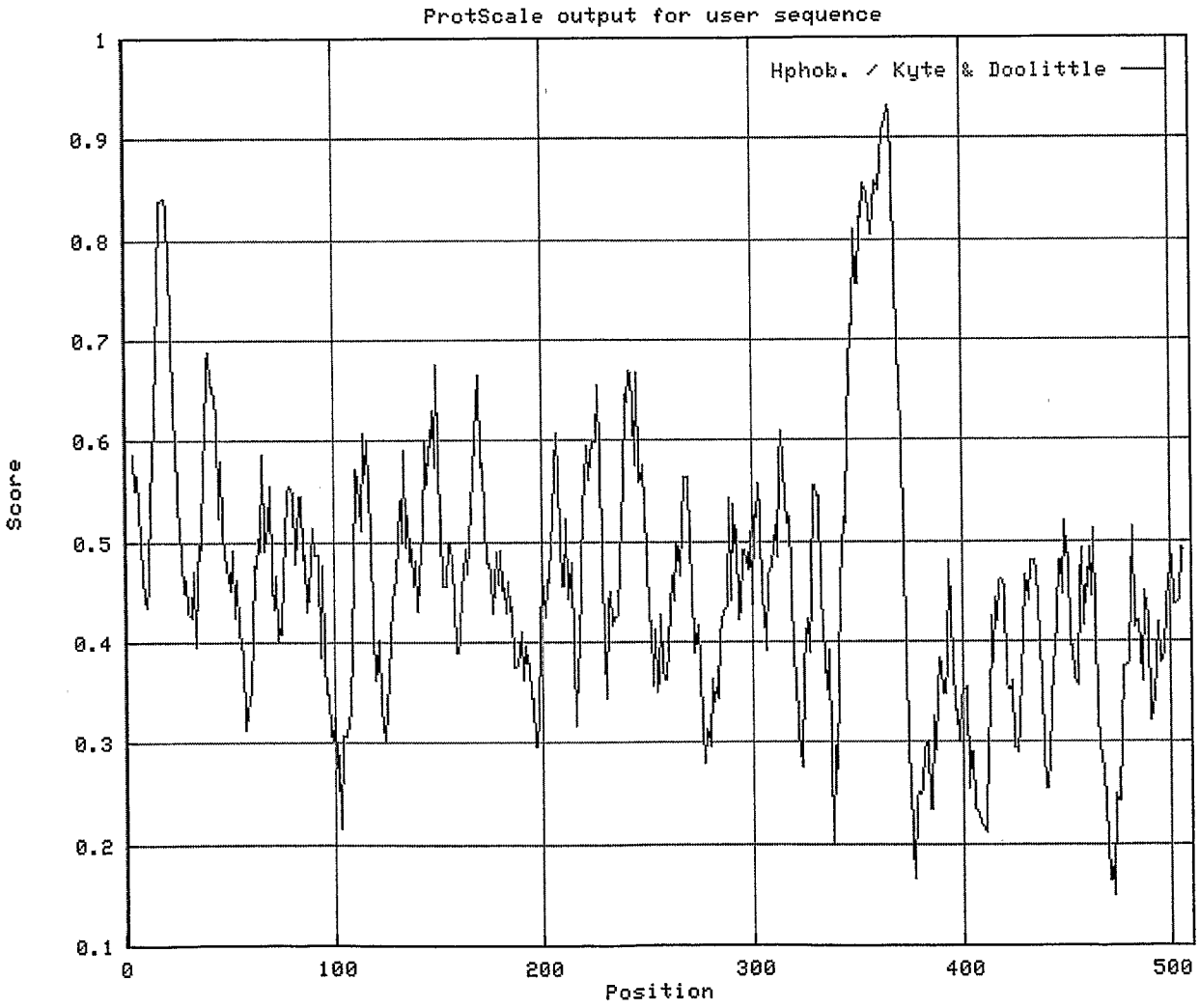

Figure 6b: 191P4D12B variant 7 Hydropathicity Profile (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

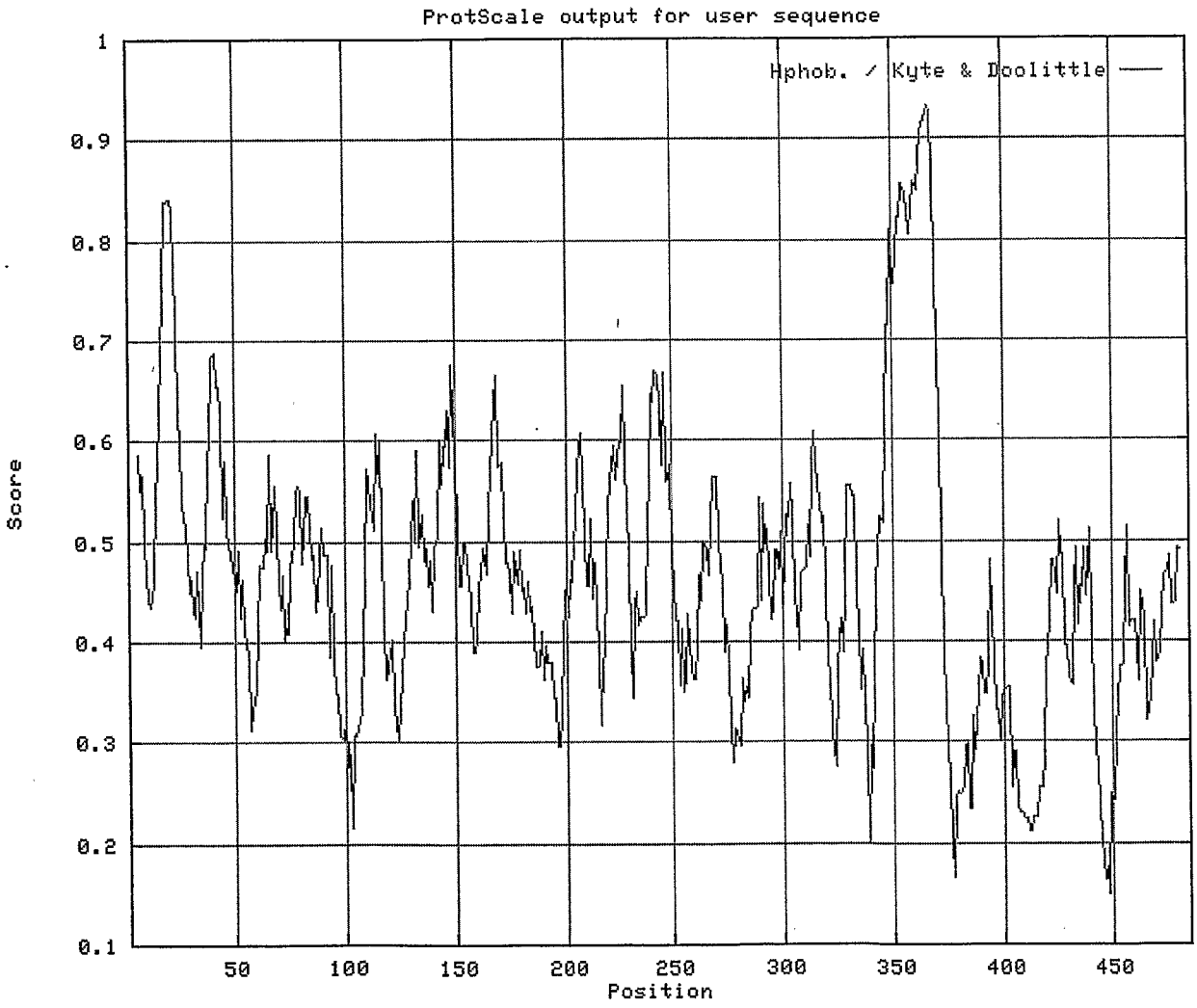

Figure 6c: 191P4D12B variant 9 Hydropathicity Profile (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

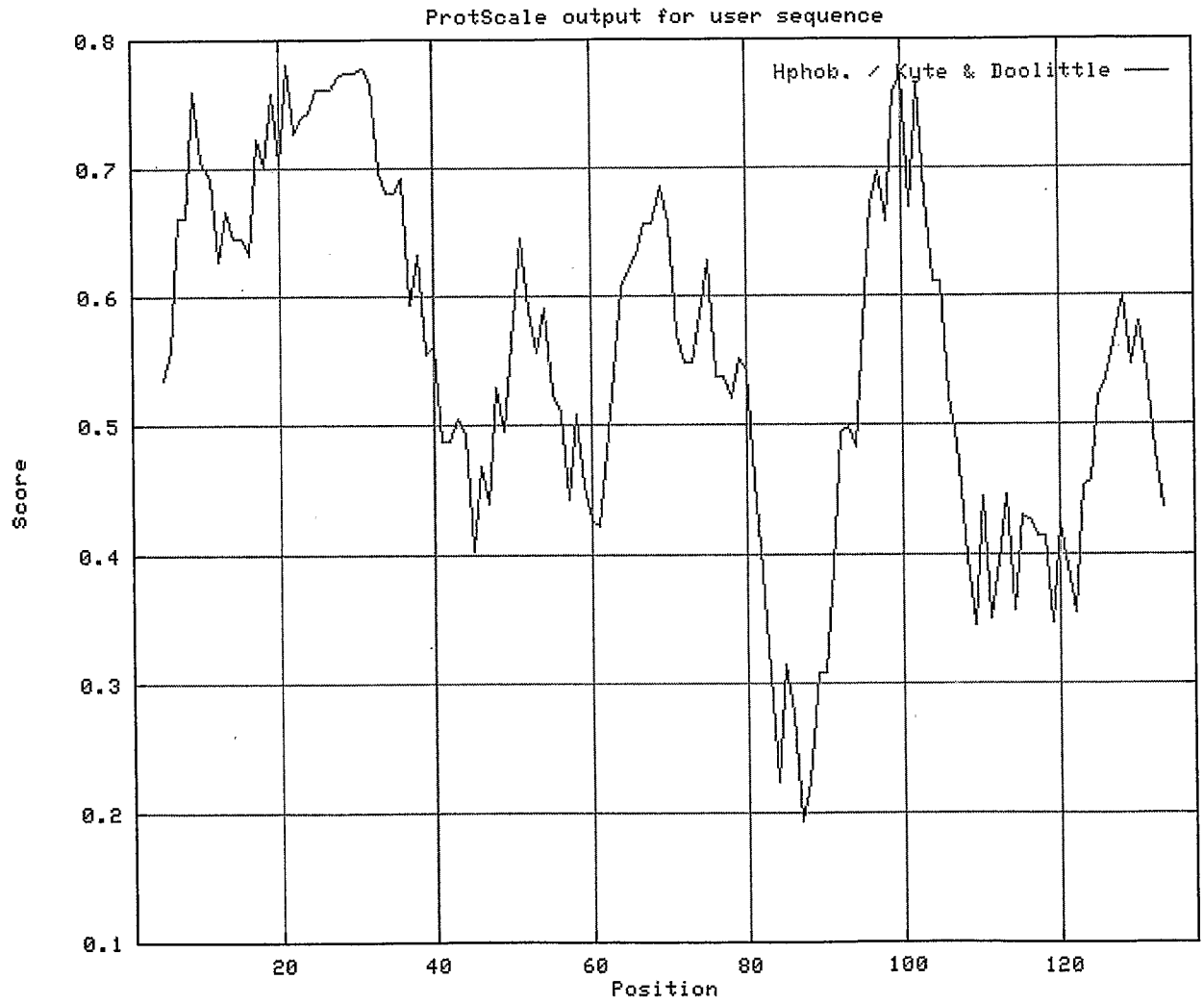

Figure 7a: 191P4D12B variant 1 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

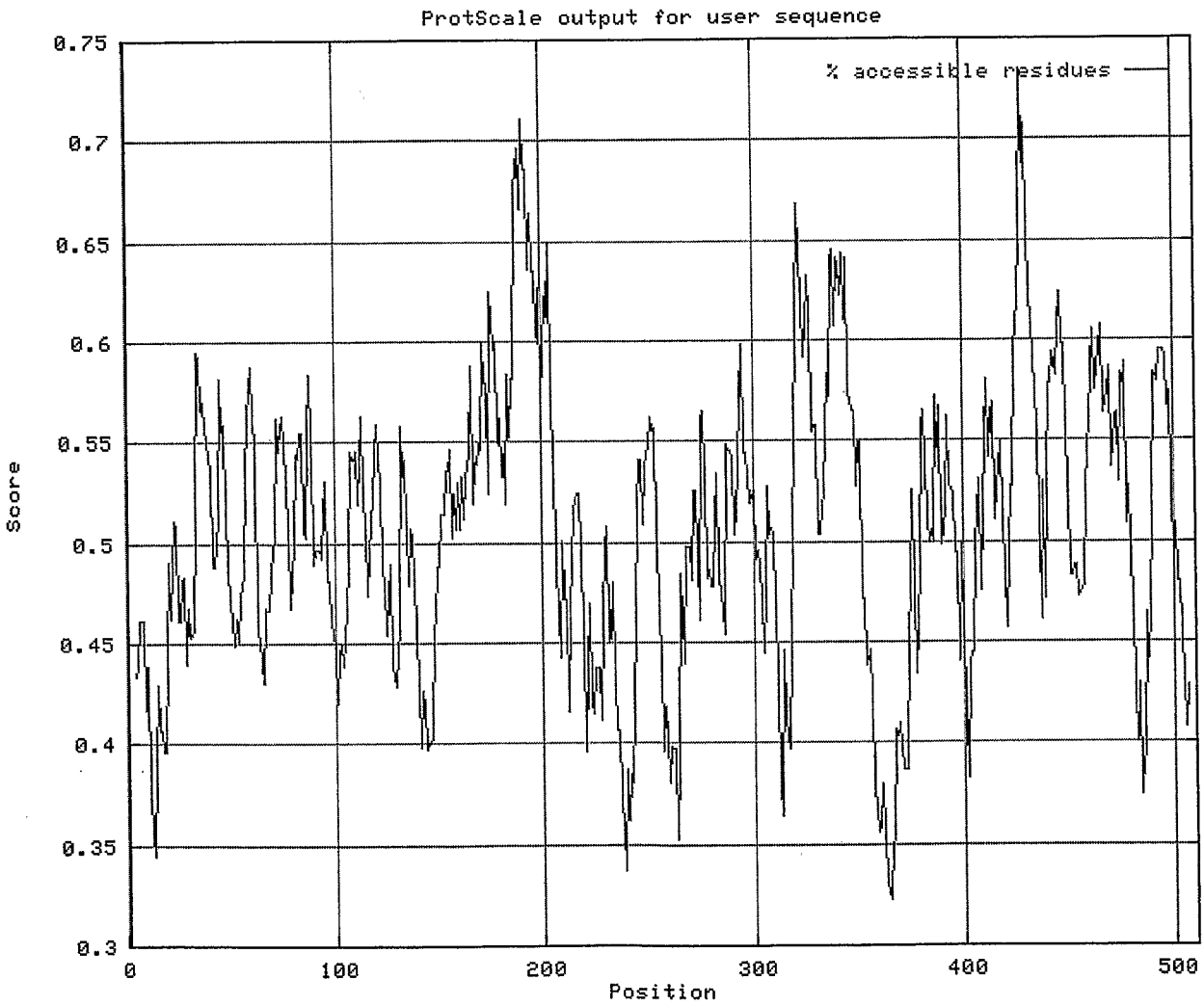

Figure 7b: 191P4D12B variant 7 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

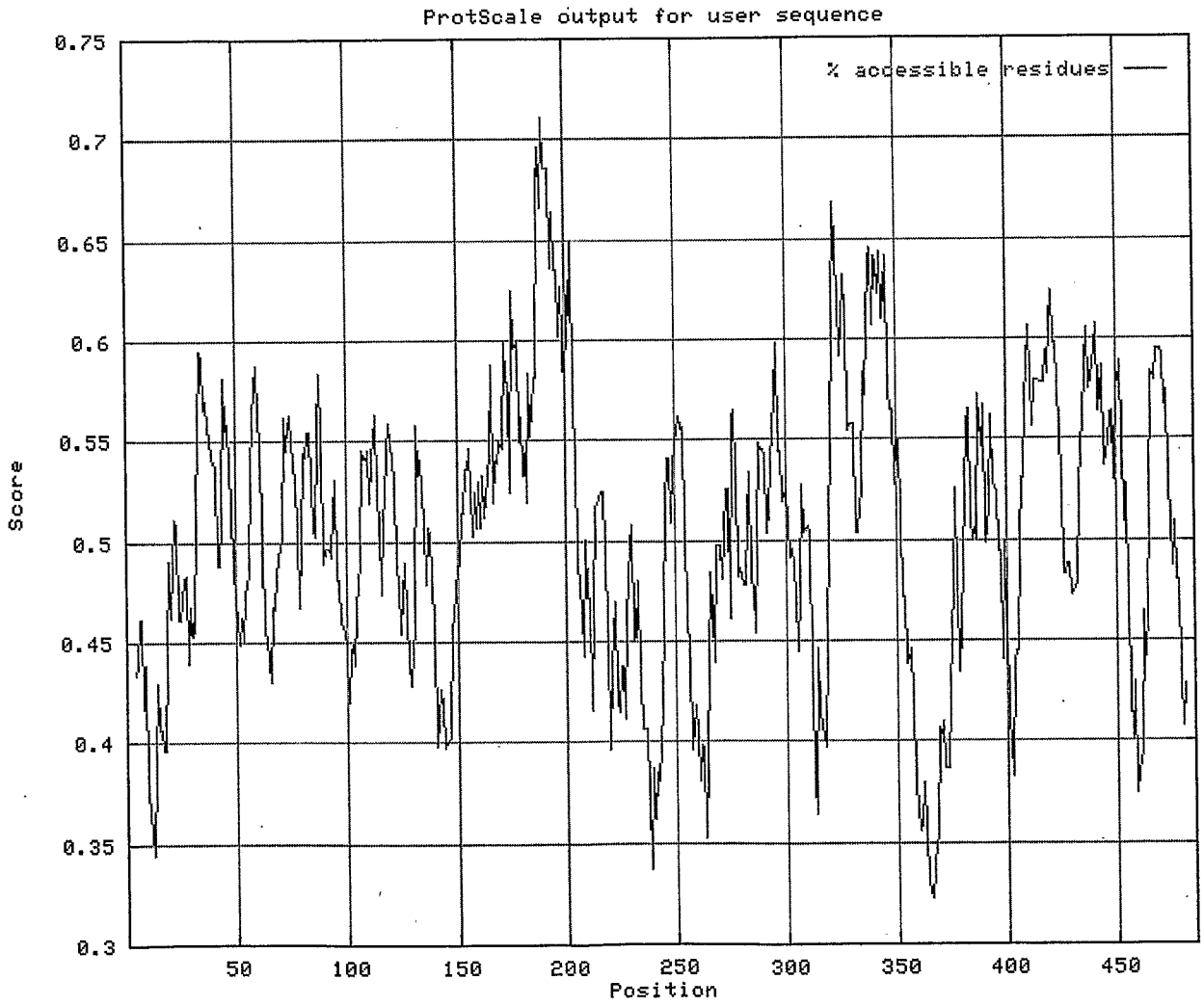

Figure 7c: 191P4D12B variant 9 % Accessible Residues Profile (Janin J., 1979. Nature 277:491-492)

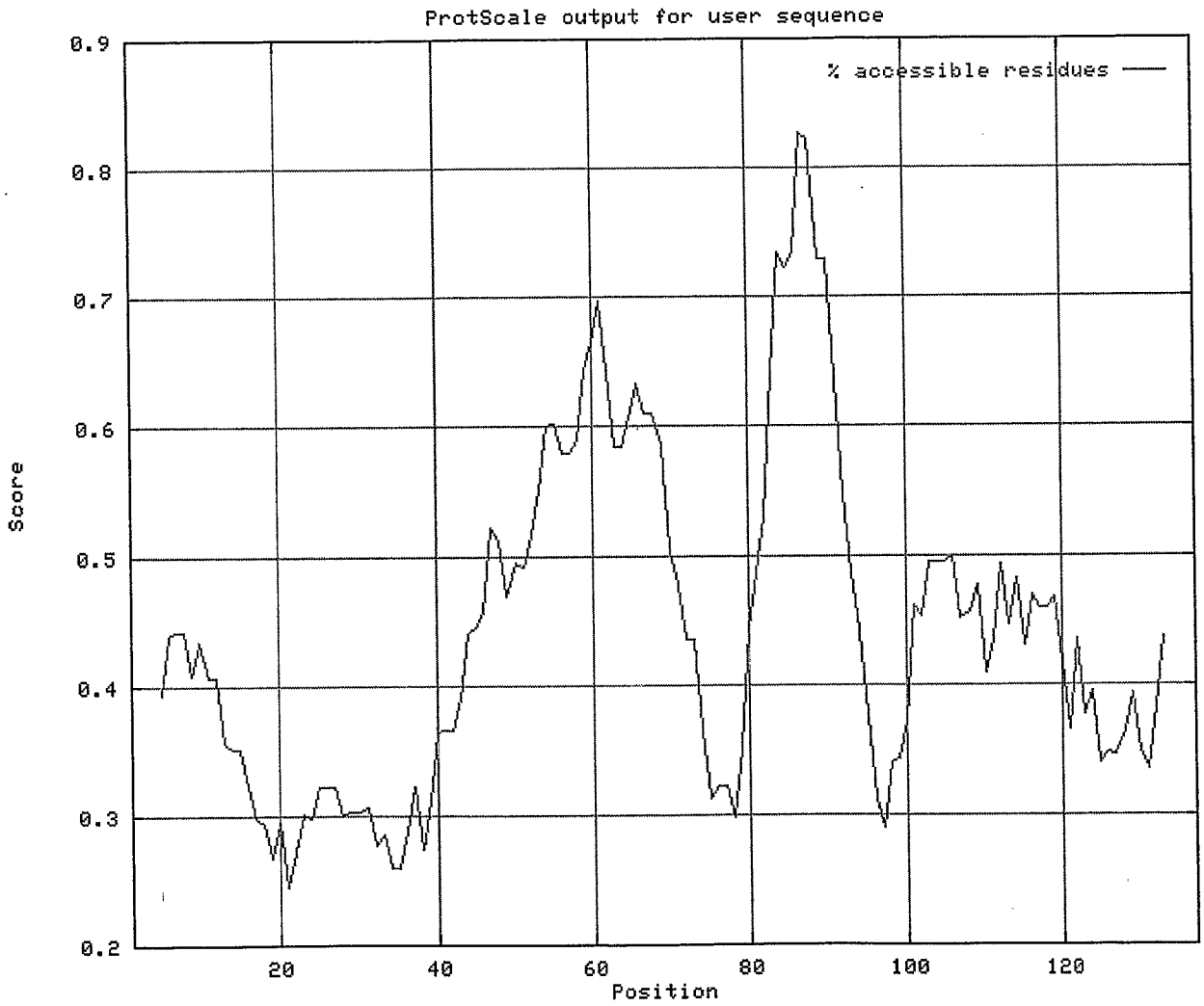

Figure 8a: 191P4D12B variant 1 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

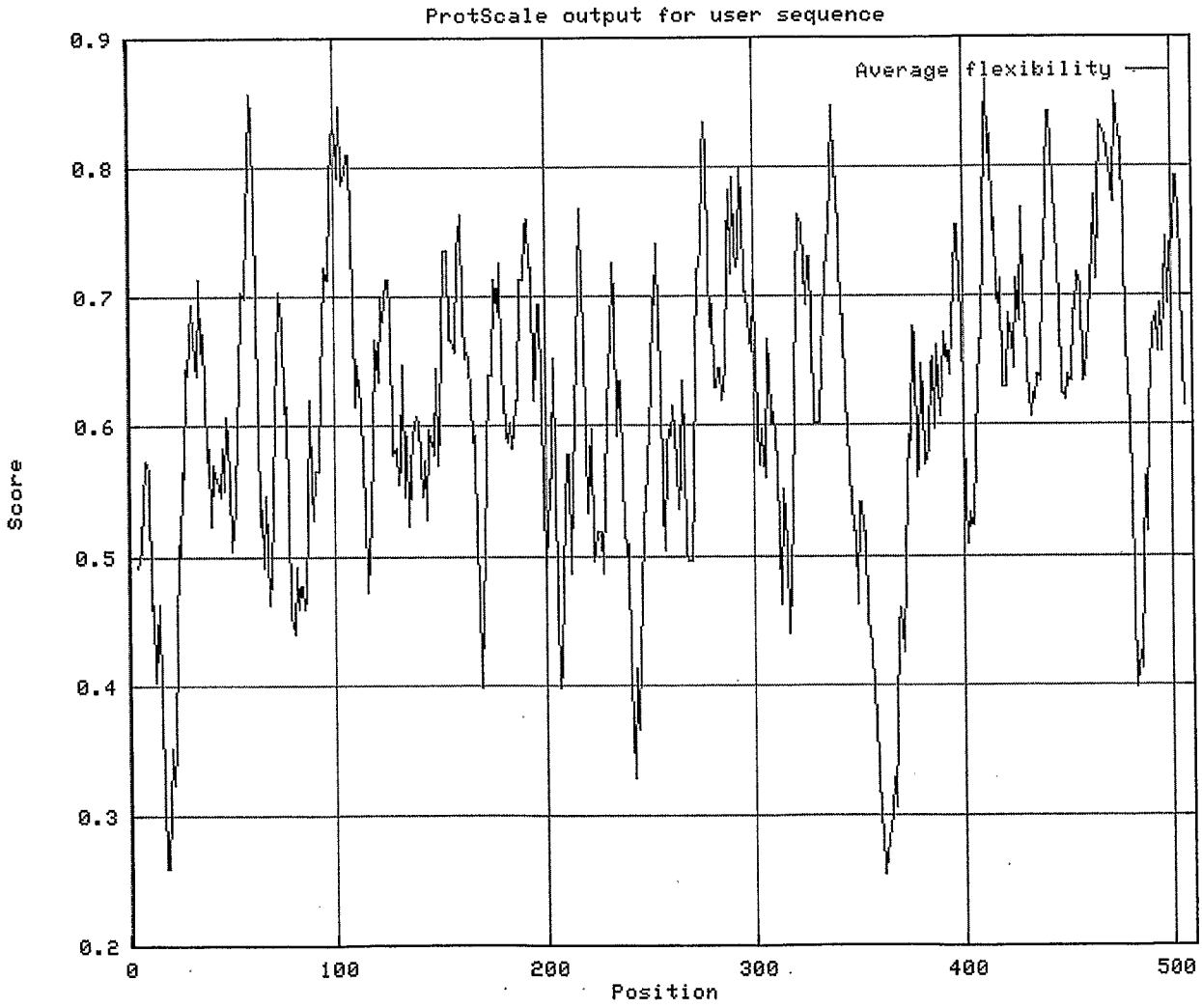

Figure 8b: 191P4D12B variant 7 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

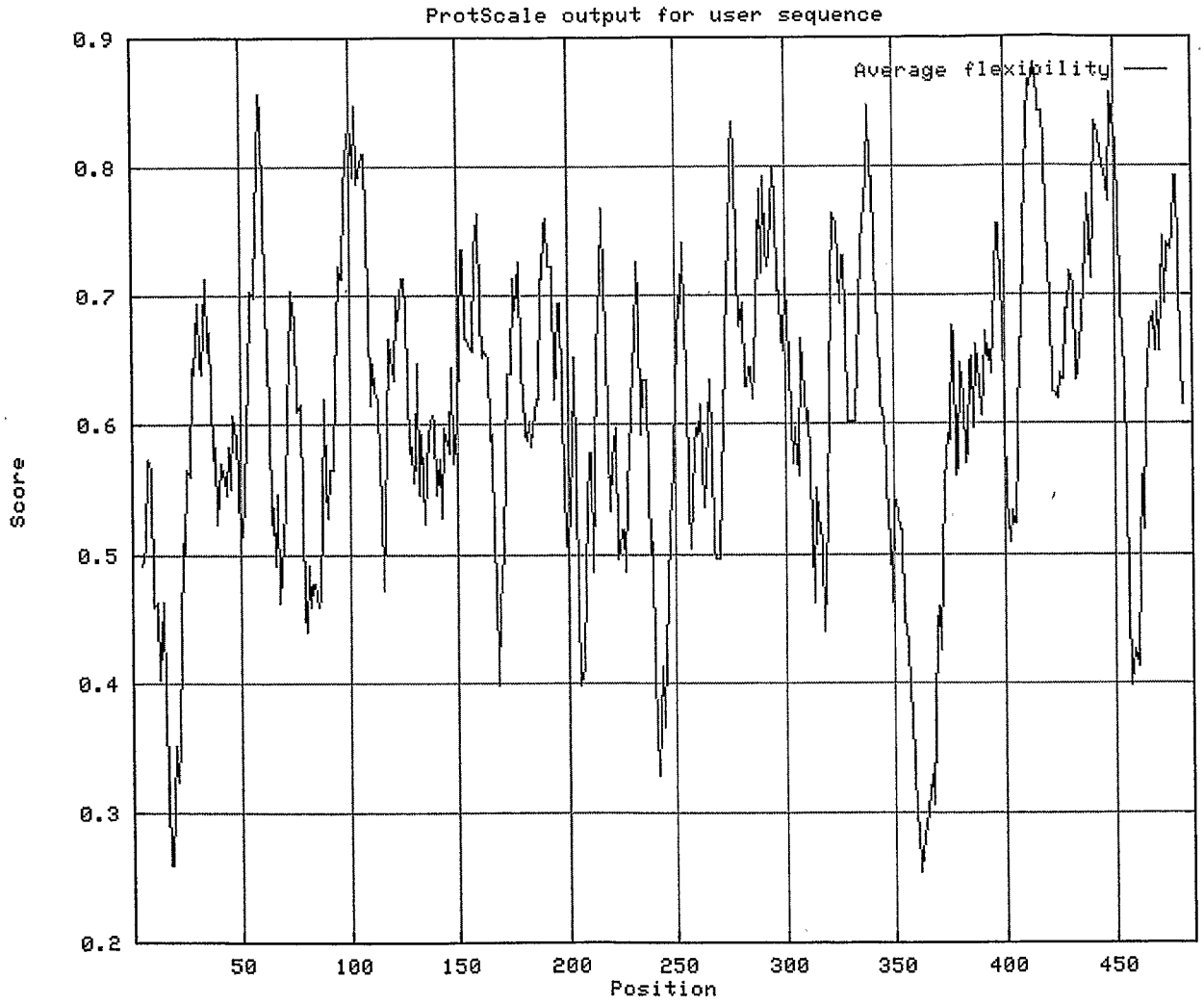

Figure 8c: 191P4D12B variant 9 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988. Int. J. Pept. Protein Res. 32:242-255)

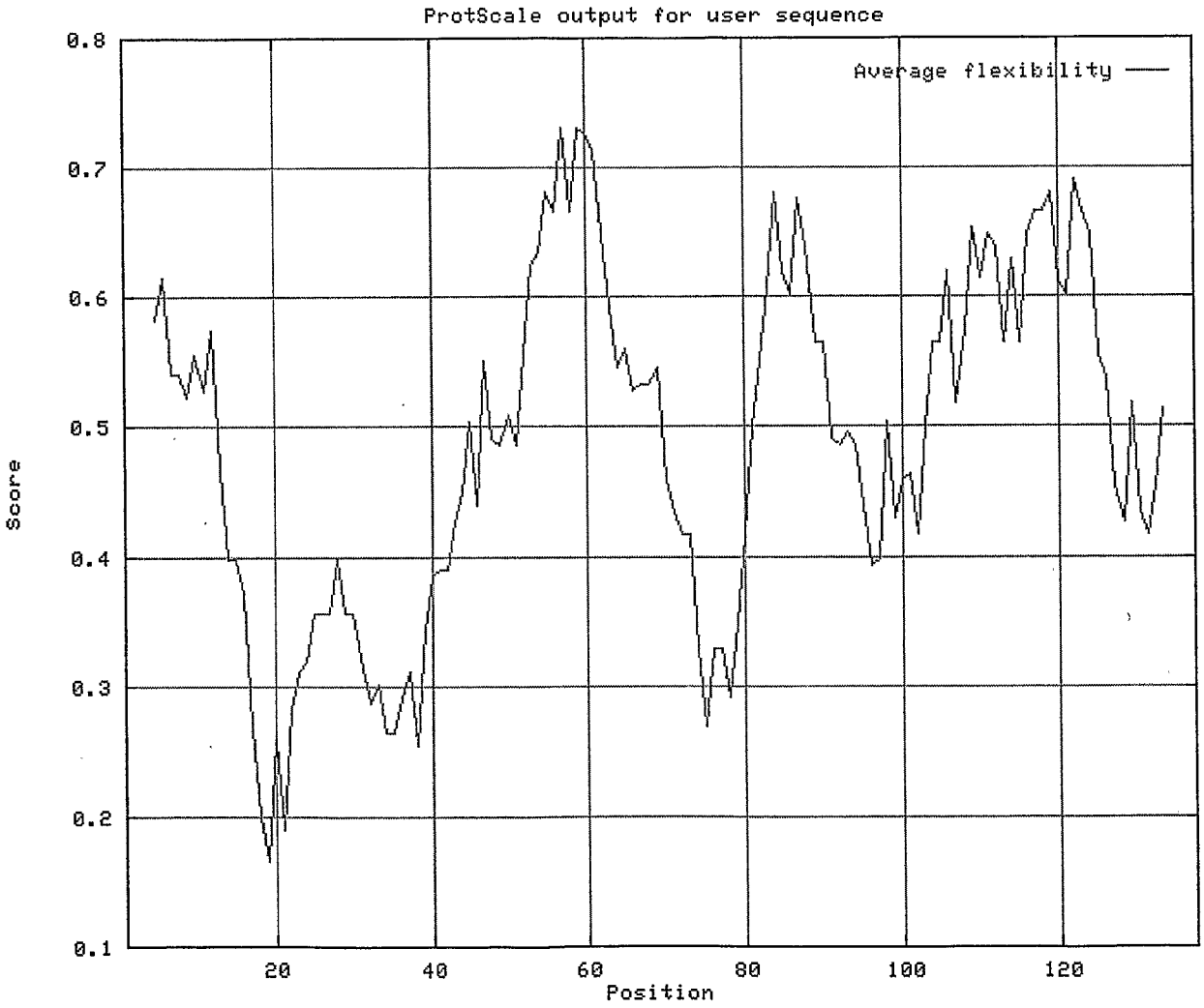

Figure 9a: 191P4D12B variant 1 Beta-turn Profile

(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

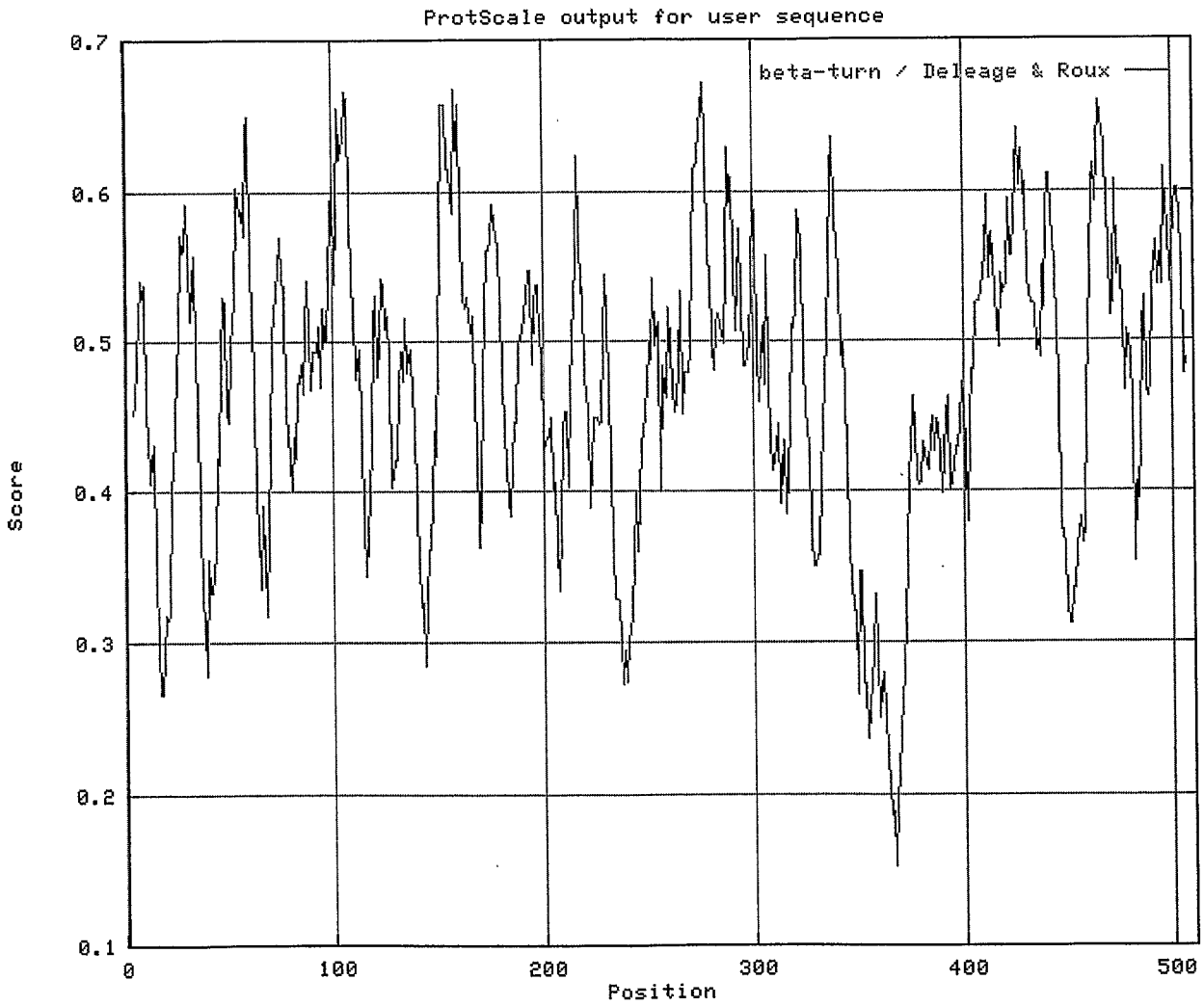

Figure 9b: 191P4D12B variant 7
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

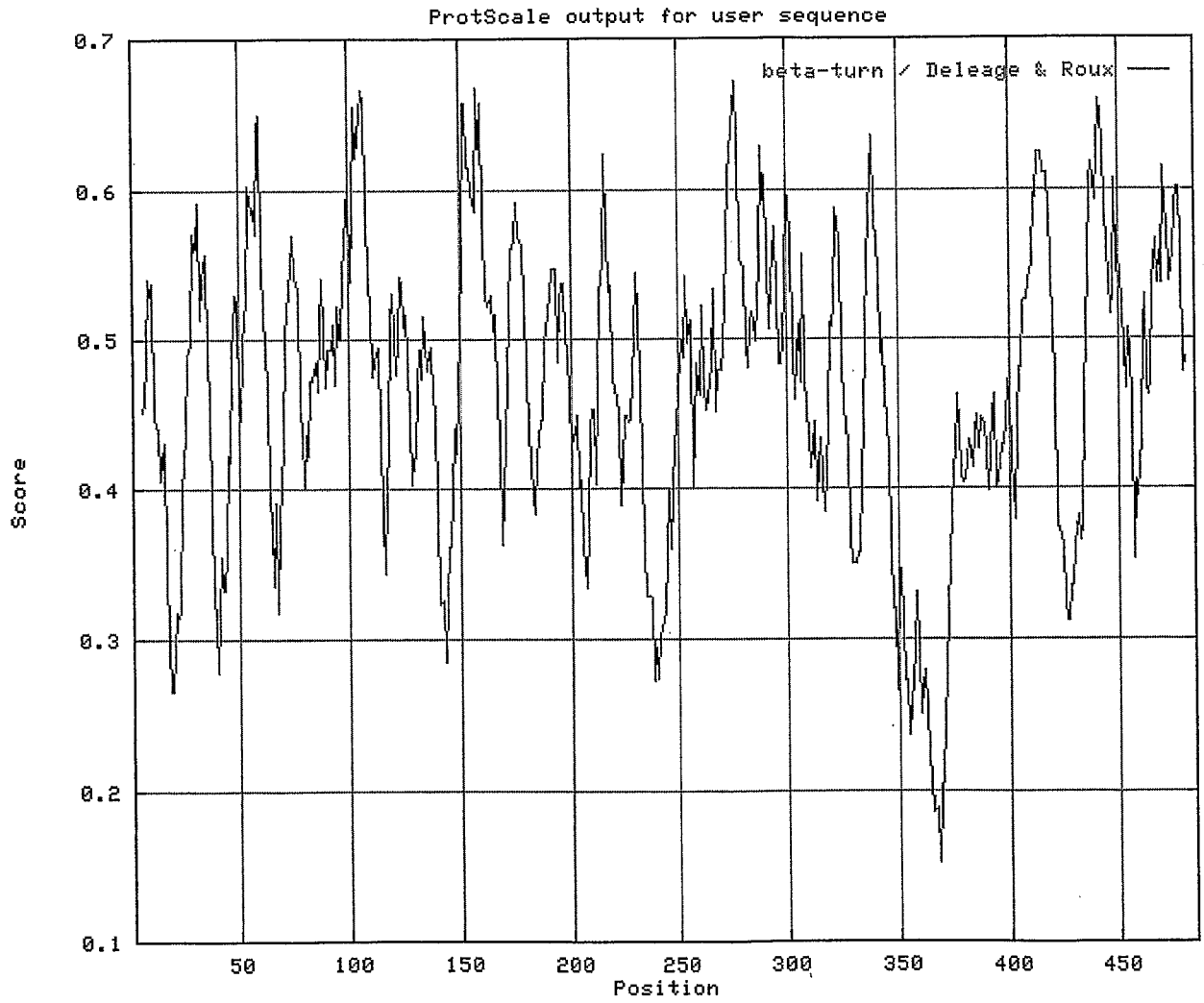

Figure 9c: 191P4D12B variant 9
Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

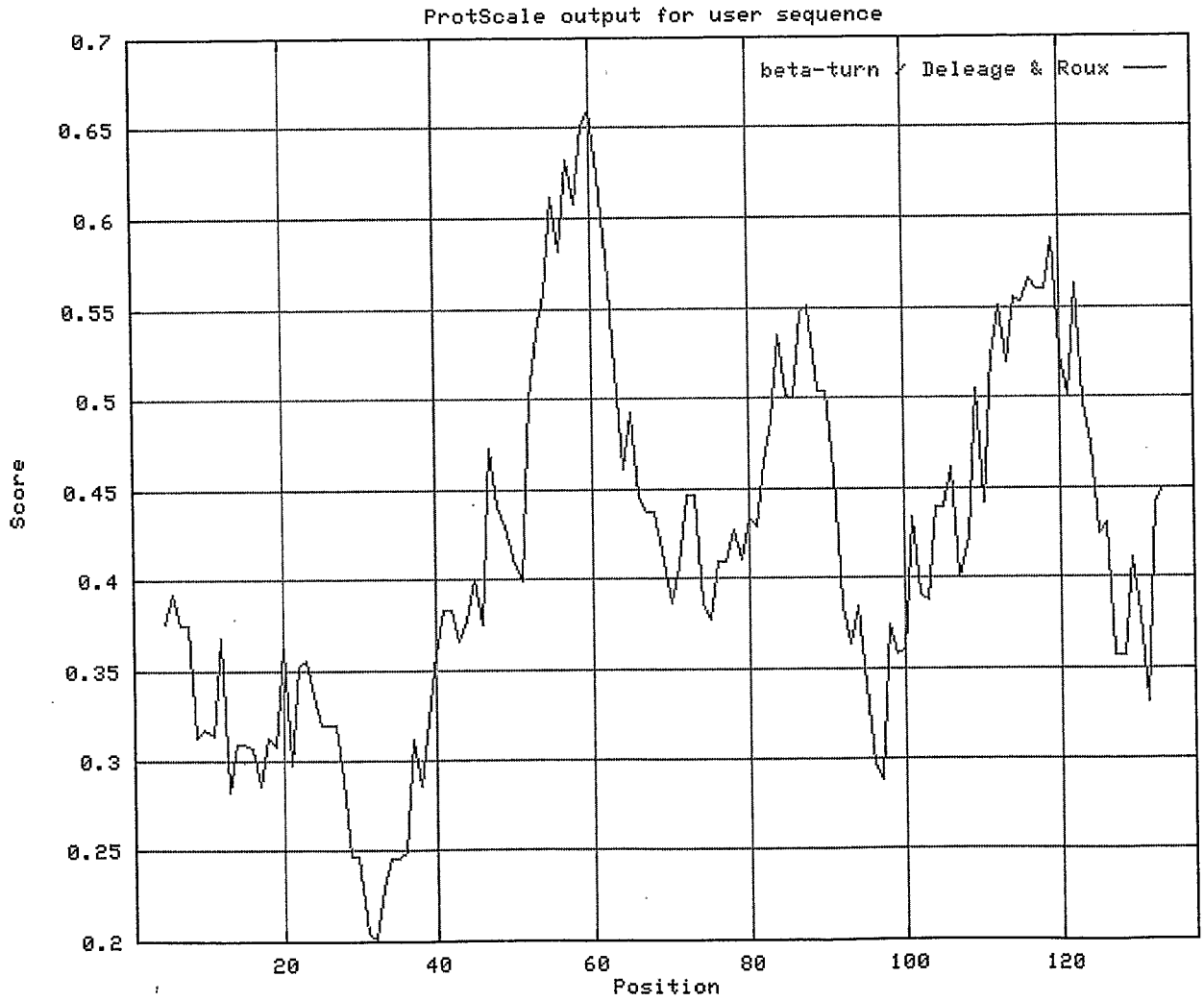

Figure 10

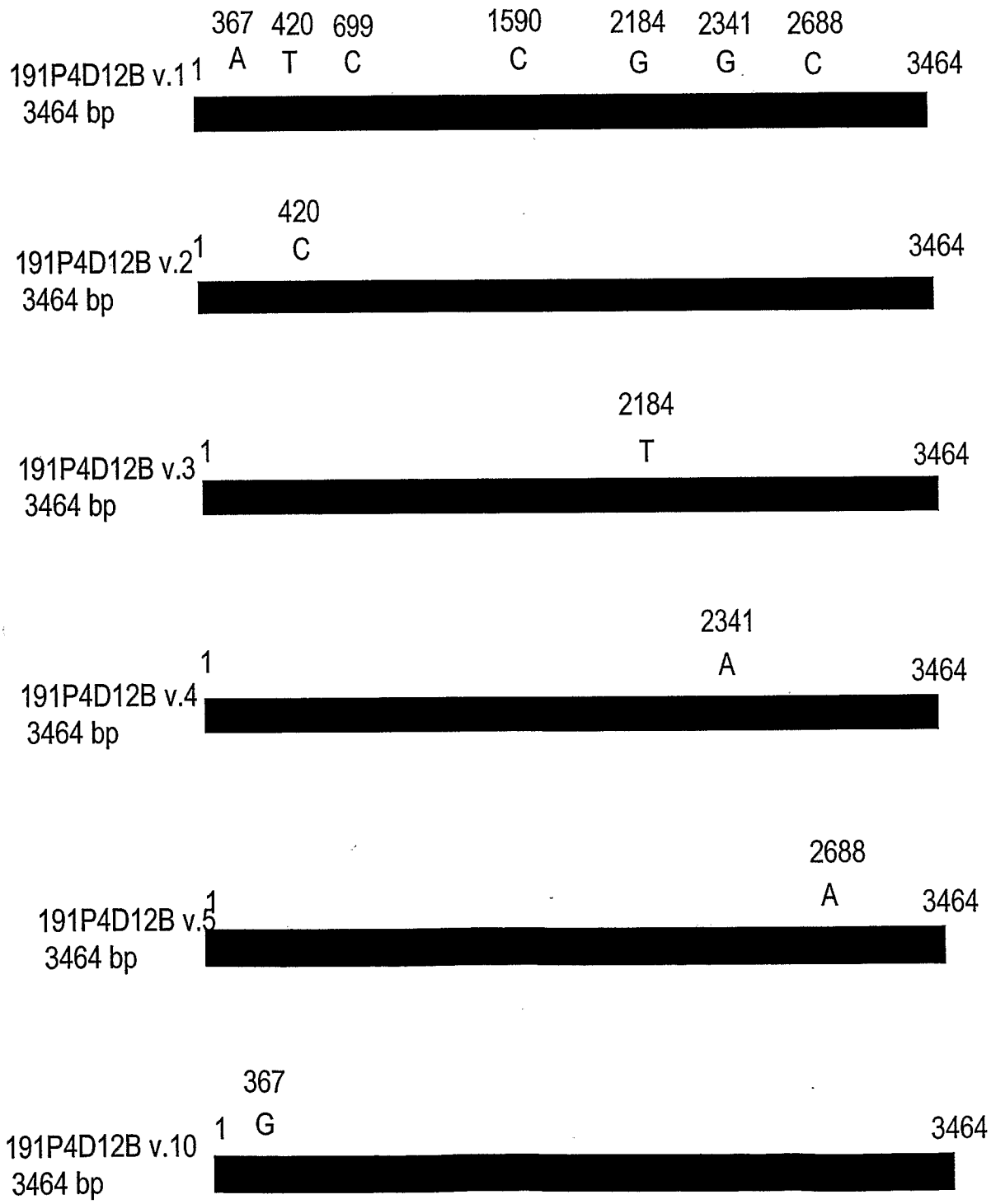
367 420 699 1590 2184 2341 2688
A T C C G G C
191P4D12B v.1 1 3464
3464 bp
420
C
191P4D12B v.2 1 3464
3464 bp
2184
T
191P4D12B v.3 1 3464
3464 bp
2341
A
191P4D12B v.4 1 3464
3464 bp
2688
A
191P4D12B v.5 1 3464
3464 bp
367
G
191P4D12B v.10 1 3464
3464 bp

Figure 10 (con'd)

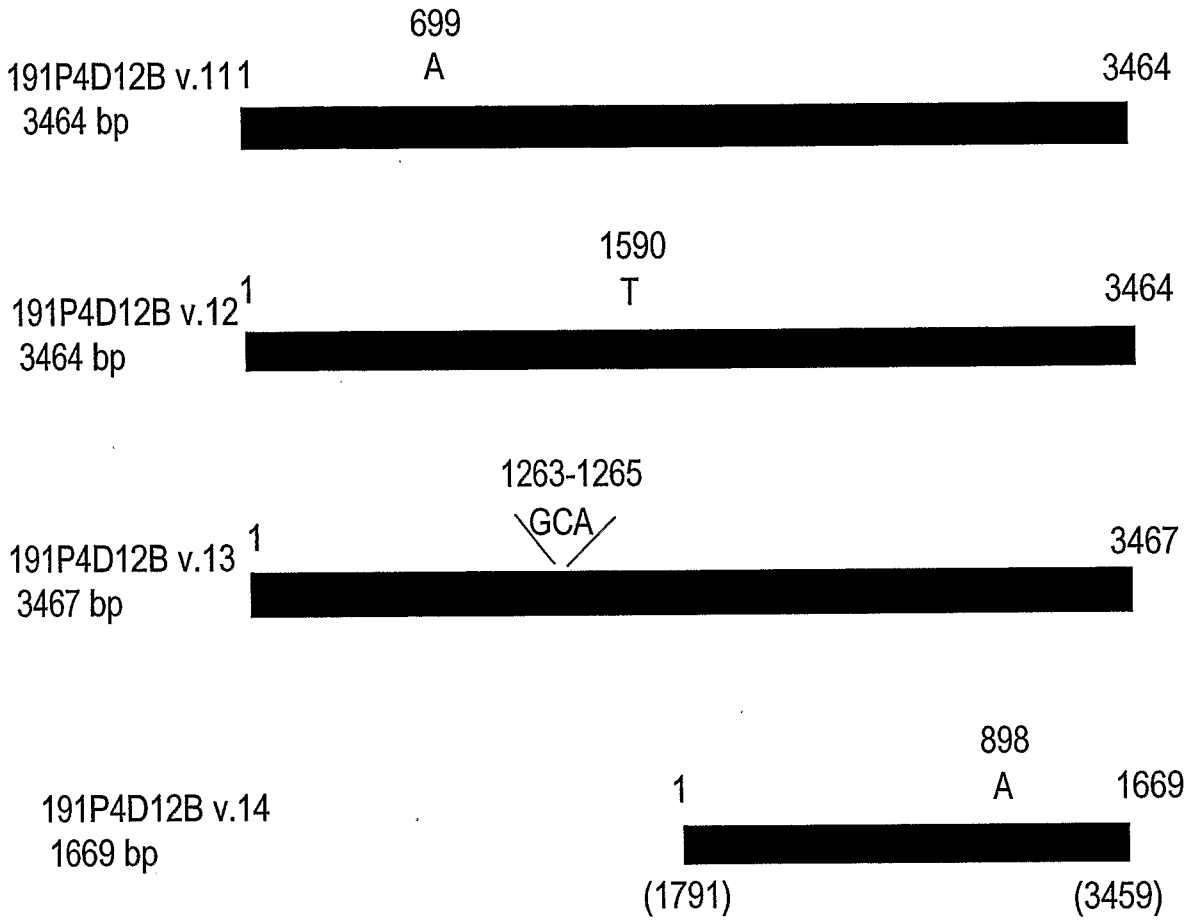

Figure 10. Schematic alignment of SNP variants of 191P4D12B.

Figure 11

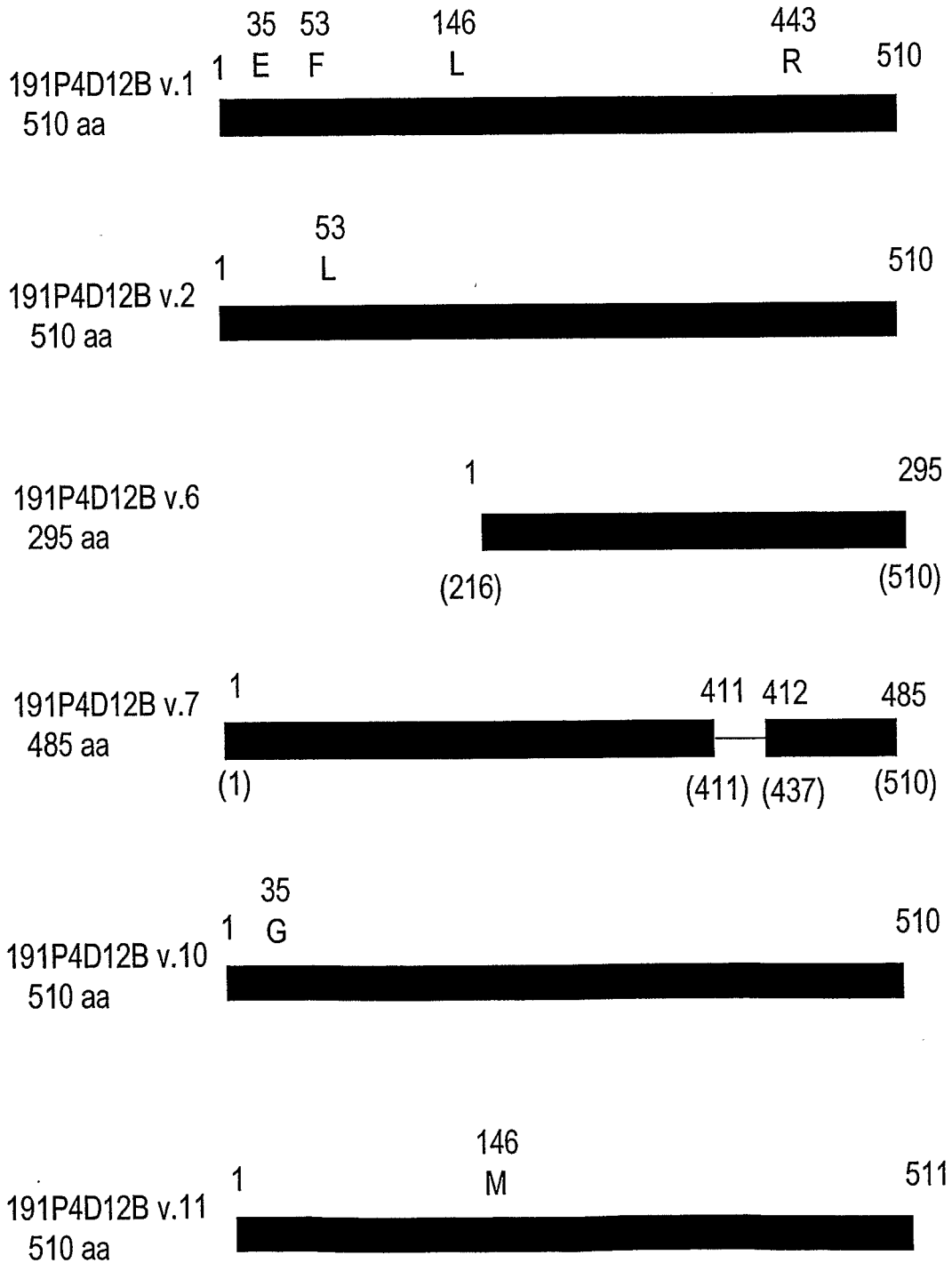
191P4D12B v.1
510 aa
1
35 E
53 F
146 L
443 R
510
191P4D12B v.2
510 aa
1
53 L
510
191P4D12B v.6
295 aa
1
295
(216)
(510)
191P4D12B v.7
485 aa
1
411 412
485
(1)
(411) (437)
(510)
191P4D12B v.10
510 aa
1
35 G
510
191P4D12B v.11
510 aa
1
146 M
511

Figure 11 (con'd)

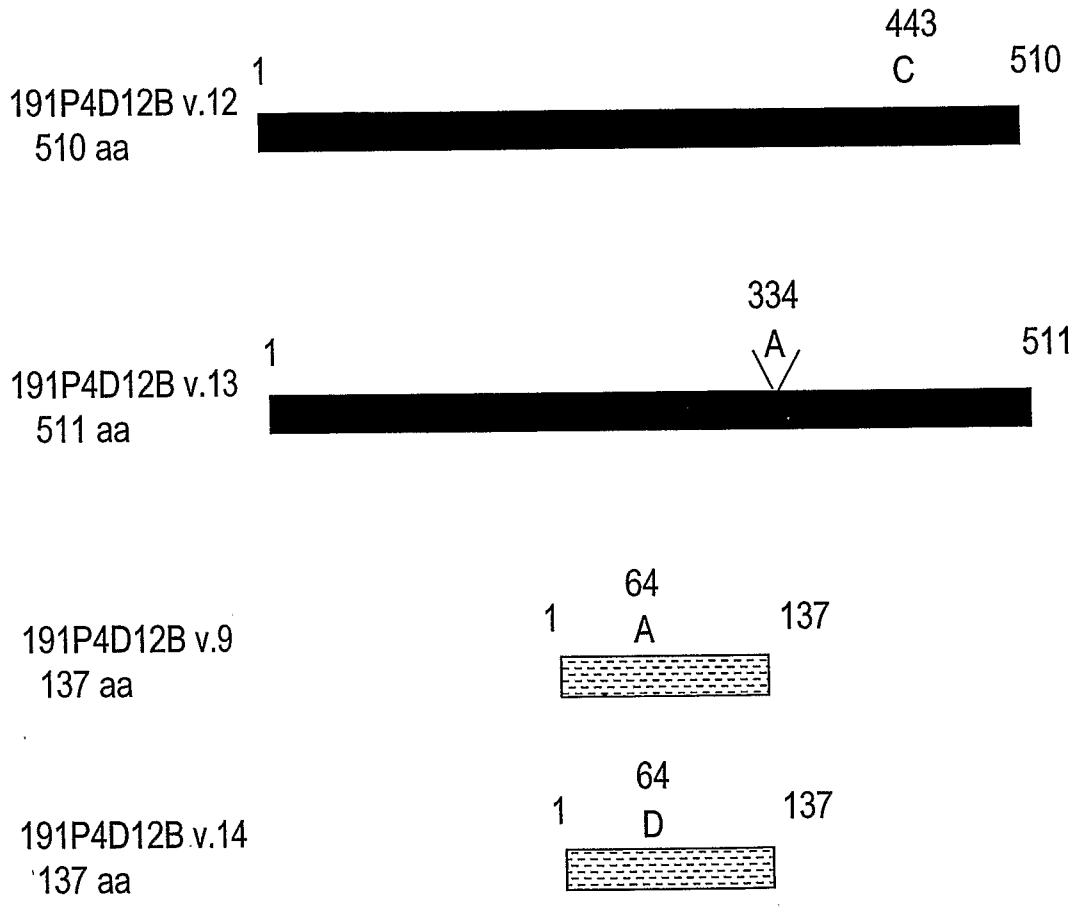

Figure 11. Schematic alignment of protein variants of 191P4D12B.

Figure 12

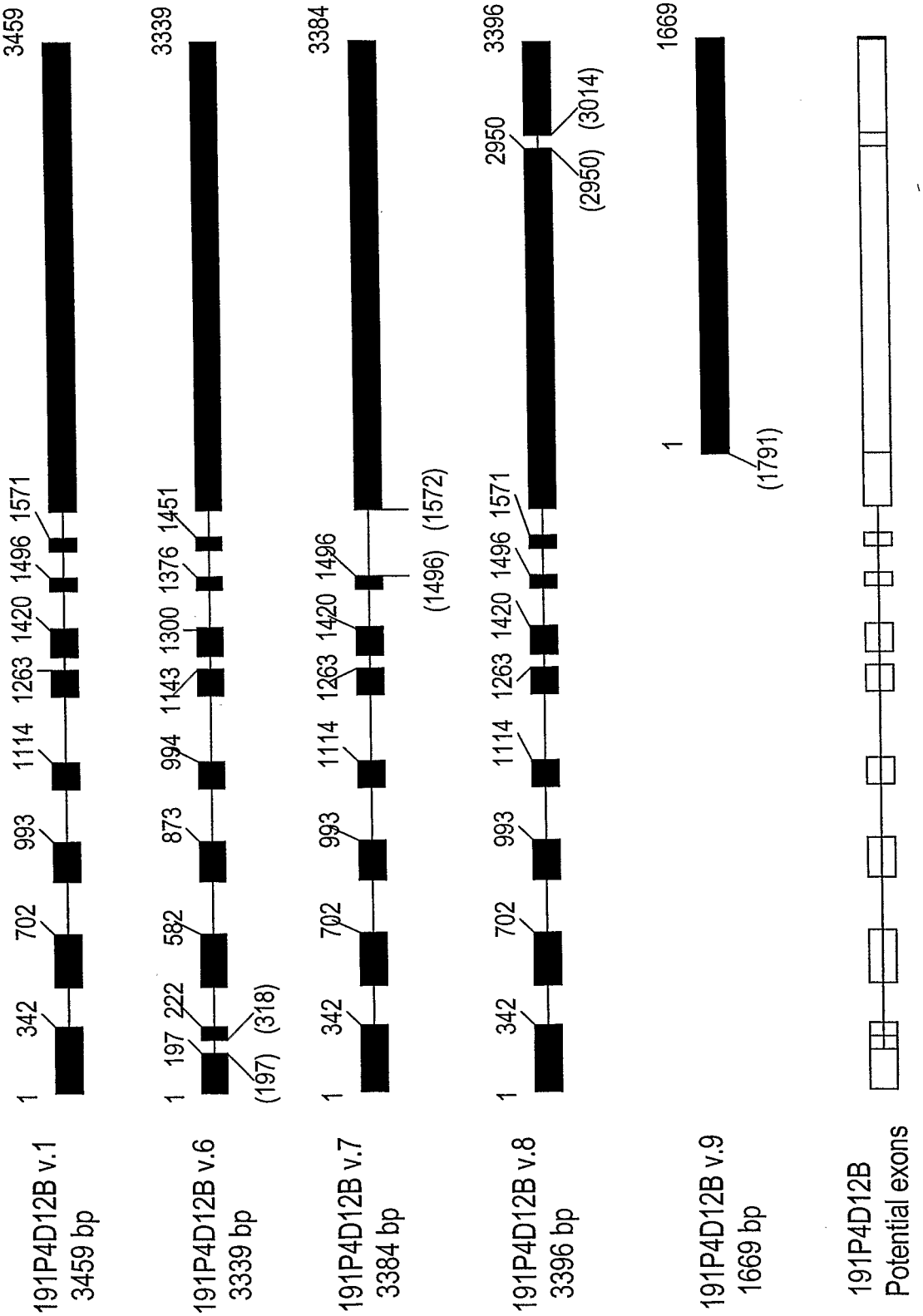
191P4D12B v.1
3459 bp
1
342
702
993
1114
1263
1420
1496
1571
3459
191P4D12B v.6
3339 bp
1
197
222
582
873
994
1143
1300
1376
1451
3339
(197)
(318)
191P4D12B v.7
3384 bp
1
342
702
993
1114
1263
1420
1496
3384
(1496)
(1572)
191P4D12B v.8
3396 bp
1
342
702
993
1114
1263
1420
1496
1571
2950
3396
(2950)
(3014)
191P4D12B v.9
1669 bp
1
1669
(1791)
191P4D12B
Potential exons

Fig: 13A Secondary structure prediction of 191P4D12B variant 1

```
          10        20        30        40        50        60        70
          |         |         |         |         |         |         |
MPLSLGAEMWGPEAWLLLLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWARV
ccccccccccchhhhhhhhhhhhhcccccccccecccceeeeeeeccccccceeeeccccccchhhhhhhhhc
DAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQAR
ccccchhhhhhhhhhcccceccccccccccccccccccccceehhhhhcccccccceeeeeccccccchhhh
LRLRVLVPPLPSLNPGPALEEGQGLTLAASCTAEGSPAPSVTWDTEVKGTTSSRSFKHSRSAAVTSEFHL
heeeeeccccccccccccccccccceeeeeeccccccccccccccccccccccccccccccccceeeccceee
VPSRSMNGQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY
ccccccccccceeeeeeccccccchhhhhhehhhhhhhhhhcccccccheehhcchehehhccccccccc
NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLDPQEDSGKQVDLVSASV
ccccccccccccccccccccccccccccccceeeeeeeccccccccceeeeeeccccccccccceeeeeeeh
VVVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQPEESVGLRA
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccchhhhhhhccccccccccccccecc
EGHPDSLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQENG
ccccccccccccceeeccccccccceeeeeeeeeeccceeccccccccccccchhhhhhhhhhheeeccc
TLRAKPTGNGIYINGRGHLV
ceeeccccceeeeeccccccc
```

Alpha helix (h): 24.90%
Extended strand (e): 18.63%
Random coil (c) : 56.47%

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13B Secondary structure prediction of 191P4D12B variant 6

```
        10        20        30        40        50        60        70
        |         |         |         |         |         |         |
MNGQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSYNWTRL
ccccccceeeeeccccccchhhhhhehhhhhhhhhhcccccccheehhcchehehhccccccccccccc
DGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLDPQEDSGKQVDLVSASVVVVGV
ccccccccccccccccccccccccceeeeeeeccccccccceeeeeeccccccccccceeeeeeehhhhhh
IAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQPEESVGLRAEGHPD
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccchhhhhhhccccccccccccccceccccccc
SLKDNSSCSVMSEEPEGRSYSTLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQENGTLRAK
ccccccccceeeccccccccceeeeeeeeeeccceeccccccccccccchhhhhhhhhhheeeccccceeec
PTGNGIYINGRGHLV
ccccceeeeeccccc
```

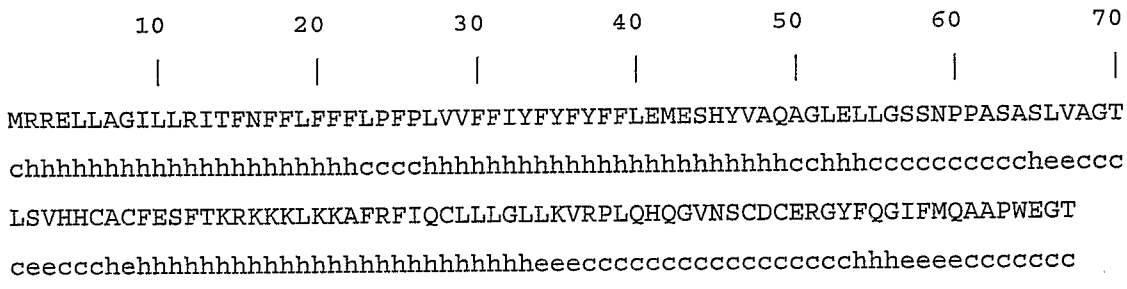
Alpha helix (h): 28.47%
Extended strand (e): 19.32%
Random coil (c) : 52.20%

13C **Secondary structure prediction of 191P4D12B variant 7**

```
         10        20        30        40        50        60        70
         |         |         |         |         |         |         |
MPLSLGAEMWGPEAWLLLLLLLLASFTGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWARV
ccccccccccchhhhhhhhhhhhhhcccccccccecccceeeeeeeccccccceeeeccccccchhhhhhhhhc
DAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQAR
ccccchhhhhhhhhhcccceccccccccccccccccccccceehhhhhcccccceeeeeccccchhhh
LRLRVLVPPLPSLNPGPALEEGQGLTLAASCTAEGSPAPSVTWDTEVKGTTSSRSFKHSRSAAVTSEFHL
heeeeeccccccccccccccccceeeeeeccccccccccccccccccccccccccccccccceeeccceee
VPSRSMNGQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPPPSY
ccccccccceeeeeeccccccchhhhhhehhhhhhhhhhcccccccheehhcchehehhccccccccc
NWTRLDGPLPSGVRVDGDTLGFPPLTTEHSGIYVCHVSNEFSSRDSQVTVDVLDPQEDSGKQVDLVSASV
ccccccccccccccccccccccccccccceeeeeeeccccccccceeeeeeccccccccccceeeeeeeh
VVVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEELTLTRENSIRRLHSHHTDPRSQSEEPEGRSY
hhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhhcccchhhhhhhccccccccccccccccc
STLTTVREIETQTELLSPGSGRAEEEEDQDEGIKQAMNHFVQENGTLRAKPTGNGIYINGRGHLV
eeeeeeeeeeccceeccccccccccccchhhhhhhhhhheeeccccceeeccccceeeeeccccc
```

Alpha helix (h): 26.19%
Extended strand (e):18.76%
Random coil (c) : 55.05%

13D Secondary structure prediction of 191P4D12B variant 9



Alpha helix (h): 56.20%
Extended strand (e): 8.76%
Random coil (c) : 35.04%

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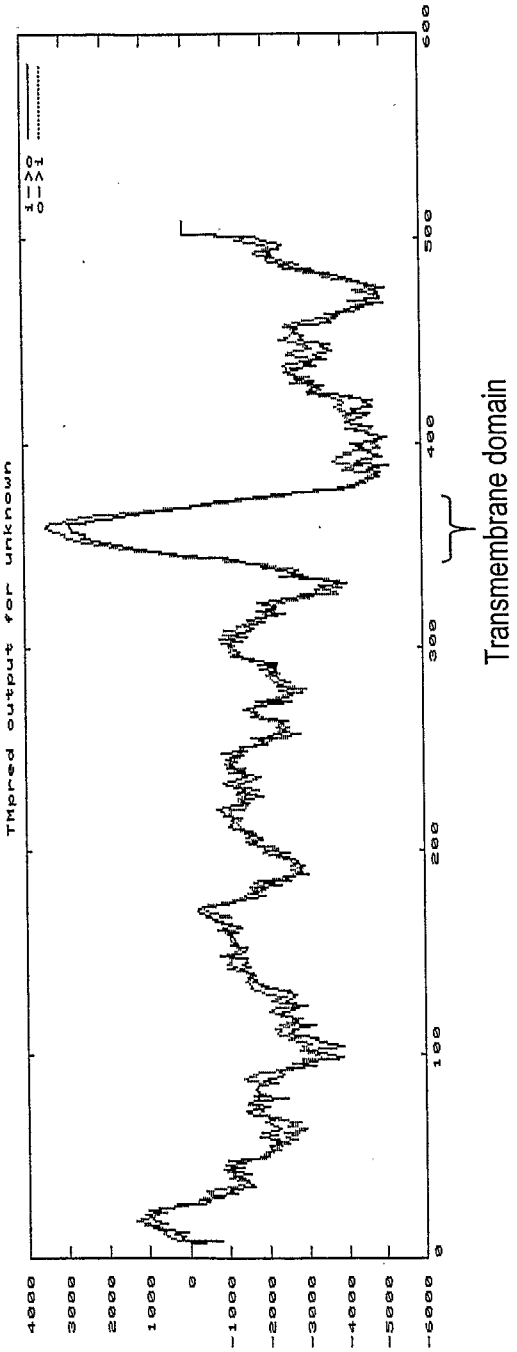
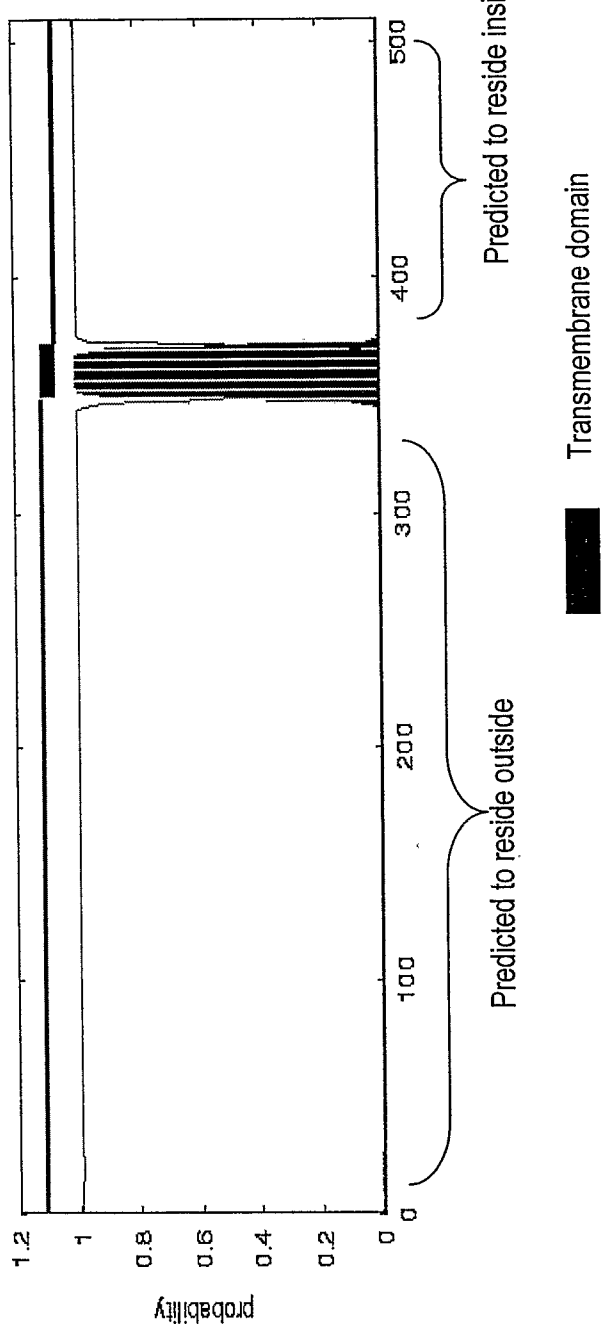
Transmembrane prediction for 191P4D12B variant 1

13E



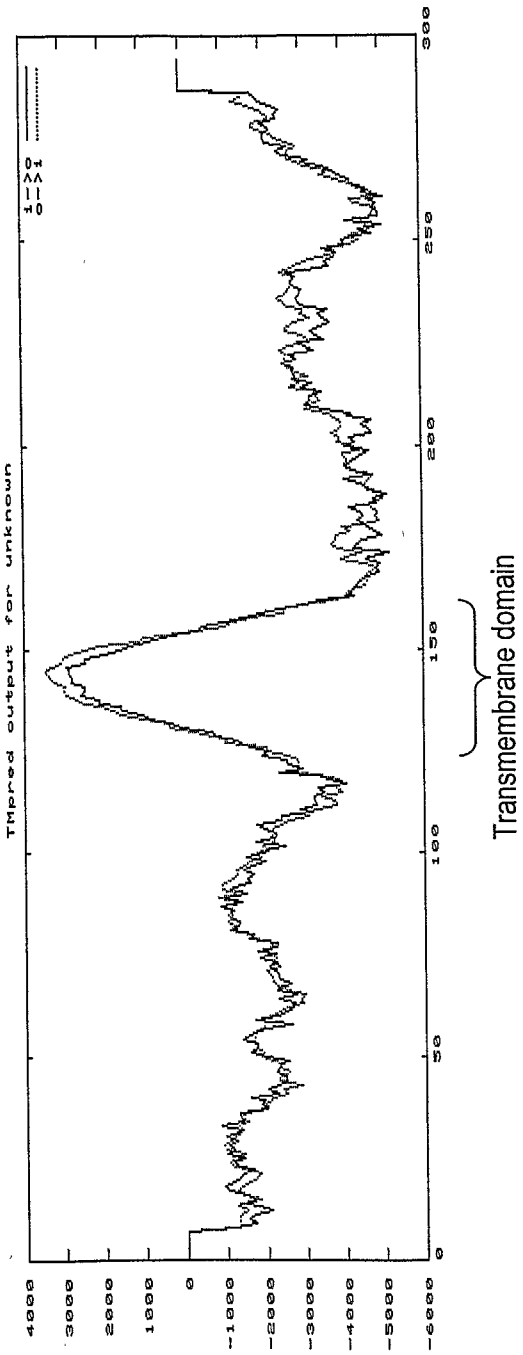
1 transmembrane domair predicted

13F



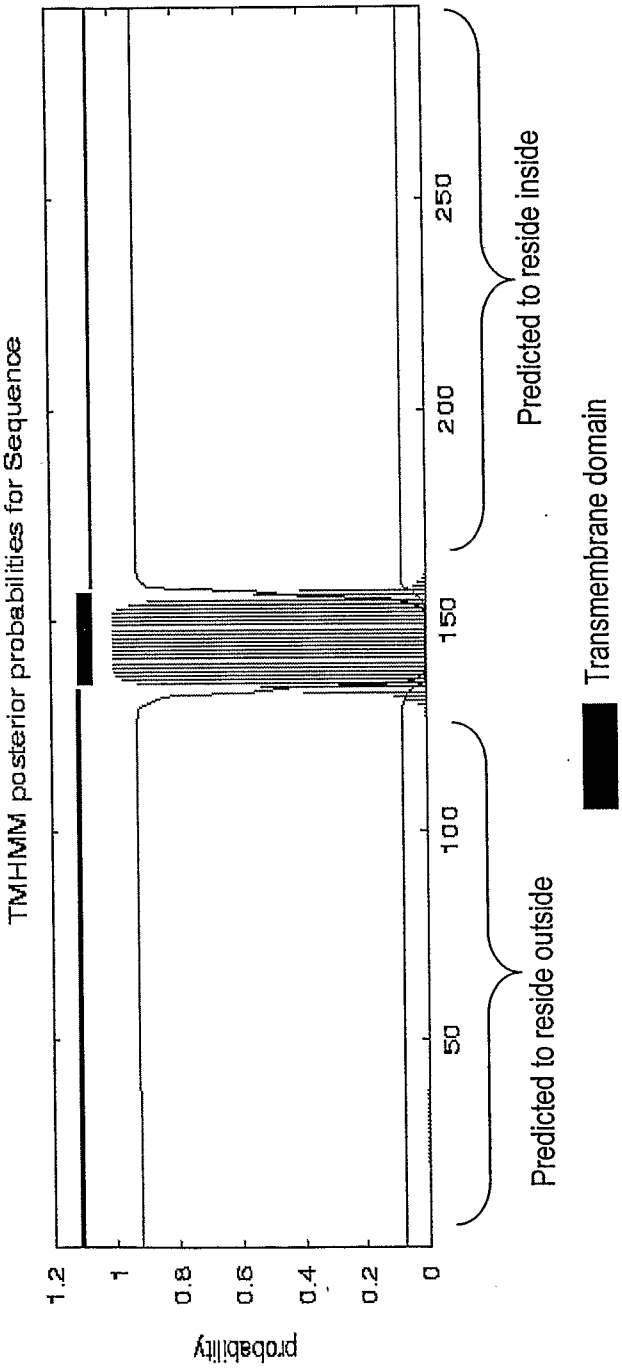
1 transmembrane domain predicted

13G Transmembrane prediction for 191P4D12B variant 6



1 transmembrane domain predicted

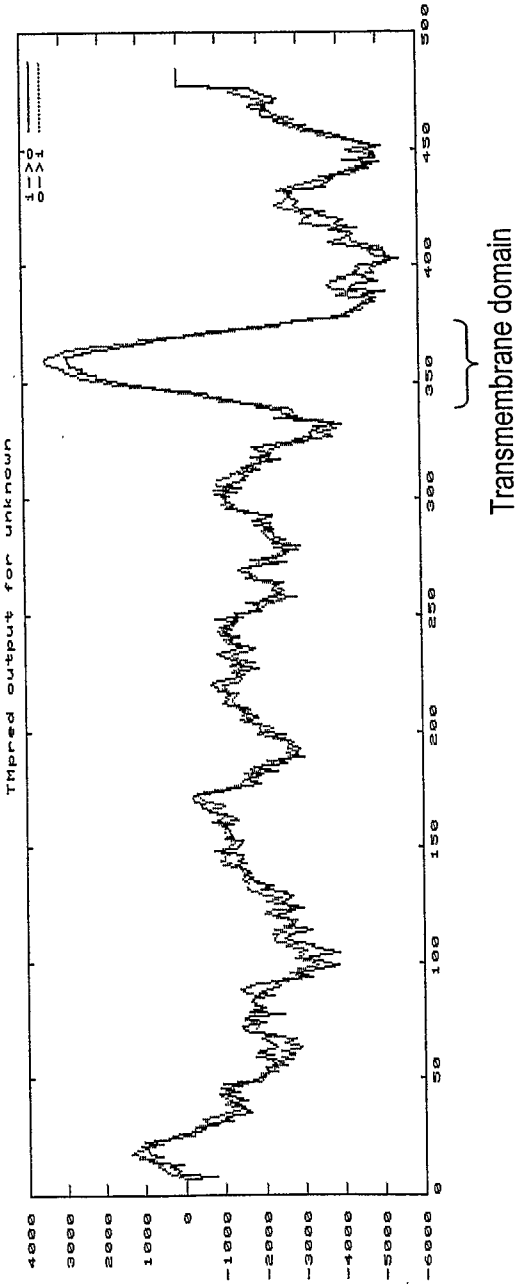
13H



1 transmembrane domain predicted

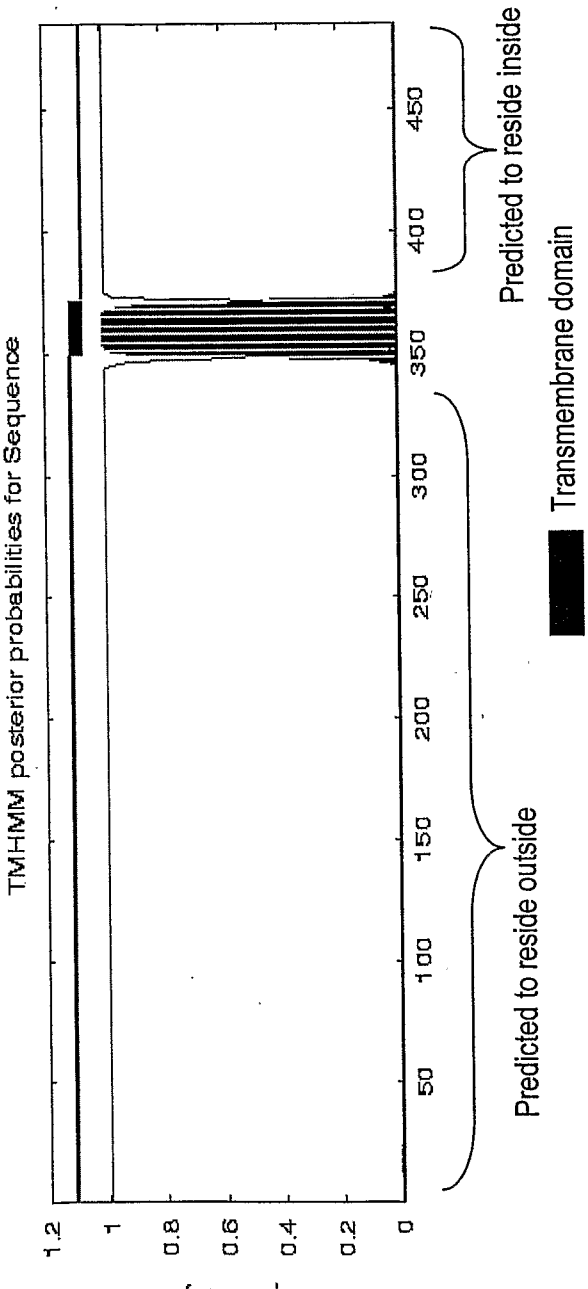
Transmembrane prediction for 191P4D12B variant 7

13I



1 transmembrane domain predicted

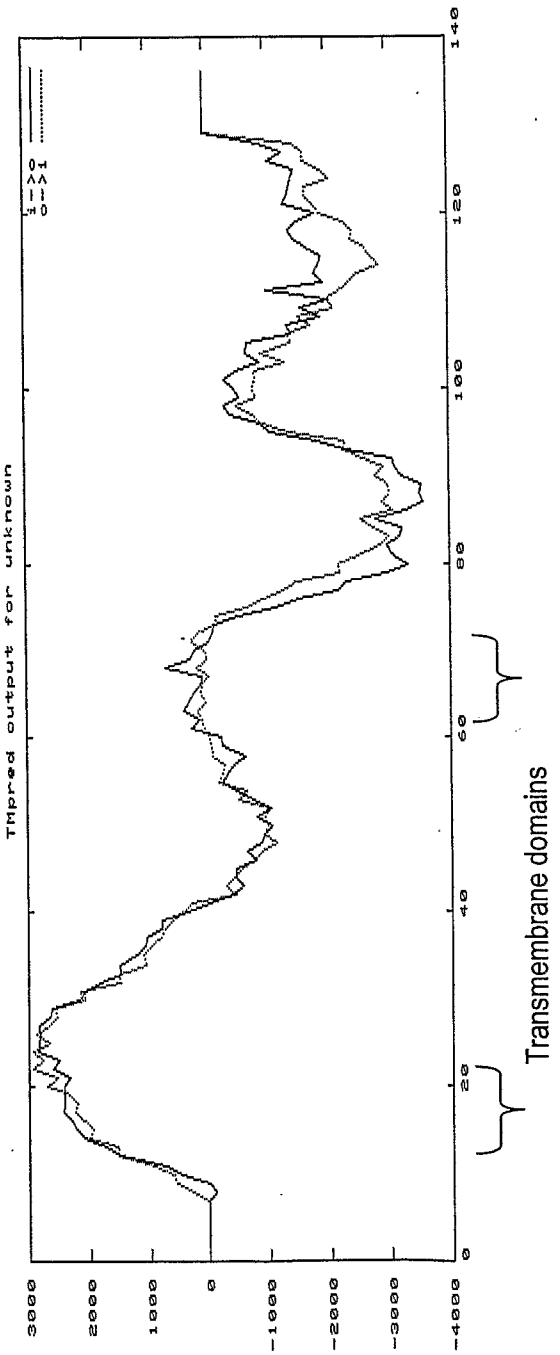
13J



1 transmembrane doma predicted

Transmembrane prediction for 191P4D12B variant 9

13K



13L

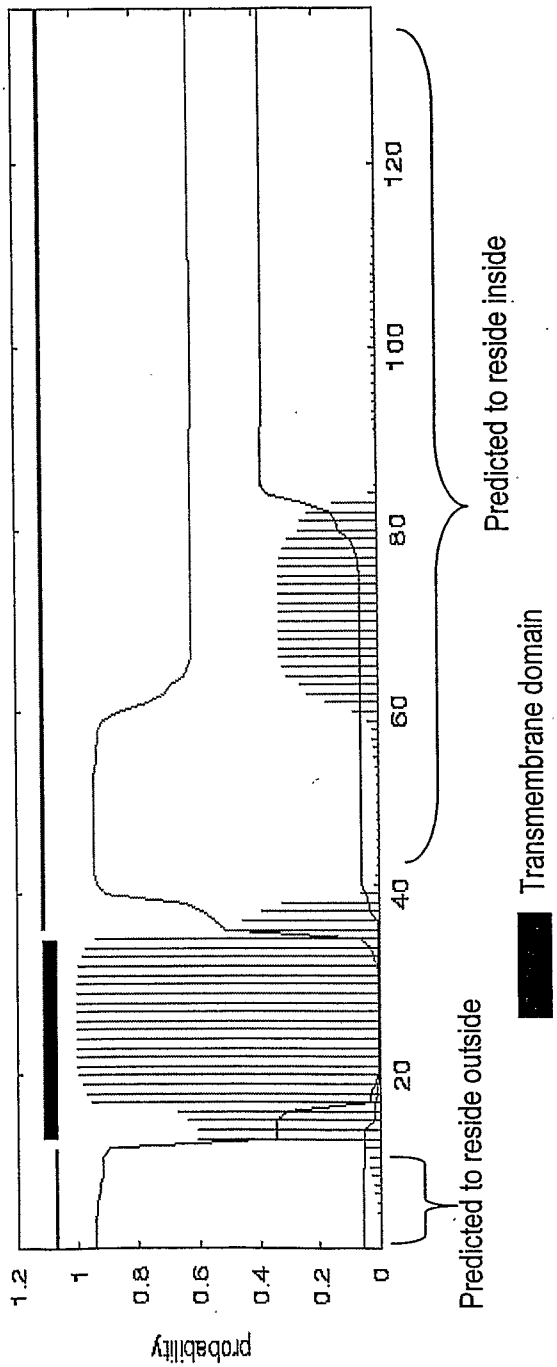


Figure 14A 191P4D12 Expression by RT-PCR

1. Vital Pool 1
2. Vital Pool 2
3. Normal kidney
4. Prostate Cancer Pool
5. Bladder cancer pool
6. Colon Cancer Pool
7. Lung Cancer Pool
8. Breast Cancer Pool
9. Metastasis Cancer Pool

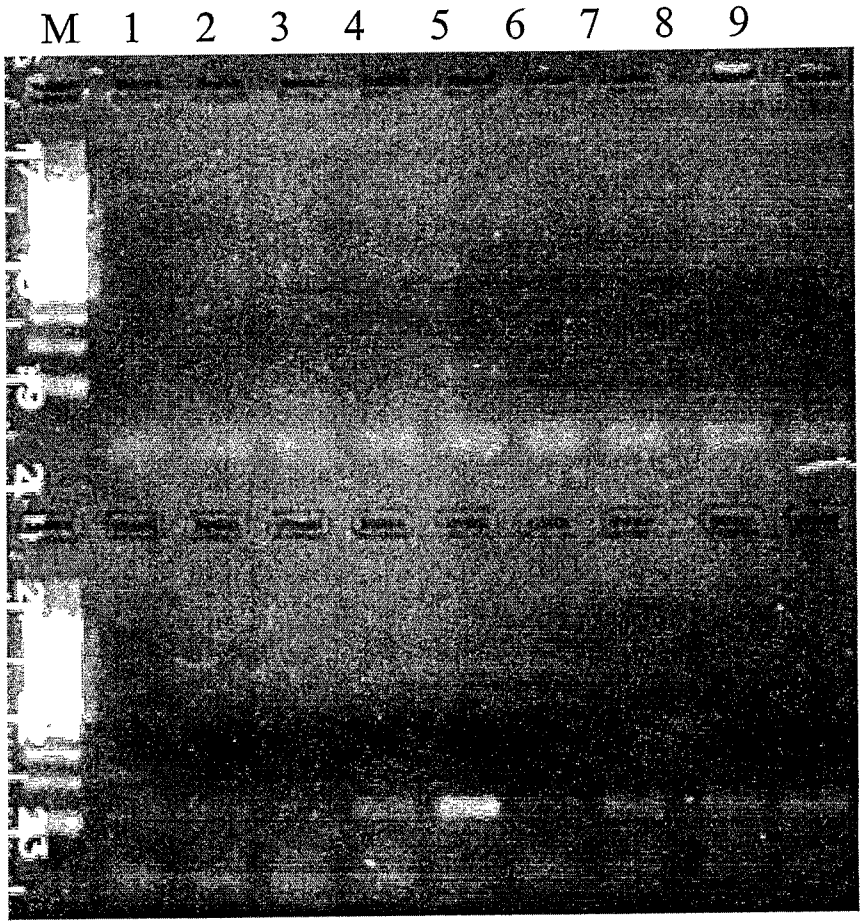
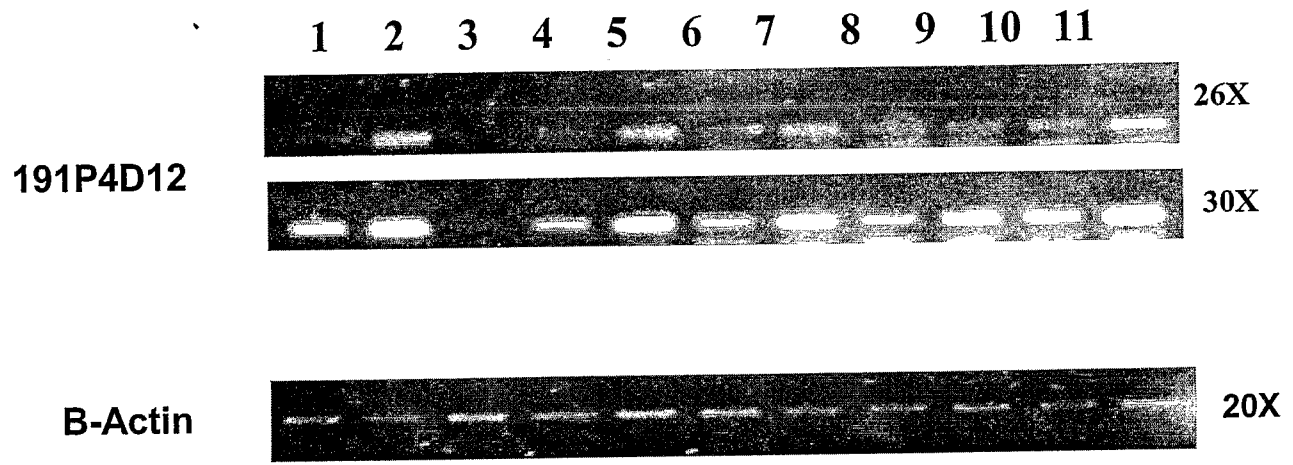
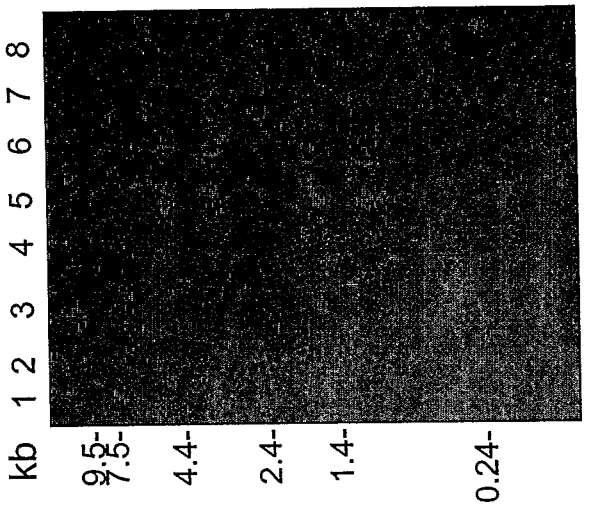


Figure 14B

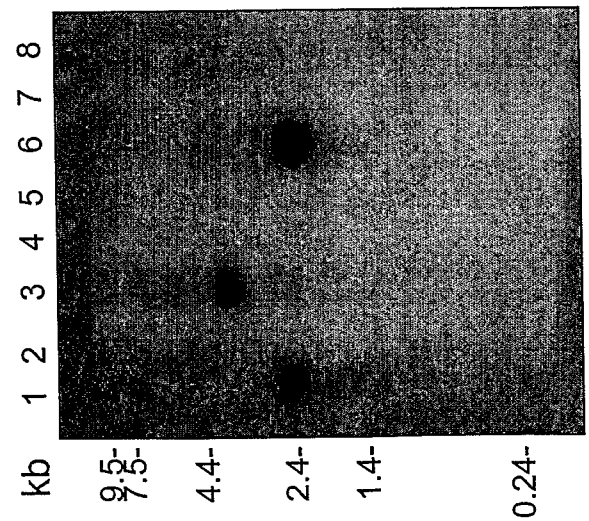


1. Prostate cancer pool
2. Bladder cancer pool
3. Kidney cancer pool
4. Colon cancer pool
5. Lung cancer pool
6. Ovary cancer pool
7. Ovary cancer pool
8. Breast cancer pool
9. Metastasis pool
10. Pancreas cancer pool
11. LAPC prostate cancer xenografts

Figure 15 191P4D12 Expression in Normal Tissues

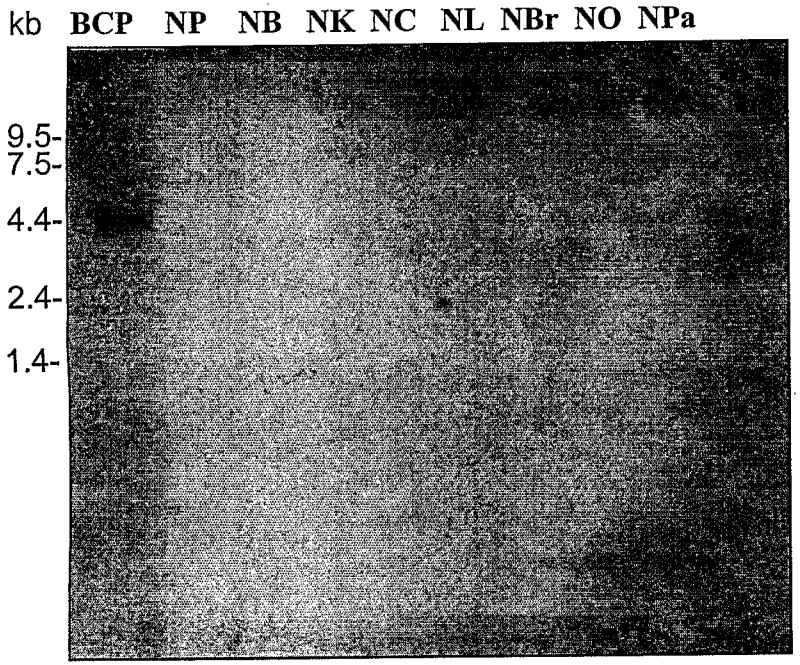


1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Uterus
6. Small Intestine
7. Colon
8. Leukocytes



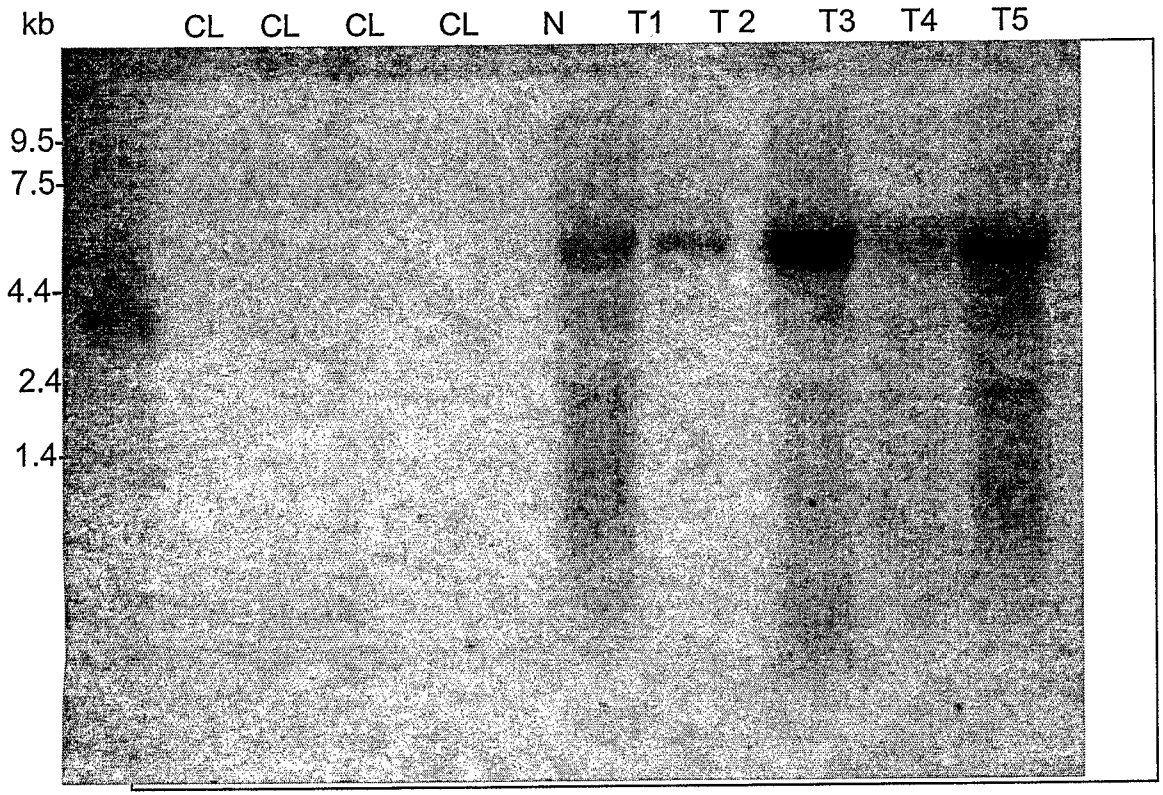
1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

Figure 16 Expression of 191P4D12 in Bladder Cancer Patient Specimens and in Normal Tissues



BCP = Bladder cancer pool: Pool of 3 different bladder cancer specimens
NP = normal prostate
NB = normal bladder
NK = normal kidney
NC = normal colon
NL = normal lung
NBr = normal breast
NO = normal ovary
NPa = normal pancreas

Figure 17 Expression of 191P4D12 in Bladder Cancer Patient Specimens



T1 = Invasive transitional papillary, grade 2

T2 = Transitional papillary, grade 2

T3 = Transitional, grade 3

T4 = Poorly diff. Transitional

T5 = Mod. to poorly diff. Squamous cell

CL = Cell lines (from left to right): HT1197, UM-U
3, TCCSUP, J82

N = Normal Bladder

T = Tumor

Figure 18 191P4D12 Expression in Prostate Cancer Xenografts

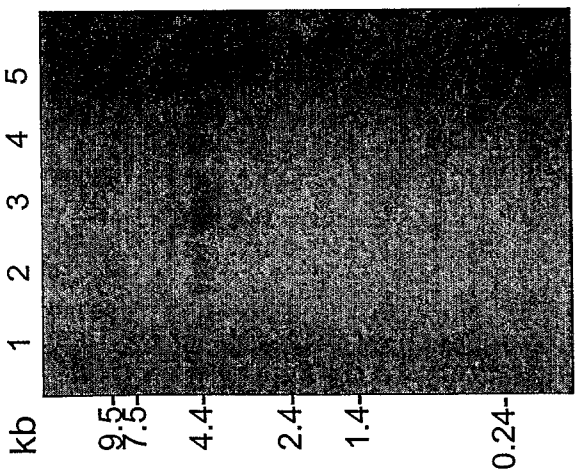
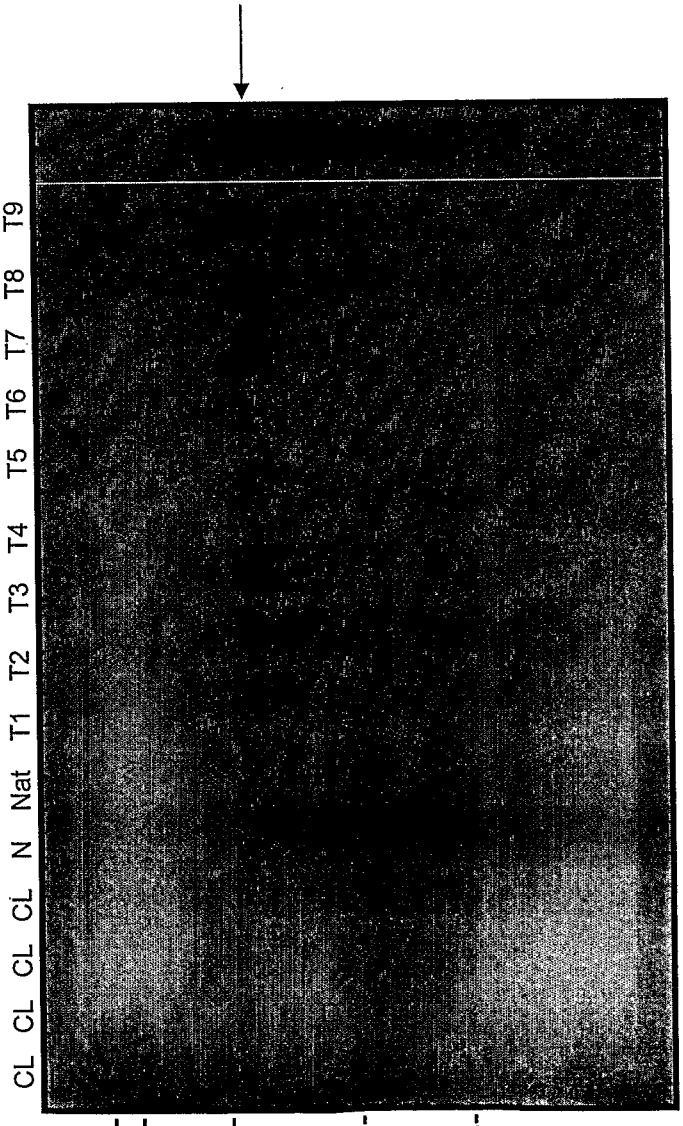


Figure 19 191P4D12 Expression in Cervical Cancer Patient Specimens

1. Normal Cervix
2. Hela Cell Line
3. Cervix Tumor #1
4. Cervix Tumor #2
5. Cervix Tumor #3

Figure 20 191P4D12 Expression in Lung Cancer Patient Specimens



CL = Cell lines (in order from left to right): A427, NCI H146, NCI H82, SKLU1
N = Normal lung
Nat = Normal adjacent to tumor
T = Tumor

T1 = Adeno I B
T2 = Adeno I B
T3 = Adeno I B
T4 = Squamous stage IB
T5 = Squamous stage IIB
T6 = Squamouse stage IIIA
T7 = Squamous stage IIIA
T8 = Large cell stage IIIA
T9 = Large cell stage IB

Figure 21A 191P4D12 Expression in Lung Cancer.

	Pathology	Grade	Expression Level
1	Bronchioalveolar	IA	3
2	Squamous		3
3	Adeno	Mod Diff	3
4	Adeno	Mod Diff	3
5	Non-small cell		3
6	Adeno	3	3
7	Squamous		3
8	Adeno	IB	2
9	Squamous		3
10	Small Cell	I	1
11	Small Cell	I	1
12	Small Cell	I	1
13	Large Cell	IV	1
14	Squamous	IIB	2
15	Squamous	IB	3
16	Squamous	IIIA	2
17	Papillary	IV	1
18	Papillary	IB	2
19	Adeno	IIIA	2
20	Adeno	IIIA	2
21	Squamous	IIB	3
22	Squamous	IB	3
23	Adeno	IB	3
24	Large Cell	IIIA	0
25	Small Cell	IIB	1
26	Squamous	IB	3
27	Squamous	IIIA	3
28	Papillary	I	3
29	Adeno	I	3
30	Large Cell	IIB	3
31	Large Cell	I	3
Percentage positive			**96.8%**

Figure 21B 191P4D12 Expression in Bladder Cancer

	Pathology	Grade	Expression Level
1	Normal		0
2	Transitional	3	1
3	Transitional	3	3
4	Transitional	3	3
5	Squamous		3
6	Papillary	3	3
7	Transitional	3	1
8	Transitional	3	0
9	Transitional	2	1
10	Transitional	2	3
11	Papillary	1	3
12	Transitional	3	3
13			3
14	Transitional	2	3
15	Papillary	3	3
16	Transitional		3
17	Squamous		2
18	Not determined	3	1
19	Transitional	3	1
Percentage positive			**94.4%**

Figure 21C 191P4D12 Expression in Prostate Cancer.

	Gleason	Expression Level
1	5	2
2	5	3
3	5	2
4	5	2
5	6	3
6	6	2
7	6	3
8	6	2
9	6	2
10	7	2
11	7	3
12	7	2
13	7	2
14	7	3
15	7	3
16	7	3
17	7	2
18	8	3
19	9	2
20	not determined	3
21	LAPC-4AD	2
22	LAPC-4AI	2
23	LAPC-9AD	2
24	LAPC-9AI	2
Percentage positive		**100.0%**

Figure 21D 191P4D12 Expression in Colon Cancer.

Patient #	Stage	Expression Level
1	I	2
2	I	2
3	II	2
4	II	2
5	II	1
6	II	2
7	II	1
8	II	1
9	II	2
10	II	2
11	II	2
12	III	2
13	III	3
14	III	2
15	III	2
16	III	2
17	III	2
18	III	1
19	III	2
20	III	2
21	IV	2
22	IV	1
Percent Positive		100%

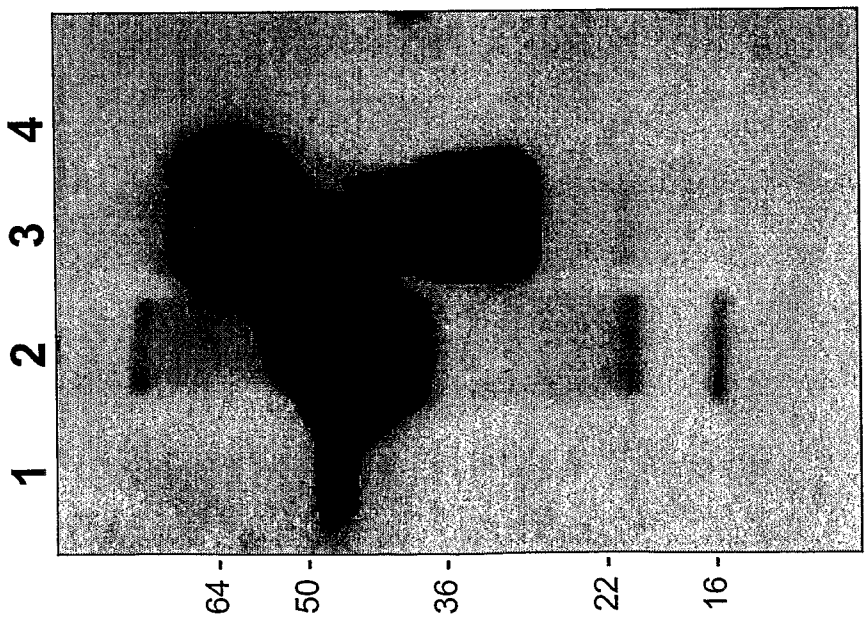
Figure 21E 191P4D12 Expression in Uterus Cancer.

Patient #	Diagnosis	Grade	Expression Level
1	AdenoCA	G1	3
2	AdenoCA	G1	2
3	AdenoCA	G1	2
4	AdenoCA	G2	3
5	AdenoCA	G2	3
6	AdenoCA	G2	2
7	AdenoCA	G2	3
8	AdenoCA	G2	3
9	AdenoCA	G3A	3
10	AdenoCA	Well diff.	3
11	Carcinosarcoma	G3	2
12	Stromal sarcoma	High grade	1
Percentage Positive			100.0%

Figure 21F 191P4D12 Expression in Cervical Cancer.

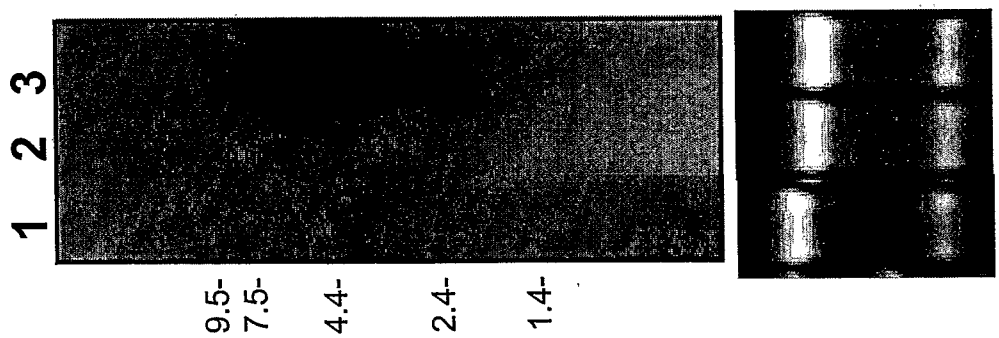
Patient #	Expression Level
1	3
2	2
3	3
4	3
5	3
6	3
7	3
8	3
9	3
10	3
11	3
12	3
13	3
14	3
Percentage Positive	100%

Figure 22 Transient Expression of 191P4D12 in Transfected 293T Cells



1. 293T-191P4D12.pTag5 supernatant
2. 293T-191P4D12.pTag5 lysate
3. 293T-191P4D12.pcDNA3.1/MycHis lysate
4. 293T-pcDNA3.1/MycHis negative control

Figure 23 Expression of 191P4D12 in Transduced Cells Following Retroviral Gene Transfer



191P4D12(b) SSH sequence of 223 nucleotides. (SEQ ID NO: 1)

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 61 TTTATTTTTA GCTGGCCCAC CCAGATACAC TCAGCCAGAA TACCTAGATT TAGTACCCAA
121 ACTCTTCTTA GTCTGAAATC TGCTGGATTT CTGGCCTAAG GGAGAGGCTC CCATCCTTCG
181 TTCCCCAGCC AGCCTAGGAC TTCGAATGTG GAGCCTGAAG ATC
```