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(54) **PROSTATE CANCER VACCINE**
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7,910,565 B2 3/2011 McNeel et al.
8,513,210 B2 8/2013 McNeel et al.
2004/0142890 A1 7/2004 McNeel

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A61K 31/70 (2006.01)
G01N 33/569 (2006.01)
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A61K 38/19 (2006.01)

(52) **U.S. Cl.**

CPC **A61K 39/0011** (2013.01); **A61K 31/70** (2013.01); **A61K 38/193** (2013.01); **G01N 33/56972** (2013.01); **G01N 33/57434** (2013.01); **A61K 2039/53** (2013.01); **A61K 2039/55516** (2013.01); **A61K 2039/585** (2013.01); **G01N 2800/52** (2013.01)

(58) **Field of Classification Search**

None
See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

6,548,064 B1 4/2003 Tureci et al.
6,562,798 B1 5/2003 Schwartz
6,800,730 B1 10/2004 Tureci et al.
6,821,767 B1 11/2004 French et al.
7,129,078 B2 10/2006 French et al.
7,179,797 B2 2/2007 McNeel
7,223,741 B2 5/2007 Krieg
7,238,778 B2 7/2007 Apolito et al.

OTHER PUBLICATIONS

Acsadi, et al., Direct Gene Transfer and Expression into Rat Heart In Vivo, *The New Biologist*, 1991, 3(1):71-81.
Ayyoub, et al., Identification of an SSX-2 Epitope Presented by Dendritic Cells to Circulating Autologous CD4+ T Cells, *Journal of Immunology*, 2004, 172:7206-7211.
Budker, et al., Naked DNA Delivered Intraportally Expresses Efficiently in Hepatocytes, *Gene Therapy*, 1996, 3:593-598.
Budker, et al., pH-Sensitive, Cationic Liposomes: A New Synthetic Virus-Like Vector, *Nature Biotechnology*, 1996, 14:760-764.
Budker, et al., The Efficient Expression of Intravascularly Delivered DNA in Rat Muscle, *Gene Therapy*, 1998, 5:272-276.
Chang, et al., Fusion Proteins Containing Androgen Receptor Sequences and Their Use in the Production of Poly- and Monoclonal Anti-Androgen Receptor Antibodies, *Endocrinology*, 1989, 123(2):1097-1099.
Chen, et al., Molecular Determinants of Resistance to Antiandrogen Therapy, *Nature Medicine*, 2004, 10:33-39.
Chen, et al., Induction of CD8+ T Cell Responses to Dominant and Subdominant Epitopes and Protective Immunity to Sendai Virus Infection by DNA Vaccination, *Journal of Immunology*, 1998, 160:2425-2432.
Chichet, et al., Androgen Receptor Distribution, PAS and Alcyan Blue Reaction in the Vomeronasal Organ and the Nasal Septum Mucosa of the Developing Male Rat, *Int. J. Morphol.*, 2007, 25(3):579-585.
Cho, et al., Immunostimulatory DNA-Based Vaccines Induce Cytotoxic Lymphocyte Activity by a T-Helper Cell-Independent Mechanism, *Nature Biotechnology*, 2000, 18:509-514.
Costagliola, et al., Genetic Immunization Against the Human Thyrotropin Receptor Causes Thyroiditis and Allows Production of Monoclonal Antibodies Recognizing the Native Receptor, *Journal of Immunology*, 1998, 160:1458-1465.
Danko, et al., Pharmacological Enhancement of In Vivo Foreign Gene Expression in Muscle, *Gene Therapy*, 1994, 1 (2):114-121.
Davis, et al., Direct Gene Transfer into Skeletal Muscle In Vivo: Factors Affecting Efficiency of Transfer and Stability of Expression, *Human Gene Therapy*, 1993, 4:151-159.
Eder, et al., Targeting the Androgen Receptor in Hormone-Refractory Prostate Cancer—New Concepts, *Future Oncology*, 2005, 1(1):93-101.
Hartmann, et al., Delineation of a CpG Phosphorothioate Oligodeoxynucleotide for Activating Primate Immune Responses In Vitro and In Vivo, *Journal of Immunology*, 2000, 164:1617-1624.
Irvine, et al., The Next Wave of Recombinant and Synthetic Anticancer Vaccines, *Cancer Biology*, 1995, 6:337-347.
Iwasaki, et al., The Dominant Role of Bone Marrow-Derived Cells in CTL Induction Following Plasmid DNA Immunization at Different Sites, *Journal of Immunology*, 1997, 159:11-14.

(Continued)

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(57) **ABSTRACT**

Androgen receptor-based vaccines for eliciting an immune reaction in vivo against cells expressing androgen receptor are disclosed. The vaccines are useful in the treatment of prostate cancer. Also disclosed are methods for inducing immune reaction to androgen receptor or treating prostate cancer in a mammal, using the vaccines and pharmaceutical compositions comprising the vaccines.

8 Claims, 15 Drawing Sheets

Specification includes a Sequence Listing.

(56)

References Cited

OTHER PUBLICATIONS

- Kaczmarczyk, et al., Induction of cre Recombinase Activity Using Modified Androgen Receptor Ligand Binding Domains: A Sensitive Assay for Ligand-Receptor Interactions, *Nucleic Acids Research*, 2003, 31(15):e86, 8 pages.
- Kaplan-Lefko, et al., Pathobiology of Autochthonous Prostate Cancer in a Pre-Clinical Transgenic Mouse Model, *The Prostate*, 2003, 55:219-237.
- Lee, et al., Comparison of Various Expression Plasmids for the Induction of Immune Response by DNA Immunization, *Mol. Cells*, 1997, 7(4):495-501.
- Manthorpe, et al., Gene Therapy by Intramuscular Injection of Plasmid DNA: Studies on Firefly Luciferase Gene Expression in Mice, *Human Gene Therapy*, 1993, 4:419-431.
- Meidenbauer, et al., Direct Visualization of Antigen-Specific T Cells Using Peptide-MHC-Class I Tetrameric Complexes, *Methods*, 2003, 31:160-171.
- Mincheff et al., Naked DNA and Adenoviral Immunizations for Immunotherapy of Prostate Cancer: A Phase I/II . *Clinical Trial*, *European Urology*, 2000, 38:208-217.
- Olson, et al., Antibody and T-Cell Responses Specific for the Androgen Receptor in Patients With Prostate Cancer, *The Prostate*, 2007, 67:1729-1739.
- Palmowski, et al., The Use of HLA Class I Tetramers to Design a Vaccination Strategy for Melanoma Patients, *Immunological Reviews*, 2002, 188:155-163.
- Prikler, et al., Adaptive Immunotherapy of the Advanced Prostate Cancer—Cancer Testis Antigen (CTA) as Possible Target Antigens, *Aktuel Urol.*, 2004, 35:326-330.
- Raz, et al., Intradermal Gene Immunization: The Possible Role of DNA Uptake in the Induction of Cellular Immunity to Viruses, *Proc. Natl. Acad. Sci. USA*, 1994, 91:9519-9523.
- Scanlan, et al., The Cancer/Testis Genes: Review, Standardization, and Commentary, *Cancer Immunity*, 2004, 4:1, 15 pages.
- Scher, et al., Targeting the Androgen Receptor: Improving Outcomes for Castration-Resistant Prostate Cancer, *Endocrine-Related Cancer*, 2004, 11:459-476.
- Suarez-Quian, et al., Androgen Receptor Distribution in Adult Human Testis, *Journal of Clinical Endocrinology and Metabolism*, 1999, 84(1):350-358.
- Thomson, et al., Delivery of Multiple CD8 Cytotoxic T Cell Epitopes by DNA Vaccination, *Journal of Immunology*, 1998, 160:1717-1723.
- Tighe, et al., Gene Vaccination: Plasmid DNA is More Than Just a Blueprint, *Immunology Today*, 1998, 19(2):89-97.
- Tureci, et al., Identification of a Meiosis-Specific Protein as a Member of the Class of Cancer/Testis Antigens, *Proc. Natl. Acad. Sci. USA*, 1998, 95:5211-5216.
- Wagner, et al., Identification of an HLA-A*02 Restricted Immunogenic Peptide Derived from the Cancer Testis Antigen HOM-MEL-40/SSX2, *Cancer Immunity*, 2003, 3:18, 15 pages.
- Wolff, et al., Direct Gene Transfer Into Mouse Muscle in Vivo, *Science*, 1990, 247:1465-1468.
- Wolff, et al., Conditions Affecting Direct Gene Transfer Into Rodent Muscle In Vivo, *Biotechniques*, 1991, 11 (4):474-485.
- Zhang, et al., Efficient Expression of Naked DNA Delivered Intraarterially to Limb Muscles of Nonhuman Primates, *Human Gene Therapy*, 2001, 12:427-438.
- Zhu, et al., Mass Spectrometric Characterization of the Human Androgen Receptor Ligand-Binding Domain Expressed in *Escherichia coli*, *Biochemistry*, 2001, 40:10756-10763.

A.

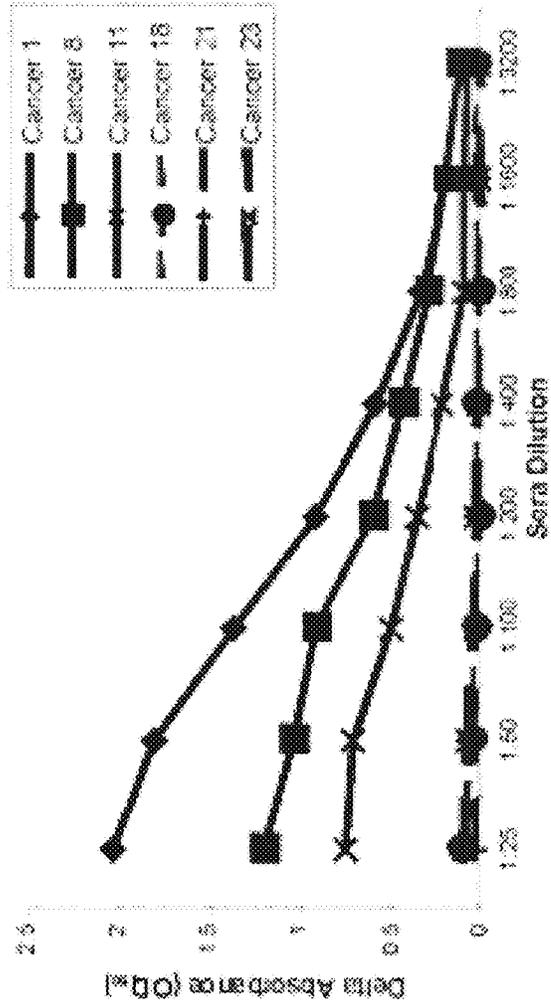


FIG. 1

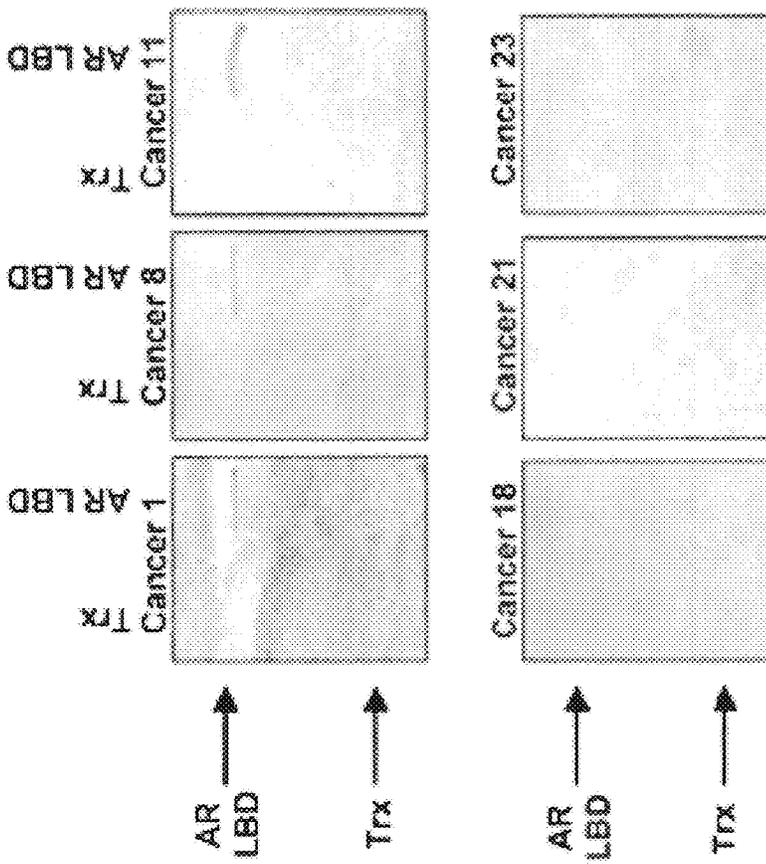


FIG. 1

B.

C.

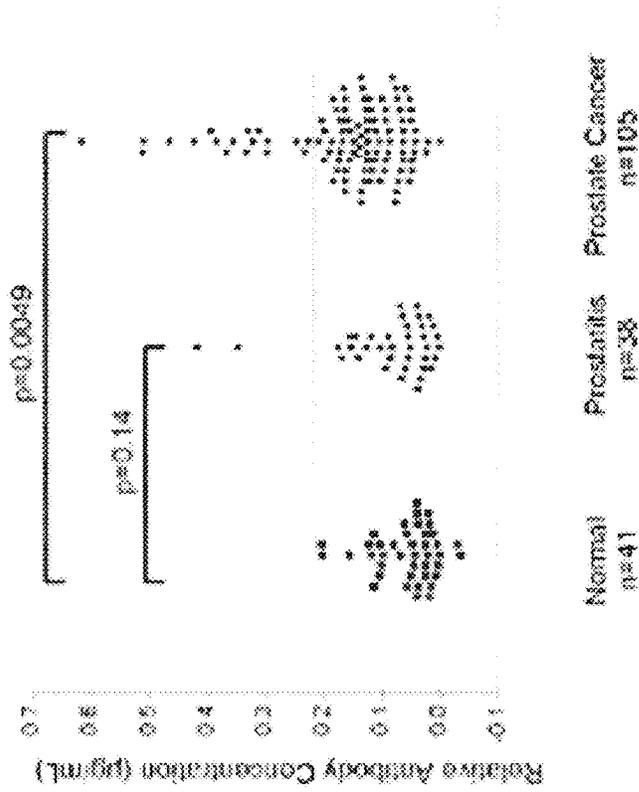


FIG. 1

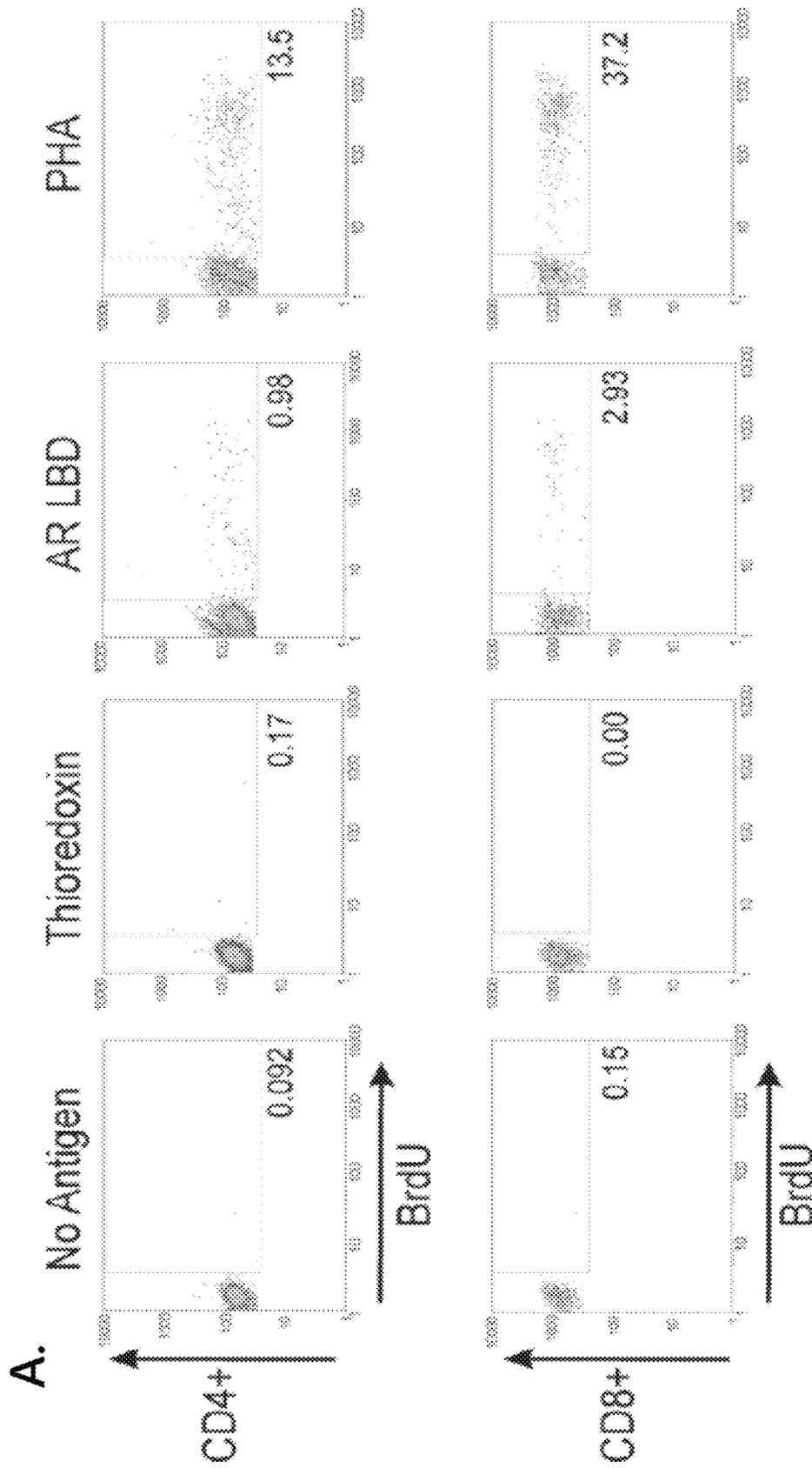


FIG. 2

B.

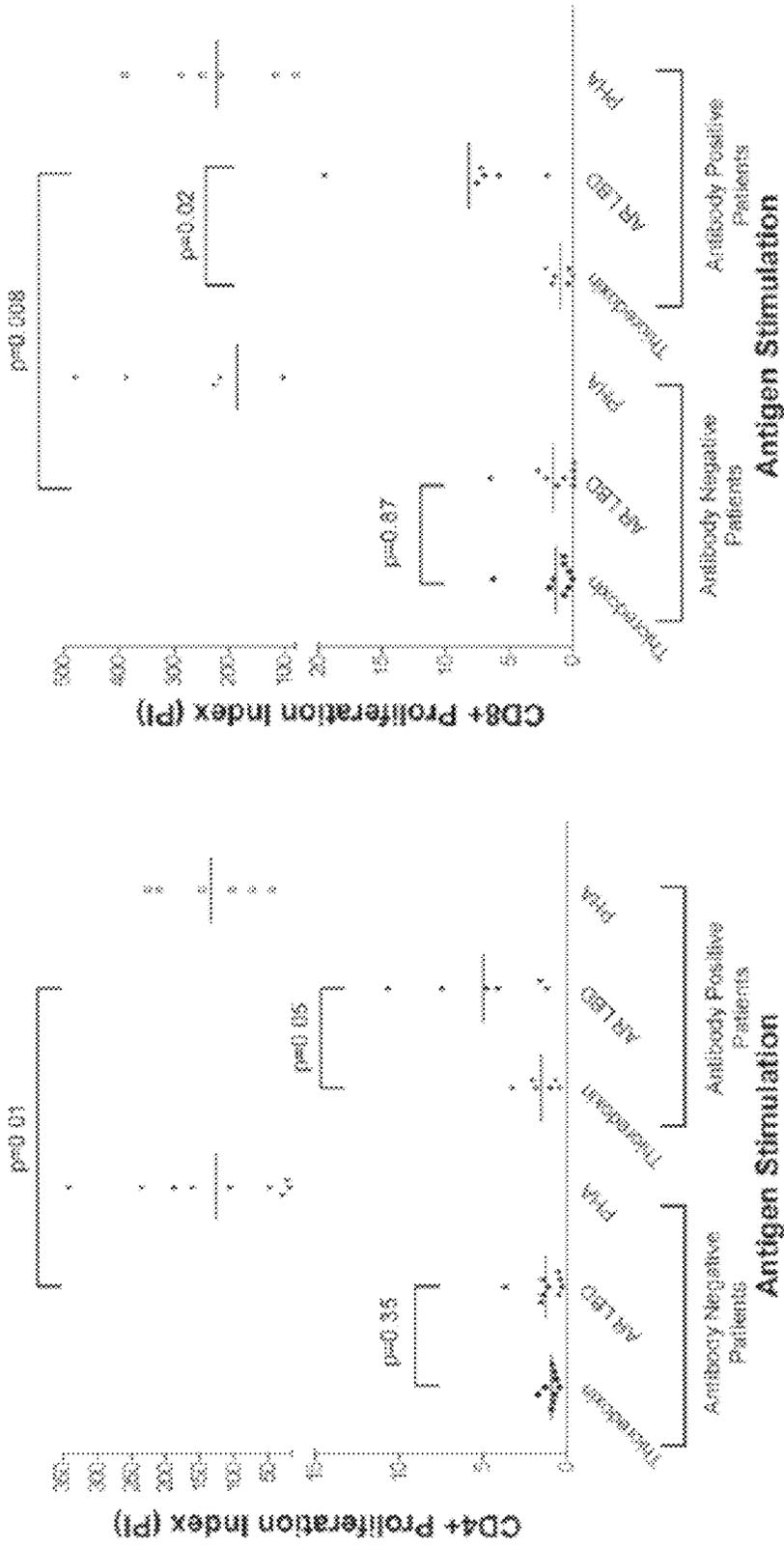


FIG. 2

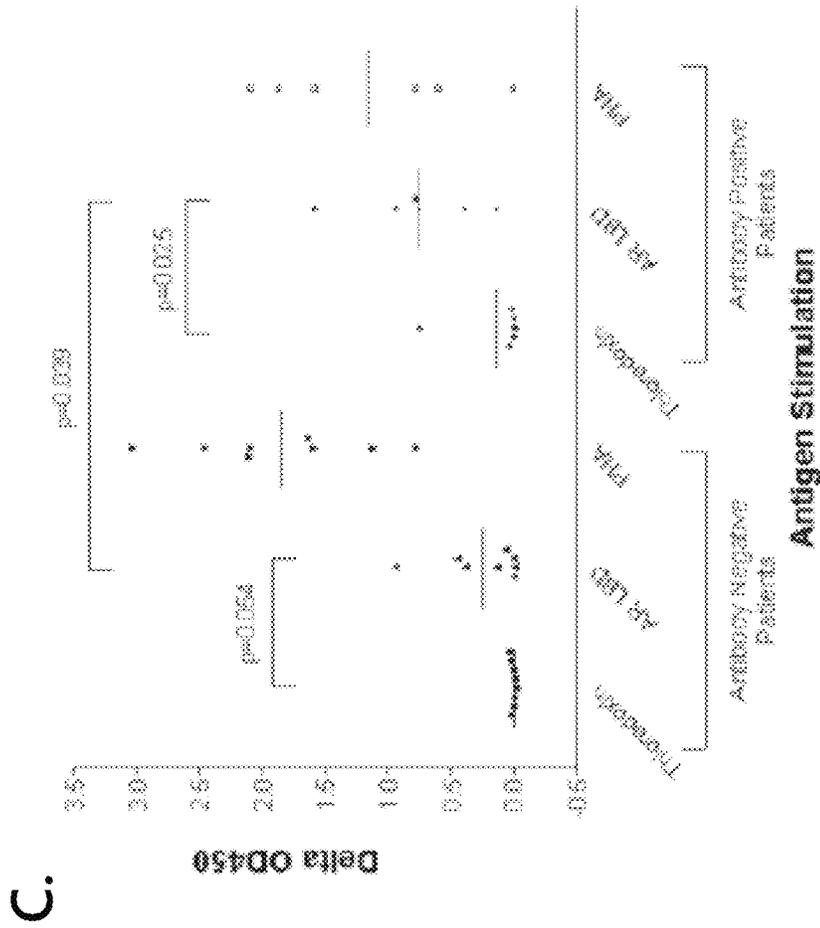


FIG. 2

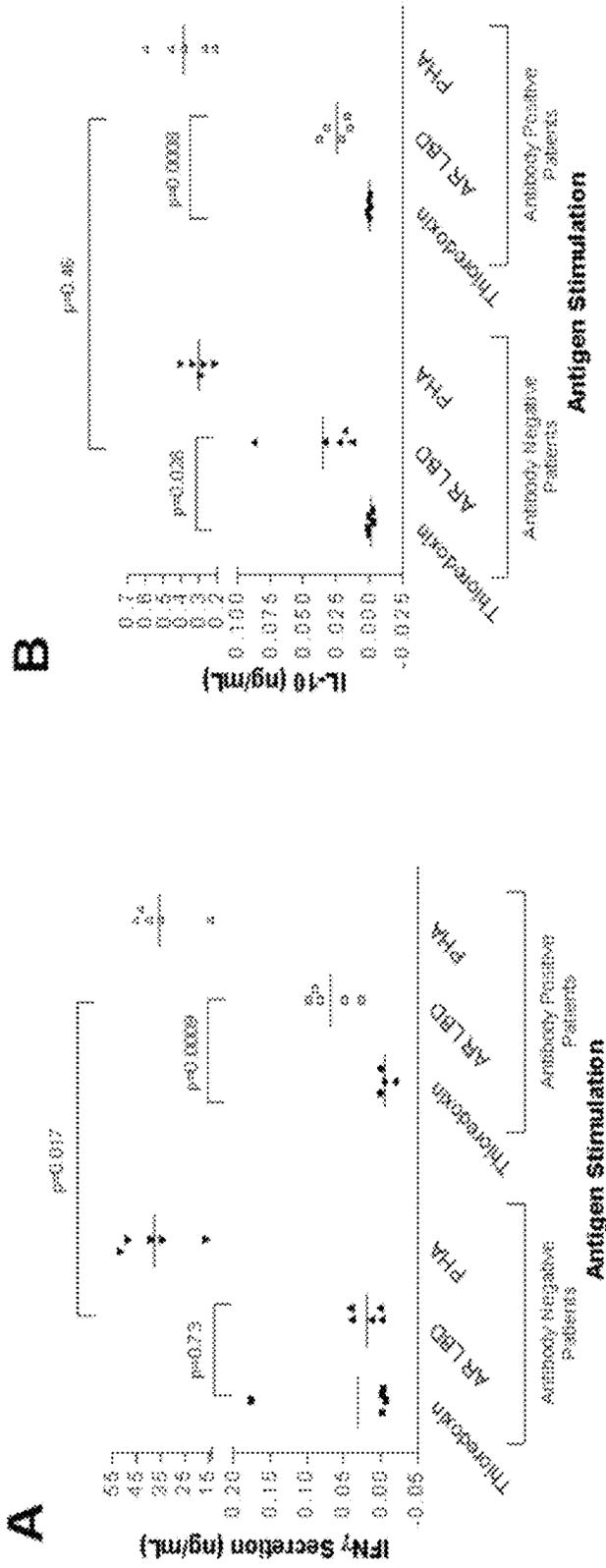


FIG. 3

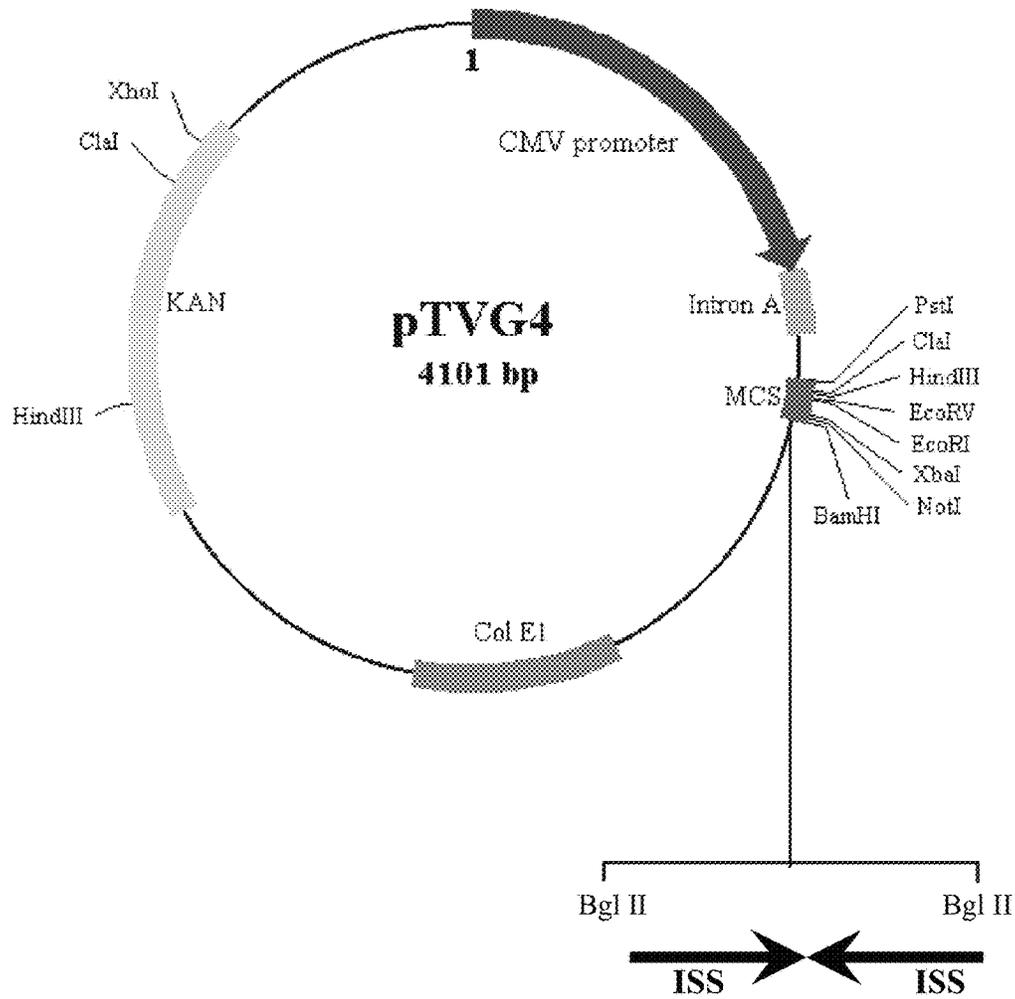


FIG. 4

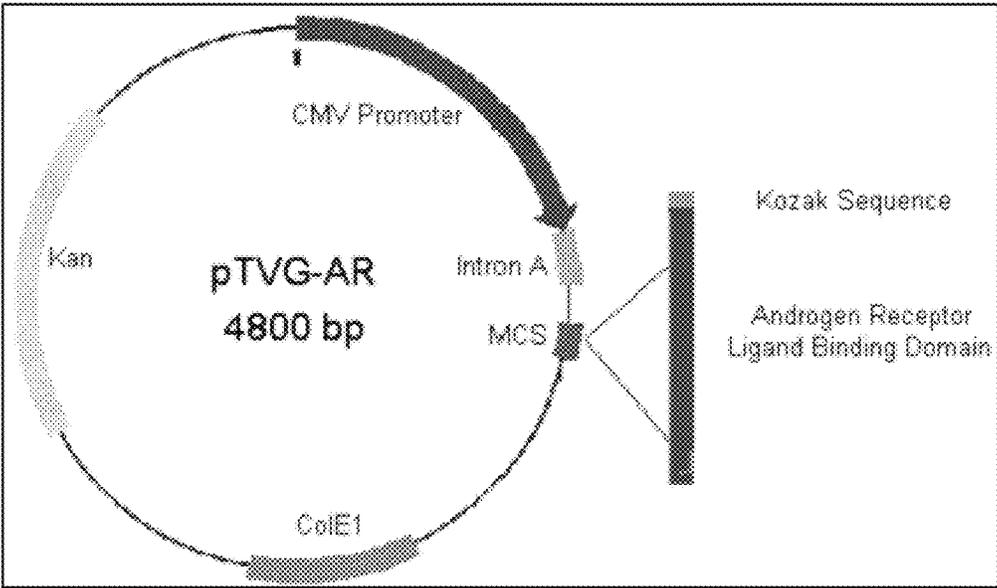


FIG. 5

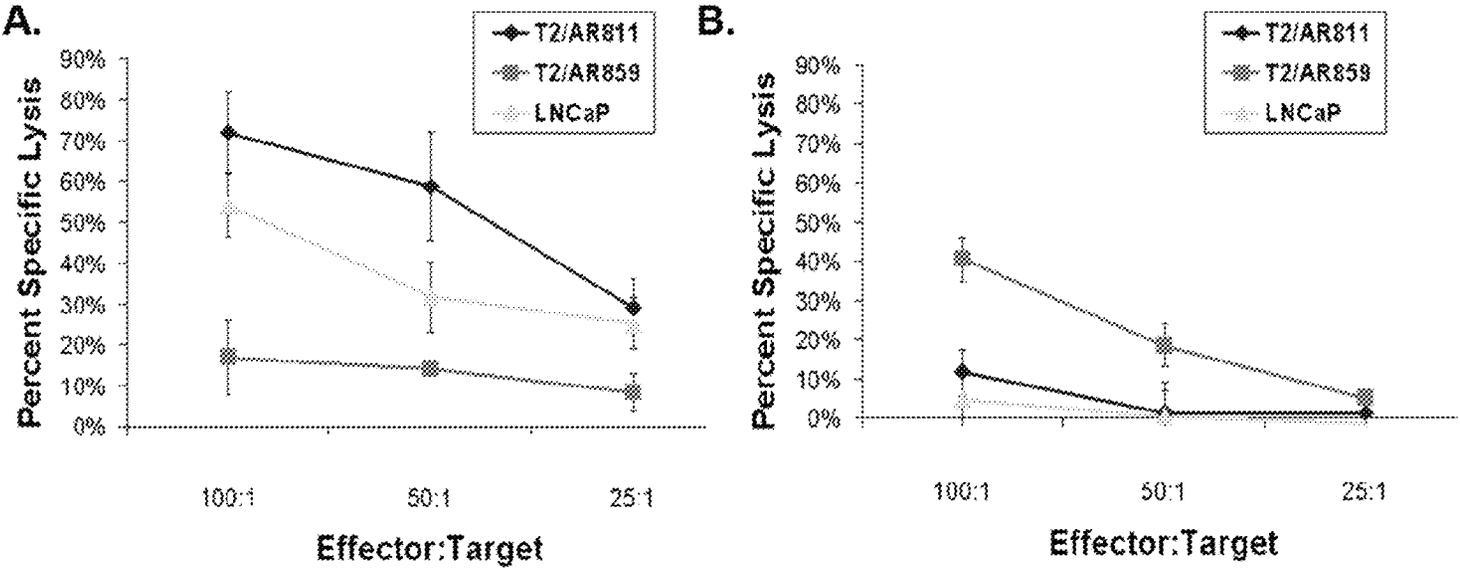


FIG. 6

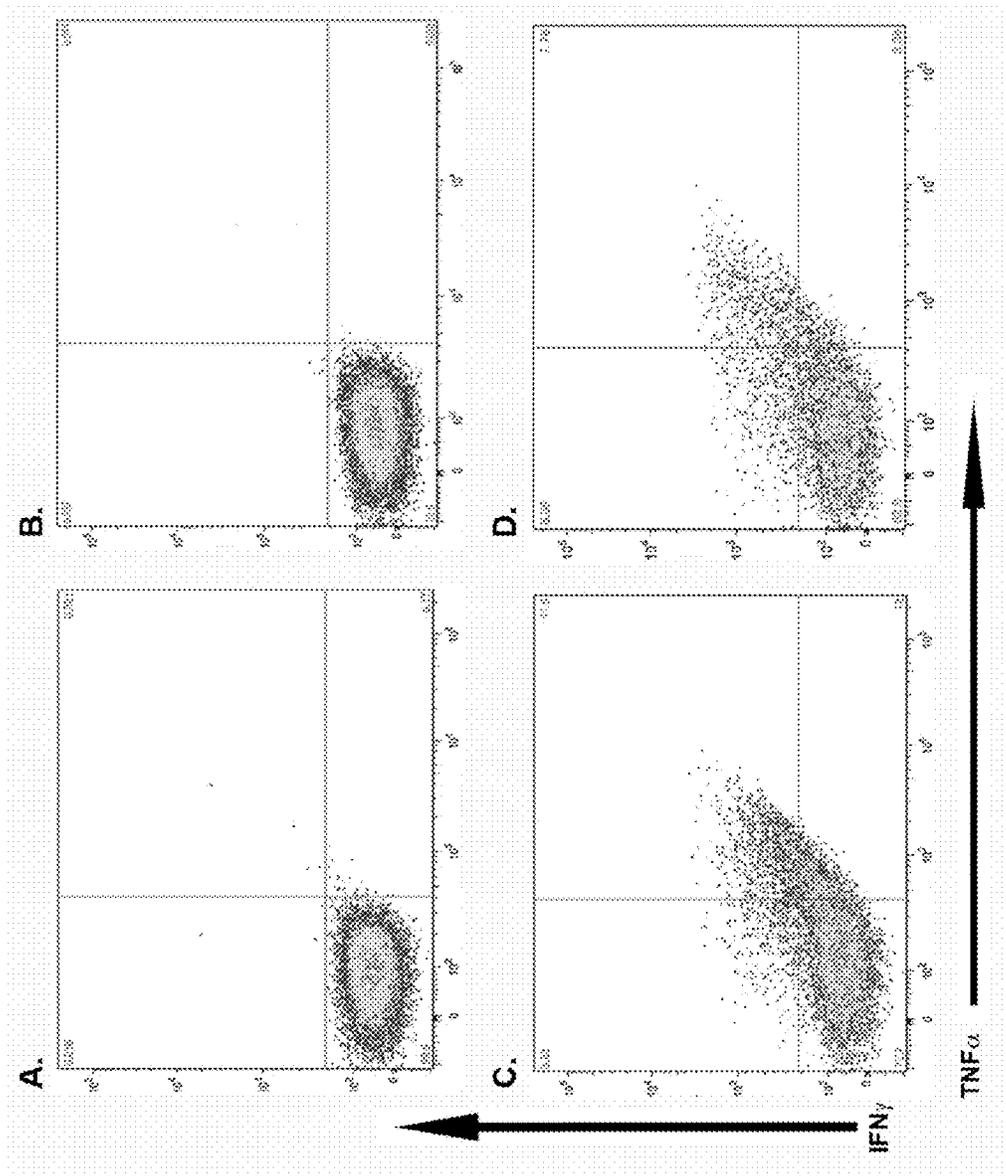


FIG. 7

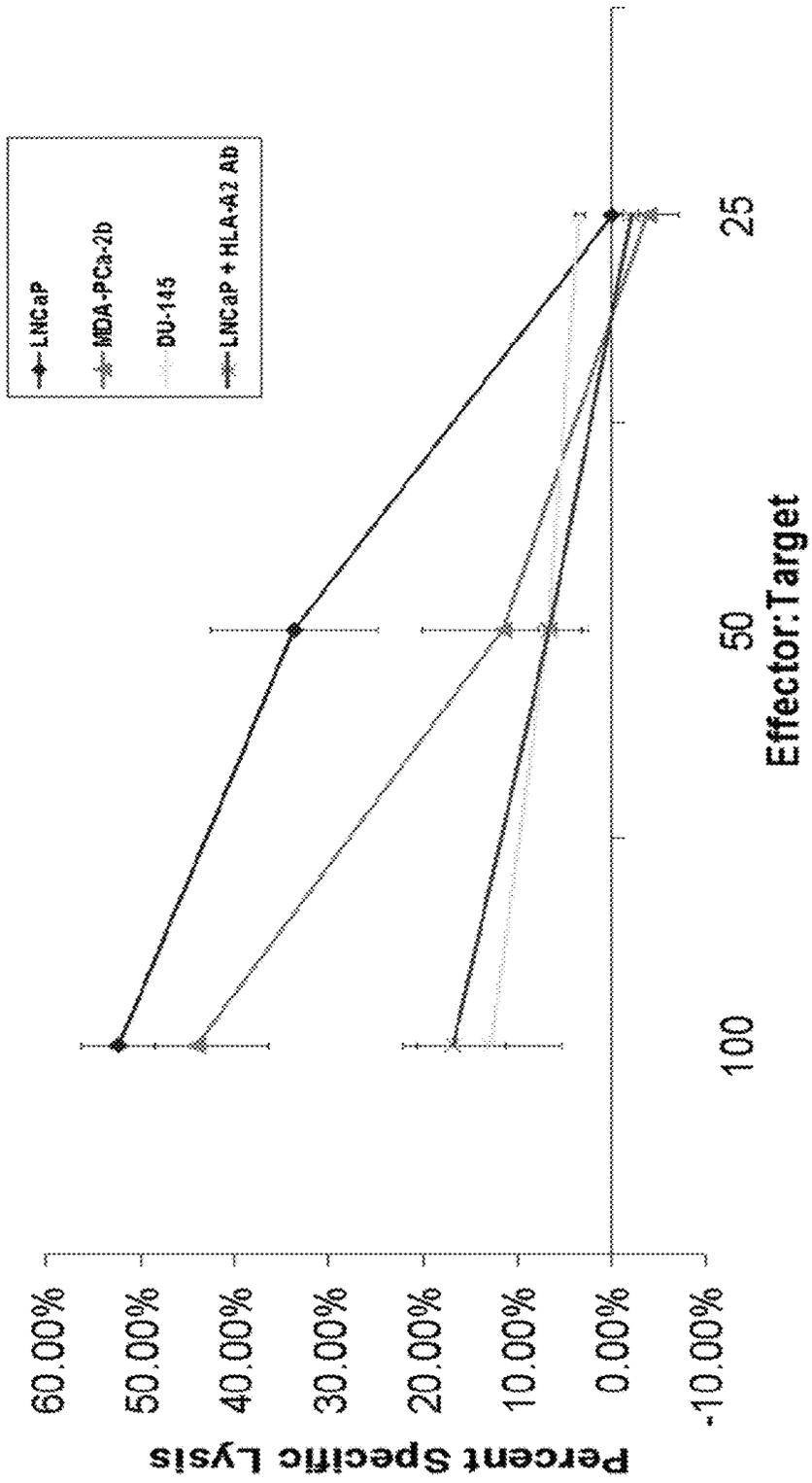


FIG. 8

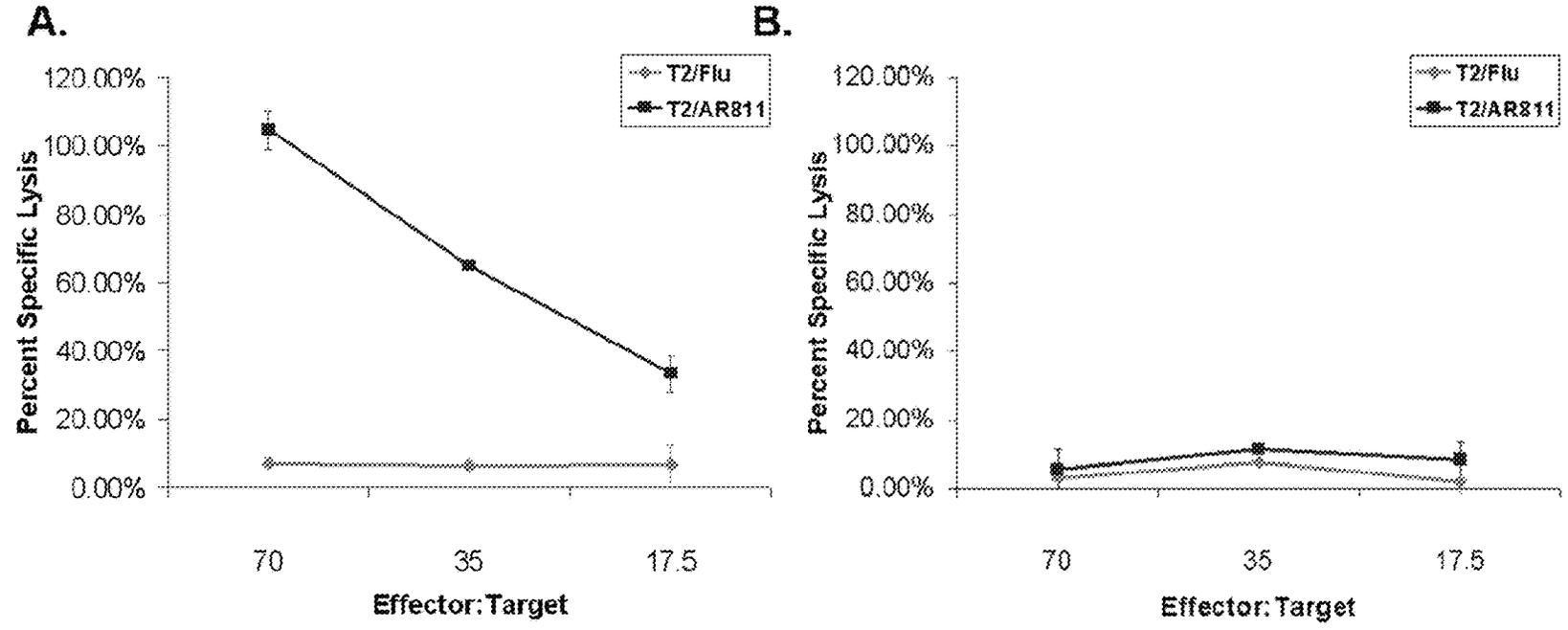


FIG. 9

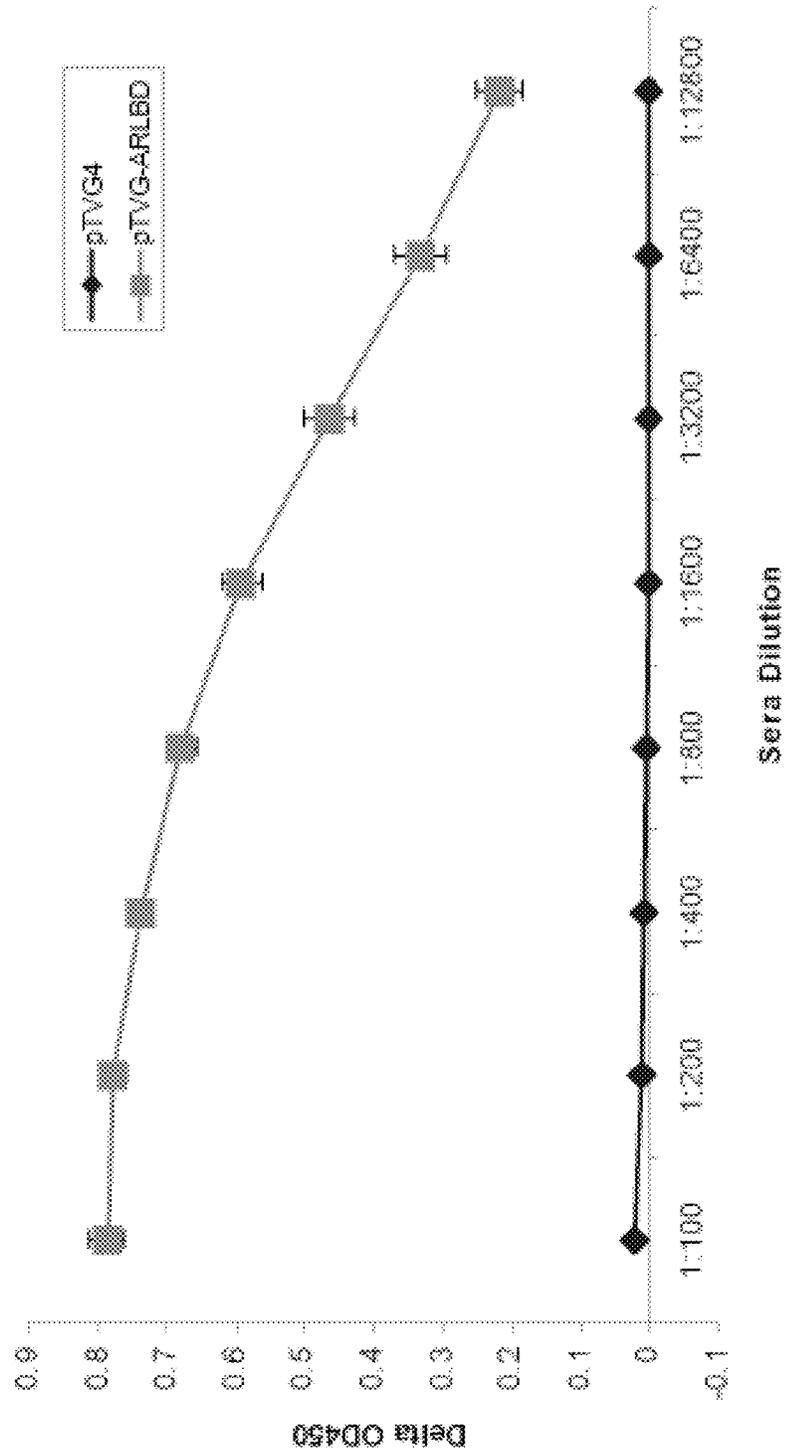


FIG. 10

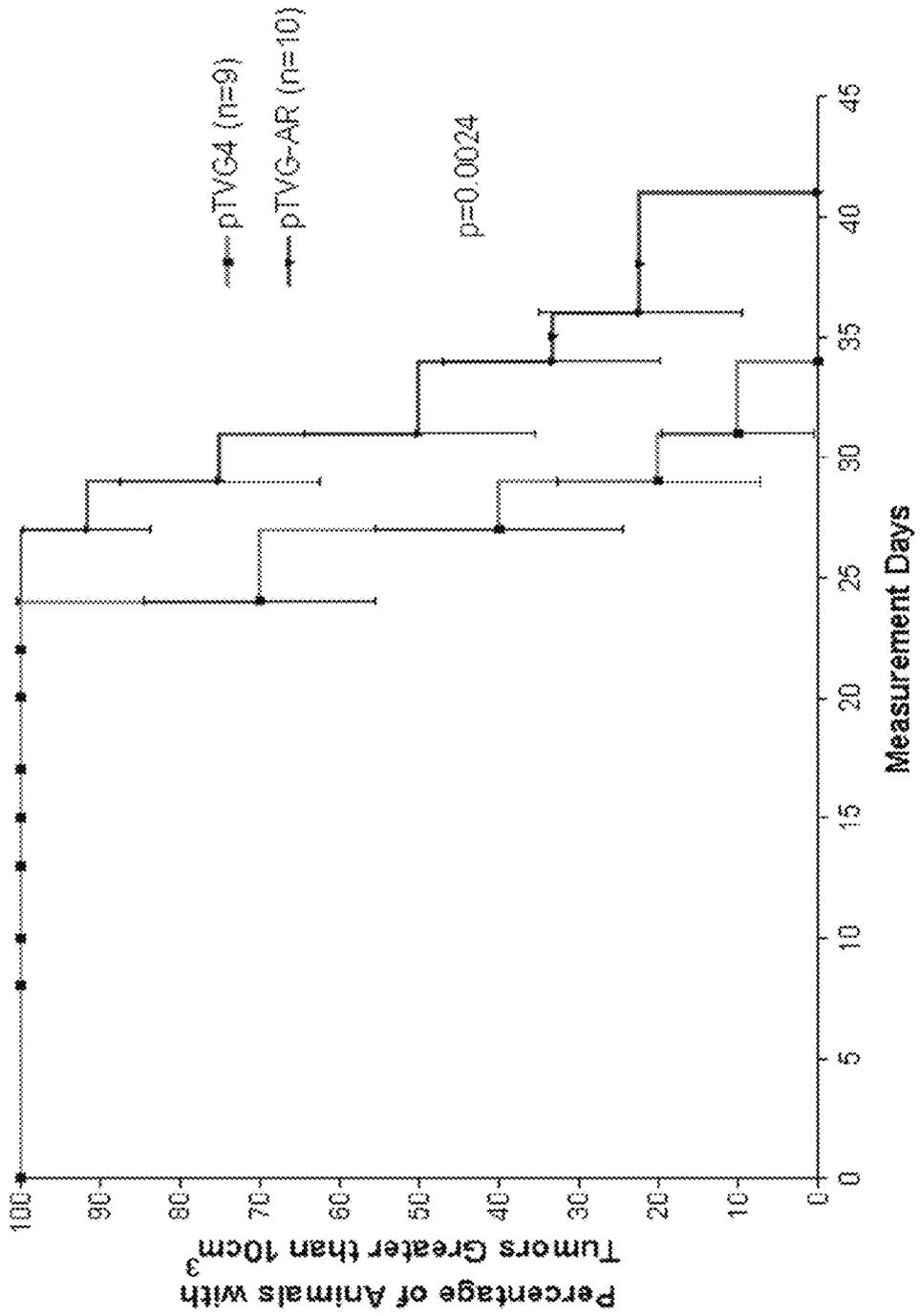


FIG. 11

PROSTATE CANCER VACCINE**CROSS-REFERENCE TO RELATED APPLICATIONS**

This application is a continuation of U.S. patent application Ser. No. 14/614,137, filed on Feb. 4, 2015, which is a continuation of U.S. patent application Ser. No. 13/968,854, filed on Aug. 16, 2013, now U.S. Pat. No. 8,962,590, which is a continuation of U.S. patent application Ser. No. 13/031,396 filed on Feb. 21, 2011, now U.S. Pat. No. 8,513,210, which is a divisional of U.S. patent application Ser. No. 11/848,607 filed on Aug. 31, 2007, now U.S. Pat. No. 7,910,565 and claims the benefit of U.S. provisional application Ser. No. 60/841,769, filed on Sep. 1, 2006, all of which are herein incorporated by reference in their entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

This invention was made with government support under RR016489 awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

Prostate cancer is a significant health risk for men over the age of 50, with about 200,000 newly diagnosed cases each year in the United States (Jemal A. et al., *Cancer Statistics, 2005* (2005) *CA Cancer J Clin*, 55:10-30). It is the most common tumor diagnosed among men and the second leading cause of male cancer-related death in the United States (Jemal et al., *Cancer Statistics, 2003* (2003) *CA Cancer J Clin*, 53:5-26). Despite advances in screening and early detection, approximately 30% of patients undergoing definitive prostatectomy or ablative radiation therapy will have recurrent disease at 10 years (Oefflein et al., 1997, *J Urol*, 158:1460-1465). At present, there is no accepted adjuvant treatment for patients undergoing radical prostatectomy or ablative radiation therapy that has been shown to prevent the progression to metastatic disease. In addition to new treatments for metastatic disease, new strategies are needed to eradicate microscopic disease to prevent the progression to clinically apparent metastasis.

In patients who have undergone definitive ablative therapy for prostate cancer, the presence of detectable serum levels of prostate-specific antigen (PSA) has provided a valuable indicator of microscopic metastatic disease. In a retrospective review of 1,997 men treated with radical prostatectomy, 15% were found to have evidence of a PSA-only recurrence over a median 5-year follow up, so-called stage D0 disease (Pound et al., 1999, *JAMA* 281:1591-7). Of these, 34% developed radiographically apparent metastatic disease, with a median time to development of metastatic disease of 8 years. In all patients with metastatic disease, the median time to death was 5 years (Pound et al., 1999, *JAMA* 281:1591-7). These findings suggest that patients with stage D0 disease are at high risk for progressive disease, however with a long window of time to test adjuvant therapies. Similarly, many patients are found to have microscopic pelvic lymph node metastases at the time of radical prostatectomy, so-called stage D1 disease. At present, the best treatment for these patients is controversial, with most treated with androgen deprivation, and others are expectantly observed without specific treatment. In retrospective studies, 10-year disease-specific recurrence and mortality is on the order of 50 to 66% for patients with stage

D1 disease (Sgrignoli et al., 1994, *J Urol*, 152:1077-81; and Cadeddu et al., 1997, *Urology*, 50:251-5). This high-risk stage of minimal residual disease also provides an opportunity to test novel adjuvant therapies.

Immunological therapies, and vaccines in particular, are appealing as possible treatment options for prostate cancer for several reasons. Such therapies may be relatively safe and inexpensive treatments compared with chemotherapies for a disease for which no standard adjuvant treatments exist (Kent et al., *Immunity of prostate specific antigens in the clinical expression of prostatic carcinoma* (1976) In: Crispen R G, ed. *Neoplasm immunity: mechanisms*. Chicago, ITR, pp. 85-95; Guinan et al., 1984, *Prostate*, 5:221-230; and McNeel et al., 2000, *Arch. Immunol. Ther. Exp.*, 48:85-93). Moreover, prostate cancer is a slow-growing disease, with typically over five years from the time of diagnosis of organ-confined disease to the development of clinically apparent metastatic disease. Such a slow-growing disease might be more amenable to vaccine-based treatments than a rapidly growing tumor, assuming that microscopic amounts of disease would be easier to treat than bulky or rapidly growing disease by vaccines. In fact, vaccines have already entered clinical trials for prostate cancer targeting a variety of prostate-specific proteins, with at least two dendritic cell-based vaccines suggesting clinical benefit in patients with low-volume metastatic disease (Murphy et al., 1999, *Prostate*, 39:54-59; and Small et al., 2000, *J. Clin. Oncol.* 18:3894-3903).

The use of plasmid DNA alone as a means of in vivo gene delivery by direct injection into muscle tissue was first described by Wolff et al. (Wolff et al., 1990, *Science*, 247:1465-1468). It was subsequently found that intramuscular or intradermal administration of plasmids expressing foreign genes elicited immune responses (Tang, et al., 1992, *Nature*, 356:152-154; Wang et al., 1993, *Proc Natl. Acad. Sci. USA*, 90:4156-4160; and Raz et al., 1994, *Proc Natl. Acad. Sci. USA*, 91:9519-9523). This has quickly led to numerous investigations into the use of plasmid DNA as a means of vaccine antigen delivery, both in animal and human models. DNA vaccines, like peptide-based vaccines, are relatively easy and inexpensive to manufacture, and are not individualized for patients as are dendritic cell-based vaccines. With recombinant protein vaccines, the antigen is taken up by antigen presenting cells and expressed predominantly in the context of MHC class II. DNA in nucleic acid vaccines is taken up and expressed by antigen-presenting cells directly, leading to antigen presentation through naturally processed MHC class I and II epitopes (Iwasaki, et al. 1997, *J Immunol*, 159:11-14). This direct expression by host cells, including MHC class I expressing bystander cells, has been demonstrated to lead to vigorous CD8+CTL responses specific for the targeted antigen (Iwasaki et al., 1997, *J. Immunol.* 159:11-14; Chen et al., 1998, *J. Immunol.*, 160:2425-2432; Thomson et al., 1998, *J. Immunol.*, 160:1717-1723; and Cho et al., 2000, *Nat. Biotechnol.* 18:509-514).

Clinical trials have suggested that plasmid DNA vaccines are safe and immunologically effective in humans. Boyer and colleagues reported that doses of 300 µg of plasmid DNA encoding HIV rev and env proteins administered intramuscularly were capable of eliciting antigen-specific, IFN γ -secreting T cell responses in HIV-seronegative patients (Boyer et al., 2000, *J. Infect. Dis.* 181:476-83). In addition, results of a clinical trial targeting prostate-specific membrane antigen (PSMA) in patients with prostate cancer by means of plasmid DNA and adenovirus have been reported (Mincheff et al., 2000, *Eur. Urol.*, 38:208-217). In this study, 26 patients were immunized either in a prime/

boost strategy with an adenoviral vector expressing PSMA followed by immunization with plasmid DNA expressing PSMA, or with plasmid DNA alone. The authors report no significant toxicity with doses of 100-800 µg of plasmid DNA administered intradermally, and suggest that patients receiving plasmid DNA expressing PSMA and CD86 with soluble GM-CSF as an adjuvant were all successfully immunized.

A DNA vaccine for the treatment of prostate cancer based on prostatic acid phosphatase (PAP) has also been described (US 2004/0142890).

BRIEF SUMMARY OF THE INVENTION

The present invention is based, in part, on the inventors' discovery that patients with prostate cancer have antibodies specific for the androgen receptor, that androgen receptor ligand-binding domain as well as four fragments thereof (SEQ ID NO:9-12) can elicit immune responses *in vivo*, and that animals vaccinated with a DNA vaccine encoding the androgen receptor (AR) ligand-binding domain (LBD) inhibited prostate tumor growth *in vivo*.

In one aspect, the invention relates a method for inducing an immune reaction to androgen receptor in a mammal in need thereof, the method comprising administering to the mammal an effective amount of a recombinant DNA construct comprising a polynucleotide operatively linked to a transcriptional regulatory element (e.g., a promoter such as a heterologous promoter) wherein the polynucleotide encodes a member selected from (i) a mammalian androgen receptor (e.g., a human androgen receptor), (ii) a fragment of the androgen receptor that comprises the ligand-binding domain, (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11, and (vi) a fragment of the ligand-binding domain defined by SEQ ID NO:12, whereby the mammal develops immune reaction against the androgen receptor. In one form, the polynucleotide employed in the method encodes the ligand-binding domain of a mammalian androgen receptor. In another form, multiple DNA constructs with each comprising a polynucleotide that encodes a different fragment selected from (iii)-(vi) are administered. For example, two DNA constructs covering fragments (iii) and (iv) can be administered together. As another example, four DNA constructs covering all four fragments (iii)-(vi) can be administered together. The method disclosed can be practiced with a mammal, preferably a human, who either currently has or previously had prostate cancer.

In one embodiment, the polynucleotide encodes a human androgen receptor or a fragment of the human androgen receptor that comprises the ligand-binding domain. The polynucleotide is preferably a nucleotide sequence of the human androgen receptor gene. In one form of this embodiment, the polynucleotide encodes the ligand-binding domain of a human androgen receptor.

The above method employing the DNA construct induces cytotoxic immune reaction against cells expressing androgen receptor. Preferably, both humoral and cellular immune reactions against androgen receptor are induced.

In another aspect, the present invention relates to a method for inducing an immune reaction to androgen receptor in a mammal in need thereof, the method comprising administering to the mammal an effective amount of a polypeptide selected from (i) a mammalian androgen receptor (e.g., a human androgen receptor), (ii) a fragment of the

androgen receptor that comprises the ligand-binding domain, (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11, and (vi) a fragment of the ligand-binding domain defined by SEQ ID NO:12, whereby the mammal develops immune reaction against the androgen receptor. In one form, the polypeptide employed is the ligand-binding domain of a mammalian androgen receptor. In another form, multiple fragments of the ligand-binding domain (e.g. SEQ ID NO:9 and SEQ ID NO:10, and optionally SEQ ID NO:11 and SEQ ID NO:12) are administered. The method disclosed can be practiced with a mammal, preferably a human, who either currently has or previously had prostate cancer.

In one embodiment, the human androgen receptor or a fragment of the human androgen receptor that comprises the ligand-binding domain is administered. In one form of this embodiment, the ligand-binding domain of the human androgen receptor is administered.

The above method employing the polypeptide induces cellular or humoral immune reaction against cells expressing androgen receptor. Preferably, both humoral and cellular immune reactions against androgen receptor are induced.

According to one embodiment of the invention, the recombinant DNA construct or the polypeptide is administered to the mammal intradermally, intramuscularly, subcutaneously, or intravascularly, including intravenously and intraarterially. Preferably, the recombinant DNA construct is administered intradermally, intramuscularly, or intravascularly and the polypeptide is administered subcutaneously.

In another aspect, the present invention relates to an isolated polypeptide selected from SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12. In another aspect, the present invention relates to a composition that comprises one or more of the above polypeptides and a pharmaceutically acceptable carrier.

According to another aspect of the present invention, a DNA vaccine is contemplated which comprises a plasmid vector comprising a polynucleotide operatively linked to a transcriptional regulatory element (e.g., a promoter such as a heterologous promoter) wherein the polynucleotide encodes a member selected from (i) a mammalian androgen receptor (e.g., a human androgen receptor), (ii) a fragment of the androgen receptor that comprises the ligand-binding domain, (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11, and (vi) a fragment of the ligand-binding domain defined by SEQ ID NO:12, wherein upon administration of said vaccine to a mammal a cytotoxic immune reaction against cells expressing androgen receptor is induced. The vaccine of the present invention preferably is suitable for intradermal, intramuscular, subcutaneous, or intravascular (including intravenous and intraarterial) administration to a mammal such as a human. According to a preferred embodiment, the plasmid vector comprises (a) a backbone of pNGV3, (b) a polynucleotide operably inserted therein wherein the polynucleotide encodes a member selected from (i) a mammalian androgen receptor (e.g., a human androgen receptor), (ii) a fragment of the androgen receptor that comprises the ligand-binding domain, (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11, and (vi) a fragment of the ligand-binding domain

defined by SEQ ID NO:12, and, optionally, (c) one or a plurality of an immunostimulatory sequence (ISS) motif.

Preferably, the DNA vaccine according to the invention comprises a plasmid vector that comprises (a) a polynucleotide operatively linked to a CMV promoter wherein the polynucleotide encodes a member selected from (i) a mammalian androgen receptor (e.g., a human androgen receptor), (ii) a fragment of the androgen receptor that comprises the ligand-binding domain, (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11, and (vi) a fragment of the ligand-binding domain defined by SEQ ID NO:12, (b) a CMV intron A operatively linked to the polynucleotide for enhancing expression of the polynucleotide, and, optionally, (c) at least one copy of an immunostimulatory fragment comprising 5'-GTCGTT-3'. In one embodiment, the plasmid construct does not express in eukaryotic cells any gene other than a member selected from (i) a mammalian androgen receptor, (ii) a fragment of the androgen receptor that comprises the ligand-binding domain, (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11, and (vi) a fragment of the ligand-binding domain defined by SEQ ID NO:12. The plasmid vector pTVG4 is particularly preferred.

According to another aspect of the present invention, a peptide vaccine is contemplated which comprises a member selected from (i) a mammalian androgen receptor (e.g., a human androgen receptor), (ii) a fragment of the androgen receptor that comprises the ligand-binding domain, (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11, and (vi) a fragment of the ligand-binding domain defined by SEQ ID NO:12. The peptide vaccine also comprises a pharmaceutically acceptable carrier. The peptide vaccine preferably is suitable for intradermal, intramuscular, subcutaneous, or intravascular (including intravenous and intraarterial) administration to a mammal such as a human.

Also disclosed are pharmaceutical compositions comprising a DNA or peptide vaccine of the invention (the polypeptides or recombinant plasmid vectors described above), and a pharmaceutically acceptable carrier. Preferably, the pharmaceutical composition further comprises a suitable amount of immuno-stimulant such as GM-CSF.

A kit containing the DNA or peptide vaccine of the invention and an instruction manual directing administering the vaccine to a mammal that has or previously had prostate cancer (e.g., a human prostate cancer patient) is also within the scope of the invention.

In another aspect, the present invention relates to a method for determining the effectiveness of a treatment for prostate cancer. The method includes the steps of (a) measuring the frequency or amount of cytotoxic T lymphocytes (CTLs) specific for a peptide selected from SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12 prior to providing at least a portion of the treatment to a mammal (e.g., a human) having prostate cancer, (b) measuring the frequency or amount of CTLs specific for the peptide after said portion of the treatment is provided to the mammal, and (c) comparing the frequency or amount of CTLs of (a) and

that of (b) wherein the frequency or amount of CTLs of (b) being higher than that of (a) indicates that the treatment is effective.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

FIG. 1 shows that patients with prostate cancer have antibodies specific for the androgen receptor. Panel A: Sera from patients with various stages of prostate cancer were analyzed for the presence of AR-specific antibodies by screening titrated sera samples using ELISA. Panel B: The presence or absence of AR-specific antibodies was confirmed using Western blotting against thioredoxin-tagged AR LBD or thioredoxin (trx) alone, followed by incubation with patient's sera. Panel C: ELISA was used to evaluate sera samples for the presence of AR-specific antibodies. Samples were analyzed from healthy male blood donors (n=41), patients with prostatitis (n=38), or patients with prostate cancer (n=105), and relative antibody concentrations were calculated by referencing delta absorbance values to titrated Ig protein standards. Positive antibody responses were defined by values higher than three standard deviations above the mean of the healthy donor group (greater than 0.22 $\mu\text{g/mL}$, indicated by the line). Statistically significant differences were calculated using the Chi square test.

FIG. 2 shows that patients with AR LBD-specific IgG antibodies have concurrent AR-specific cellular immune responses. PBMC were analyzed for the presence of AR-specific T cells and IFN γ -secreting cells among patients with antibody responses specific for the AR (n=6) or patients with no detectable antibody responses (n=9). PBMC were stimulated with thioredoxin-tagged AR LBD, thioredoxin alone, media only, or PHA. After a 96-hour stimulation, these cells were analyzed for the presence of CD4+ and CD8+ T cell proliferation in response to antigen stimulation. Example data is shown in panel A from a subject with a strong IgG₂ response. The numbers in the upper-right corner of each panel indicate the percentage of CD4+ or CD8+ T cells that co-stained with BrdU. Proliferation indexes (PI) were calculated by normalizing experimental values to values obtained from PBMCs stimulated with media alone, and compiled PI values are shown for CD4+ (panel B, left) and CD8+ (panel B, right) T-cells. Supernatants from cultured PBMC were also analyzed for the presence of IFN γ secretion by capture ELISA (panel C). A comparison of results among different antigen-stimulation conditions was performed using the Student's T test.

FIG. 3 shows that patients with AR LBD-specific IgG antibodies have a mixed Th1/Th2-type immune response. PBMC from prostate cancer patients with (n=5) or without (n=5) antibody responses specific for the AR were analyzed for the presence of antigen-specific IFN γ or IL-10-secretion. PBMC were stimulated with thioredoxin-tagged AR LBD, thioredoxin alone, media only, or PHA. After a 96-hour stimulation, supernatants were analyzed for the presence of IFN γ (panel A) and IL-10 (panel B) secretion by quantitative ELISA. A comparison of results among different antigen-stimulation conditions was performed using a Student's T test. The results shown are representative of duplicate experiments with the same peripheral blood samples.

FIG. 4 shows the plasmid map of pTVG4.

FIG. 5 shows the plasmid map of pTVG-ARLBD (pTVG-androgen receptor ligand-binding domain).

FIG. 6 shows that AR LBD peptide-specific T-cells can lyse peptide-pulsed and prostate cancer cell line target cells. Peptide-specific T-cell lines were cultured from the periph-

eral blood of HLA-A2-expressing patients with prostate cancer using peptides AR811 (LLFSIIPV, SEQ ID NO:9, panel A) or AR859 (QLTKLLDSV, SEQ ID NO:12, panel B). After several *in vitro* restimulations, cultures were tested for cytolytic activity to T2 cells loaded with AR811 peptide (diamond), AR859 (square), or the LNCaP HLA-A2 expressing prostate cancer cell line (triangle). Shown is a representative graph results obtained from the cytotoxicity assay of T-cell cultures performed in triplicate at three different effector-to-target ratios as indicated.

FIG. 7 shows that a T-cell clone specific for the AR811 peptide secretes IFN γ and TNF α in response to peptide stimulation. A clonal T-cell line specific for the AR811 peptide was derived by limited dilution following multiple restimulations *in vitro*. This line was restimulated for 5 hours *in vitro* with T2 cells and media only (panel A), an irrelevant peptide (panel B), AR811 peptide (panel C), or PMA/Ionomycin (panel D). IFN γ and TNF α cytokine accumulation were assessed by intracellular flow cytometric analysis (Cytotfix/cytoperm kit, BD Pharmingen). Cells were first stained for CD3 and CD8 expression and CD3+/CD8+ cells were analyzed for IFN γ and TNF α expression. Shown are the plots gated on CD3+/CD8+ cells.

FIG. 8 shows that the AR811 epitope is a naturally processed HLA-A2-restricted T-cell epitope. The AR811 T-cell clone was tested for its ability to lyse prostate cancer cell lines (expressing the AR) that express HLA-A2 (LNCaP, diamond and MDA-Pca-2B, triangle), or do not express HLA-A2 (DU145, X). In addition, lysis was evaluated following pre-treatment of LNCaP with an HLA-A2 blocking monoclonal antibody (starburst). Shown is a cytotoxicity assay of an AR811 CD8+ cell clone. Cells were restimulated for seven days using peptide-pulsed antigen presenting cells, followed on day seven by a rest period of three days before they were analyzed for their cytotoxic activity.

FIG. 9 shows that HHD-II mice immunized with AR811 peptide develop peptide-specific CTL (contain splenocytes that can specifically lyse AR811 target cells). Male HHD-II mice (n=3 per group) were immunized once with 100 μ g AR811 peptide in CFA or with CFA alone. One week after immunization, splenocytes were collected and stimulated *in vitro* with 10 μ g/mL peptide for two hours, and on the second day, recombinant murine IL-2 and IL-7 (Fitzgerald Industries) were added to 10 U/mL and 30 U/mL, respectively. The cultures were then allowed to incubate an additional six days before analysis. Cultured cells from AR811-immunized animals (panel A) or control immunized animals (panel B) were then tested for cytolytic activity to T2 cells pulsed with the AR811 peptide (square) or T2 cells pulsed with an influenza matrix peptide (diamond). Shown are the mean and standard deviation of triplicate wells at three effector-to-target ratios as indicated, each from a single animal per group, and representative of the other animals per group.

FIG. 10 shows that rats immunized with a plasmid vector encoding AR LBD develop AR LBD-specific antibody responses. Copenhagen rats were immunized 4 times at 14-day intervals with pTVG4 control vector or pTVG-ARLBD. Two weeks after the fourth immunization, blood was collected and assessed for antibody responses to the AR-LBD protein by ELISA. Shown are the mean and standard error for 10 animals per experimental group.

FIG. 11 shows tumor growth in pTVG4 control vector or pTVG-ARLBD immunized rats (Kaplan-Meier analysis of animal endpoint survival following treatment with the pTVG4 control vector or pTVG-ARLBD). Male Copenhagen rats were immunized four times every other week with

pTVG4 control vector or pTVG-ARLBD. Two weeks after immunization, the rats were challenged with 1×10^4 syngeneic Mat-LyLu prostate cancer cells given with Matrigel. Tumors were measured every other day, and rats were sacrificed when tumors grew larger than 10 cm³ (Kaplan-Meier survival end point being tumor volume over 10 cm³).

DETAILED DESCRIPTION OF THE INVENTION

This invention provides pharmaceutical compositions and methods that relate to the use of plasmid DNA and peptide vaccines for the treatment of prostate cancer. Specifically, this invention provides polypeptides such as the ligand-binding domain of an androgen receptor or certain fragments thereof and recombinant plasmid vectors comprising genes or polynucleotide molecules encoding the polypeptides for preventing or treating prostate cancer, including metastatic tumors thereof. In a preferred embodiment, the polypeptides or recombinant plasmid vectors are administered to prostate cancer patients to treat prostate cancer. In another preferred embodiment, the polypeptides or recombinant plasmid vectors are administered to stage D0 or D1 prostate cancer patients to prevent recurrence or metastasis of prostate cancer.

A polypeptide vaccine of the present invention, which comprises a pharmaceutically acceptable carrier and an effective amount of a mammalian androgen receptor, a fragment of the mammalian androgen receptor that comprises the ligand-binding domain, or certain fragments of the ligand-binding domain, can be administered into a mammal such as a human being to elicit an immune response against androgen receptor in the mammal. An "effective amount" or an "immunologically effective amount" means that the administration of that amount to a subject, either in a single dose or as part of a series, is effective for inducing an immune reaction and preferably for treating or preventing prostate cancer. Pharmaceutically acceptable carriers are well known to those of ordinary skill in the art (Arnon, R. (Ed.) *Synthetic Vaccines* 1:83-92, CRC Press, Inc., Boca Raton, Fla., 1987). They include liquid media suitable for use as vehicles to introduce the peptide into a patient but should not in themselves induce the production of antibodies harmful to the individual receiving the composition. An example of such liquid media is saline solution. Moreover, the vaccine formulation may also contain an adjuvant for stimulating the immune response and thereby enhancing the effect of the vaccine.

The plasmid DNA vaccines of the present invention, when directly introduced into mammals such as humans *in vivo*, induce the expression of encoded polypeptides within the mammals, and cause the mammals' immune system to become reactive against the polypeptides. The vaccines may be any polynucleotides that are capable of eliciting immune responses to an encoded polypeptide.

The instant invention also provides a method of using a polynucleotide which, upon introduction into a mammal, induces the expression, *in vivo*, of the polynucleotide thereby producing the encoded polypeptide, and causes the mammal to become immune reactive against the polypeptide so produced.

DNA vaccines, like peptide-based vaccines, are relatively easy and inexpensive to manufacture, and are not individualized for patients, as are dendritic cell-based vaccines. With recombinant protein vaccines, the antigen is taken up by antigen presenting cells and expressed predominantly in the context of MHC class II. DNA in nucleic acid vaccines is

taken up and expressed by antigen-presenting cells directly, leading to antigen presentation through naturally processed MHC class I and II epitopes (Iwasaki, et al. 1997, J Immunol, 159:11-14).

Given their potential ability to elicit antigen-specific cytotoxic T lymphocytes (CTL) immunity in an MHC class I diverse population, DNA-based vaccines for various diseases have recently entered human clinical trials (Mincheff et al., 2000, Eur. Urol., 38:208-217). This method of immunization is similar to the use of viral immunization vectors, but without the additional foreign antigens introduced with a viral vector and therefore with less risk of an overwhelming immune response to the vector itself (Irvine and Restifo, 1995, Seminars in Canc. Biol. 6:337-347). Direct expression by host cells, including MHC class I-expressing bystander cells, has been demonstrated to lead to vigorous CD8+CTL responses specific for the targeted antigen (Iwasaki et al., 1997, J. Immunol. 159:11-4; Chen et al., 1998, J. Immunol. 160:2425-2432; Thomson et al., 1998, J. Immunol. 160:1717-1723; and Cho et al., 2000, Nat. Biotechnol, 18:509-14). In addition, plasmid DNA used for immunization may remain within cells at the site of immunization, providing a constant source of antigenic stimulation. Persistent antigen expression may lead to long-lived immunity (Raz et al., 1994, Proc. Natl. Acad. Sci. USA 91:9519-23).

The present invention provides DNA-based vaccines that express a polypeptide antigen, the ligand-binding domain of a mammalian androgen receptor or certain fragments thereof, and methods for treating prostate cancers in a human or non-human animal using the vaccines. In addition to the reasons explained above, plasmid vaccines are advantageous over viral vaccines. For example, viral vaccines are not amenable to repeated immunizations. With viral vectors, one is trying to elicit an immune response against a "self" protein encoded by a foreign virus. The immune system preferentially recognizes the foreign proteins, sometimes hundreds of proteins, encoded by the virus. For example, the inventors have found in rats that repeated immunizations with a vaccinia virus encoding human prostatic acid phosphatase (hPAP) elicits a strong vaccinia response but no hPAP-specific response (Johnson et al., 2007, Canc. Immunol. Immunoth. 56:885). That same finding was also shown in humans, in a trial in which repeated immunization with the vaccinia virus encoding human prostate-specific antigen (PSA) elicited weak PSA-specific immunity, but potent vaccinia immunity (Sanda et al., 1999, Urology 53:260). The direction in the field of viral-based vaccines is to "prime" with a virus encoding the antigen, and then "boost" with a different virus (like adenovirus or fowl pox) encoding the same antigen. The advantage of plasmid DNA vaccines is that they encode a defined, often small, number of proteins. Therefore, one can repetitively immunize the animal or patient. Furthermore, a virus may kill cells, incorporate into the genome, or potentially induce other unwanted immune responses. All these are disadvantages that are likely avoided by DNA plasmid vaccines.

It is readily recognizable that the ligand-binding domain of an androgen receptor of any origin, or any of the ligand-binding domain's derivatives, equivalents, variants, mutants etc., is suitable for the instant invention, as long as the ligand-binding domain or derivatives, equivalents, variants, or mutants thereof is able to induce an immune reaction in the host human or non-human animal substantially similar to that induced by an autoantigenic or xenoantigenic ligand-binding domain of the androgen receptor in the animal. Similarly, a polynucleotide sequence of an androgen receptor gene of any origin that encodes the ligand-binding

domain of the receptor, or any of the polynucleotide's derivatives, equivalents, variants, mutants etc., is suitable for the instant invention, as long as the polynucleotide sequence and the polypeptide or protein encoded by the polynucleotide sequence, or derivatives, equivalents, variants, or mutants thereof is able to induce an immune reaction in the host human or non-human animal substantially similar to that induced by an autoantigenic or xenoantigenic ligand-binding domain of the androgen receptor in the animal.

Androgen receptor genes are known and have been cloned from many species. For example, the human, mouse, rat, dog, chimpanzee, macaque, and lemur androgen receptor cDNA along with amino acid sequences can be found at GenBank Accession Nos. NM_000044 (cDNA-SEQ ID NO:1 and amino acid sequence-SEQ ID NO:2), NM_013476 (cDNA-SEQ ID NO:3 and amino acid sequence-SEQ ID NO:4), NM_012502 (cDNA-SEQ ID NO:5 and amino acid sequence-SEQ ID NO:6), NM_001003053, NM_001009012, U94179, and U94178, respectively. Androgen receptor genes from other species are also known. These species include but are not limited to *Sus scrofa*, *Astatotilapia burtoni*, *Gallus gallus*, *Kryptolebias marmoratus*, *Alligator mississippiensis*, *Leucoraja erinacea*, *Haplochromis burtoni*, *Pimephales promelas*, *Dicentrarchus labrax*, *Gambusia affinis*, *Micropogonias undulatus*, *Oryzias latipes*, *Acanthopagrus schlegelii*, *Rana catesbeiana*, *Crocota crocata*, *Eulemur fulvus collaris*, and *Anguilla japonica* (see GenBank Accession Nos. NM_214314 (or AF161717), AY082342, NM_001040090, DQ339105, AB186356, DQ382340, AF121257, AY727529, AY647256, AB099303, AY701761, AB076399, AY219702, AY324231, AY128705, U94178, and AB023960, respectively). The ligand-binding domains of androgen receptors are well known in the art. For the purpose of the present invention, the ligand-binding domain of the human androgen receptor refers to a polypeptide that starts at any amino acid from amino acid positions 651 to 681 and ends at any amino acid from amino acid positions 900 to 920. For example, human androgen receptor or a fragment of the human androgen receptor that comprises amino acids 681-900 as well as DNA vaccines containing a polynucleotide encoding the above are suitable vaccines. The corresponding ligand-binding domains of androgen receptors from other species can be readily determined by sequence alignment (to the human sequence) (e.g., by the methods described below in connection with sequence identity or homology). In a preferred embodiment, a polypeptide from the human androgen receptor that starts at any amino acid from amino acid positions 661 to 671 and ends at any amino acid from amino acid positions 910 to 920 is used in the present invention. In a more preferred embodiment, a polypeptide containing amino acids 661 to 920 or 664 to 920 of the human androgen receptor is used in the present invention. To help determine the corresponding fragments of the androgen receptors from other species, it is noted here that the amino acid positions on rat, dog, chimpanzee, macaque, and lemur androgen receptors that correspond to amino acid positions 661 to 920 of the human androgen receptor are 640 to 899, 643 to 902, 648 to 907, 652 to 910, 636 to 895, and 625 to 884, respectively. It is noted that the above fragments of the human, mouse, rat, dog, chimpanzee, macaque, and lemur androgen receptors have the same amino acid sequence. The ligand-binding domains of the androgen receptors of other species are also known or can be readily identified through sequence alignment. As will be readily recognized by one of ordinary skill in the art, any DNA sequence that encodes a ligand-binding domain or a larger fragment of an androgen

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receptor including the full-length receptor from one of the above species as well as other animals is suitable for the present invention.

As is well-known to those skilled in the art, polypeptides having substantial sequence similarities cause identical or very similar immune reaction in a host animal. As discussed below, this phenomenon is the basis for using a xenoantigen for inducing autoreactive reaction to an otherwise tolerated autoantigen. Accordingly, a derivative, equivalent, variant, fragment, or mutant of the ligand-binding domain of any of the known or to-be-identified androgen receptors or any DNA sequence encoding the above is also suitable for the present invention. The polypeptides encoded by these DNA sequences are useful as long as the polypeptides encoded by the DNA sequences are structurally similar to the ligand-binding domain of the autologous androgen receptor, and are sufficiently immunogenic.

It is readily apparent to those ordinarily skilled in the art that variations or derivatives of the nucleotide sequence encoding the polypeptide or protein antigen can be produced which alter the amino acid sequence of the encoded polypeptide or protein. The altered polypeptide or protein may have an altered amino acid sequence, for example by conservative substitution, yet still elicits immune responses which react with the unaltered protein antigen, and are considered functional equivalents. According to a preferred embodiment, the derivative, equivalents, variants, or mutants of the ligand-binding domain of an androgen receptor are polypeptides that are at least 85% homologous to the ligand-binding domain of a human androgen receptor. More preferably, the homology is at least 88%, at least 90%, at least 95%, or at least 98%.

As used in this application, "percent identity" between amino acid or nucleotide sequences is synonymous with "percent homology," which can be determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87, 2264-2268, 1990), modified by Karlin and Altschul (Proc. Natl. Acad. Sci. USA 90, 5873-5877, 1993). The noted algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al. (*J. Mol. Biol.* 215, 403-410, 1990). BLAST nucleotide searches are performed with the NBLAST program, score=100, wordlength=12, to obtain nucleotide sequences homologous to a polynucleotide of the invention. BLAST protein searches are performed with the XBLAST program, score=50, wordlength=3, to obtain amino acid sequences homologous to a reference polypeptide. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (*Nucleic Acids Res.* 25, 3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) are used.

As used herein, the term "conservative substitution" denotes the replacement of an amino acid residue by another, biologically similar residue. It is well known in the art that the amino acids within the same conservative group can typically substitute for one another without substantially affecting the function of a protein. For the purpose of the present invention, such conservative groups are set forth in Table 1 based on shared properties.

TABLE 1

Conservative substitution.	
Original Residue	Conservative Substitution
Ala (A)	Val, Leu, Ile
Arg (R)	Lys, Gln, Asn
Asn (N)	Gln, His, Lys, Arg

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TABLE 1-continued

Conservative substitution.	
Original Residue	Conservative Substitution
Asp (D)	Glu
Cys (C)	Ser
Gln (Q)	Asn
Glu (E)	Asp
His (H)	Asn, Gln, Lys, Arg
Ile (I)	Leu, Val, Met, Ala, Phe
Leu (L)	Ile, Val, Met, Ala, Phe
Lys (K)	Arg, Gln, Asn
Met (M)	Leu, Phe, Ile
Phe (F)	Leu, Val, Ile, Ala
Pro (P)	Gly
Ser (S)	Thr
Thr (T)	Ser
Trp (W)	Tyr, Phe
Tyr (Y)	Trp, Phe, Thr, Ser
Val (V)	Ile, Leu, Met, Phe, Ala

In addition, fragments of a ligand binding domain of an androgen receptor such as those that can bind to HLA-A2 are also useful antigens which elicit cytotoxic responses against cells expressing the androgen receptor or its ligand binding domain. Polynucleotides that encode these fragments are considered functional equivalents. Examples of these fragments are provided in the examples below. In particular, the use of the following four fragments are contemplated: SEQ ID NO:9 (amino acids 811-819 of SEQ ID NO:2), SEQ ID NO:10 (amino acids 761-770 of SEQ ID NO:2), SEQ ID NO:11 (amino acids 805-813 of SEQ ID NO:2), and SEQ ID NO:12 (amino acids 859-867 of SEQ ID NO:2).

A polynucleotide useful in the present invention is preferably ligated into an expression vector which has been specifically optimized for polynucleotide vaccinations. Elements include a transcriptional promoter, immunogenic epitopes, and additional cistrons encoding immunoenhancing or immunomodulatory genes, with their own promoters, transcriptional terminator, bacterial origin of replication and antibiotic resistance gene, as well known to those skilled in the art. Optionally, the vector may contain internal ribosome entry sites (IRES) for the expression of polycistronic mRNA.

In one embodiment of this invention, a polynucleotide useful in the present invention is directly linked to a transcriptional promoter. The use of tissue-specific promoters or enhancers, for example the muscle creatine kinase (MCK) enhancer element, may be desirable to limit expression of the polynucleotide to a particular tissue type. For example, myocytes are terminally differentiated cells which do not divide. Integration of foreign DNA into chromosomes appears to require both cell division and protein synthesis. Thus, limiting protein expression to non-dividing cells such as myocytes may be preferable. In addition, a PSA promoter may be used to limit expression of the protein to prostate tissue. In one embodiment, tissue- or cell-specific promoters may be used to target the expression of the protein to antigen-presenting cells. For example, an α -fetoprotein (AFP) promoter (see e.g., Peyton et al. 2000, Proc. Natl. Acad. Sci., USA. 97:10890-10894) may be used to limit expression to liver tissues. However, use of the CMV promoter is adequate for achieving expression in many tissues into which the plasmid DNA vaccine is introduced.

Suitable vectors include any plasmid DNA construct encoding an androgen receptor, a fragment of the androgen receptor that comprises the ligand-binding domain, a suit-

able fragment of the ligand-binding domain, or a functional equivalent or derivative thereof, operatively linked to a suitable promoter. Examples of such vectors include the pCMV series of expression vectors, commercially available from Stratagene (La Jolla, Calif.); or the pCDNA or pREP series of expression vectors by Invitrogen Corporation (Carlsbad, Calif.).

A preferred vector is pNGVL3 available from the National Gene Vector Laboratory at the University of Michigan. This vector, similar to the pCDNA3.1 eukaryotic expression vector of Invitrogen Corp. (Carlsbad, Calif.), drives transcription from the CMV promoter, but also includes the CMV intron A sequence to enhance protein expression (Lee et al., 1997, *Mol. Cells* 7:495-501). The vector also contains a multi-cloning site, and does not express a eukaryotic antibiotic resistance gene, such that the only protein expression expected in a eukaryotic system is the one driven from the CMV promoter, unlike the pCDNA vector. Another preferred vector is the pTVG4 vector described in US 2004/0142890, which is herein incorporated by reference in its entirety. The pTVG4 vector can be made by incorporating 2 copies of a 36-bp immunostimulatory (ISS) fragment containing the 5'-GTCGTT-3' motif previously identified (Hartmann et al., 2000, *J. Immunol.* 164: 1617-24) into pNGVL3.

There are many embodiments of the instant invention which those skilled in the art can appreciate from the specification. Thus, different transcriptional promoters, terminators, and other transcriptional regulatory elements may be used successfully. Examples of other eukaryotic transcription promoters include the Rous sarcoma virus (RSV) promoter, the simian virus 40 (SV40) promoter, the human elongation factor-1 α (EF-1 α) promoter, and the human ubiquitin C (UbC) promoter.

A Kozak sequence can be provided upstream of the polynucleotide useful in the present invention to enhance the translation of the corresponding mRNA from the polynucleotide. For vertebrates, the Kozak sequence is (GCC)NC-CATGG (SEQ ID NO:7) wherein N is A or G and GCC is less conserved. For example, ACCATGG can be used. See Kozak, M. *Nucleic Acids Res.* 1987, 15:8125-48.

The vectors of the present invention may be delivered intradermally, intramuscularly, subcutaneously, or intravascularly (including intravenously and intraarterially). In preferred embodiments, delivery may be a combination of two or more of the various delivery methods.

"Naked" plasmid DNA expressing a transgene could be directly injected intradermally or intramuscularly, taken up, and expressed (see e.g., Wolff et al., 1990, *Science* 247: 1465-8). The efficiency of this approach may be low, with only a small percentage of myocytes being directly transformed *in vivo*, and within only a limited area of muscle tissue targeted by this directed delivery. Various alternative approaches yielding a higher gene delivery efficiency are known (see e.g., Acsadi et al., 1991, *New Biol.* 3:71-81). Subsequent work on strategies that increase uptake of plasmid DNA by muscle tissue focused on various carrier solutions and molecules (Wolff et al., 1991, *Biotechniques* 11:474-85; and Budker et al., 1996, *Nat. Biotechnol.* 14:760-4), the use of myotoxic agents to enhance DNA uptake (Davis et al., 1993, *Hum. Gene Ther.* 4:151-9; and Danko et al., 1994, *Gene Ther.* 1:114-21), and the use of various transcriptional promoters and plasmid DNA backbones (Manthorpe et al., 1993, *Hum. Gene Ther.* 4:419-31).

In a preferred embodiment, plasmid vectors of the present invention may be delivered to the patient in need thereof intravascularly. Plasmid DNA delivered intravascularly

resulted in 100-fold higher uptake in downstream tissues in rodent studies (Budker et al., 1996, *Gene Ther.* 3:593-8). Intravascular delivery may be intravenous, e.g. by direct injection of plasmid DNA into the portal vein of rodents with uptake and expression demonstrated in hepatocytes (Budker et al., 1996, *Gene Ther.* 3:593-8; and Zhang et al., 1997, *Hum. Gene Ther.* 8:1763-72). Intravascular delivery may also be performed more directly by intraarterial delivery. For example, initial studies in rodents demonstrated that high levels of gene expression in hind limb muscle could be obtained by rapid injection of plasmid DNA into the femoral artery (Budker et al., 1998, *Gene Ther.* 5:272-276). This approach is efficient and safe in non-human primates as well, with an average of 7% of downstream myofibers expressing a β -galactosidase reporter construct two weeks after intraarterial DNA administration (Zhang et al., 2001, *Hum. Gene Ther.* 12:427-438). Parallel studies in T cell immunosuppressed rats showed that gene expression was stable for at least 10 weeks (Zhang et al., 2001, *Hum. Gene Ther.* 12:427-438).

Accordingly, delivery of plasmid DNA vaccines of the present invention can be done by direct intraarterial administration. This method provides more effective delivery to MHC class I expressing cells. Administrations of plasmid DNA vaccines intravascularly may result in increased antigen expression and subsequently lead to enhanced immune responses, and increased antigen expression in MHC class I expressing cells by means of intraarterial delivery of DNA plasmid may lead to a more robust immune response with androgen receptor-specific CTL. An intraarterial method of DNA delivery has been shown to be at least as effective as or more effective than traditional intradermal administration of DNA in eliciting prostatic acid phosphatase-specific immunity.

In another embodiment, intravenous delivery may also be used, employing methods well known to those skilled in the art (See e.g., Budker et al., 1998, *Gene Ther.* 5:272-276; and Budker et al., 1996, *Gene Ther.* 3:593-598). This delivery method may lead to a high level of antigen expression in hepatocytes. Expression of the antigen in liver, a tissue more rich with antigen-presenting cells, may lead to a more pronounced Th1/CTL response than expression in muscle tissue.

The DNA or peptide vaccines of the present invention can be used in a prime-boost strategy to induce robust and long-lasting immune response to androgen receptor. Priming and boosting vaccination protocols based on repeated injections of the same antigenic construct are well known and result in strong CTL responses. In general, the first dose may not produce protective immunity, but only "primes" the immune system. A protective immune response develops after the second or third dose.

In one embodiment, the DNA or peptide vaccines of the present invention may be used in a conventional prime-boost strategy, in which the same antigen is administered to the animal in multiple doses. In a preferred embodiment, the DNA or peptide vaccine is used in one or more inoculations. These boosts are performed according to conventional techniques, and can be further optimized empirically in terms of schedule of administration, route of administration, choice of adjuvant, dose, and potential sequence when administered with another vaccine, therapy or homologous vaccine.

The peptide or DNA vaccines of the present invention may be used in a prime-boost strategy using an alternative administration of xenoantigen and autoantigen or xenoantigen- and autoantigen-encoding vectors. Specifically, according to the present invention, the animal is first treated, or

“primed,” with a peptide antigen of foreign origin (a “xeno-antigen”) or DNA vaccine encoding the antigen of foreign origin. The animal is then treated with another peptide antigen which corresponds to the xenoantigen but is of self origin (“autoantigen”) or another DNA vaccine encoding the autoantigen. This way, the immune reaction to the antigen is boosted. The boosting step may be repeated one or more times.

A xenoantigen, as compared to a self-antigen or an autoantigen, is an antigen originated in or derived from a species different from the species that generates an immune reaction against the antigen. Xenoantigens usually are highly homologous molecules to a corresponding autoantigen. Xenoantigens have been shown to be able to elicit auto-reactive immunity. For example, molecular mimicry by highly homologous viral antigens has been one theory to explain the occurrence of several autoimmune diseases (von Herrat and Oldstone, 1996, *Curr. Opin. Immunol.* 8:878-885; and Oldstone, 1998, *Faseb J.* 12:1255-1265). That is, the induction of immune responses following infection by viral antigens that closely resemble normal autologous proteins may then lead to an autoimmune reaction to the autologous protein.

The use of highly homologous foreign antigens or xenoantigens as vaccine antigens to elicit autoreactive immunity has been explored in animal models. For example, xenoantigens derived from zona pellucida of foreign species can elicit autoreactive T cell responses and disrupt ovarian function in a variety of animal species studied (Mahi-Brown et al., 1992, *J. Reprod. Immunol.* 21:29-46; and Mahi-Brown, 1996, *J. Reprod. Fertil. Suppl.* 50:165-74). While not wishing to be bound by any theory on mechanism, it is believed that because T cells involved in autoimmune processes recognize peptide epitopes presented in the context of MHC molecules, the uptake and MHC presentation of a homologous foreign antigen presumably exposes T cell epitopes with enhanced MHC binding or unmasks cryptic epitopes of the native antigen not normally recognized.

While the prime-boost strategy is known to work with antigens of different origins, it is readily apparent to those ordinarily skilled in the art that variants, derivatives or equivalents, as discussed above, of the nucleotide sequence encoding a self-antigen can also be used to achieve the same results as xenoantigens.

The peptide or DNA vaccines of the present invention may be used together with prostate cancer vaccines based on other antigens such as prostatic acid phosphatase-based antigens. The androgen receptor-based vaccines and vaccines based on other antigens can be used simultaneously or at different times. Each may be used in a prime-boost strategy.

The present invention also provides a method for determining the effectiveness of a treatment for prostate cancer. The method includes the steps of (a) measuring the frequency or amount of cytotoxic T lymphocytes (CTLs) specific for a peptide selected from SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, and SEQ ID NO:12 prior to providing at least a portion of the treatment to a mammal having prostate cancer; (b) measuring the frequency or amount of CTLs specific for the peptide after said portion of the treatment is provided to the mammal, and (c) comparing the frequency or amount of CTLs of (a) and that of (b) wherein the frequency or amount of CTLs of (b) being higher than that of (a) indicates that the treatment is effective. For example, a biological sample containing CTLs such as a blood sample or a sample of peripheral blood mononuclear cells (PBMC) can be taken from the mammal and

the frequency or amount of CTLs in the blood sample can be measured. In one embodiment, the method is used to determine the effectiveness of a treatment provided to a human prostate cancer patient.

One of ordinary skill in the art is familiar with the techniques for functional and quantitative measurements of antigen-specific T cells. Examples include but are not limited to limited dilution assays (LDA), enzyme linked immunosorbent assay on a single cell level (ELISPOT), intracellular staining, and MHC/HLA multimer (e.g., dimer, tetramer, and pentamer) staining. Description on the MHC/HLA multimer staining technique can be found, for example, in Arnold H Bakker and Ton N M Schumacher (*Current Opinion in Immunology*, 2005, 17:428-433), Meidenbauer N et al. (*Methods*, 2003, 31:160-171), and U.S. patent application publication 20072036812.

In one embodiment, a biological sample (e.g., a blood sample or PBMC sample) containing CTLs from a patient is obtained and the sample is brought into contact with an HLA multimer (e.g., an HLA tetramer). The frequency or amount of CTLs specific for a peptide antigen bound to the HLA tetramer can then be measured by known techniques such as flow cytometry.

The invention will be more fully understood upon consideration of the following non-limiting examples.

Example 1

Immune Responses to Androgen Receptor Ligand-Binding Domain can Exist in Patients with Prostate Cancer

We evaluated whether or not patients with prostate cancer have existing immune responses to the androgen receptor (AR). We focused these studies on responses specific for the AR ligand-binding domain (LBD). As shown in FIG. 1, we found that prostate cancer patients, but not healthy male blood donors, have antibodies that are specific for the AR LBD. These antibodies were predominantly of the IgG isotype and IgG₂ sub-isotype (data not shown). Moreover, we identified that patients with antibody responses to the AR LBD have CD4+ and CD8+ T cells that proliferate, as well as cells that secrete interferon-gamma (IFN γ), in response to stimulation with the AR LBD (FIG. 2). Antigen-specific IL-10 secretion was observed in many patients who did not have evidence of antibody responses to AR LBD (FIG. 3). Taken together, these results demonstrate that some patients with prostate cancer can have pre-existing cellular immune responses specific for the AR. These findings further suggest that tolerance against the AR, which may be prevalent, is not absolute and can be overcome in some patients with prostate cancer.

Example 2

Materials and Methods

Subject Population:

Peripheral blood mononuclear cells (PBMC) were obtained from eleven patients with prostate cancer at the University of Wisconsin Hospital and Clinics between 2001 and 2007. All subjects gave Institutional Review Board-approved written informed consent for their blood products to be used for immunological research. PBMC were prepared from heparinized blood by gradient centrifugation.

T2 Binding Assay:

After passing T2 cells into fresh media the day before the assay, these cells were pulsed with 50 μ g/mL peptide overnight at 37° C./5% CO₂. The next day, the levels of HLA-A2 expression on the surface of these cells were measured using

a fluorescently-labeled HLA-A2 antibody (Clone BB7.2, BD Biosciences, San Jose, Calif.) followed by flow cytometry using FACSCaliber system (BD Biosciences). The reported “fold change” in fluorescence intensity was calculated by averaging the mean fluorescent intensity results from triplicate samples and dividing these values by the average mean fluorescent intensity of the negative control (media only) samples.

T-Cell Culturing:

Human prostate cancer patients underwent leukapheresis, and PBMCs were isolated using a Ficoll-Paque gradient (Pharmacia, Kirkland, Quebec). Immature dendritic cells (iDCs) were generated by incubating flask-adherent PBMCs with 20 ng/mL granulocyte-macrophage colony stimulating factor and 10 ng/mL interleukin four (IL-4) for six days at 37° C./5% CO₂ (cytokines from: Fitzgerald Industries, Concord, Mass.). These iDCs were then treated with 150 ng/mL IL-6, 10 ng/mL IL-1β, 10 ng/mL tumor necrosis factor alpha (TNF-α), and 1 mg/mL prostaglandin E2 (Fitzgerald Industries) to generate mature dendritic cells (mDCs). These mDCs were then pulsed with 20 μg/mL AR LBD-derived peptide, and after being irradiated were co-incubated with CD4+ and CD8+ T-cells negatively isolated from autologous PBMCs (Invitrogen, Carlsbad, Calif.). After incubating for 24 hours, these cultures were then treated with 10 U/mL IL-2 and 30 U/mL IL-7 (Fitzgerald Industries), and incubated for another 6 days. These cultured T-cells were re-stimulated weekly using peptide-pulsed antigen presenting cells (either mDCs or the TK6 lymphoma cell line).

Lactate Dehydrogenase Cytotoxicity Assay:

T-cell cultures that underwent at least two stimulations (or splenocyte cultures that had undergone one stimulation) were collected and incubated for four hours with target cells (either T2 cells pulsed for two hours with a specific or non-specific peptide, the LNCaP prostate cancer cell line, or media alone) at various effector-to-target ratios. After incubation, supernatants were collected and levels of lactate dehydrogenase were measured using the CytoTox 96 Non-Radioactive Assay (Promega). The relative percentage of peptide-specific lysis was quantitated using the following equation:

$$\% \text{ Cytotoxicity} = \frac{\text{Experimental} - \text{Effector Spontaneous} - \text{Target Spontaneous}}{\text{Target Maximum} - \text{Target Spontaneous}}$$

To conduct a mini-cytotoxicity assay of limited-dilution clones, 50 μl (1/4) of the cultured clones were incubated for four hours with either T2 cells pulsed with the specific peptide, a non-specific peptide, or media alone. For the subsequent characterization of CTL clone cytotoxicity against prostate cancer cells, cryopreserved CTL clones were thawed, washed 3 times, and restimulated by incubating the clones with peptide-pulsed irradiated TK6 cells for 7 days. These clones were then resuspended in 10 U/mL IL-2, and allowed to incubate for three days at 37° C./5% CO₂. They were then analyzed for cytotoxicity (as described above) against four prostate cancer cell lines: LNCaP, DU145, LAPC4, and MDAPCa-2b cell lines. To characterize HLA-A2-restriction of observed cytotoxicity, a HLA-A2 antibody was added to the reaction (Clone BB7.2, BD Biosciences, 1 μg/mL).

Limited-Dilution T-Cell Cloning and T-Cell Expansion:

After T-cell cultures containing AR LBD peptide-specific T-cells were identified, peptide-specific T-cell clones were

isolated using limited-dilution cloning. Briefly, cultured T-cells were diluted to 400 cells/mL, and were diluted at a 1:1 ratio down the rows of a 96-well plate. These T-cells were mixed with 2×10⁵ autologous PBMCs, as well as an anti-CD3 antibody (Clone UCHT1, BD Biosciences, 120 ng/mL) and IL-2 (Fitzgerald Industries, 200 U/mL), and were incubated at 37° C./5% CO₂ for 12-14 days. Cultures generated from a single cell were identified, and their peptide-specificity was analyzed using a mini-cytotoxicity assay (as above). Peptide-specific T-cell clones were then expanded in the presence of autologous PBMCs, TK6 cells, and an anti-CD3 antibody (30 ng/mL). The next day, 50 U/mL IL-2 was added to the cultures. Six days later, CTL clones were resuspended in media with 80 U/mL IL2, and three days later were again resuspended in 20 U/mL IL-2. After three additional days, expanded T-cell clones were analyzed for cytotoxicity against peptide-specific or non-specific T2-pulsed cells (as described above).

Surface Molecule Staining:

T-cell clones were thawed, washed 3 times, and resuspended in media supplemented with 10 U/mL IL-2 for 18 hours at 37° C./5% CO₂. These recovered clones were then resuspended in staining buffer (phosphate-buffered saline+5% fetal bovine serum) and incubated with fluorescently-labeled antibodies specific for CD3, CD4, CD8, and CD56 (clones SK7, RPA-T4, RPA-T8, or NCAM16.2, respectively; BD Biosciences) or the appropriate controls, for 30 minutes on ice. Cells were subsequently analyzed using an LSR II flow cytometer (BD Biosciences), counting 100,000 events. Cells were gated based on CD3+/CD56+ expression and CD4+/CD8+ expression.

Intracellular Cytokine Staining:

Recovered CTL clones were restimulated for one hour with media alone, the specific peptide, a non-specific peptide (peptides both at 2 μg/mL), or Phorbol Myristate Acetate (Sigma-Aldrich, St. Louis, Mo.; 10 μg/mL) and Ionomycin (MP Biomedicals, Solon, Ohio; 1 μg/mL). Cells were then treated with monensin (BD Biosciences; 1 μl per 1.5 mL cell culture) for four hours at 37° C./5% CO₂, followed by a brief blocking treatment with mouse IgG. Cells were then resuspended in staining buffer (phosphate-buffered saline+5% fetal bovine serum) and incubated with fluorescently-labeled CD3- and CD8-specific antibodies (BD Biosciences), or the appropriate controls, for 30 minutes on ice. After fixation and permeabilization, intracellular staining was conducted using fluorescently-labeled IFNγ and TNFα antibodies (Clones 4S.B3 and MAb11, respectively; BD Biosciences), or the appropriate isotype controls. Cells were subsequently analyzed using an LSR II flow cytometer, counting 100,000 events. IFNγ and TNFα-positive events were determined by gating CD3+/CD8+ cells and analyzing this population for co-expression of IFNγ and TNFα.

Immunization of HLA-A2/HLA-DR1 Mice:

Groups of four 6-10 week old HLA-A2/DR1 transgenic male mice (Charles River Laboratory—France with the permission of Dr. François Lemmonier) were immunized subcutaneously with 100 μg AR811 peptide with Complete Freund’s Adjuvant (CFA) or with CFA alone (Sigma-Aldrich), and seven days later, the mice were euthanized. Spleens were collected, and splenocytes were isolated by gradient centrifugation (Histopaque 3130, Sigma-Aldrich). Splenocytes were stimulated with 10 μg/mL peptide for two hours, and on the second day, recombinant murine IL-2 and IL-7 (Fitzgerald Industries) were added to 10 U/mL and 30 U/mL, respectively. The cultures were then allowed to incubate an additional six days before analysis.

Construction of pTVG4 and pTVG-ARLBD:
 Plasmid DNA expression vectors have been developed for use in human vaccines. Shown in FIG. 4 is a plasmid map of the pTVG4 vector as constructed for animal (e.g., rat and mouse) and human immunization. The coding sequence for the ligand-binding domain of the human androgen receptor gene has been inserted into the pTVG4 vector to create the immunization vector pTVG-ARLBD (see below).

The plasmid vector pNGVL3 was obtained from the National Gene Vector Laboratory at the University of Michigan (courtesy, Dr. Robert Gerard). This vector, similar to the pCDNA3.1 expression vector from Invitrogen Corp. (Carlsbad, Calif.), drives transcription from the CMV promoter, but also includes the CMV intron A sequence to enhance transcription (Lee et al., 1997, Mol. Cells 7:495-501). The vector also contains a multi-cloning site, and does not express a eukaryotic antibiotic resistance gene, such that the only protein expression expected in a eukaryotic system is the one driven from the CMV promoter, unlike the pCDNA vector. To this vector has been added 2 copies of a 36-bp immunostimulatory (ISS) fragment containing the 5'-GTCGTT-3' motif previously identified (Hartmann et al., 2000, J. Immunol. 164:1617-24), to create the vector pTVG4 (FIG. 4). ColE1, the DNA sequence for Colicin E1 which can be used for cloning purpose, is provided in the vector. Kan, the DNA sequence encoding a kanamycin resistance gene which can also be used for cloning purpose, is also provided in the vector. The coding sequence for the ligand-binding domain of the human androgen receptor gene has been cloned into this vector and a Kozak sequence has been provided directly upstream of the coding sequence to enhance the translation of the corresponding mRNA (FIG. 5). Expression of the ligand-binding domain has been confirmed by in vitro expression studies (not shown). This construct, named pTVG-ARLBD, is used for the immunization of animals and humans.

Immunization and Tumor Protection of Copenhagen Rats:
 Groups of ten 9-11 week old Copenhagen rats (Harlan) were immunized intradermally with 100 µg pTVG-ARLBD or 100 µg pTVG4 alone with 1 µg rat GM-CSF. Rats received three booster immunizations (100 µg) every 14 days, and 14 days after the last immunization, rats were challenged with 10,000 syngeneic Mat-LyLu prostate tumor cells, given along with Matrigel Matrix (BD Biosciences). Tumors (long and short diameters) were measured every two days, and volumes were calculated using the following equation:

$$\text{Tumor volume} = (\pi/6) \times (d_{\text{short}})^2 \times (d_{\text{long}})$$

Results

AR LBD-Specific CD8+ T-Cells from Prostate Cancer Patients can Lyse Prostate Cancer Cells:

To characterize CD8+ T-cell responses to the AR LBD, the amino acid sequence of the AR LBD was evaluated for potential HLA-A2-binding epitopes that fit the consensus peptide binding sequence of X-L/M-X-X-X-V-X-X-V/L (SEQ ID NO:8), using the algorithm of Parker and colleagues (Parker K C et al., 1994, J. Immunol. 152:163-175). As demonstrated in Table 1, ten unique peptides were identified. These peptides were synthesized and then characterized for their affinity for HLA-A2 in vitro using T2 binding assays. The results from these binding studies are also shown in Table 1. As demonstrated, several potential epitopes were predicted and found experimentally to bind strongly to HLA-A2. Peptide-specific T-cell lines were then cultured from the peripheral blood of 11 HLA-A2+ patients with prostate cancer, using each of these peptides, and then

tested for their cytolytic activity against both peptide-pulsed HLA-A2-expressing target cells and the HLA-A2+ LNCaP prostate cancer cell line. Specifically, naive T cells were isolated by magnetic negative selection (Dyna) from the peripheral blood mononuclear cells (PBMCs) of HLA-A2-expressing prostate cancer patients, and cultured in the presence of autologous cytokine-matured irradiated dendritic cells (mDC) that had been loaded with individual peptides. These cultures received interleukin 2 (IL-2) and IL-7 the day after the culture, and were re-stimulated weekly with peptide-pulsed mDCs. Beginning after two weeks of stimulation, the T-cell cultures were tested weekly for their cytolytic activity using peptide-loaded T2 cells as target cells. Peptide-specific T-cells could be cultured from the majority of patients to at least one of these peptides, and peptide-specific T-cell lines could be cultured from the majority (7/11) of HLA-A2-expressing patients against the AR811 peptide in particular (Table 2).

TABLE 1

Prediction of AR LBD-derived HLA-A2-specific peptide epitopes.			
Peptide	Sequence	Predicted Binding Affinity (t _{1/2} (min) of Dissociation)	In Vitro HLA-A2 Expression (Relative Mean Fluorescent Intensity)
AR677	VLEAIEPGV (SEQ ID NO: 13)	7.6	1.37 ± 0.14
AR700	ALLSSLNEL (SEQ ID NO: 14)	182	2.66 ± 0.28
AR708	LGERQLVHVV (SEQ ID NO: 15)	0.114	1.16 ± 0.06
AR742	WMGLMVFAM (SEQ ID NO: 16)	220	1.32 ± 0.06
AR761	RMLYFAPDLV (SEQ ID NO: 10)	217	2.15 ± 0.13
AR805	FLCMKALLL (SEQ ID NO: 11)	98	2.19 ± 0.14
AR811	LLFSIIPV (SEQ ID NO: 9)	1006	2.54 ± 0.25
AR814	FSIIPVDGL (SEQ ID NO: 17)	111	1.01 ± 0.12
AR859	QLTKLLDSV (SEQ ID NO: 12)	78	1.33 ± 0.15
AR862	KLLDSVQPI (SEQ ID NO: 18)	1274	1.65 ± 0.19
Influenza	GILGFVFTL (SEQ ID NO: 19)	30	1.88 ± 0.24
Negative Control		0	1.00 ± 0.07

AR LBD peptide epitopes were identified by scanning the protein sequence of the AR LBD for 9-mer or 10-mer peptides that fit the HLA-A2 consensus binding sequence X-L/M-X-X-X-V-X-X-V/L (SEQ ID NO: 8) and by their predicted binding affinity to HLA-A2 (Bioinformatics and Molecular Analysis Section). These peptides were synthesized and then analyzed for their affinity for HLA-A2 using a T2 binding assay. Shown is the ratio of the mean fluorescent intensity, calculated from triplicate samples, of peptide-loaded T cells normalized against unloaded T cells. Influenza: positive control influenza matrix protein peptide; negative control: vehicle.

TABLE 2

Compiled results of T cell culturing and cytotoxicity assays.		
Peptide	Peptide-specific lysis (Number of patients)	Prostate cancer cell lysis
AR677	2/11	-
AR700	1/11	-
AR708	1/11	-
AR742	2/11	-
AR761	6/11	+/-
AR805	3/11	+/-
AR811	7/11	+
AR814	3/11	-
AR859	2/11	+/-
AR862	5/11	-

Shown in this table are the results obtained from cytotoxicity assays of T cell cultures from eleven HLA-A2-expressing patients with prostate cancer. In the second column is the number of patients for which peptide-specific T cells could be identified following 2-4 in vitro stimulations. The third column shows results as to whether those peptide-specific T cells were able to lyse the HLA-A2+ LNCaP prostate cancer cell line (+: positive lysis, -: no lysis, +/-: inconclusive).

As shown in FIG. 6, AR811 peptide-specific T-cells were found to lyse T2 cells in a peptide-specific fashion, and could lyse the LNCaP cell line. Several other peptides demonstrated peptide-specific lysis and variable amounts of lysis against the LNCaP cell line (Table 2). In contrast, T-cells specific for the AR859 peptide could be cultured, and while these showed peptide-specific lysis they did not lyse the LNCaP cell line (FIG. 6B). AR811-specific T-cells were cloned by limited dilution and found to be CD8+, and to secrete both IFN γ and TNF α in response to peptide stimulation (FIG. 7). Moreover, these cells lysed prostate cancer cells in an MHC class I-restricted fashion (FIG. 8). These findings confirm that the AR811 peptide is a naturally processed and presented HLA-A2 epitope from the AR.

HLA A2 Transgenic Mice Immunized with the AR811 Peptide Developed Peptide-Specific CTL:

Human HLA transgenic mice have become a valuable tool for the identification and study of human MHC class I-specific epitopes and CTL responses. In work published by others, transgenic mice expressing human HLA-A201 have been immunized directly with peptides, or with DNA encoding antigens, or protein antigens, to identify HLA-A2-specific epitopes (Carralot J P et al., 2005, *Int Immunol* 17:591-7; Gallez-Hawkins G et al., 2003, *J Virol* 77:4457-62; and Loirat D et al., 2000, *J Immunol* 165:4748-55). Unfortunately, many of the early studies with these transgenic strains were complicated by the preference to develop H-2-restricted murine responses rather than HLA-A2-restricted CTL responses, thus limiting the usefulness of these strains. This led to the development of the HHD strains by Dr. François Lemonnier and colleagues at the Institut Pasteur, in which the mouse MHC class I H-2Db was knocked out, and mice express human β 2-microglobulin and HLA-A201 monochains fused to the α 3, transmembrane and cytoplasmic domains of the mouse MHC class I molecule (Pascolo S et al., 1997, *J Exp Med* 185:2043-51). These strains and derivatives have been particularly useful as these mice are forced to use a diverse repertoire of CD8+ T-cells specific for HLA-A2 (Pascolo S et al., 1997, *J Exp Med* 185:2043-51), and have been demonstrated to be superior in eliciting HLA-A2-restricted CTL (Ramage J M et al., 2004, *Vaccine* 22:1728-31). The HHD-II transgenic mouse strain developed by Dr. Lemonnier expresses both human HLA-A0201 and HLA-DR1, and has both the murine H-2 class I and MHC class II knocked out (Pajot A et al., 2004, *Eur J Immunol* 34:3060-9). This particular strain has been used for the identification of HLA-DR1-restricted CD4+ T-cell epitopes as well as HLA-A2-restricted epitopes (Pajot A et

al., 2006, *Microbes Infect* 8:2783-90). HHD-II mice were immunized once with 100 μ g of the AR811 peptide in complete Freund's adjuvant (CFA) or with CFA alone. As shown in FIG. 9, AR811 peptide-specific CTL could be identified after immunization.

DNA Vaccine Encoding AR LBD can Elicit Antigen-Specific Responses and Retard Prostate Cancer Cell Growth In Vivo:

cDNA was prepared from a prostate cancer cell line, and AR LBD (amino acids 664-920) was cloned into the pTVG4 vector as described above (similar to cloning prostatic acid phosphatase into the pTVG4 vector described in Johnson L E, et al., 2007, *Canc Immunol Immunoth* 56:885-895, which is herein incorporated by reference in its entirety). CHO cells transiently transfected with this pTVG-ARLBD construct produced AR LBD mRNA and protein that could be detected by RT-PCR and by Western blot analysis (data not shown). Male Copenhagen rats, 2-3 months of age, were then immunized with 100 μ g of pTVG-ARLBD four times at 14-day intervals, intradermally with 5 μ g rat GM-CSF given as a vaccine adjuvant. Two weeks after the final immunization, blood was collected for immunological analysis. As shown in FIG. 10, animals immunized with pTVG-ARLBD, but not the pTVG4 vector, developed AR LBD-specific IgG antibody responses. To assess anti-tumor efficacy, Copenhagen rats that had been immunized four times at 14-day intervals were then challenged with 1×10^4 syngeneic Mat-LyLu prostate tumor cells implanted subcutaneously. As shown in FIG. 11, immunization with pTVG-ARLBD, but not the pTVG4 vector, retarded the growth of these Mat-LyLu prostate tumors.

Example 3 (Prophetic)

Prostate Cancer Therapy with pTVG-ARLBD DNA Vaccine

Groups of ten suitable rats or mice such as Copenhagen rats are challenged with a suitable number of prostate cancer cells (e.g., 1×10^4 Mat-LyLu prostate cancer cells). These rats or mice are then immunized with either the pTVG4 (negative control) or pTVG-ARLBD constructs. One example is to immunize the rats or mice at days 2, 9, and 16 after the tumor challenge with 100 μ g injected intradermally along with 5 μ g rat or mouse GM-CSF as an adjuvant. Suitable schemes with fewer or additional immunizations may be used as alternatives. Optionally, boosts (e.g., on weekly basis) can be provided. Other suitable amounts of DNA or adjuvant can be used, as can different adjuvants (such as Freund's adjuvant) or additional vaccines (such as those targeting prostatic acid phosphatase or the synovial sarcoma X chromosome family of proteins). In addition, other suitable routes of administration may be used (such as intravenously). Tumor growth is monitored daily using bi-dimensional measurements. Sera from these rats or mice may be obtained and used to evaluate the presence of AR LBD antibodies. It is expected that immunization with pTVG-ARLBD DNA vaccine will elicit therapeutic anti-tumor response.

The present invention is not intended to be limited to the foregoing examples, but encompasses all such modifications and variations as come within the scope of the appended claims.

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Ser	Gly	Ala	Pro	Thr	Ser	Ser	Lys	Asp	Asn	Tyr	Leu	Gly	Gly	Thr	Ser	
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acc	att	tct	gac	aac	gcc	aag	gag	ttg	tgt	aag	gca	gtg	tcg	gtg	tcc	1853
Thr	Ile	Ser	Asp	Asn	Ala	Lys	Glu	Leu	Cys	Lys	Ala	Val	Ser	Val	Ser	
			235					240					245			
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Met	Gly	Leu	Gly	Val	Glu	Ala	Leu	Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	
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ctt	cgg	ggg	gat	tgc	atg	tac	gcc	cca	ctt	ttg	gga	ggt	cca	ccc	gct	1949
Leu	Arg	Gly	Asp	Cys	Met	Tyr	Ala	Pro	Leu	Leu	Gly	Val	Pro	Pro	Ala	
		265				270					275					
gtg	cgt	ccc	act	cct	tgt	gcc	cca	ttg	gcc	gaa	tgc	aaa	ggt	tct	ctg	1997
Val	Arg	Pro	Thr	Pro	Cys	Ala	Pro	Leu	Ala	Glu	Cys	Lys	Gly	Ser	Leu	
	280				285					290						
cta	gac	gac	agc	gca	ggc	aag	agc	act	gaa	gat	act	gct	gag	tat	tcc	2045
Leu	Asp	Asp	Ser	Ala	Gly	Lys	Ser	Thr	Glu	Asp	Thr	Ala	Glu	Tyr	Ser	
	295			300					305					310		
cct	ttc	aag	gga	ggt	tac	acc	aaa	ggg	cta	gaa	ggc	gag	agc	cta	ggc	2093
Pro	Phe	Lys	Gly	Tyr	Thr	Lys	Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Gly	
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tgc	tct	ggc	agc	gct	gca	gca	ggg	agc	tcc	ggg	aca	ctt	gaa	ctg	ccg	2141
Cys	Ser	Gly	Ser	Ala	Ala	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Leu	Pro	
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tct	acc	ctg	tct	ctc	tac	aag	tcc	gga	gca	ctg	gac	gag	gca	gct	gcg	2189
Ser	Thr	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	
		345				350						355				
tac	cag	agt	cgc	gac	tac	tac	aac	ttt	cca	ctg	gct	ctg	gcc	gga	ccg	2237
Tyr	Gln	Ser	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ala	Gly	Pro	
	360				365				370							
ccg	ccc	oct	ccg	ccg	cct	ccc	cat	ccc	cac	gct	cgc	atc	aag	ctg	gag	2285
Pro	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu							
	375			380					385					390		
aac	ccg	ctg	gac	tac	ggc	agc	gcc	tgg	gcg	gct	gcg	gcg	gcg	cag	tgc	2333
Asn	Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	
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cgc	tat	ggg	gac	ctg	gcg	agc	ctg	cat	ggc	gcg	ggt	gca	gcg	gga	ccc	2381
Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Ala	Gly	Ala	Ala	Gly	Pro	
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ggg	tct	ggg	tca	ccc	tca	gcc	gcc	gct	tcc	tca	tcc	tgg	cac	act	ctc	2429

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Gly	Ser	Gly	Ser	Pro	Ser	Ala	Ala	Ala	Ser	Ser	Ser	Trp	His	Thr	Leu	
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ttc	aca	gcc	gaa	gaa	ggc	cag	ttg	tat	gga	ccg	tgt	ggg	ggt	ggt	ggg	2477
Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Cys	Gly	Gly	Gly	Gly	
	440					445					450					
ggg	ggg	ggc	2525													
Gly																
	455				460					465					470	
ggc	ggc	ggc	gag	gag	gga	gct	gta	gcc	ccc	tac	ggc	tac	act	cgg	ccc	2573
Gly	Gly	Gly	Glu	Ala	Gly	Ala	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	
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cct	cag	ggg	ctg	gag	ggc	cag	gaa	agc	gac	ttc	acc	gca	cct	gat	gtg	2621
Pro	Gln	Gly	Leu	Ala	Gly	Gln	Glu	Ser	Asp	Phe	Thr	Ala	Pro	Asp	Val	
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tgg	tac	cct	ggc	ggc	atg	gtg	agc	aga	gtg	ccc	tat	ccc	agt	ccc	act	2669
Trp	Tyr	Pro	Gly	Gly	Met	Val	Ser	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Thr	
		505				510							515			
tgt	gtc	aaa	agc	gaa	atg	ggc	ccc	tgg	atg	gat	agc	tac	tcc	gga	cct	2717
Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Asp	Ser	Tyr	Ser	Gly	Pro	
	520					525						530				
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Tyr	Gly	Asp	Met	Arg	Leu	Glu	Thr	Ala	Arg	Asp	His	Val	Leu	Pro	Ile	
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gac	tat	tac	ttt	cca	ccc	cag	aag	acc	tgc	ctg	atc	tgt	gga	gat	gaa	2813
Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	
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gct	tct	ggg	tgt	cac	tat	gga	gct	ctc	aca	tgt	gga	agc	tgc	aag	gtc	2861
Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys	Val	
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ttc	ttc	aaa	aga	gcc	gct	gaa	ggg	aaa	cag	aag	tac	ctg	tgc	gcc	agc	2909
Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala	Ser	
		585						590					595			
aga	aat	gat	tgc	act	att	gat	aaa	ttc	cga	agg	aaa	aat	tgt	cca	tct	2957
Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro	Ser	
	600					605							610			
tgt	cgt	ctt	cgg	aaa	tgt	tat	gaa	gca	ggg	atg	act	ctg	gga	gcc	cgg	3005
Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala	Arg	
	615				620					625					630	
aag	ctg	aag	aaa	ctt	ggg	aat	ctg	aaa	cta	cag	gag	gaa	gga	gag	gct	3053
Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu	Glu	Gly	Glu	Ala	
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tcc	agc	acc	acc	agc	ccc	act	gag	gag	aca	acc	cag	aag	ctg	aca	gtg	3101
Ser	Ser	Thr	Thr	Ser	Pro	Thr	Glu	Glu	Thr	Thr	Gln	Lys	Leu	Thr	Val	
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Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe	Leu	Asn	Val	Leu	
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gaa	gcc	att	gag	cca	ggg	gta	gtg	tgt	gct	gga	cac	gac	aac	aac	cag	3197
Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn	Gln	
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ccc	gac	tcc	ttt	gca	gcc	ttg	ctc	tct	agc	ctc	aat	gaa	ctg	gga	gag	3245
Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly	Glu	
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aga	cag	ctt	gta	cac	gtg	gtc	aag	tgg	gcc	aag	gcc	ttg	cct	ggc	ttc	3293
Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala	Leu	Pro	Gly	Phe	
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cgc	aac	tta	cac	gtg	gac	gac	cag	atg	gct	gtc	att	cag	tac	tcc	tgg	3341
Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile	Gln	Tyr	Ser	Trp	
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Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn Val	
745 750 755	
aac tcc agg atg ctc tac ttc gcc cct gat ctg gtt ttc aat gag tac	3437
Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr	
760 765 770	
cgc atg cac aag tcc cgg atg tac agc cag tgt gtc cga atg agg cac	3485
Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg His	
775 780 785 790	
ctc tct caa gag ttt gga tgg ctc caa atc acc ccc cag gaa ttc ctg	3533
Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu	
795 800 805	
tgc atg aaa gca ctg cta ctc ttc agc att att cca gtg gat ggg ctg	3581
Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly Leu	
810 815 820	
aaa aat caa aaa ttc ttt gat gaa ctt cga atg aac tac atc aag gaa	3629
Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu	
825 830 835	
ctc gat cgt atc att gca tgc aaa aga aaa aat ccc aca tcc tgc tca	3677
Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser	
840 845 850	
aga cgc ttc tac cag ctc acc aag ctc ctg gac tcc gtg cag cct att	3725
Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile	
855 860 865 870	
gcg aga gag ctg cat cag ttc act ttt gac ctg cta atc aag tca cac	3773
Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His	
875 880 885	
atg gtg agc gtg gac ttt ccg gaa atg atg gca gag atc atc tct gtg	3821
Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val	
890 895 900	
caa gtg ccc aag atc ctt tct ggg aaa gtc aag ccc atc tat ttc cac	3869
Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His	
905 910 915	
acc cag tga agcattggaa accctatttc cccaccccag ctcatgcccc	3918
Thr Gln	
920	
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<210> SEQ ID NO 2

<211> LENGTH: 920

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

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Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
35 40 45

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Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
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 Gln
 65 70 75 80
 Glu Thr Ser Pro Arg Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser
 85 90 95
 Pro Gln Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu
 100 105 110
 Glu Gln Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu
 115 120 125
 Arg Gly Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly
 130 135 140
 Leu Pro Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala
 145 150 155 160
 Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser
 165 170 175
 Cys Ser Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln
 180 185 190
 Leu Leu Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser
 195 200 205
 Gly Arg Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn
 210 215 220
 Tyr Leu Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys
 225 230 235 240
 Lys Ala Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His
 245 250 255
 Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu
 260 265 270
 Leu Gly Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala
 275 280 285
 Glu Cys Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu
 290 295 300
 Asp Thr Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu
 305 310 315 320
 Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser
 325 330 335
 Gly Thr Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala
 340 345 350
 Leu Asp Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro
 355 360 365
 Leu Ala Leu Ala Gly Pro Pro Pro Pro Pro Pro Pro His Pro His
 370 375 380
 Ala Arg Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala
 385 390 395 400
 Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly
 405 410 415
 Ala Gly Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser
 420 425 430
 Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly
 435 440 445
 Pro Cys Gly
 450 455 460
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro

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Ala Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val
 900 905 910

Lys Pro Ile Tyr Phe His Thr Gln
 915 920

<210> SEQ ID NO 3
 <211> LENGTH: 2998
 <212> TYPE: DNA
 <213> ORGANISM: Mus musculus
 <220> FEATURE:
 <221> NAME/KEY: CDS
 <222> LOCATION: (33)..(2732)

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gga agg gtc tac cca cgg ccc cca tcc aag acc tat cga gga gcg ttc 101
 Gly Arg Val Tyr Pro Arg Pro Pro Ser Lys Thr Tyr Arg Gly Ala Phe
 10 15 20

cag aat ctg ttc cag agc gtg cgc gaa gcg atc cag aac ccg ggc ccc 149
 Gln Asn Leu Phe Gln Ser Val Arg Glu Ala Ile Gln Asn Pro Gly Pro
 25 30 35

agg cac cct gag gcc gct aac ata gca cct ccc ggc gcc tgt tta cag 197
 Arg His Pro Glu Ala Ala Asn Ile Ala Pro Pro Gly Ala Cys Leu Gln
 40 45 50 55

cag agg cag gag act agc ccc cgg cgg cgg cgg cag cag cac act 245
 Gln Arg Gln Glu Thr Ser Pro Arg Arg Arg Arg Gln Gln His Thr
 60 65 70

gag gat ggt tct cct caa gcc cac atc aga ggc ccc aca ggc tac ctg 293
 Glu Asp Gly Ser Pro Gln Ala His Ile Arg Gly Pro Thr Gly Tyr Leu
 75 80 85

gcc ctg gag gag gaa cag cag cct tca cag cag cag gca gcc tcc gag 341
 Ala Leu Glu Glu Glu Gln Gln Pro Ser Gln Gln Gln Ala Ala Ser Glu
 90 95 100

ggc cac cct gag agc agc tgc ctc ccc gag cct ggg gcg gcc acc gct 389
 Gly His Pro Glu Ser Ser Cys Leu Pro Glu Pro Gly Ala Ala Thr Ala
 105 110 115

cct ggc aag ggg ctg ccg cag cag cca cca gct cct cca gat cag gat 437
 Pro Gly Lys Gly Leu Pro Gln Gln Pro Pro Ala Pro Pro Asp Gln Asp
 120 125 130 135

gac tca gct gcc cca tcc acg ttg tcc ctg ctg ggc ccc act ttc cca 485
 Asp Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro
 140 145 150

ggc tta agc agc tgc tcc gcc gac att aaa gac att ttg aac gag gcc 533
 Gly Leu Ser Ser Cys Ser Ala Asp Ile Lys Asp Ile Leu Asn Glu Ala
 155 160 165

ggc acc atg caa ctt ctt cag cag cag caa caa cag cag cag cac caa 581
 Gly Thr Met Gln Leu Leu Gln Gln Gln Gln Gln Gln Gln His Gln
 170 175 180

cag cag cac caa cag cac caa cag cag cag gag gta atc tcc gaa ggc 629
 Gln Gln His Gln Gln His Gln Gln Gln Gln Glu Val Ile Ser Glu Gly
 185 190 195

agc agc gca aga gcc agg gag gcc acg ggg gct ccc tct tcc tcc aag 677
 Ser Ser Ala Arg Ala Arg Glu Ala Thr Gly Ala Pro Ser Ser Ser Lys
 200 205 210 215

gat agt tac cta ggg ggc aat tca acc ata tct gac agt gcc aag gag 725
 Asp Ser Tyr Leu Gly Gly Asn Ser Thr Ile Ser Asp Ser Ala Lys Glu
 220 225 230

ttg tgt aaa gca gtg tct gtg tcc atg gga ttg ggt gtg gaa gca ttg 773

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Glu	His	Leu	Ser	Pro	Gly	Glu	Gln	Leu	Arg	Gly	Asp	Cys	Met	Tyr	Ala		
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tcg	ctc	ctg	gga	ggt	cca	ccc	gcg	gtg	cgt	ccc	act	cct	tgt	gcg	ccg	869	
Ser	Leu	Leu	Gly	Gly	Pro	Pro	Ala	Val	Arg	Pro	Thr	Pro	Cys	Ala	Pro		
	265					270					275						
ctg	ccc	gaa	tgc	aaa	ggt	ctt	ccc	ctg	gac	gaa	ggc	cca	ggc	aaa	agc	917	
Leu	Pro	Glu	Cys	Lys	Gly	Leu	Pro	Leu	Asp	Glu	Gly	Pro	Gly	Lys	Ser		
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Thr	Glu	Glu	Thr	Ala	Glu	Tyr	Ser	Ser	Phe	Lys	Gly	Gly	Tyr	Ala	Lys		
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gga	ttg	gaa	ggt	gag	agc	ttg	ggg	tgc	tct	ggc	agc	agt	gaa	gca	ggt	1013	
Gly	Leu	Glu	Gly	Glu	Ser	Leu	Gly	Cys	Ser	Gly	Ser	Ser	Glu	Ala	Gly		
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Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser	Ser	Leu	Ser	Leu	Tyr	Lys	Ser		
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gga	gca	cta	gac	gag	gca	gca	gca	tac	cag	aat	cgc	gac	tac	tac	aac	1109	
Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr	Gln	Asn	Arg	Asp	Tyr	Tyr	Asn		
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Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro	His	Pro	Pro	Pro	Pro	Thr	His		
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cca	cac	gcc	cgt	atc	aag	ctg	gag	aac	cca	ttg	gac	tac	ggc	agc	gcc	1205	
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Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Gly	Ser	Leu		
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cat	gga	ggg	agt	gta	gcc	ggg	ccc	agc	act	gga	tgc	ccc	cca	gcc	acc	1301	
His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser	Thr	Gly	Ser	Pro	Pro	Ala	Thr		
	410					415						420					
acc	tct	tct	tcc	tgg	cat	act	ctc	ttc	aca	gct	gaa	gaa	ggc	caa	tta	1349	
Thr	Ser	Ser	Ser	Trp	His	Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu		
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tat	ggg	cca	gga	ggc	ggg	ggc	ggc	agc	agc	agc	cca	agc	gat	gcc	ggg	1397	
Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser	Ser	Ser	Pro	Ser	Asp	Ala	Gly		
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Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Thr	Ser		
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Gln	Glu	Ser	Asp	Tyr	Ser	Ala	Ser	Glu	Val	Trp	Tyr	Pro	Gly	Gly	Val		
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Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro	Asn	Cys	Val	Lys	Ser	Glu	Met		
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Gly	Pro	Trp	Met	Glu	Asn	Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu		
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gac	agt	acc	agg	gac	cat	gtt	tta	ccc	atc	gac	tat	tac	ttt	cca	ccc	1637	
Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro		
520					525					530					535		
cag	aag	acc	tgc	ctg	atc	tgt	gga	gat	gaa	gct	tct	ggc	tgt	cac	tac	1685	
Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr		
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Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile	
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gat aaa ttt cgg agg aaa aat tgc cca tct tgt cgt ctc cgg aaa tgt	1829
Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys	
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tat gaa gca ggg atg act ctg gga gct cgt aag ctg aag aaa ctt gga	1877
Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly	
600 605 610 615	
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Asn Leu Lys Leu Gln Glu Gly Glu Asn Ser Asn Ala Gly Ser Pro	
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Thr Glu Asp Ser Gln Lys Met Thr Val Ser His Ile Glu Gly Tyr	
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Val Val Cys Ala Gly His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala	
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Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu Val His Val	
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Val Lys Trp Ala Lys Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp	
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Asp Gln Met Ala Val Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe	
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Phe Ala Pro Asp Leu Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg	
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Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln Glu Phe Gly	
760 765 770 775	
tgg ctc caa ata acc ccc cag gaa ttc ctg tgc atg aaa gca ctg ctg	2405
Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu	
780 785 790	
ctc ttc agc att att cca gtg gat ggg ctg aaa aat caa aaa ttc ttt	2453
Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe	
795 800 805	
gat gaa ctt cga atg aac tac atc aag gaa ctc gat cgc atc att gca	2501
Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala	
810 815 820	
tgc aaa aga aag aat ccc aca tcc tgc tca agg cgc ttc tac cag ctc	2549
Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu	
825 830 835	
acc aag ctc ctg gat tct gtg cag cct att gca aga gag ctg cat cag	2597
Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln	
840 845 850 855	
ttc act ttt gac ctg cta atc aag tcc cat atg gtg agc gtg gac ttt	2645
Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser Val Asp Phe	
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cct gaa atg atg gca gag atc atc tct gtg caa gtg ccc aag atc ctt 2693
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tct ggg aaa gtc aag ccc atc tat ttc cac aca cag tga agatttgaa 2742
 Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln
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accctaatac ccaaaaccoa ccttggtccc tttccagatg tcttctgctt gttatataac 2802

tctgcactac ttctctgcag tgccctgggg gaaattcctc tactgatgta cagtctgtcg 2862

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Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
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Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
 65 70 75 80

Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
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Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
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Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
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Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
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Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
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Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
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Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln
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Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
 195 200 205

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

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Ser	Gly	Ser	Ser	Glu	Ala	Gly	Ser	Ser	Gly	Thr	Leu	Glu	Ile	Pro	Ser
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Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Leu	Asp	Glu	Ala	Ala	Ala	Tyr
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Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser	Gly	Pro	Pro
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His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys	Leu	Glu	Asn
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Pro	Leu	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala	Gln	Cys	Arg
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Tyr	Gly	Asp	Leu	Gly	Ser	Leu	His	Gly	Gly	Ser	Val	Ala	Gly	Pro	Ser
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Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Ser
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Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly	Tyr	Thr	Arg
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Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr	Pro	Ser	Pro
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Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His	Val	Leu	Pro
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Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile	Cys	Gly	Asp
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Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly	Ser	Cys	Lys
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Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr	Leu	Cys	Ala
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Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys	Asn	Cys	Pro
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Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr	Leu	Gly	Ala
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Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His	Asp	Asn	Asn
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Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn	Glu	Leu	Gly
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Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
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Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
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Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
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Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
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His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
 770 775 780

Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
 785 790 795 800

Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
 805 810 815

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

Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
 835 840 845

Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
 850 855 860

His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
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Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
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His Thr Gln

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cgcccctcac cctgtgtgtg cagctagaat tgaaaagatg aaaagacagt tggggcttca 600

gtagtcgaaa gcaaaaacaa agcaaaaaga aaacaaaag aaaatagccc agttcttatt 660

tgcacctgct tcagtggaca ttgactttgg aaggcagaga attttccttc cccccagtca 720

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gggcagatcc tgtctagcgc gtgccttctt ttacaggaga ctttgaggct atctgggcgc 840

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Met Glu Val Gln Leu Gly Leu	
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Gly Arg Val Tyr Pro Arg Pro Pro Ser Lys Thr Tyr Arg Gly Ala Phe	
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Gln Asn Leu Phe Gln Ser Val Arg Glu Ala Ile Gln Asn Pro Gly Pro	
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Arg His Pro Glu Ala Ala Ser Ile Ala Pro Pro Gly Ala Cys Leu Gln	
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Gln Arg Gln Glu Thr Ser Pro Arg Arg Arg Arg Arg Gln Gln His Pro	
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Glu Asp Gly Ser Pro Gln Ala His Ile Arg Gly Thr Thr Gly Tyr Leu	
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Pro Gly Lys Gly Leu Pro Gln Gln Pro Pro Ala Pro Pro Asp Gln Asp	
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Asp Ser Ala Ala Pro Ser Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro	
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Gly Leu Ser Ser Cys Ser Ala Asp Ile Lys Asp Ile Leu Ser Glu Ala	
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Gly Thr Met Gln Leu Leu Gln Gln Gln Gln Gln Gln Gln Gln Gln	
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Gln Glu Val Ile Ser	
185 190 195	
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Glu Gly Ser Ser Ser Val Arg Ala Arg Glu Ala Thr Gly Ala Pro Ser	
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Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr Ile Ser Asp Ser	
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Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met Gly Leu Gly Val	
235 240 245	
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Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu Arg Gly Asp Cys	
250 255 260	
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Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val Arg Pro Thr Pro	
265 270 275	
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Tyr Ala Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys Ser Gly Ser Ser	
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Glu Ala Gly Ser Ser Gly Thr Leu Glu Ile Pro Ser Ser Leu Ser Leu	
330 335 340	
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Tyr Lys Ser Gly Ala Val Asp Glu Ala Ala Ala Tyr Gln Asn Arg Asp	
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Tyr Tyr Asn Phe Pro Leu Ala Leu Ser Gly Pro Pro His Pro Pro Pro	
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Pro Thr His Pro His Ala Arg Ile Lys Leu Glu Asn Pro Ser Asp Tyr	
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Gly Ser Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg Tyr Gly Asp Leu	
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Pro Ala Thr Ala Ser Ser Ser Trp His Thr Leu Phe Thr Ala Glu Glu	
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Asp Ala Gly Pro Val Ala Pro Tyr Gly Tyr Thr Arg Pro Pro Gln Gly	
460 465 470	
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Leu Ala Ser Gln Glu Gly Asp Phe Ser Ala Ser Glu Val Trp Tyr Pro	
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Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly	
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Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys	
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Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala Ser Arg Asn Asp	
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tgc acc att gat aaa ttt cgg agg aaa aat tgt cca tcg tgt cgt ctc	2790
Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro Ser Cys Arg Leu	
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Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala Arg Lys Leu Lys	
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Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr Val Ser His Ile	
635 640 645	
gaa ggc tat gaa tgt caa cct atc ttt ctt aat gtc ctg gaa gcc att	2982
Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val Leu Glu Ala Ile	
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gag cca gga gtg gtg tgt gcc gga cat gac aac aac cag cct gat tcc	3030
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Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly Glu Arg Gln Leu	
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745 750 755	
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Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg His Leu Ser Gln	
760 765 770 775	
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Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe Leu Cys Met Lys	
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Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly Leu Lys Asn Gln	
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aaa ttc ttt gat gaa ctt cga atg aac tac atc aag gaa ctt gat cgc	3462
Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg	
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Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys Ser Arg Arg Phe	
825 830 835	
tac cag ctc acc aag ctc ctg gat tct gtg cag cct att gca aga gag	3558
Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro Ile Ala Arg Glu	
840 845 850 855	
ctg cat caa ttc act ttt gac ctg cta atc aag tcc cat atg gtg agc	3606
Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser His Met Val Ser	
860 865 870	
gtg gac ttt cct gaa atg atg gca gag atc atc tct gtg caa gtg ccc	3654
Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser Val Gln Val Pro	
875 880 885	
aag atc ctt tct ggg aaa gtc aag ccc atc tat ttc cac aca cag tga	3702
Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe His Thr Gln	
890 895 900	
agatttgaa accctaatac ccaaaccac cttgttcct ttcagatgt cttctgctg	3762
ttatataact ctgcaactact tctctggcat gggccttggg ggaaattcct ctactgatgt	3822
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tctttctctc tgcctctttt accctcccat ggcacathtt gaatccgctg cgtggtgtgg 3942
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cccagtgcca actgtgcttg tttatagcac tgtgctgtgt gccaaccaag caaatgttta 4062
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<210> SEQ ID NO 6
<211> LENGTH: 902
<212> TYPE: PRT
<213> ORGANISM: Rattus norvegicus

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<400> SEQUENCE: 6

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20 25 30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ile Ala
35 40 45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
50 55 60
Arg Arg Arg Gln Gln His Pro Glu Asp Gly Ser Pro Gln Ala His Ile
65 70 75 80
Arg Gly Thr Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
85 90 95
Gln Gln Gln Ser Ala Ser Glu Gly His Pro Glu Ser Gly Cys Leu Pro
100 105 110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
115 120 125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
130 135 140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145 150 155 160
Lys Asp Ile Leu Ser Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
165 170 175
Gln Gln
180 185 190
Gln Gln Gln Glu Val Ile Ser Glu Gly Ser Ser Ser Val Arg Ala Arg
195 200 205
Glu Ala Thr Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly
210 215 220
Asn Ser Thr Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser
225 230 235 240
Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly
245 250 255
Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro
260 265 270
Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly
275 280 285
Leu Ser Leu Asp Glu Gly Pro Gly Lys Gly Thr Glu Glu Thr Ala Glu
290 295 300
Tyr Ser Ser Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser
305 310 315 320
Leu Gly Cys Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu

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325				330				335							
Ile	Pro	Ser	Ser	Leu	Ser	Leu	Tyr	Lys	Ser	Gly	Ala	Val	Asp	Glu	Ala
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Ala	Ala	Tyr	Gln	Asn	Arg	Asp	Tyr	Tyr	Asn	Phe	Pro	Leu	Ala	Leu	Ser
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Gly	Pro	Pro	His	Pro	Pro	Pro	Pro	Thr	His	Pro	His	Ala	Arg	Ile	Lys
	370					375					380				
Leu	Glu	Asn	Pro	Ser	Asp	Tyr	Gly	Ser	Ala	Trp	Ala	Ala	Ala	Ala	Ala
385					390					395					400
Gln	Cys	Arg	Tyr	Gly	Asp	Leu	Ala	Ser	Leu	His	Gly	Gly	Ser	Val	Ala
					405					410					415
Gly	Pro	Ser	Thr	Gly	Ser	Pro	Pro	Ala	Thr	Ala	Ser	Ser	Ser	Trp	His
			420						425					430	
Thr	Leu	Phe	Thr	Ala	Glu	Glu	Gly	Gln	Leu	Tyr	Gly	Pro	Gly	Gly	Gly
		435					440							445	
Gly	Gly	Ser	Ser	Ser	Pro	Ser	Asp	Ala	Gly	Pro	Val	Ala	Pro	Tyr	Gly
	450					455					460				
Tyr	Thr	Arg	Pro	Pro	Gln	Gly	Leu	Ala	Ser	Gln	Glu	Gly	Asp	Phe	Ser
465					470					475					480
Ala	Ser	Glu	Val	Trp	Tyr	Pro	Gly	Gly	Val	Val	Asn	Arg	Val	Pro	Tyr
					485					490					495
Pro	Ser	Pro	Ser	Cys	Val	Lys	Ser	Glu	Met	Gly	Pro	Trp	Met	Glu	Asn
			500						505					510	
Tyr	Ser	Gly	Pro	Tyr	Gly	Asp	Met	Arg	Leu	Asp	Ser	Thr	Arg	Asp	His
		515					520							525	
Val	Leu	Pro	Ile	Asp	Tyr	Tyr	Phe	Pro	Pro	Gln	Lys	Thr	Cys	Leu	Ile
	530					535					540				
Cys	Gly	Asp	Glu	Ala	Ser	Gly	Cys	His	Tyr	Gly	Ala	Leu	Thr	Cys	Gly
545					550					555					560
Ser	Cys	Lys	Val	Phe	Phe	Lys	Arg	Ala	Ala	Glu	Gly	Lys	Gln	Lys	Tyr
					565					570					575
Leu	Cys	Ala	Ser	Arg	Asn	Asp	Cys	Thr	Ile	Asp	Lys	Phe	Arg	Arg	Lys
			580							585				590	
Asn	Cys	Pro	Ser	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Ala	Gly	Met	Thr
		595					600							605	
Leu	Gly	Ala	Arg	Lys	Leu	Lys	Lys	Leu	Gly	Asn	Leu	Lys	Leu	Gln	Glu
	610					615					620				
Glu	Gly	Glu	Asn	Ser	Ser	Ala	Gly	Ser	Pro	Thr	Glu	Asp	Pro	Ser	Gln
625					630					635					640
Lys	Met	Thr	Val	Ser	His	Ile	Glu	Gly	Tyr	Glu	Cys	Gln	Pro	Ile	Phe
					645					650					655
Leu	Asn	Val	Leu	Glu	Ala	Ile	Glu	Pro	Gly	Val	Val	Cys	Ala	Gly	His
			660						665					670	
Asp	Asn	Asn	Gln	Pro	Asp	Ser	Phe	Ala	Ala	Leu	Leu	Ser	Ser	Leu	Asn
			675				680							685	
Glu	Leu	Gly	Glu	Arg	Gln	Leu	Val	His	Val	Val	Lys	Trp	Ala	Lys	Ala
	690					695					700				
Leu	Pro	Gly	Phe	Arg	Asn	Leu	His	Val	Asp	Asp	Gln	Met	Ala	Val	Ile
	705				710					715					720
Gln	Tyr	Ser	Trp	Met	Gly	Leu	Met	Val	Phe	Ala	Met	Gly	Trp	Arg	Ser
					725					730					735
Phe	Thr	Asn	Val	Asn	Ser	Arg	Met	Leu	Tyr	Phe	Ala	Pro	Asp	Leu	Val
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Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val
 755 760 765
 Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro
 770 775 780
 Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro
 785 790 795 800
 Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn
 805 810 815
 Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro
 820 825 830
 Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser
 835 840 845
 Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu
 850 855 860
 Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu
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 Ile Tyr Phe His Thr Gln
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 <223> OTHER INFORMATION: synthetic oligonucleotide
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 <221> NAME/KEY: misc_feature
 <222> LOCATION: (4)..(4)
 <223> OTHER INFORMATION: n is a or g

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<210> SEQ ID NO 8
 <211> LENGTH: 9
 <212> TYPE: PRT
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 <223> OTHER INFORMATION: X can be any amino acid
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 <222> LOCATION: (2)..(2)
 <223> OTHER INFORMATION: X is Leu or Met
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 <223> OTHER INFORMATION: X can be any amino acid
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 <223> OTHER INFORMATION: X can be any amino acid
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 <222> LOCATION: (9)..(9)
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<400> SEQUENCE: 8

Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa

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5

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<210> SEQ ID NO 9
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<212> TYPE: PRT
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<220> FEATURE:
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<400> SEQUENCE: 9

Leu Leu Leu Phe Ser Ile Ile Pro Val
1 5

<210> SEQ ID NO 10
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: synthetic peptide

<400> SEQUENCE: 10

Arg Met Leu Tyr Phe Ala Pro Asp Leu Val
1 5 10

<210> SEQ ID NO 11
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<212> TYPE: PRT
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<220> FEATURE:
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<400> SEQUENCE: 11

Phe Leu Cys Met Lys Ala Leu Leu Leu
1 5

<210> SEQ ID NO 12
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<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: synthetic peptide

<400> SEQUENCE: 12

Gln Leu Thr Lys Leu Leu Asp Ser Val
1 5

<210> SEQ ID NO 13
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<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: synthetic peptide

<400> SEQUENCE: 13

Val Leu Glu Ala Ile Glu Pro Gly Val
1 5

<210> SEQ ID NO 14
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: synthetic peptide

<400> SEQUENCE: 14

Ala Leu Leu Ser Ser Leu Asn Glu Leu
1 5

5. The method of claim 1, wherein both a humoral and cellular immune reactions against the androgen receptor are induced.

6. The method of claim 1, wherein the method comprises administering to the mammal an effective amount of the combination of (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9 and (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10. 5

7. The method of claim 1, wherein the method comprises administering to the mammal an effective amount of the combination of (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, and (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11. 10 15

8. The method of claim 1, wherein the method comprises administering to the mammal an effective amount of the combination of (iii) a fragment of the ligand-binding domain defined by SEQ ID NO:9, (iv) a fragment of the ligand-binding domain defined by SEQ ID NO:10, (v) a fragment of the ligand-binding domain defined by SEQ ID NO:11, and (vi) a fragment of the ligand-binding domain defined by SEQ ID NO:12, whereby the mammal develops immune reaction against androgen receptor. 20

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