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(54) **IDENTIFICATION OF MHC CLASS I PHOSPHO-PEPTIDE ANTIGENS FROM BREAST CANCER UTILIZING SHLA TECHNOLOGY AND COMPLEMENTARY ENRICHMENT STRATEGIES**

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(63) Continuation of application No. 16/806,374, filed on Mar. 2, 2020, now Pat. No. 11,414,458, which is a continuation of application No. 14/403,350, filed on

(57) **ABSTRACT**

The present invention describes novel tumor-specific phosphorylated peptides, nucleic acids encoding those peptides, and antibodies generated against said peptides. The genes, peptides, and antibodies described herein may be used as diagnostic indicators of the presence of breast cancer and/or used in therapeutics to treat breast cancer.

Specification includes a Sequence Listing.

Figure 1A

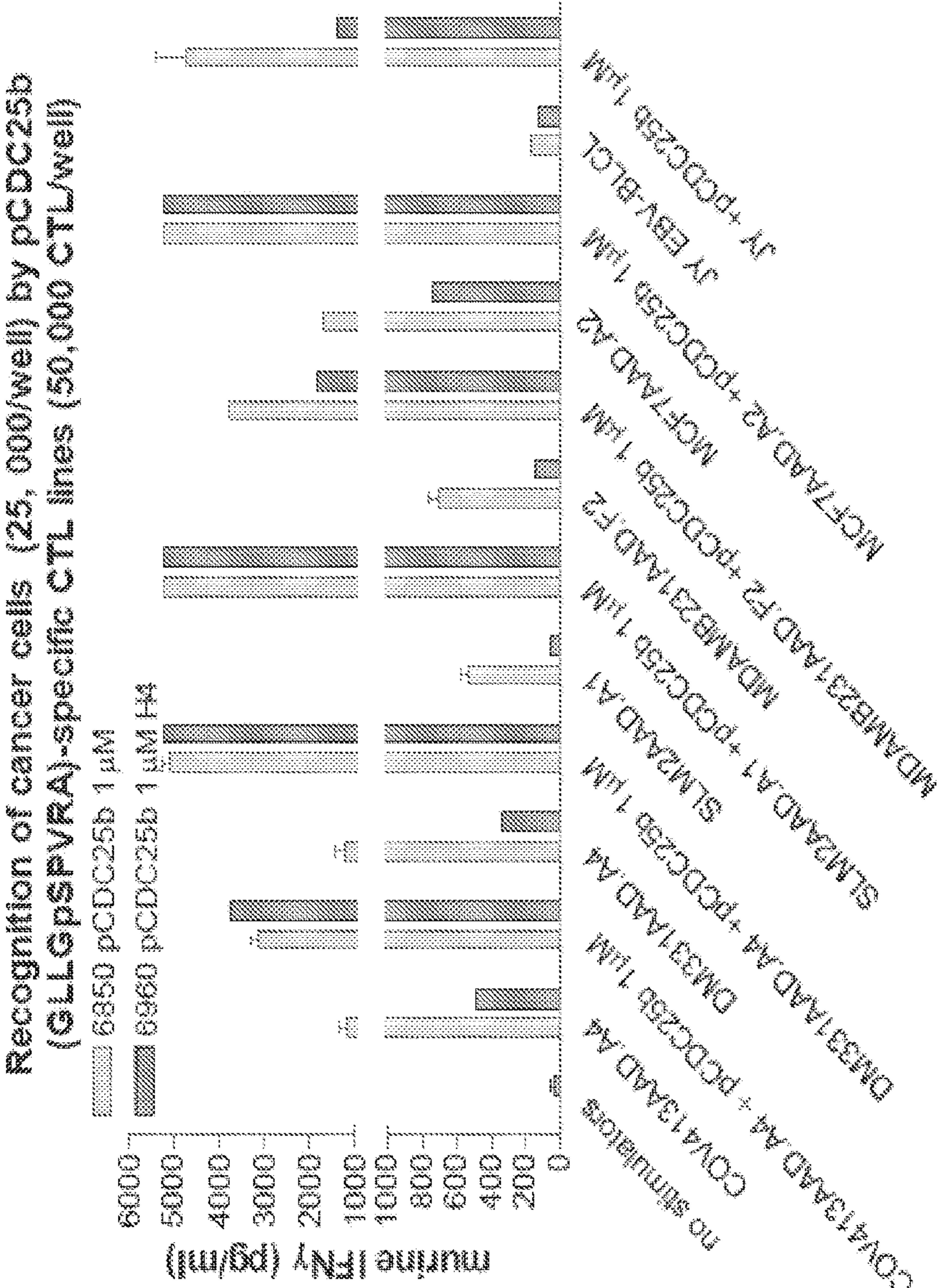


Figure 1B

Recognition of cancer cells (25, 000/well) by RvApSPTSGV-specific CTL lines
(50,000 CTL/well)

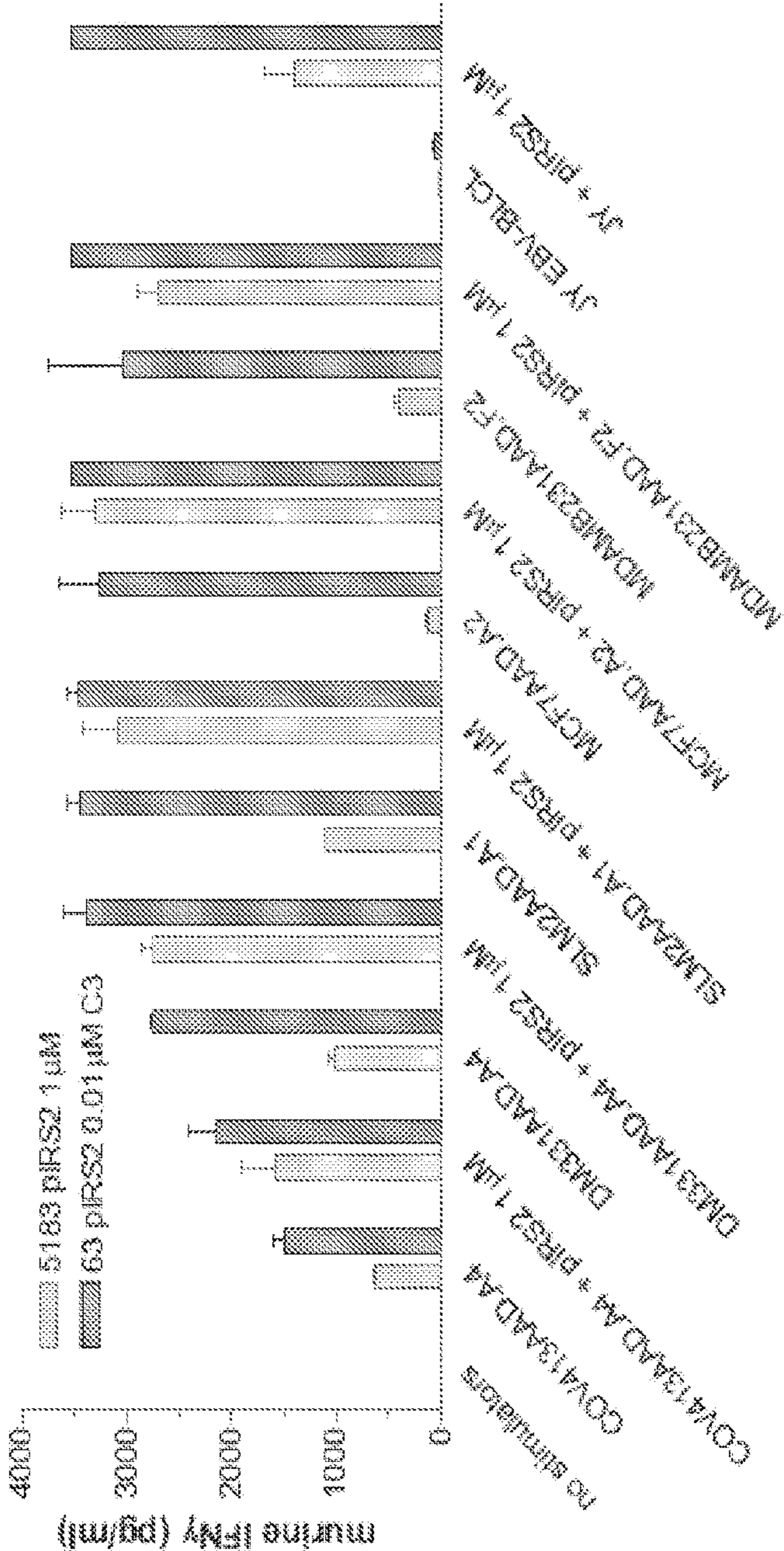


Figure 2

TABLE 1						
Phosphopeptides Presented on Breast Cancer by the Class I MHC Molecule, HLA B*0702						
Breast Cancer Cell Lines: 184B5 (A), BT20 (B) and MCF7 (C)						
#	Sequence	Start	Stop	A/B/C	UniProt	
70	APRKGSFSALM	5	14	A/B	Q13619	Cullin-4A
71	ALDSGASLLHL	482	492	A	P57078	Receptor-interacting serine/threonine-protein kinase 4
72	APLARASsL	249	257	A	Q15477	Helicase SK12W
73	APRAPsASPLAL	479	490	A	Q8N3F8	MICAL-like protein 1
74	APRKGSFSAL	5	14	A/B	Q13619	Cullin-4A
75	APSVRSLSL	278	286	A/B	Q9Y446	Plakophilin-3
76	APSVRSLSL	278	286	A/B	Q9Y446	Plakophilin-3
77	FPHsLLSVI	662	670	B	Q9H9Y6	DNA-directed RNA polymerase 1 135 kDa polypeptides/POLR1B
78	GPRPGsPSAL	266	275	A/B	Q91Z73	RNA Pseudouridylate synthase domain
79	GPRsPPVTL	147	155	B	Q15735	Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A
80	GRIGLPDL	271	278	A	P56036	26S Proteasome non-ATPase regulatory subunit 4
81	HPKRSVsL	160	167	A	Q60238	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like
82	HPRsPNVLSV	684	693	A	Q16665	Hypoxia-inducible factor 1-alpha
83	HPRsPTPTL	341	349	A	P02812	Basic salivary proline rich protein 2
84	KAFsPVRSV	2	10	A	Q02363	DNA-binding protein inhibitor ID-2
85	KARsPGRAL	6	14	A	Q14767	Latent transforming growth factor-beta-binding protein-2
86	KPEsRRSsLL	428	437	A	Q6WKZ4	Rab11 family-interacting protein 1
87	KPLIRSQsL	217	225	A/B/C	Q9LIGH4	Receptor expression-enhancing protein 4
88	KPRPPPLsP	328	336	A/B	Q15162	Cdc42-interacting protein 4
89	KPRsPDHVL	859	867	A	Q9UPN3	Microtubule-actin cross-linking factor 1
90	KPRsPPRAL	249	257	A/C	Q86TG8	Retrotransposon-derived protein PEG11

Figure 2 (cont.)

91	KPRsPPRALVL	249	259	A	Q86TG8	Retrotransposon-derived protein PEG11
92	KPRsPVVEL	667	675	A/B/C	P25098	Beta-Adrenergic receptor kinase 1
93	KPSsPRGSLL	134	143	A	Q96IF1	Protein aluba
94	KRPEsPPSI	254	262	A	Q6P2C6	AF-17 protein/ MLLT6 protein
95	LPAsPRARL	443	451	A/B	Q3KQU3	Map 7 domain-containing protein 1
96	LPFSRLSI	483	491	A/B	P47974	Zinc finger protein 36, C2H1 type-like 2
97	LPKsPPY1AF	90	99	A	P23588	Eukaryotic translation initiation factor 4B
98	LPRGSsPSVL	105	114	A/B	Q9GZN2	Hormobox protein, TGFβ induced factor 2/TGF2
99	LPRMISHSEL	22	31	A	Q15172	Putative phosphoserine phosphatase-like
100	PARsPVTEI	187	195	B	Q86YC2	Partner and localizer of BRCA2, PALB2
101	QPSFPsVLPALPA			A		No data base hit
102	RAHsSPASL	124	132	B	P46937	Yorkie homolog
103	RAPsPSSRM	2423	2431	A	Q9UQ35	Sennelarginine repetitive matrix protein 2
104	RARGIsPIVF	303	312	B	Q96MU7	YTH domain containing protein 1
105	RLlsPQQPAL	177	185	A	Q14814	Myocyte-specific enhancer factor 2D
106	RPAKsMDSL	323	331	A	Q7Z5I6	Rho GTPase-activating protein 30
107	RPAsAGAML	198	206	B	Q14814	Monocyte-specific enhancer factor 2D
108	RPAsARADPGL	57	67	A	Q9NPB0	Uncharacterized protein C6orf64
109	RPAsPAAKL	512	520	A/B	Q9P2N6	KIAA1310
110	RPAsPGPSL	646	654	A/B	Q8IY33	MICAL-like protein 2
111	RPAsPQRAQL			A/B		No data base hit
112	RPAsPSLQL	277	285	A/B	Q8WUF5	RelA-associated inhibitor
113	RPAsPSLQLL	277	285	A/B	Q8IY33	MICAL-like protein 2
114	RPAsRFEVL	384	392	B	Q8IZ52	Chondroitin sulfate synthase 2
115	RPDsPTRPTL	1646	1655	A	Q7RTP6	Protein MICAL-3

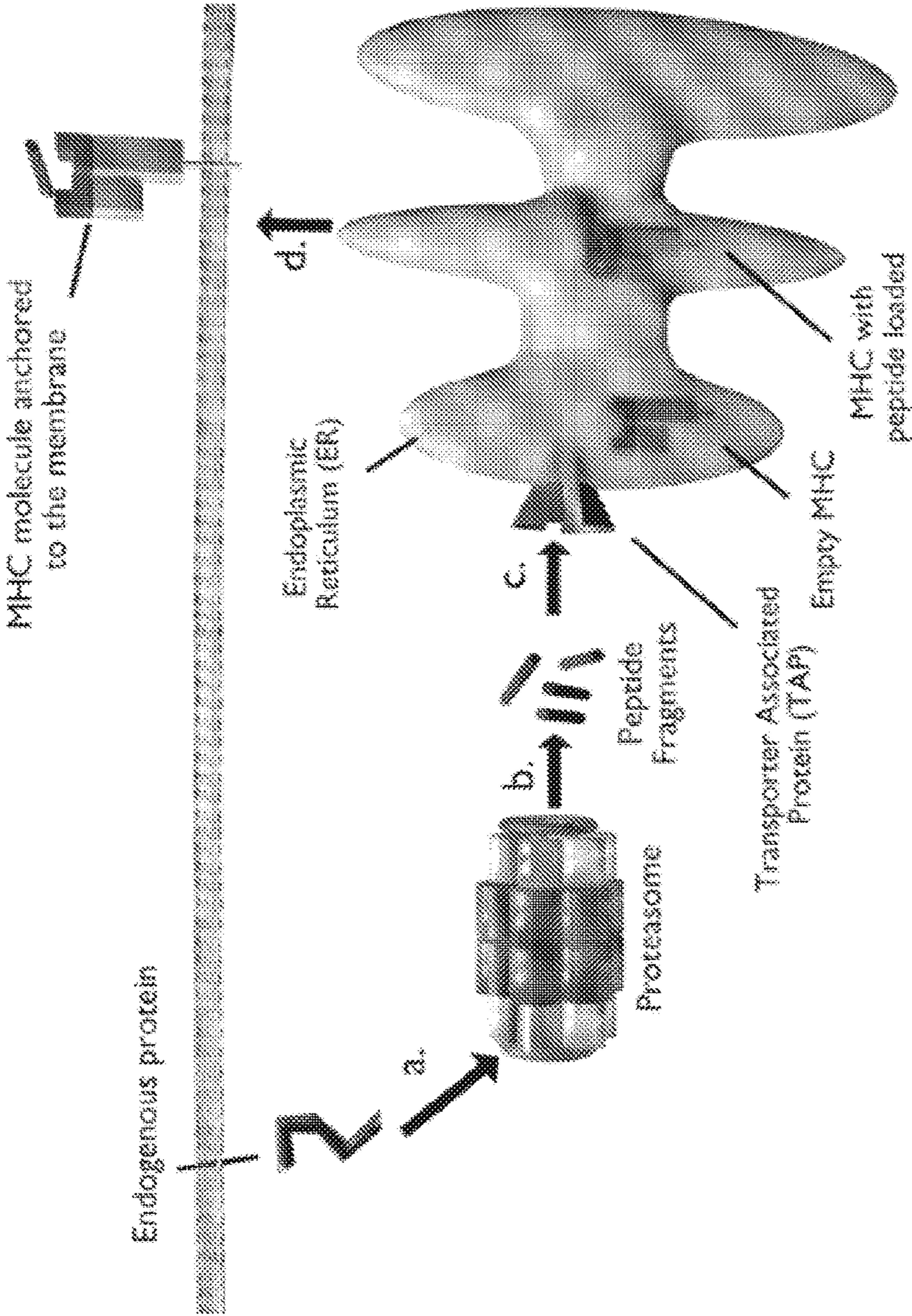
Figure 2 (cont.)

116	RPD _s RLGKTEL	1225	1235	A	Q9BYW2	Histone-lysine N-methyltransferase, SEID2
117	RPFAR _s HSF/RPFARSHsF	1534	1542	A	Q98X84	Transient receptor potential cation channel, sub M, mem 6 TRPM6
118	RPFHGISTVSL	1417	1427	B	Q5VZ89	DENN domain containing protein 4C
119	RPFsPREAL	742	750	A/B/C	Q86V48	Leucine zipper protein 1
120	RPHIPTGIYM	198	208	B	P62995	Transformer-2 protein homolog beta
121	RPIsPGLSY	364	372	B/C	Q16204	Coiled-coil domain containing protein 6
122	RPNsPSPTAL	185	194	A/B	Q9UK18	Serine/threonine-protein kinase fousled-like 1
123	RPFsPGPVL	934	942	A/B	Q12770	SREPB cleavage-activating protein
124	RPPsSEFLDL	476	485	A/B	Q9P2R6	Arginine-glutamic acid dipeptide repeats protein
125	RQQRAlSNVF	13	22	A/B	P19105	Myosin regulatory light chain 12A
126	RPRARsVDAL	488	497	A/B/C	Q86X29	Lipolysis-stimulated lipoprotein receptor
127	RPLSsTNSSRF			A		No data base hit
128	RPRPVsPSSL	430	439	A/B	P57059	Serine/threonine-protein kinase SIK1
129	RPRSLsSPTV	443	452	A	Q96PU5	E3 ubiquitin-protein ligase NEDD4-like
130	RPRSLsSPTVTL	443	454	A	Q96PU5	E3 ubiquitin-protein ligase NEDD4-like
131	RPRsPGSNSKV	671	681	A/B/C	P76347	General transcription factor III
132	RPRsPNMQDL	214	223	B	Q6T310	Ras-like protein family member 11A
133	RPRsPRENSI	689	698	A/B	Q99700	Ataxin-2
134	RPRsPRQNSI	689	698	A/B/C	Q99700	Ataxin-2 with point mutation
135	RPRSTsQSIVSL	841	852	A	Q70EL4	Ubiquitin carboxyl-terminal hydrolase 43
136	RPSsLPDL	661	668	A	Q6NFD5	AT-rich interactive domain-containing protein 1B
137	RPSPALYF	261	269	A	Q9Y3Q8	TSC22 domain family protein 4
138	RPTsRLNRL	860	868	A/B/C	Q15798	Nuclear receptor coactivator 1
139	RPV _s PFOEL			A/B/C		No database hit
140	RPV _s PGKDI	406	414		P31629	Transcription factor HIVEP2

Figure 2 (cont.)

141	RPVtPVSDL	63	71	A	Q13118	KLF10/ Krueppel-like factor 10
142	RPWSPAVSA	380	388	A	P12755	Ski oncogene
143	RPYsPSQYAL/RPYSPsQAL	575	584	A	F5H1B7	Nuclear factor erythroid 2-related factor-1, NFE2L1
144	RSRsPRPAL			A		No data base hit
145	RTRsPSPTL	515	523	B	Q86UU1	Pleckstrin homology-like domain family B
146	SKRGyIGL			A		No data base hit
147	SPAsPKISL	493	501	A/B	Q8WVM7	Ataxin-2-like protein
148	SPFKRQLsL	317	325	A/B/C	Q9Y6R0	Numb homolog (Drosophila)- like
149	SPGsPRPAL	391	399	A	Q9H211	DNA replication factor Cdt1
150	SPKsPTAAL	425	433	A/B	Q53EZ4	Centrosomal protein of 55 kDa, mitotic exit and cytokinesis
151	SPLTKSISL	1683	1691	A/B	Q12802	A-kinase anchor protein 13
152	SPRERsPAL	243	251	A	Q9Y2W1	Thyroid hormone receptor associated protein 3
153	SPRPPNsPSI	222	231	A	Q8IZW8	Tensin-4
154	SPRRsLGLAL	1382	1391	A	Q8NEY1	Neuron navigator 1
155	SPRRsRSISL	159	168	A/B/C	Q16629	Serine/Arginine-rich splicing factor 7
156	SPRsITSTP	290	298	A	Q9P0K7	Ankyrin
157	SPRsPGKPM			A/C		No data base hit
158	SPRsPGRSL			A/B/C		No data base hit
159	SPRsPSSTTYL	772	781	A/C	Q13111	Chromatin assembly factor 1 subunit A
160	SPVsPMKEL	22	30	B	Q3KP66	Uncharacterized protein C1orf106
161	SPVsTRPLEP/SPVsIRPLEP	1534	1542	A	Q9BX84	Transient receptor potential cation channel, sub M, mem 6 TRPM6
162	SRSSsSVLSL	636	644	A	A1L390	PLEKHG3/ Pleckstrin homology domain-containing family G member 3
163	SVRsLSLSL	280	288	A	Q9Y446	Plakophilin3
164	TPRsPPLGL	755	763	A/B/C	Q16584	Mitogen-activated protein kinase kinase kinase 11
165	TPRsPPLGLI	755	764	A/B/C	Q16584	Mitogen-activated protein kinase kinase kinase 11

Figure 3



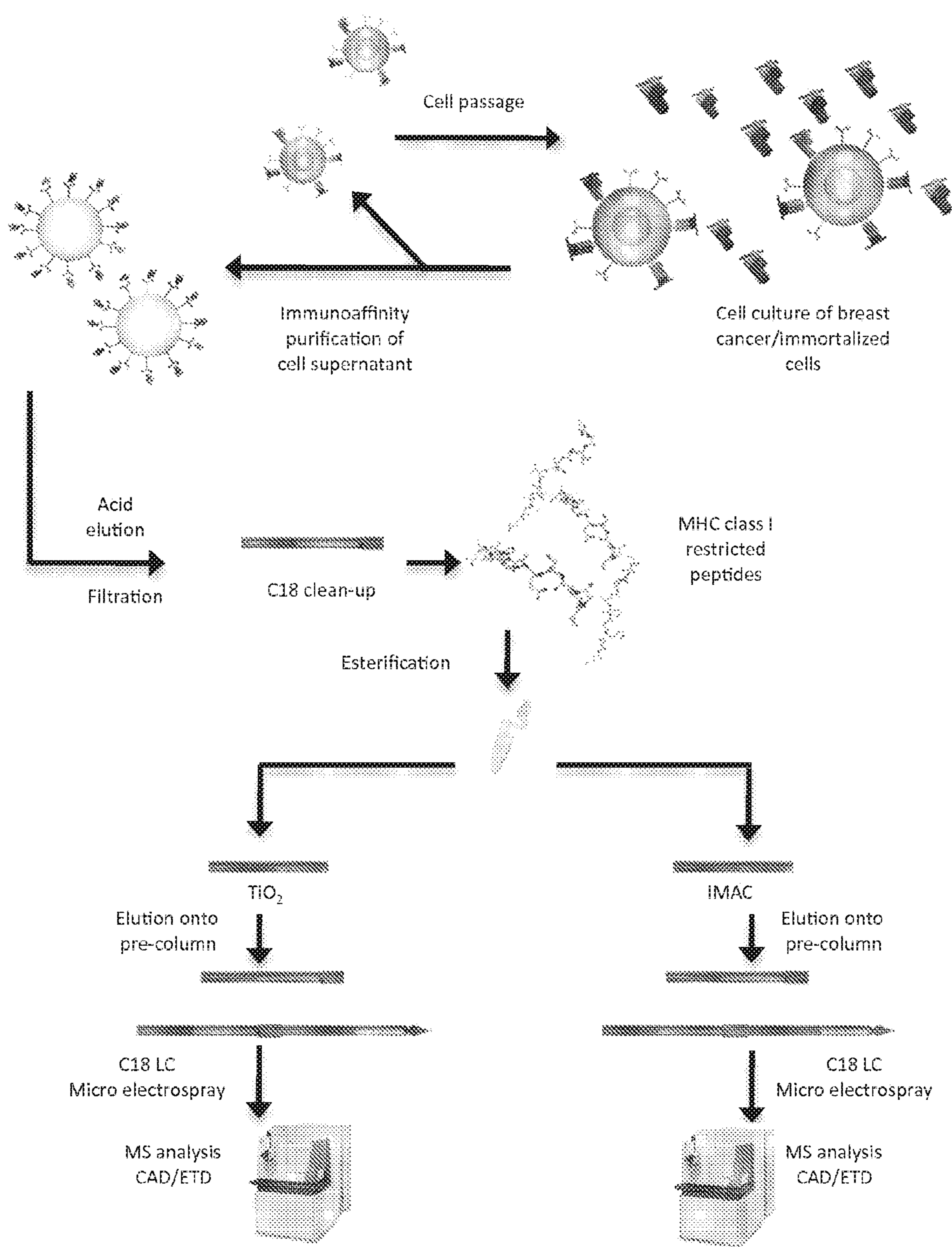


Figure 4

1	2	3	4	5	6	7	8	9
	P							L

Figure 5

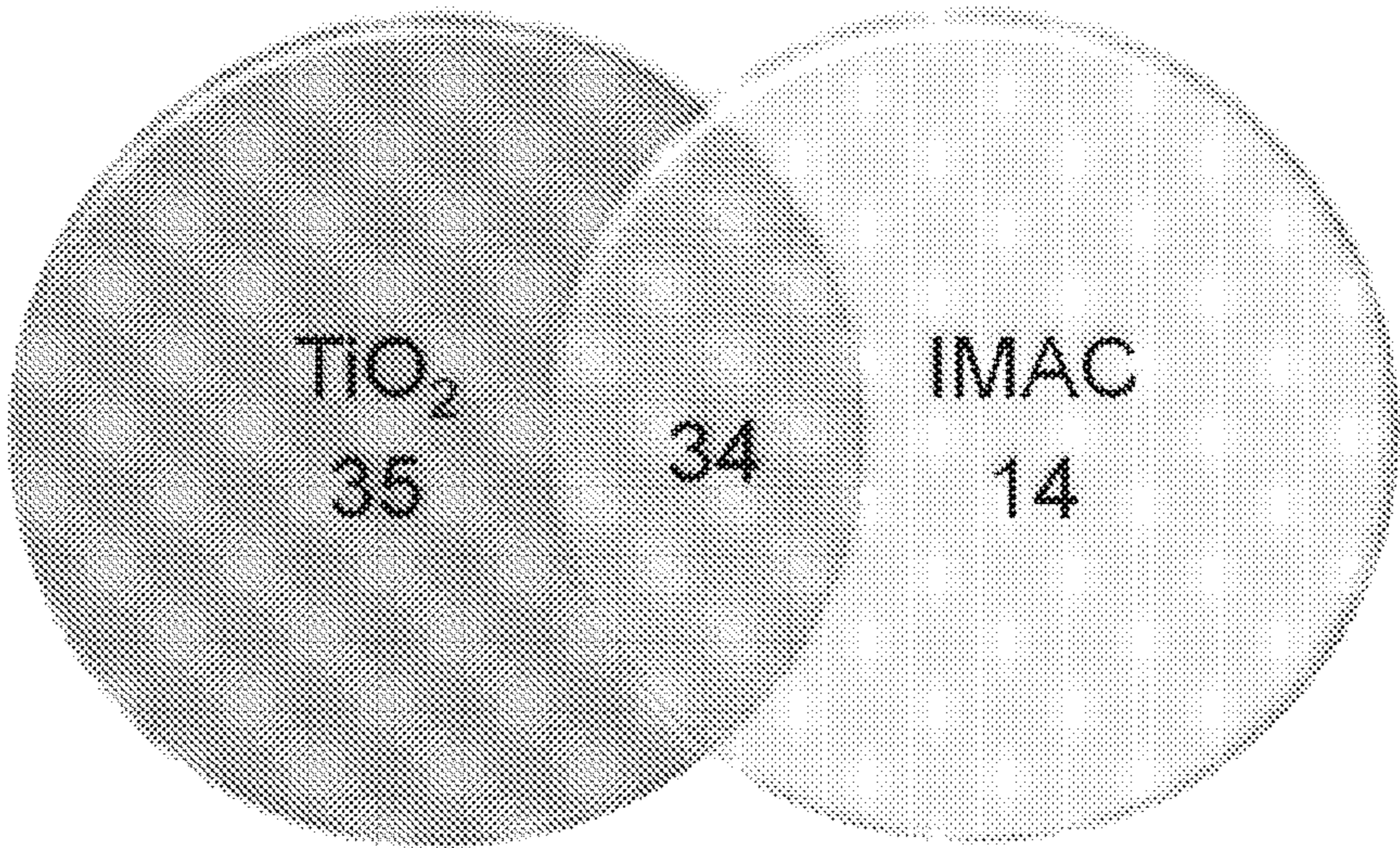


Figure 6

**IDENTIFICATION OF MHC CLASS I
PHOSPHO-PEPTIDE ANTIGENS FROM
BREAST CANCER UTILIZING SHLA
TECHNOLOGY AND COMPLEMENTARY
ENRICHMENT STRATEGIES**

**CROSS-REFERENCE TO RELATED
APPLICATIONS**

[0001] This application is a continuation of U.S. patent application Ser. No. 14/403,350, filed Mar. 12, 2015, which is a 35 U.S.C. § 371 filing of International Patent Application No. PCT/US2013/042908, filed May 28, 2013, which claims priority to U.S. Provisional Patent Application Serial Nos. 61/652,028, filed May 25, 2012; and 61/667,697, filed Jul. 3, 2012, the disclosures of each of which are incorporated by reference herein in their entireties.

U.S. GOVERNMENT RIGHTS

[0002] This invention was made with United States Government support under Grant No. R01 AI33993 awarded by the National Institutes of Health. The United States Government has certain rights in the invention.

SEQUENCE LISTING

[0003] The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Mar. 2, 2020, is named 702696_AGBW-075USCON_ST25.txt and is 39,295 bytes in size.

BACKGROUND

[0004] The mammalian immune system has evolved a variety of mechanisms to protect the host from cancerous cells. An important component of this response is mediated by cells referred to as T cells. Cytotoxic T lymphocytes (CTL) are specialized T cells that primarily function by recognizing and killing cancerous cells or infected cells, but they can also function by secreting soluble molecules referred to as cytokines that can mediate a variety of effects on the immune system. T helper cells primarily function by recognizing antigen on specialized antigen presenting cells, and in turn secreting cytokines that activate B cells, T cells, and macrophages.

[0005] A variety of evidence suggests that immunotherapy designed to stimulate a tumor-specific CTL response would be effective in controlling cancer. For example, it has been shown that human CTL recognize sarcomas (Slovin et al., 1986, J Immunol 137, 3042-3048), renal cell carcinomas (Schendel et al., 1993, J Immunol 151, 4209-4220), colorectal carcinomas (Jacob et al., 1997, Int J Cancer 71, 325-332), ovarian carcinomas (Peoples et al., 1993, Surgery 114, 227-234), pancreatic carcinomas (Peiper et al., 1997, Eur J Immunol 27, 1115-1123), squamous tumors of the head and neck (Yasumura et al., 1993, Cancer Res 53, 1461-1468), and squamous carcinomas of the lung (Slingluff et al., 1994, Cancer Res 54, 2731-2737; Yoshino et al., 1994, Cancer Res 54, 3387-3390). The largest number of reports of human tumor-reactive CTLs, however, has concerned melanomas (Boon et al., 1994, Annu Rev Immunol 12, 337-365). The ability of tumor-specific CTL to mediate tumor regression, in both human (Parmiani et al., 2002, J Natl Cancer Inst 94, 805-818; Weber, 2002, Cancer Invest 20, 208-221) and

animal models, suggests that methods directed at increasing CTL activity would likely have a beneficial effect with respect to tumor treatment.

[0006] Melanoma, or skin cancer, is a disease that is diagnosed in approximately 54,200 persons per year. Conventional therapy for the disease includes surgery, radiation therapy, and chemotherapy. In spite of these approaches to treatment, approximately 7,600 individuals die in the United States every year due to melanoma. Overall, the 5-year survival rate for the disease is 88%. The survival rate drops, however, in more advanced stages of the disease with only about 50% of Stage III patients, and 20-30% of Stage IV patients surviving past five years. In patients where the melanoma has metastasized to distant sites, the 5-year survival dips to only 12%. Clearly, there is a population of melanoma patients that is in need of better treatment options. More recently, in an attempt to decrease the number of deaths attributed to melanoma, immunotherapy has been added to the arsenal of treatments used against the disease.

[0007] In order for CTL to kill or secrete cytokines in response to a cancer cell, the CTL must first recognize the cancer cell (Townsend and Bodmer, 1989). This process involves the interaction of the T cell receptor, located on the surface of the CTL, with what is generically referred to as an MHC-peptide complex which is located on the surface of the cancerous cell. MHC (major histocompatibility-complex)-encoded molecules have been subdivided into two types, and are referred to as class I and class II MHC-encoded molecules. In the human immune system, MHC molecules are referred to as human leukocyte antigens (HLA). Within the MHC complex, located on chromosome six, are three different loci that encode for class I MHC molecules. MHC molecules encoded at these loci are referred to as HLA-A, HLA-B, and HLA-C. The genes that can be encoded at each of these loci are extremely polymorphic, and thus, different individuals within the population express different class I MHC molecules on the surface of their cells. HLA-A1, HLA-A2, HLA-A3, HLA-B7, and HLA-B8 are examples of different class I MHC molecules that can be expressed from these loci.

[0008] The peptides which associate with the MHC molecules can either be derived from proteins made within the cell, in which case they typically associate with class I MHC molecules (Rock and Goldberg, 1999, Annu Rev Immunol 17, 739-779); or they can be derived from proteins which are acquired from outside of the cell, in which case they typically associate with class II MHC molecules (Watts, 1997, Annu Rev Immunol 15, 821-850). The peptides that evoke a cancer-specific CTL response most typically associate with class I MHC molecules. The peptides themselves are typically nine amino acids in length, but can vary from a minimum length of eight amino acids to a maximum of twelve amino acids in length. Tumor antigens may also bind to class II MHC molecules on antigen presenting cells and provoke a T helper cell response. The peptides that bind to class II MHC molecules are generally twelve to nineteen amino acids in length, but can be as short as ten amino acids and as long as thirty amino acids.

[0009] The process by which intact proteins are degraded into peptides is referred to as antigen processing. Two major pathways of antigen processing occur within cells (Rock and Goldberg, 1999, Annu Rev Immunol 17, 739-779). One pathway, which is largely restricted to cells that are antigen presenting cells such as dendritic cells, macrophages, and B

cells, degrades proteins that are typically phagocytosed or endocytosed into the cell. Peptides derived in this pathway typically bind to class II MHC molecules. A second pathway of antigen processing is present in essentially all cells of the body. This second pathway primarily degrades proteins that are made within the cells, and the peptides derived from this pathway primarily bind to class I MHC molecules. Antigen processing by this latter pathway involves polypeptide synthesis and proteolysis in the cytoplasm, followed by transport of peptides to the plasma membrane for presentation. These peptides, initially being transported into the endoplasmic reticulum of the cell, become associated with newly synthesized class I MHC molecules and the resulting complexes are then transported to the cell surface. Peptides derived from membrane and secreted proteins have also been identified. In some cases these peptides correspond to the signal sequence of the proteins which is cleaved from the protein by the signal peptidase. In other cases, it is thought that some fraction of the membrane and secreted proteins are transported from the endoplasmic reticulum into the cytoplasm where processing subsequently occurs.

[0010] Once bound to the class I MHC molecule, the peptides are recognized by antigen-specific receptors on CTL. Several methods have been developed to identify the peptides recognized by CTL, each method of which relies on the ability of a CTL to recognize and kill only those cells expressing the appropriate class I MHC molecule with the peptide bound to it. Mere expression of the class I MHC molecule is insufficient to trigger the CTL to kill the target cell if the antigenic peptide is not bound to the class I MHC molecule. Such peptides can be derived from a non-self source, such as a pathogen (for example, following the infection of a cell by a bacterium or a virus) or from a self-derived protein within a cell, such as a cancerous cell. The tumor antigens from which the peptides are derived can broadly be categorized as differentiation antigens, cancer/testis antigens, mutated gene products, widely expressed proteins, and viral antigens (Castelli et al., 2000, J Cell Physiol 182, 323-331).

[0011] Immunization with melanoma-derived, class I or class II MHC-encoded molecule associated peptides, or with a precursor polypeptide or protein that contains the peptide, or with a gene that encodes a polypeptide or protein containing the peptide, are forms of immunotherapy that can be employed in the treatment of melanoma. This form of immunotherapy requires that immunogens be identified so that they can be formulated into an appropriate vaccine. Although a large number of tumor-associated peptide antigens recognized by tumor reactive CTL have been identified, there are few examples of antigens that are derived from proteins that are selectively expressed on a broad array of tumors, as well as associated with cellular proliferation and/or transformation. Attractive candidates for this type of antigen are peptides derived from proteins that are differentially phosphorylated on serine (Ser), threonine (Thr), and tyrosine (Tyr) (Zarling et al., 2000, J Exp Med 192 1755-1762). Due to the increased phosphorylation of cellular proteins in transformed cells as compared to normal cells, there are likely to be new phosphorylated peptides presented on the cell surface available for recognition by CTL. However, these are not predictable from simple inspection of protein sequences, and the exact phosphorylation sites of many proteins, as well as their phosphorylation state in a tumor cell, remain unknown.

[0012] There is a long felt need in the art for methods of identifying tumor antigens, and for methods of treating or preventing cancer based on the use of such tumor antigens. The present invention satisfies these needs.

SUMMARY OF THE INVENTION

[0013] The present invention describes novel tumor-specific peptides and antibodies generated against said peptides. The peptides and antibodies described herein may be used as diagnostic indicators of the presence of cancer and/or used in therapeutics to treat and prevent cancer. For the present invention, mass spectrometry has been used to identify phosphorylated peptides associated with the class I MHC molecule HLA-A*0201 and HLA-B*0702 and displayed on melanoma cells. The invention also provides novel methods for identifying such peptides.

[0014] In one aspect, the cancer is breast cancer.

[0015] Various aspects and embodiments of the invention are described in further detail below.

BRIEF DESCRIPTION OF THE DRAWINGS

[0016] FIG. 1, comprising FIGS. 1A and 1B, is a graphic illustration of the recognition of naturally processed and presented phosphorylated peptides on cancer cells by the phosphopeptide-specific CTL. Phosphopeptide-specific CTL were incubated with the following cancer cell lines or EBV-transformed B lymphoblastoid cell lines (BLCL): COV413.AAD.A4 ovarian carcinoma, DM331.AAD.A4 and SLM2.AAD.A1 melanomas, MCF7.AAD.A2 and MDAMB231.AAD breast carcinomas, and JY EBV-BLCL. Supernatants were harvested and evaluated for the presence of murine IFN γ (produced by murine CTL lines). As a positive control, cancer cells were pulsed with the specific phosphopeptide to show that they are capable of presenting exogenously added peptide. In FIG. 1A, two phosphopeptide-specific CTL cell lines, 6850 and 6960 that are specific for the phosphopeptide GLLGpSPVRA, recognize the phosphopeptide on all the cancer cell lines, but not the control cell line. In FIG. 1B, two phosphopeptide-specific CTL cell lines, 5183 and 63 that are specific for the phosphopeptide RVApSPTSGV, recognize the phosphopeptide on all the cancer cell lines, but not the control cell line. The ordinate indicates murine IFN γ in pg/ml. The abscissa indicates each cell line.

[0017] FIG. 2 presents a Table of phosphopeptides identified for breast cancer by the Class I MHC Molecule on the HLA B*0702 allele.

[0018] FIG. 3 graphically demonstrates the MHC class I pathway.

[0019] FIG. 4 schematically illustrates an overview of sample analysis.

[0020] FIG. 5 describes the B*0702 motif showing amino acid anchors.

[0021] FIG. 6 shows the total number of peptides in IMAC and TiO₂ experiments and schematically depicts the overlap between the peptides identified in an IMAC analysis of 184B5 and a TiO₂ analysis.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

[0022] In describing and claiming the invention, the following terminology will be used in accordance with the definitions set forth below.

[0023] As used herein, the articles “a” and “an” refer to one or to more than one, i.e., to at least one, of the grammatical object of the article. By way of example, “an element” means one element or more than one element.

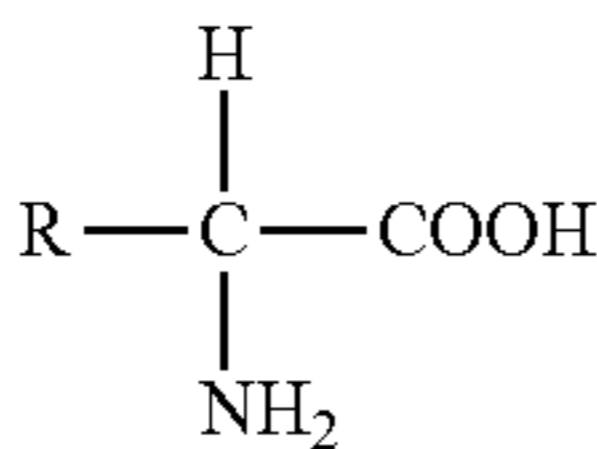
[0024] As used herein, amino acids are represented by the full name thereof, by the three letter code corresponding thereto, or by the one-letter code corresponding thereto, as indicated in the following table:

Full Name	Three-Letter Code	One-Letter Code
Aspartic Acid	Asp	D
Glutamic Acid	Glu	E
Lysine	Lys	K
Arginine	Arg	R
Histidine	His	H
Tyrosine	Tyr	Y
Cysteine	Cys	C
Asparagine	Asn	N
Glutamine	Gln	Q
Serine	Ser	S
Threonine	Thr	T
Glycine	Gly	G
Alanine	Ala	A
Valine	Val	V
Leucine	Leu	L
Isoleucine	Ile	I
Methionine	Met	M
Proline	Pro	P
Phenylalanine	Phe	F
Tryptophan	Trp	W

[0025] The expression “amino acid” as used herein is meant to include both natural and synthetic amino acids, and both D and L amino acids. “Standard amino acid” means any of the twenty standard L-amino acids commonly found in naturally occurring peptides. “Nonstandard amino acid residue” means any amino acid, other than the standard amino acids, regardless of whether it is prepared synthetically or derived from a natural source. As used herein, “synthetic amino acid” also encompasses chemically modified amino acids, including but not limited to salts, amino acid derivatives (such as amides), and substitutions. Amino acids contained within the peptides of the present invention, and particularly at the carboxy- or amino-terminus, can be modified by methylation, amidation, acetylation or substitution with other chemical groups which can change the peptide’s circulating half-life without adversely affecting their activity. Additionally, a disulfide linkage may be present or absent in the peptides of the invention.

[0026] The term “amino acid” is used interchangeably with “amino acid residue,” and may refer to a free amino acid and to an amino acid residue of a peptide. It will be apparent from the context in which the term is used whether it refers to a free amino acid or a residue of a peptide.

[0027] Amino acids have the following general structure:



[0028] Amino acids may be classified into seven groups on the basis of the side chain R: (1) aliphatic side chains, (2) side chains containing a hydroxylic (OH) group, (3) side chains containing sulfur atoms, (4) side chains containing an

acidic or amide group, (5) side chains containing a basic group, (6) side chains containing an aromatic ring, and (7) proline, an imino acid in which the side chain is fused to the amino group. The nomenclature used to describe the peptide compounds of the present invention follows the conventional practice wherein the amino group is presented to the left and the carboxy group to the right of each amino acid residue. In the formulae representing selected specific embodiments of the present invention, the amino- and carboxy-terminal groups, although not specifically shown, will be understood to be in the form they would assume at physiologic pH values, unless otherwise specified.

[0029] The term “basic” or “positively charged” amino acid as used herein, refers to amino acids in which the R groups have a net positive charge at pH 7.0, and include, but are not limited to, the standard amino acids lysine, arginine, and histidine.

[0030] A disease or disorder is “alleviated” if the severity of a symptom of the disease or disorder, the frequency with which such a symptom is experienced by a patient, or both, are reduced. The term “antigen” as used herein is defined as a molecule that provokes an immune response. This immune response may involve either antibody production, or the activation of specific immunologically-competent cells, or both.

[0031] As used herein, the term “antibody” refers to a polyclonal or monoclonal antibody or a binding fragment thereof such as Fab, F(ab')₂ and Fv fragments.

[0032] As used herein, the term “antigen peptide” refers to a phosphorylated amino acid sequence derived from a cancer cell, such as the sequences selected from the group consisting of SEQ ID NOs:70-171 or a peptide at least or about 80, 85, 90, 95, 98, 99, or 100% identical thereto.

[0033] As used herein, the term “cancer cell-specific phosphopeptide” refers to a phosphopeptide, which is expressed at higher levels in said cancer cell compared to its normal counterpart cell or tissue.

[0034] A “control” cell, tissue, sample, or subject is a cell, tissue, sample, or subject of the same type as a test cell, tissue, sample, or subject. The control may, for example, be examined at precisely or nearly the same time the test cell, tissue, sample, or subject is examined. The control may also, for example, be examined at a time distant from the time at which the test cell, tissue, sample, or subject is examined, and the results of the examination of the control ay be recorded so that the recorded results may be compared with results obtained by examination of a test cell, tissue, sample, or subject.

[0035] A “test” cell, tissue, sample, or subject is one being examined.

[0036] A “pathoindicative” cell, tissue, or sample is one which, when present, is an indication that the animal in which the cell, tissue, or sample is located (or from which the tissue was obtained) is afflicted with a disease or disorder. By way of example, the presence of one or more breast cells in a lung tissue of an animal is an indication that the animal is afflicted with metastatic breast cancer.

[0037] A tissue “normally comprises” a cell if one or more of the cell are present in the tissue in an animal not afflicted with a disease or disorder.

[0038] As used herein, a “functional” biological molecule is a biological molecule in a form in which it exhibits a property or activity by which it is characterized. A functional enzyme, for example, is one which exhibits the character-

istic catalytic activity by which the enzyme is characterized. “Homologous” as used herein, refers to the subunit sequence similarity between two polymeric molecules, e.g., between two nucleic acid molecules, e.g., two DNA molecules or two RNA molecules, or between two polypeptide molecules. When a subunit position in both of the two molecules is occupied by the same monomeric subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then they are homologous at that position. The homology between two sequences is a direct function of the number of matching or homologous positions, e.g., if half (e.g., five positions in a polymer ten subunits in length) of the positions in two compound sequences are homologous then the two sequences are 50% homologous, if 90% of the positions, e.g., 9 of 10, are matched or homologous, the two sequences share 90% homology. By way of example, the DNA sequences 3'ATTGCC5' and 3'TATGGC share 50% homology.

[0039] As used herein, “homology” is used synonymously with “identity.”

[0040] The determination of percent identity between two nucleotide or amino acid sequences can be accomplished using a mathematical algorithm. For example, a mathematical algorithm useful for comparing two sequences is the algorithm of Karlin and Altschul (1990, Proc. Natl. Acad. Sci. USA 87:2264-2268), modified as in Karlin and Altschul (1993, Proc. Natl. Acad. Sci. USA 90:5873-5877). This algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990, J. Mol. Biol. 215:403-410), and can be accessed, for example at the National Center for Biotechnology Information (NCBI) world wide web site. BLAST nucleotide searches can be performed with the NBLAST program (designated “blastn” at the NCBI web site), using the following parameters: gap penalty=5; gap extension penalty=2; mismatch penalty=3; match reward=1; expectation value 10.0; and word size=11 to obtain nucleotide sequences homologous to a nucleic acid described herein. BLAST protein searches can be performed with the XBLAST program (designated “blastp” at the NCBI web site) or the NCBI “blastp” program, using the following parameters: expectation value 10.0, BLOSUM62 scoring matrix to obtain amino acid sequences homologous to a protein molecule described herein. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al. (1997, Nucleic Acids Res. 25:3389-3402). Alternatively, PSI-Blast or PHI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.) and relationships between molecules which share a common pattern. When utilizing BLAST, Gapped BLAST, PSI-Blast, and PHI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

[0041] The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, typically exact matches are counted.

[0042] By the term “immunizing a subject against an antigen” is meant administering to a subject a composition, a peptide, a polypeptide, or a fragment, derivative, or modification thereof, a protein complex, a DNA encoding a protein complex, an antibody or a DNA encoding an antibody, which elicits an immune response in the human which

immune response provides protection to the human against a disease caused by the antigen or an organism which expresses the antigen.

[0043] As used herein, an “instructional material” includes a publication, a recording, a diagram, or any other medium of expression, which can be used to communicate the usefulness of the composition of the invention for its designated use. The instructional material of the kit of the invention may, for example, be affixed to a container, which contains the composition or be shipped together with a container which contains the composition. Alternatively, the instructional material may be shipped separately from the container with the intention that the instructional material and the composition be used cooperatively by the recipient.

[0044] As used herein, a “ligand” is a compound that specifically binds to a target compound or molecule. A ligand “specifically binds to” or “is specifically reactive with” a compound when the ligand functions in a binding reaction which is determinative of the presence of the compound in a sample of heterogeneous compounds.

[0045] As used herein, a “peptide” encompasses a sequence of 3 or more amino acids wherein the amino acids are naturally occurring or synthetic (non-naturally occurring) amino acids. Peptide mimetics include peptides having one or more of the following modifications:

[0046] 1. peptides wherein one or more of the peptidyl —C(O)NR— linkages (bonds) have been replaced by a non-peptidyl linkage such as a —CH₂-carbamate linkage (—CH₂OC(O)NR—), a phosphonate linkage, a —CH₂-sulfonamide (—CH₂-S(O)₂NR—) linkage, a urea (—NHC(O)NH—) linkage, a —CH₂-secondary amine linkage, or with an alkylated peptidyl linkage (—C(O)NR—) wherein R is C1-C4 alkyl;

[0047] 2. peptides wherein the N-terminus is derivatized to a —NRR₁ group, to a —NRC(O)R group, to a —NRC(O)OR group, to a —NRS(O)R₂ group, to a —NHC(O)NHR group where R and R₁ are hydrogen or C1-C4 alkyl with the proviso that R and R₁ are not both hydrogen;

[0048] 3. peptides wherein the C terminus is derivatized to —C(O)R₂ where R₂ is selected from the group consisting of C1-C4 alkoxy, and —NR₃R₄ where R₃ and R₄ are independently selected from the group consisting of hydrogen and C1-C4 alkyl.

[0049] “Polypeptide” refers to a polymer composed of amino acid residues, related naturally occurring structural variants, and synthetic non-naturally occurring analogs thereof linked via peptide bonds, related naturally occurring structural variants, and synthetic non-naturally occurring analogs thereof. Synthetic polypeptides can be synthesized, for example, using an automated polypeptide synthesizer.

[0050] The term “protein” typically refers to large polypeptides.

[0051] Naturally occurring amino acid residues in peptides are abbreviated as recommended by the IUPAC-IUB Biochemical Nomenclature Commission as follows: Phenylalanine is Phe or F; Leucine is Leu or L; Isoleucine is Ile or I; Methionine is Met or M; Norleucine is Nle; Valine is Val or V; Serine is Ser or S; Proline is Pro or P; Threonine is Thr or T; Alanine is Ala or A; Tyrosine is Tyr or Y; Histidine is His or H; Glutamine is Gln or Q; Asparagine is Asn or N; Lysine is Lys or K; Aspartic Acid is Asp or D; Glutamic Acid is Glu or E; Cysteine is Cys or C; Tryptophan is Trp or W; Arginine is Arg or R; Glycine is Gly or G, and

Xaa or X is any amino acid. Other naturally occurring amino acids include, by way of example, 4-hydroxyproline, 5-hydroxylysine, and the like.

[0052] Synthetic or non-naturally occurring amino acids refer to amino acids which do not naturally occur in vivo but which, nevertheless, can be incorporated into the peptide structures described herein. The resulting “synthetic peptide” contains amino acids other than the 20 naturally occurring, genetically encoded amino acids at one, two, or more positions of the peptides. For instance, naphthylalanine can be substituted for tryptophan to facilitate synthesis. Other synthetic amino acids that can be substituted into peptides include L-hydroxypropyl, L-3,4-dihydroxyphenylalanyl, alpha-amino acids such as L-alpha-hydroxylysyl and D-alpha-methylalanyl, L-alpha-methylalanyl, beta-amino acids, and isoquinolyl. D amino acids and non-naturally occurring synthetic amino acids can also be incorporated into the peptides. Other derivatives include replacement of the naturally occurring side chains of the 20 genetically encoded amino acids (or any L or D amino acid) with other side chains.

[0053] As used herein, the term “conservative amino acid substitution” is defined herein as an amino acid exchange within one of the following five groups:

[0054] I. Small aliphatic, nonpolar or slightly polar residues: Ala, Ser, Thr, Pro, Gly;

[0055] II. Polar, negatively charged residues and their amides: Asp, Asn, Glu, Gln;

[0056] III. Polar, positively charged residues: His, Arg, Lys;

[0057] IV. Large, aliphatic, nonpolar residues: Met, Leu, Ile, Val, Cys

[0058] V. Large, aromatic residues: Phe, Tyr, Trp

[0059] As used herein, the term “purified” and like terms relate to an enrichment of a molecule or compound relative to other components normally associated with the molecule or compound in a native environment. The term “purified” does not necessarily indicate that complete purity of the particular molecule has been achieved during the process. A “highly purified” compound as used herein refers to a compound that is greater than 90% pure.

[0060] As used herein, the term “pharmaceutically acceptable carrier” includes any of the standard pharmaceutical carriers, such as a phosphate buffered saline solution, water, emulsions such as an oil/water or water/oil emulsion, and various types of wetting agents. The term also encompasses any of the agents approved by a regulatory agency of the US Federal government or listed in the US Pharmacopeia for use in animals, including humans.

[0061] A “subject” of diagnosis or treatment is a mammal, including a human.

[0062] As used herein, the term “treating” includes prophylaxis of the specific disorder or condition, or alleviation of the symptoms associated with a specific disorder or condition and/or preventing or eliminating said symptoms. A “prophylactic” treatment is a treatment administered to a subject who does not exhibit signs of a disease or exhibits only early signs of the disease for the purpose of decreasing the risk of developing pathology associated with the disease.

[0063] A “therapeutic” treatment is a treatment administered to a subject who exhibits signs of pathology for the purpose of diminishing or eliminating those signs.

[0064] A “therapeutically effective amount” of a compound is that amount of compound which is sufficient to provide a beneficial effect to the subject to which the compound is administered.

[0065] By the term “vaccine,” as used herein, is meant a composition, which when inoculated into a mammal has the effect of stimulating a cellular immune response comprising a T cell response or a humoral immune response comprising a B cell response generally resulting in antibody production. The T cell response may be a cytotoxic T cell response directed against macromolecules produced by the bacteria. However, the induction of a T cell response comprising other types of T cells by the vaccine of the invention is also contemplated. A B cell response results in the production of antibody which binds to the antigen. The “vaccine” has the effect of stimulating an immune response in the subject, which serves to fully or partially protect the subject against a disease or its symptoms. The term vaccine encompasses prophylactic as well as therapeutic vaccines. A combination vaccine is one which combines two or more vaccines.

EMBODIMENTS OF THE INVENTION

[0066] The present invention is directed to novel phosphorylated peptides that give rise to cancer antigens. In one embodiment, for example, the phosphopeptides are those described in the tables of the invention, including Table 1, associated with Examples 1 and 2. Example 3 and Appendix have different Tables with other peptides, and all 5 sequences cited below are for Table 1 of Examples 1 and 2, but the embodiments cited are also useful for the results and sequences of Example 3 and Appendix A. In one aspect, the peptides bind to MHC molecules. In another aspect, the peptides of the invention stimulate an immune response. In yet another aspect, the peptides of the invention are recognized by a cell or molecule which is a product of, or is stimulated as a result of, an immune response.

TABLE 1

Cancer Antigen Phosphopeptides				
Protein	GI number	Sequence	HLA type	SEQ ID
MUM-2	20177848	RLDpSYVRSL	HLA-A2.1	1
Orphan nuclear receptor T2	136117	RQDpSTPGKVFL	HLA-A2.1	2
Riken ORF 32, chromosome 10	58864795	VLKGpSRSSSEL	HLA-A2.1	3
ORF 17, chromosome 2	40787650	RLpSSPLHFV	HLA-A2.1	4
ATP-dependent metalloprotease	14248493	RLQpSTSERL	HLA-A2.1	5

TABLE 1-continued

Cancer Antigen Phosphopeptides				
Protein	Gi number	Sequence	HLA type	SEQ ID
Heterogeneous nuclear ribonucleoprotein: A0	13938287	AMAApSPHAV	HLA-A2.1	6
Jun-b/c/d	49456463	KLApSPELERL	HLA-A2.1	7
Ribosomal protein L4	22002063	ILKpSPEIQRA	HLA-A2.1	8
Ub-carboxyl terminal hydrolase-10 (USP-10)	2501458	KLLpSPSNEKL	HLA-A2.1	9
Ribosomal protein S17	51476007	KLLDFGSLpSNLQV	HLA-A2.1	10
Krueppel-like zinc finger protein	903598	KLLSSAQRpTL	HLA-A2.1	11
B-Catenin	20384898	YLDpSGIHSGA	HLA-A2.1	12
CDC25b: p63	14602917	GLLGpSPVRA	HLA-A2.1	13
Insulin receptor substrate-2	55663292	RVApSPTSGV	HLA-A2.1	14
Breast cancer anti-estrogen resistance-3 (BCAR3)	55663999	IMDRpTPEKL	HLA-A2.1	15
Tumor endothelial marker-6, thyroid specific PTB domain protein	23451123	VMIGpSPKKV	HLA-A2.1	16
Hypothetical protein FAM65A protein	32493393	RTLpSHISEA	HLA-A2.1	17
Nedd4 binding protein 2, BCL3 binding protein	31742492	KMDpSFLDMQL	HLA-A2.1	18
Unknown (protein gi: 22902182)	22902182	LMFpSVTS (L/I)	HLA-A2.1	19
Pleckstrin homology domain-containing protein family A member 6	46397654	SLQPRSHpSV	HLA-A2.1	20
Predicted: similar to RAVR1	55648233	RLlpSPLSSA	HLA-A2.1	21
SRp46 splicing factor	14141201	SMpTRSPPRV	HLA-A2.1	22
Adenosine monophosphate deaminase 2 (isoform L)	56206061	RQIpSQDVKL	HLA-A2.1	23
B lymphocyte signal transduction gene	4261606	RQApSIELPSM	HLA-A2.1	24
B lymphocyte signal transduction gene	4261606	RQApSIELPSMAV	HLA-A2.1	25
Carcinoembryonic antigen 2b	3702267	SLLTFWNL	HLA-A2.1	26
SLTP004	20146522	KVQVpTSLSV	HLA-A2.1	27
Tsg24 protein	11967711	VLLpSPVPEL	HLA-A2.1	28
YME1-like 1, isoform 2	14043646	RLQpSTSERL	HLA-A2.1	29
FLJ22624 protein	55661789	TLApSPSVFKST	HLA-A2.1	30
Premature ovarian failure, 1B	57284143	RTYpSGPMNKV	HLA-A2.1	31
Serine/threonineprotein kinase Chk1.	7531055	KLIDIVpSSQKV	HLA-A2.1	32
Desmuslin, synemin	20137613	RTFpSPTYGL	HLA-A2.1	33
FLJ20297 protein, KIAA1418 protein	40674045	ALYpSPAQPSL	HLA-A2.1	34

TABLE 1-continued				
Cancer Antigen Phosphopeptides				
Protein	Gi number	Sequence	HLA type	SEQ ID
Adenosine monophosphate deaminase 2 (isoform L)	56206061	RQIpSQDVKL	HLA-A2.1	35
BRD4_Human bromodomain containing protein 4	20141192	AVVpSPPALHNA	HLA-A2.1	36
MUM-2	20177848	RLDpSYVRS	HLA-A2.1	37
Pro-apoptotic protein/BCL2adenovirus E1B interacting protein 3like/My020 protein		HPKRSVpSL	HLA-B7	38
KIAA1187/FLJ10350/Hypothetical protein		LPApSPRARL	HLA-B7	39
FLJ11029 protein/unnamed protein		HPRpSPTPTL	HLA-B7	40
signal-induced proliferation-associated 1 like 1/high-risk human papilloma viruses E6 oncoproteins targeted protein		YPSpSPRKAL	HLA-B7	41
Paternally expressed gene 10 ORF1		KPRpSPPRAL	HLA-B7	42
Novel protein/similar to cdc42 GTPase activating protein		RPAKpSMDSL	HLA-B7	43
Beta-adrenergi c-receptor kinase		KPRpSPVVEL	HLA-B7	44
No direct database hit- (X = L/I)				
Suppressor of cytokine signaling protein		APRpSPPPSRP	HLA-B7	46
inositol 1,4,5-triphosphate receptor, type 1		RPSGRREpSL	HLA-B7	47
Tumor necrosis factor receptor superfamily, member 8 (CD30 antigen)		RPRRpSSTQL	HLA-B7	48
LIM domain only 6		RPRpSPPPRAP	HLA-B7	49
General transcription factor 2-1		RPRpSPGSNSKV	HLA-B7	50
Ajuba (a novel LIM protein required for mitotic commitment)		GAQPGRHpSV	HLA-B7	51
novel retinal pigment epithelial cell protein/retinoic acid induced 14		SPRpSITSTP	HLA-B7	52
latent transforming growth factor-beta-binding protein-2		KARpSPGRAL	HLA-B7	53
No direct database hit- (X = L/I)		SPRpSPGRS (L/I)	HLA-B7	54
TGFB-induced factor 2/TGIF2		LPRGSpSPSVL	HLA-B7	55
DNA-directed RNA polymerase 1135 kDa polypeptide/POLR1B protein		FPHpSLLSVI	HLA-B7	56

TABLE 1-continued

Cancer Antigen Phosphopeptides				
Protein	Gi number	Sequence	HLA type	SEQ ID
thyroid hormone receptor associated protein 3		SPRERpSPAL	HLA-B7	57
RhoGAP protein/Nadrlin		APRRYpSSSL	HLA-B7	58
Synemin/desmuslin		RTFpSPTYGL	HLA-B7	59
numb homolog (Drosophila)-like		SPFKRQLpSL	HLA-B7	60
Chromatin assembly factor 1, subunit A (p150)		SPRSPpSTTYL	HLA-B7	61
No direct database hit- (X = L/I) -MIX?		RPApSP (K/Q) RA (K/Q) (L/I)	HLA-B7	62
Interleukin enhancer-binding factor 3 (Nuclear factor of activated T-cells 90 kDa)	62512150	KLFPDpTPLAL	HLA-A2.1	63
Predicted: similar to RAVR1	55648233	RLlpSPLSSA	HLA-A2.1	64
MUM-2 (truncated)	20177848	RLDpSYVR	HLA-A2.1	65
B lymphocyte signal transduction gene	4261606	RQApSIELPSM	HLA-A2.1	66
KIAA1328 protein-hypothetical protein	20521886	KLmpSPKADVKL	HLA-A2.1	67
SRp46 splicing factor	14141201	SMpTRSPPRV	HLA-A2.1	68
TFIID Transcription initiation factor	5032155	RLFpSKELRG	HLA-A2.1	69

[0067] In accordance with one embodiment of the present invention, a purified polypeptide is provided comprising the amino acid sequence of SEQ ID NO: 70-171, or an amino acid sequence that differs from any of those sequences by one or more conservative amino acid substitutions. In another embodiment the purified polypeptide comprises an amino acid sequence that differs from SEQ ID NO: 70-171 by less than 5 conservative amino acid substitutions, and in a further embodiment, by 2 or less conservative amino acid substitutions. In accordance with one embodiment of the present invention, a purified polypeptide is provided comprising the amino acid sequence of SEQ ID NO: 70-171, or a bioactive fragment of SEQ ID NO: 70-171, or an amino acid sequence that differs from SEQ ID NO: 70-171 by one to ten conservative amino acid substitutions. In one aspect, a peptide of the invention is an unphosphorylated peptide having a sequence identical with, or highly homologous with, one of the peptides having SEQ ID NOs:70-171. The present invention is also directed to isolated nucleic acids, which comprise nucleic acid sequences encoding the non-phosphorylated homologs of the phosphopeptides of the invention. The polypeptides of the present invention may include additional amino acid sequences to assist in the stabilization and/or purification of recombinantly produced polypeptides. These additional sequences may include intra- or inter-cellular targeting peptides or various peptide tags known to those skilled in the art. In one embodiment, the purified polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 70-171

and a peptide tag, wherein the peptide tag is linked to the phosphorylated peptide sequence. Suitable expression vectors for expressing such fusion proteins and suitable peptide tags are known to those skilled in the art and commercially available. In one embodiment the tag comprises a His tag. In another embodiment, the present invention is directed to a purified polypeptide that comprises an amino acid fragment of a phosphorylated polypeptide.

[0068] More particularly the phosphorylated polypeptide fragment consists of natural or synthetic portions of a full-length polypeptide selected from the group consisting of SEQ ID NO: 70-171 that are capable of specific binding to their natural ligand. Alternatively, the fragment may comprise an antigenic fragment, including fragments of 10-30, 12-19, 8-12 or 9 amino acids in length, of a polypeptide selected from the group consisting of SEQ ID NO: 70-171.

[0069] In accordance with one embodiment, a composition is provided for inducing an immune response against a cancer-associated phosphopeptide as described herein. In one embodiment, the composition consists of a peptide comprising a sequence selected from the group consisting of SEQ ID NO: 70-171, and antigenic fragments of those sequences. The compositions can be combined with a pharmaceutically acceptable carrier or adjuvant and administered to a mammalian species to induce an immune response. The immune response can take the form of an antibody response, a T helper response, or a CTL response. The immune response may be generated in vitro or in vivo.

[0070] In accordance with one embodiment, the peptides can be used to immunize a non-human recipient such as a mouse, rat, or goat for the production of antibodies that specifically recognize the peptides. Antibodies to peptides may be generated using methods that are well known in the art. In one embodiment, recombinantly produced peptides, or fragments thereof are used to generate antibodies against the phosphorylated peptides.

[0071] In accordance with one embodiment, an antibody is provided which binds to a polypeptide of the invention. In one aspect, the polypeptide is selected from the group consisting of SEQ ID NOs: 70-171. In one embodiment the antibody is a monoclonal antibody. The antibodies may be used with or without modification, and may be labeled by joining them, either covalently or non-covalently, with a reporter molecule. In addition, the antibodies can be formulated with standard carriers and optionally labeled to prepare therapeutic or diagnostic compositions.

[0072] Antibodies to peptides may be generated using methods that are well known in the art. For the production of antibodies, various host animals, including rabbits, mice, rats, goats and other mammals, can be immunized by injection with a peptide. They may be conjugated to carrier proteins such as KLH or tetanus toxoid. Various adjuvants may be used to increase the immunological response, depending on the host species, and including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*. Methods of immunization to achieve a polyclonal antibody response are well known in the art, as are the methods for generating hybridomas and monoclonal antibodies.

[0073] For preparation of monoclonal antibodies, any technique, which provides for the production of antibody molecules by continuous cell lines in culture may be used. For example, the hybridoma technique originally developed by Kohler and Milstein (1975, *Nature* 256:495-497), as well as the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, *Immunology Today* 4:72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). In an additional embodiment of the invention, monoclonal antibodies can be produced in germ-free animals utilizing recent technology (PCT/US90/02545). According to the invention, human antibodies may be used and can be obtained by using human hybridomas (Cote et al., 1983, *Proc. Natl. Acad. Sci. U.S.A.* 80:2026-2030) or by transforming human B cells with EBV virus in vitro (Cole et al., 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, pp. 77-96). In fact, according to the invention, techniques developed for the production of "chimeric antibodies" (Morrison et al., 1984, *Proc. Natl. Acad. Sci. U.S.A.* 81:6851-6855; Neuberger et al., 1984, *Nature* 312:604-608; Takeda et al., 1985, *Nature* 314:452-454) by splicing the genes from a mouse antibody molecule specific for epitopes of TAG polypeptides together with genes from a human antibody molecule of appropriate biological activity can be used; such antibodies are within the scope of this invention.

[0074] Antibodies generated in accordance with the present invention may include, but are not limited to, polyclonal,

monoclonal, chimeric (i.e., "humanized" antibodies), single chain (recombinant), Fab fragments, and fragments produced by a Fab expression library. These antibodies can be used as diagnostic agents for the diagnosis of conditions or diseases characterized by expression or overexpression of antigen peptides (such as cancer), or in assays to monitor a patient's responsiveness to an anti-cancer therapy. In one embodiment antibodies specific for one or more of the antigen peptides are used as diagnostics for the detection of the antigen peptides in cancer cells.

[0075] The antibodies or antibody fragments of the present invention can be combined with a carrier or diluent to form a composition. In one embodiment, the carrier is a pharmaceutically acceptable carrier. Such carriers and diluents include sterile liquids such as water and oils, with or without the addition of a surfactant and other pharmaceutically and physiologically acceptable carrier, including adjuvants, excipients or stabilizers. Illustrative oils are those of petroleum, animal, vegetable, or synthetic origin, for example, peanut oil, soybean oil, or mineral oil. In general, water, saline, aqueous dextrose, and related sugar solution, and glycols such as, propylene glycol or polyethylene glycol, are preferred liquid carriers, particularly for injectable solutions.

[0076] In accordance with one embodiment, the detection of antigen peptides is used as a diagnostic mark for detecting cancer. In another embodiment the antigen peptides can be used to immunize an individual to induce an immune response. The induced response may include T helper cells or CTL specific for the antigen peptides. The induced immune response may be useful in preventing the development of cancer in an individual without cancer, and it may be useful in eliminating or preventing the further spread of the disease in an individual with cancer. In one embodiment the antigen peptides may be added to antigen presenting cells. The antigen presenting cells will now present antigen peptides, which can be used to stimulate an in vitro T helper cell or CTL response. The T helper cells or CTL can then be used as diagnostics to detect the presence of tumor cells. The T helper cells or CTL can also be infused into a cancer patient as a treatment for cancer.

[0077] Accordingly, one embodiment of the invention is directed to the use of antigen peptides as diagnostic markers for neoplastic disease such as cancer. The method comprises the steps of screening for elevated levels or inappropriate expression of antigen peptides, including the expression of antigen peptides in somatic tissues. The term "inappropriate expression" includes any non-typical expression that is deleterious to the cell or host organism, including for example, expression in a cell type that normally does not express the peptide, or expression of a modified form of the peptide that impacts cell function. Such screens could be conducted using antibodies specific for the antigen. Alternatively, antibodies directed against antigen peptides can be used in assays to monitor patients being treated with anti-cancer therapies to monitor the effectiveness of the therapy.

[0078] The antigen peptides are known to be expressed in melanoma, ovarian, breast, colorectal, or squamous carcinoma of the lung, and thus may be used as immunogens to prevent, eliminate, or delay the progression of, inter alia, these types of cancer.

[0079] In one aspect, the cancer is, inter alia, sarcoma, renal cell carcinoma, pancreatic carcinomas, squamous tumors of the head and neck.

[0080] These same antigen peptides may also be expressed in untested forms of cancer and thus may be useful in their ability to prevent, eliminate, or delay the progression of additional cancers.

[0081] Antibodies generated with specificity for the antigen peptides are used in accordance with one embodiment to detect the corresponding peptides in biological samples. The biological sample could come from an individual whom is suspected of having cancer and thus detection would serve to diagnose the cancer. Alternatively, the biological sample may come from an individual known to have cancer, and detection of the antigen peptides would serve as an indicator of disease prognosis or treatment efficacy. Appropriate immunoassays are well known in the art and include, but are not limited to, immunohistochemistry, flow cytometry, radioimmunoassay, western blotting, and ELISA. Biological samples suitable for such testing would include, but are not limited to, cells, tissue biopsy specimens, whole blood, plasma, serum, sputum, cerebrospinal fluid, pleural fluid, and urine.

[0082] Antigens recognized by T cells, whether helper T lymphocytes or CTL, are not recognized as intact proteins, but rather as small peptides that associate with class I or class II MHC proteins on the surface of cells. During the course of a naturally occurring immune response antigens that are recognized in association with class II MHC molecules on antigen presenting cells are acquired from outside the cell, internalized, and processed into small peptides that associate with the class II MHC molecules. Conversely, the antigens that give rise to proteins that are recognized in association with class I MHC molecules are generally proteins made within the cells, and these antigens are processed and associate with class I MHC molecules. It is now well known that the peptides that associate with a given class I or class II MHC molecule are characterized as having a common binding motif, and the binding motifs for a large number of different class I and II MHC molecules have been determined. It is also well known that synthetic peptides can be made which correspond to the sequence of a given antigen and which contain the binding motif for a given class I or II MHC molecule. These peptides can then be added to appropriate antigen presenting cells, either in vitro or in vivo, and be used to stimulate a T helper cell or CTL response. The binding motifs, methods for synthesizing the peptides, and methods for stimulating a T helper cell or CTL response are all well known and readily available.

[0083] The antigens of this invention may take the form of antigen peptides added to autologous dendritic cells and used to stimulate a T helper cell or CTL response in vitro. The in vitro generated T helper cells or CTL can then be infused into a patient with cancer (Yee et al., 2002), and specifically a patient with a form of cancer that expresses one or more of antigen peptides. The antigen peptides may also be used to vaccinate an individual. The antigen peptides may be injected alone, but most often they would be administered in combination with an adjuvant. The proteins may also be added to dendritic cells in vitro, with the dendritic cells being subsequently transferred into an individual with cancer with the intent of stimulating an immune response.

[0084] Peptide analogs can readily be synthesized that retain their ability to stimulate a particular immune response, but which also gain several beneficial features which include, but are not limited to the following: (i)

Substitutions may be made in the peptide at residues known to interact with the MHC molecule. Such substitutions can have the effect of increasing the binding affinity of the peptide for the MHC molecule and can also increase the lifespan of the peptide-MHC complex, the consequence of which is that the analog is a more potent stimulator of an immune response than is the original peptide. (ii) The substitutions may be at positions in the peptide that interact with the receptor on the T helper cells or CTL, and have the effect of increasing the affinity of interaction such that a stronger immune response is generated. (iii) Additionally, the substitutions may have no effect on the immunogenicity of the peptide per se, but rather than may prolong its biological half-life or prevent it from undergoing spontaneous substitutions or alternations which might otherwise negatively impact on the immunogenicity of the peptide.

[0085] The antigen peptides of this invention can also be used as a vaccine for cancer, and more specifically for melanoma, ovarian, breast, colorectal, or lung squamous cancer. The antigens may take the form of genes, proteins, or peptides. The vaccine may include only the antigens of this invention or they may include other cancer antigens that have been identified.

[0086] Pharmaceutical carriers, diluents and excipients are generally added that are compatible with the active ingredients and acceptable for pharmaceutical use. Examples of such carriers include, but are not limited to, water, saline solutions, dextrose, or glycerol. Combinations of carriers may also be used. The vaccine compositions may further incorporate additional substances to stabilize pH, or to function as adjuvants, wetting agents, or emulsifying agents, which can serve to improve the effectiveness of the vaccine.

[0087] The composition may be administered parenterally or orally, and, if parenterally, either systemically or topically. Parenteral routes include subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, transdermal, or buccal routes. One or more such routes may be employed. Parenteral administration can be, for example, by bolus injection or by gradual perfusion over time. Alternatively, or concurrently, administration may be by the oral route.

[0088] It is understood that the suitable dosage of an immunogen of the present invention will depend upon the age, sex, health, and weight of the recipient, the kind of concurrent treatment, if any, the frequency of treatment, and the nature of the effect desired, however, the most preferred dosage can be tailored to the individual subject, as determined by the researcher or clinician. The total dose required for any given treatment will commonly be determined with respect to a standard reference dose based on the experience of the researcher or clinician, such dose being administered either in a single treatment or in a series of doses, the success of which will depend on the production of a desired immunological result (i.e., successful production of a T helper cell and/or CTL-mediated response to the antigen, which response gives rise to the prevention and/or treatment desired). Thus, the overall administration schedule must be considered in determining the success of a course of treatment and not whether a single dose, given in isolation, would or would not produce the desired immunologically therapeutic result or effect. Thus, the therapeutically effective amount (i.e., that producing the desired T helper cell and/or CTL-mediated response) will depend on the antigenic composition of the vaccine used, the nature of the disease

condition, the severity of the disease condition, the extent of any need to prevent such a condition where it has not already been detected, the manner of administration dictated by the situation requiring such administration, the weight and state of health of the individual receiving such administration, and the sound judgment of the clinician or researcher. Needless to say, the efficacy of administering additional doses, and of increasing or decreasing the interval, may be re-evaluated on a continuing basis, in view of the recipient's immunocompetence (for example, the level of T helper cell and/or CTL activity with respect to tumor-associated or tumor-specific antigens).

[0089] The concentration of the T helper or CTL stimulatory peptides of the invention in pharmaceutical formulations are subject to wide variation, including anywhere from less than 0.01% by weight to as much as 50% or more. Factors such as volume and viscosity of the resulting composition should also be considered. The solvents, or diluents, used for such compositions include water, possibly PBS (phosphate buffered saline), or saline itself, or other possible carriers or excipients. The immunogens of the present invention may also be contained in artificially created structures such as liposomes, which structures may or may not contain additional molecules, such as proteins or polysaccharides, inserted in the outer membranes of said structures and having the effect of targeting the liposomes to particular areas of the body, or to particular cells within a given organ or tissue. Such targeting molecules may commonly be some type of immunoglobulin. Antibodies may work particularly well for targeting the liposomes to tumor cells.

[0090] The present invention is also directed to a vaccine in which a peptide or polypeptide or active fragment of the present invention is delivered or administered in the form of a polynucleotide coding the peptide or polypeptide or active fragment, whereby the peptide or polypeptide or active fragment is produced in vivo. The polynucleotide may be included in a suitable expression vector and combined with a pharmaceutically acceptable carrier.

[0091] The vaccine compositions may be used prophylactically for the purposes of preventing cancer in an individual that does not currently have cancer, or they may be used to treat an individual that already has cancer. Prevention relates to a process of prophylaxis in which the individual is immunized prior to the induction or onset of cancer. For example, individuals with a history of severe sunburn and at risk for developing melanoma, might be immunized prior to the onset of the disease. Alternatively, individuals that already have cancer can be immunized with the antigens of the present invention so as to stimulate an immune response that would be reactive against the cancer. A clinically relevant immune response would be one in which the cancer partially or completely regresses and is eliminated from the patient, and it would also include those responses in which the progression of the cancer is blocked without being eliminated.

[0092] In one embodiment, the present invention provides methods of screening for agents, small molecules, or proteins that interact with polypeptides comprising a sequence selected from the group consisting of SEQ ID NO: 1 through 69 or bioactive fragments thereof. The invention encompasses both in vivo and in vitro assays to screen small molecules, compounds, recombinant proteins, peptides, nucleic acids, antibodies, etc., which bind to or modulate the

activity of antigen peptides and are thus useful as therapeutic or diagnostic markers for cancer.

[0093] As used herein, modulating the activity of an antigen peptide includes interfering or altering the antigen peptide ligand binding properties.

EXAMPLES

[0094] The invention is now described with reference to the following examples. These examples are provided for the purpose of illustration only and the invention should in no way be construed as being limited to these examples, but rather should be construed to encompass any and all variations which become evident as a result of the teachings provided herein.

Example 1

[0095] Phosphorylated peptides were extracted from melanoma cell lines that express either or both of HLA-B7 and HLA-A*0201, identified by mass spectrometry to be differentially displayed on melanoma versus a control B cell line, and then sequenced. The peptides were identified through the following procedure. Two melanoma cell lines and one B lymphoblastoid cell line were extracted with detergent containing buffer, and HLA-A*0201 class I MHC molecules were purified by immunoaffinity chromatography. Peptides were separated from the MHC molecules by extraction in acid and filtration through a 5000 dalton cut-off filter. Phosphopeptides were identified through analysis by microcapillary reversed phase high performance liquid chromatography tandem mass spectrometry. Sequences were determined from an analysis of collision activated dissociation spectra. Source proteins were determined from a search of protein and DNA databases. SEQ ID NOs: 1 through 69 were identified (see Table 1). One of ordinary skill in the art would appreciate that such techniques can be modified and that other techniques are known to aid in identifying peptides of the invention.

[0096] These peptides represent potential targets of an immune response, either cytotoxic T lymphocyte or antibody, that could be used for either therapeutic or diagnostic purposes. While the peptides have been identified on melanoma cells, they may also be expressed on other kinds of cancer cells and the invention covers their use for cancers other than melanoma. The binding of these peptides to class I MHC molecules is necessary for their recognition by cytotoxic T lymphocytes, while recognition by antibody could occur in either a class I MHC associated or free form. The invention comprises these peptides, together with structural modifications that retain or enhance the ability: 1) to bind to MHC molecules or; 2) to stimulate an immune response or; 3) to be recognized by a product of an immune response.

[0097] The binding of the peptides to class I MHC molecules can be determined by 2-3 anchor residues within the sequence, and these peptides are generally 8-11 residues in length. For example, peptides that bind to HLA-B7 generally contain a Pro at the second position, a hydrophobic aliphatic residue at the carboxyl terminus, and are 9 residues long. However, some peptides have been identified that do not contain one of these anchor residues, and peptides up to 14 residues in length have also been identified. It has also

been shown that other residues in a sequence may augment or diminish binding, despite the presence or absence of appropriate anchor residues.

[0098] The sequences displayed on a cell are derived from proteolysis of proteins made inside the cell and transported into the lumen of the endoplasmic reticulum. The specificities of the proteases and the transporter are poorly understood, and the sequences of all proteins made by human cells, based on data from the Human Genome Project, are very incomplete. In addition, proteins may undergo modifications such as phosphorylation. However, relatively few of these sites have been identified. Thus, there is a large universe of potential peptides displayed by any given MHC molecule based on the sequences of all proteins made by the cell and the distribution of appropriate anchor motifs within those sequences. However, the exact peptides displayed by a cell are not readily predictable. The direct identification of such peptides by mass spectrometry provides information that cannot be otherwise obtained at present without undue effort.

[0099] Different MHC molecules may have similar anchor preferences, leading to the possibility that a peptide associated with, for example, HLA-A*0201, may also be displayed by HLA-A3. The existence of such “supertypes” means that the peptides identified above in association with one MHC molecule may be presented by others, broadening their utility as antigens.

Example 2

[0100] CTL specific for two of the antigen peptides were generated by long term culture with the peptides. Two CTL lines specific for the antigen peptide GLLGpSPVRA, lines 6850 and 6960, SEQ ID NO: 13, and two CTL lines specific for the antigen peptide RVApSPTSGV, SEQ ID NO: 14, lines 5183 and 63 were used to detect these two antigen peptides on cancer cells. The phosphopeptide-specific CTL (50,000 CTL/well) were incubated 24 hours with the following cancer cell lines or EBV-transformed B lymphoblastoid cell lines (BLCL) (25,000 cells/well): COV413.AAD. A4 ovarian carcinoma, DM331.AAD.A4 and SLM2.AAD. A1 melanomas, MCF7.AAD.A2 and MDAMB231.AAD breast carcinomas, and JY EBVBLCL. Supernatants were harvested 24 hours later and evaluated for the presence of murine IFN γ (produced by murine CTL lines) by ELISA (eBioscience Ready-Set-go murine IFN γ ELISA kit). As a positive control, cancer cells were pulsed with the specific antigen peptide (1 μ M) to show that they are capable of presenting exogenously added peptide. In FIG. 1A, two phosphopeptide-specific CTL cell lines, 6850 and 6960, specific for the phosphopeptide GLLGpSPVRA, recognize the phosphopeptide on all the cancer cell lines, but not the control cell line. In FIG. 1B, two phosphopeptide-specific CTL cell lines, 5183 and 63, specific for the phosphopeptide RVApSPTSGV, recognize the phosphopeptide on all the cancer cell lines, but not the control cell line.

Example 3

[0101] Over-expression of select phospho-proteins is a hallmark of malignant transformation.

[0102] Due to the low expression levels of phosphopeptides by the MHC class I pathway, identification of immunologically relevant phospho-peptides is difficult.

[0103] Secreted WIC molecule technology allows for an increase in the amounts of WIC class I peptides available for analysis.

[0104] Identification of WIC class I phosphopeptides that are unique to tumor cells provides an avenue to the production of peptide-based cancer vaccines and biomarkers

[0105] Materials, Methods, and Results

[0106] Table 2 as set forth in FIG. 2 presents phosphopeptides of the present invention on breast cancer by the Class I WIC Molecule, in particular, on the HLA B*0702 allele. Table 3, as set forth below, summarizes “Source proteins for peptides identified from analyses of samples from breast cancer and immortalized cell lines and their expression in non-tumorigenic control cell line 184B5 and the breast cancer cell lines BT20 and MCF-7”.

[0107] FIG. 3 graphically demonstrates

[0108] The MHC class I pathway—

[0109] a) Protein is marked for degradation

[0110] b) The proteasome digests the peptides into smaller fragments

[0111] c) Peptides are transported into the ER via the transporter associated protein (TAP)

[0112] d) The MHC molecule with peptide loaded is transported to the surface

[0113] FIG. 4 schematically illustrates “Sample analysis overview. Cells are grown in culture and the cell supernatant is collected. MHC molecules are immunoaffinity purified and peptides are eluted under acidic conditions. Peptides are esterified, enriched for phospho-peptides through IMAC and/or TiO₂ and analyzed via C18 micro electrospray LC/MS with high resolution full MS and low resolution MS/MS”.

[0114] FIG. 5 describes the B*0702 motif showing amino acid anchors.

[0115] FIG. 6 shows the total number of peptides in IMAC and TiO₂ experiments and schematically depicts the overlap between the peptides identified in an IMAC analysis of 184B5 and a TiO₂ analysis. The IMAC analysis was performed twice, once with ETD fragmentation (d.d. top 6) and once with CAD (d.d. top 10) fragmentation. The TiO₂ analysis was performed in a single run with toggled ETD/CAD fragmentation. We investigated each MS analysis for the presence of all identified sequences using the calculated accurate mass value.

[0116] The MHC class I pathway (FIG. 3) is classically responsible for presenting endogenous peptides to the immune system. Each MHC molecule has a binding pocket which can only accept peptides with narrowly defined motifs. The MHC molecule with peptide loaded in the binding groove is transported to the surface where the MHC molecule remains anchored to the membrane. Phosphopeptides can be processed and displayed by the MHC class I pathway.

[0117] Secreted MHC Molecules

[0118] A cDNA clone of a specific MEW molecule is altered to remove the regions that code for the transmembrane and cytoplasmic portions of the protein

[0119] Cloned into a plasmid expression vector

[0120] Cell produce endogenous MHC molecules as well as the secreted MEW molecules (sHLA)

[0121] sHLA are released into the cell culture medium as they lack the portion of the protein responsible for anchoring them to the membrane

[0122] The inventors have demonstrated that sHLA molecules successfully present phospho-peptides and that they display a similar repertoire of phospho-peptides as endogenous HLA molecules.

[0123] Phosphopeptide Analyses

[0124] Breast cancer cell lines (BT20, MCF7) and an immortalized non-malignant mammary tissue cell line (184B5) were transfected with the B*0702 sHLA cDNA1

[0125] FIG. 5 shows the motif for peptides which are presented by B*0702 MHC molecules

[0126] Samples were analyzed with both ETD fragmentation and CAD fragmentation on either an Orbitrap or FT-ICR instrument, which were in-house custom modified for front end electron transfer dissociation

[0127] Species of interest were identified by a combination of algorithm searching (OMSSA), d0/d3 methyl ester pair detection and CAD neutral loss detection

[0128] Peptide sequences were determined by manual confirmation of search data and de novo sequencing utilizing both CAD and ETD data where necessary

[0129] Source proteins were determined by BLAST2 search, and a single protein identification was determined from UniProt 3

[0130] Due to issues with non-specific binding having a negative effect on the ability to identify peptides in IMAC experiments, TiO2 was considered as an alternative. FIG. 4 shows the total number of peptides in IMAC and TiO2 experiments. The level of non-specific binding for non-phospho peptides was reduced substantially in the TiO2 experiment, however recovery of the angiotensin II phosphate (DRVyIHPF) standard peptide was much lower in the TiO2 experiment.

Conclusions—Example 3

[0131] 104 phospho-peptides have been identified, deriving from 84 different source proteins

[0132] 22 phospho-peptides were only detected in samples deriving from breast cancer cell lines

[0133] 2 peptides were identified in both cancer cell lines but not in the control cell line

[0134] Peptides from source proteins known to be involved in tumors have been identified

[0135] In a complementary TiO2/IMAC experiment, 34 peptides were common to both analyses, 14 peptides were unique to the IMAC experiment and 35 peptides were unique to the TiO2 experiment

[0136] Based on the disclosure provided herein, the present invention encompasses compositions and methods useful for submitting/testing specific peptides of immunological interest for binding and T-cell recognition assays. The present invention further encompasses compositions and methods to apply the sHLA technology to cell lines with known phospho-peptide expression patterns and the present invention has application to cells with non-ideal HLA alleles and/or cells with poor growth.

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TABLE 3

Uniprot protein identification	184B5	BT20	MCF7	Uniprot protein identification	184B5	BT20	MCF7
A-kinase anchor protein 13	X	X		Unique peptide, unidentified source 6	X	X	X
Anky corbin	X			Unique peptide, unidentified source 7	X		
Arginine- glutamic acid dipeptide repeats protein		X		Unique peptide, unidentified source 8	X	X	
Ataxin-2	X	X	X	Neuron navigator 1	X		
Ataxin-2 - with point mutation	X	X		Nuclear factor erythroid 2-related factor 1	X		
Ataxin-2-like protein	X	X		Nuclear receptor coactivator 1	X		X
AT-rich interactive domain- containing protein 1A	X	X		Numb-like protein	X	X	X
Beta- adrenergic receptor kinase 1	X	X	X	Partner and localizer of BRCA2		X	
Butyrate response factor 2	X	X		Phosphatidylinositol 4,5-bisphosphate 5phosphatase A		X	
Cdc42- interacting protein 4	X	X		Plakophilin-3	X	X	

TABLE 3-continued

Uniprot protein identification	184B5	BT20	MCF7	Uniprot protein identification	184B5	BT20	MCF7
Centrosomal protein of 55 kDa	X	X		Plakophilin-3	X	X	
Chondroitin sulfate synthase 2		X		Plakophilin-3	X		
Chromatin assembly factor 1 subunit A	X		X	Pleckstrin homology domain- containing family G	X		
Coiled-coil domain-containing protein 6		X	X	Pleckstrin homology-like domain family B member 1		X	
Cullin-4A	X	X		Proline-rich protein 11			X
Death-associated protein kinase 1	X			proteasome non- ATPase regulatory subunit 4	X		
DENN domain- containing protein 4C		X		Protein AF-17	X		
DNA replication factor Cdt1	X			Protein ajuba	X		
DNA-binding protein inhibitor ID-2	X			Protein TANC2	X	X	
DNA-directed RNA polymerase 1 subunit RPA2		X		Putative phosphoserine phosphatase-like protein	X		
Dynamin-1- like protein	X			Rab11 family- interacting protein 1	X		
E3 ubiquitin- protein ligase	X			Ras-associated and pleckstrin homology	X		X
NEDD4-like	X			domains-containing protein 1	X		X
E3 ubiquitin- protein ligase				Ras-like protein family member 11A	X		X
NEDD4-like E3 ubiquitin- protein ligase				Receptor expression- enhancing protein 4			X
UBR5				Receptor- interacting serine/threonine- protein kinase 4			X
Eukaryotic translation initiation factor 4B				RelA-associated inhibitor			X
General transcription factor II-I				Retrotransposon- derived protein PEG10	X		X
Helicase SKI2W	X			Retrotransposon- derived protein PEG10			X
Histone-lysine N-methyltransferase				Rho GTPase- activating protein 30			X
SETD2				Rho GTPase- activating protein 30			X
Homeobox protein TGIF2	X			RNA pseudouridylate synthase domain			X
Hypoxia- inducible factor 1-alpha				Serine/arginine repetitive matrix protein 2			X
Krueppel-like factor 10					X		
Latent- transforming growth factor beta-binding protein 2	X						

TABLE 3-continued

Uniprot protein identification	184B5	BT20	MCF7	Uniprot protein identification	184B5	BT20	MCF7
Leucine zipper protein 1	X	X	X	Serine/threonine- protein kinase SIK1	X		X
Lipolysis- stimulated lipoprotein receptor	X	X	X	Serine/threonine- protein kinase tousled-like 1	X	X	
MAP7 domain- containing protein 1	X	X		Signal-induced proliferation- associated 1-like protein 1	X		
MICAL-like protein 1	X			Ski oncogene	X		
MICAL-like protein 2	X	X		Splicing factor, arginine/serine-rich 7	X	X	X
MICAL-like protein 2	X	X		Sterol regulatory element-binding protein	X	X	
Microtubule- actin cross- linking factor 1	X			Targeting protein for Xklp2		X	
Mitogen-activated protein kinase kinase kinase 11		X	X	Tensin-4	X		
Mitogen- activated protein kinase kinase kinase 11		X		Thyroid hormone receptor-associated protein 3	X		
Myocyte- specific enhancer factor 2D		X		Transcription factor HIVEP2	X		
Myocyte-specific enhancer factor 2D		X		Transformer-2 protein homolog beta		X	
Myocyte- specific enhancer factor 2D	X			Transient receptor potential cation channel	X		
Myosin regulatory light chain 12A	X	X		TSC22 domain family protein 4	X		
Unique peptide, unidentified source 1	X		X	Ubiquitin carboxyl- terminal hydrolase 43	X		
Unique peptide, unidentified source 2	X			Uncharacterized protein Clorf106		X	
Unique peptide, unidentified source 3	X		X	Uncharacterized protein C6orf64	X	X	
Unique peptide, unidentified source 4	X			Uncharacterized protein CXorf66	X		
Unique peptide, unidentified source 5	X			Uncharacterized protein KIAA0819	X		
YTH domain- containing protein 1		X		Uncharacterized protein KIAA1310	X	X	
Zinc finger protein 335	X			Yorkie homolog		X	
	X					X	

[0140] The disclosures of each and every patent, patent application, and publication cited herein are hereby incorporated by reference herein in their entirety. One of skill in the art will appreciate that the superiority of the compositions and methods of the invention relative to the compositions and methods of the prior art are unrelated to the physiological accuracy of the theory explaining the superior results.

[0141] Headings are included herein for reference and to aid in locating certain sections. These headings are not intended to limit the scope of the concepts described 10 therein under, and these concepts may have applicability in other sections throughout the entire specification.

[0142] The previous description of the disclosed embodiments is provided to enable any person skilled in the art to make or use the present invention. Various modifications to these embodiments will be readily apparent to those skilled in the art, and the generic principles defined herein may be applied to other embodiments without departing from the spirit or scope of the invention. The appended claims are intended to be construed to include all such embodiments and equivalent variations. Accordingly, the present invention is not intended to be limited to the embodiments shown herein but is to be accorded the widest scope consistent with the principles and novel features disclosed herein.

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RQDSTPGKVF L		11
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MOD_RES	5	
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source	1..10	
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	organism = Homo sapiens	
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VLKGSRSSEL		10
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SEQUENCE: 8 ILKSPEIQRA		10
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source	1..13 mol_type = protein organism = Homo sapiens	
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source	1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 11 KLLSSAQRTL		10
SEQ ID NO: 12 FEATURE MOD_RES	moltype = AA length = 10 Location/Qualifiers 4 note = Phosphorylated residue	
source	1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 12 YLDSGIHSGA		10
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-continued

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	organism = Homo sapiens	
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	organism = Homo sapiens	
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SEQ ID NO: 19	moltype = AA length = 8	
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MOD_RES	8	
	note = Leu or Ile	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 19		
LMFSVTSX		8
SEQ ID NO: 20	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	

-continued

SEQUENCE: 20		
SLQPRSHSV		9
SEQ ID NO: 21	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 21		
RLLSPLSSA		9
SEQ ID NO: 22	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	3	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 22		
SMTRSPPRV		9
SEQ ID NO: 23	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 23		
RQISQDVKL		9
SEQ ID NO: 24	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 24		
RQASIELPSM		10
SEQ ID NO: 25	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 25		
RQASIELPSM AV		12
SEQ ID NO: 26	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 26		
SLLTFWNL		8
SEQ ID NO: 27	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	5	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 27		
KVQVTSLSV		9

-continued

SEQ ID NO: 28	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 28		
VLLSPVPEL		9
SEQ ID NO: 29	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 29		
RLQSTSERL		9
SEQ ID NO: 30	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 30		
TLASPSVFKS T		11
SEQ ID NO: 31	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 31		
RTYSGPMNKV		10
SEQ ID NO: 32	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	7	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 32		
KLIDIVSSQK V		11
SEQ ID NO: 33	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 33		
RTFSPTYGL		9
SEQ ID NO: 34	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 34		
ALYSPAQPSL		10

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SEQ ID NO: 35	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 35		
RQISQDVKL		9
SEQ ID NO: 36	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 36		
AVVSPPALHN A		11
SEQ ID NO: 37	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 37		
RLDSYVRS		8
SEQ ID NO: 38	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
MOD_RES	7	
	note = Phosphorylated residue	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 38		
HPKRSVSL		8
SEQ ID NO: 39	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 39		
LPASPRARL		9
SEQ ID NO: 40	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 40		
HPRSPTPTL		9
SEQ ID NO: 41	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 41		
YPSSPRKAL		9

-continued

SEQ ID NO: 42	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 42		
KPRSPPRAL		9
SEQ ID NO: 43	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	5	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 43		
RPAKSMDSL		9
SEQ ID NO: 44	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 44		
KPRSPVVEL		9
SEQ ID NO: 45	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
MOD_RES	9	
	note = Leu or Ile	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 45		
RSRSPRPAX		9
SEQ ID NO: 46	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 46		
APRSPPPSRP		10
SEQ ID NO: 47	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 47		
RPSGRRESL		9
SEQ ID NO: 48	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	5	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 48		
RPRRSSTQL		9

-continued

SEQ ID NO: 49	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 49		
RPRSPPPRAP		10
SEQ ID NO: 50	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 50		
RPRSPGSNSK V		11
SEQ ID NO: 51	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 51		
GAQPGRHSV		9
SEQ ID NO: 52	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 52		
SPRSITSTP		9
SEQ ID NO: 53	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 53		
KARSPGRAL		9
SEQ ID NO: 54	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
MOD_RES	9	
	note = Leu or Ile	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 54		
SPRSPGRSX		9
SEQ ID NO: 55	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 55		
LPRGSSPSVL		10

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SEQ ID NO: 56	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 56		
FPHSLLSVI		9
SEQ ID NO: 57	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 57		
SPRERSPAL		9
SEQ ID NO: 58	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 58		
APRRYSSSL		9
SEQ ID NO: 59	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 59		
RTFSPTYGL		9
SEQ ID NO: 60	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 60		
SPFKRQLSL		9
SEQ ID NO: 61	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 61		
SPRSPSTTYL		10
SEQ ID NO: 62	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
MOD_RES	6	
	note = Lys or Gln	
MOD_RES	9	
	note = Lys or Gln	
MOD_RES	10	
	note = Leu or Ile	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	

-continued

SEQUENCE: 62		
RPASPXRAXX		10
SEQ ID NO: 63	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
source	note = Phosphorylated residue	
	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 63		
KLFPDTPLAL		10
SEQ ID NO: 64	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
source	note = Phosphorylated residue	
	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 64		
RLLSPLSSA		9
SEQ ID NO: 65	moltype = AA length = 7	
FEATURE	Location/Qualifiers	
MOD_RES	4	
source	note = Phosphorylated residue	
	1..7	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 65		
RLDSYVR		7
SEQ ID NO: 66	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
source	note = Phosphorylated residue	
	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 66		
RQASIELPSM		10
SEQ ID NO: 67	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
source	note = Phosphorylated residue	
	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 67		
KLMSPKADV K L		11
SEQ ID NO: 68	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	3	
source	note = Phosphorylated residue	
	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 68		
SMTRSPPRV		9
SEQ ID NO: 69	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
source	note = Phosphorylated residue	
	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 69		
RLFSKELRC		9

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SEQ ID NO: 70	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 70		
APRKGSFSAL M		11
SEQ ID NO: 71	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 71		
ALDSGASLLH L		11
SEQ ID NO: 72	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 72		
APLARASSL		9
SEQ ID NO: 73	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 73		
APRAPASPL AL		12
SEQ ID NO: 74	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 74		
APRKGSFSAL		10
SEQ ID NO: 75	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 75		
APSVRSLSL		9
SEQ ID NO: 76	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 76		
APSVRSLSL		9

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SEQ ID NO: 77	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 77		
FPHSLLSVI		9
SEQ ID NO: 78	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 78		
GPRPGSPSAL		10
SEQ ID NO: 79	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 79		
GPRSPPVTL		9
SEQ ID NO: 80	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
MOD_RES	3	
	note = Phosphorylated residue	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 80		
GRTGLPDL		8
SEQ ID NO: 81	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
MOD_RES	7	
	note = Phosphorylated residue	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 81		
HPKRSVSL		8
SEQ ID NO: 82	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 82		
HPRSPNVLSV		10
SEQ ID NO: 83	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 83		
HPRSPPTPL		9

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SEQ ID NO: 84	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 84		
KAFSPVRSV		9
SEQ ID NO: 85	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 85		
KARSPGRAL		9
SEQ ID NO: 86	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 86		
KPESRRSSLL		10
SEQ ID NO: 87	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 87		
KPLIRSQSL		9
SEQ ID NO: 88	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 88		
KPRPPPLSP		9
SEQ ID NO: 89	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 89		
KPRSPDHVL		9
SEQ ID NO: 90	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 90		
KPRSPPRAL		9

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SEQ ID NO: 91	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 91		
KPRSPPRALV L		11
SEQ ID NO: 92	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 92		
KPRSPVVEL		9
SEQ ID NO: 93	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 93		
KPSSPRGSLL		10
SEQ ID NO: 94	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	5	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 94		
KRPESPPSI		9
SEQ ID NO: 95	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 95		
LPASPRARL		9
SEQ ID NO: 96	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 96		
LPIFSRLSI		9
SEQ ID NO: 97	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 97		
LPKSPPYTAF		10

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SEQ ID NO: 98	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 98		
LPRGSSPSVL		10
SEQ ID NO: 99	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 99		
LPRMISHSEL		10
SEQ ID NO: 100	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 100		
PARSPVTEI		9
SEQ ID NO: 101	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 101		
QPSFPSVLPA		10
SEQ ID NO: 102	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 102		
RAHSSPASL		9
SEQ ID NO: 103	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 103		
RAPSPSSRM		9
SEQ ID NO: 104	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 104		
RARGISPIVF		10

-continued

SEQ ID NO: 105	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 105		
RLLSPQQPAL		10
SEQ ID NO: 106	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	5	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 106		
RPAKSMDSL		9
SEQ ID NO: 107	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 107		
RPASAGAML		9
SEQ ID NO: 108	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 108		
RPASARAQPG L		11
SEQ ID NO: 109	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 109		
RPASPAAKL		9
SEQ ID NO: 110	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 110		
RPASPGPSL		9
SEQ ID NO: 111	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 111		
RPASPQRAQL		10

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SEQ ID NO: 112	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 112		
RPASPSLQL		9
SEQ ID NO: 113	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 113		
RPASPSLQLL		10
SEQ ID NO: 114	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 114		
RPASRFEVL		9
SEQ ID NO: 115	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 115		
RPDSPTRPTL		10
SEQ ID NO: 116	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 116		
RPDSRLGKTE L		11
SEQ ID NO: 117	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 117		
RPFARSHSF		9
SEQ ID NO: 118	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	10	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 118		
RPFHGISTVS L		11

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SEQ ID NO: 119	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 119		
RPFSPREAL		9
SEQ ID NO: 120	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 120		
RPHTPTGIYM		10
SEQ ID NO: 121	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 121		
RPISPGLSY		9
SEQ ID NO: 122	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 122		
RPNSPSPTAL		10
SEQ ID NO: 123	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 123		
RPPSPGPVL		9
SEQ ID NO: 124	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 124		
RPPSSEFLDL		10
SEQ ID NO: 125	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 125		
RPQRATSNVF		10

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SEQ ID NO: 126	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 126		
RPRARSVDAL		10
SEQ ID NO: 127	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 127		
RPRLSSTNSS RF		12
SEQ ID NO: 128	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 128		
RPRPVSPSSL		10
SEQ ID NO: 129	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 129		
RPRSLSSPTV		10
SEQ ID NO: 130	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 130		
RPRSLSSPTV TL		12
SEQ ID NO: 131	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 131		
RPRSPGSNSK V		11
SEQ ID NO: 132	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 132		
RPRSPNMQDL		10

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SEQ ID NO: 133	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 133		
RPRSPRENSI		10
SEQ ID NO: 134	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 134		
RPRSPRQNSI		10
SEQ ID NO: 135	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 135		
RPRSTSQSIV SL		12
SEQ ID NO: 136	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 136		
RPSSLPDL		8
SEQ ID NO: 137	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	3	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 137		
RPSSPALYF		9
SEQ ID NO: 138	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 138		
RPTSRLNRL		9
SEQ ID NO: 139	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 139		
RPVSPFQEL		9

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SEQ ID NO: 140	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 140		
RPVSPGKDI		9
SEQ ID NO: 141	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 141		
RPVTPVSDL		9
SEQ ID NO: 142	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 142		
RPWSPAUSA		9
SEQ ID NO: 143	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 143		
RPYSPSQYAL		10
SEQ ID NO: 144	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 144		
RSRSPRPAL		9
SEQ ID NO: 145	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 145		
RTRSPSPTL		9
SEQ ID NO: 146	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
MOD_RES	5	
	note = Phosphorylated residue	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 146		
SKRGYIGL		8

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SEQ ID NO: 147	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 147		
SPASPKISL		9
SEQ ID NO: 148	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 148		
SPFKRQLSL		9
SEQ ID NO: 149	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 149		
SPGSPRPAL		9
SEQ ID NO: 150	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 150		
SPKSPTAAL		9
SEQ ID NO: 151	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 151		
SPLTKSISL		9
SEQ ID NO: 152	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 152		
SPRERSPAL		9
SEQ ID NO: 153	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	7	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 153		
SPRPPNSPSI		10

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SEQ ID NO: 154	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	5	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 154		
SPRRSLGLAL		10
SEQ ID NO: 155	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	5	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 155		
SPRRSRISL		10
SEQ ID NO: 156	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 156		
SPRSITSTP		9
SEQ ID NO: 157	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 157		
SPRSPGKPM		9
SEQ ID NO: 158	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 158		
SPRSPGRSL		9
SEQ ID NO: 159	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 159		
SPRSPSTTYL		10
SEQ ID NO: 160	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 160		
SPVSPMKEL		9

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SEQ ID NO: 161	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 161		
SPVSTRPLEP		10
SEQ ID NO: 162	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 162		
SRSSSVLSL		9
SEQ ID NO: 163	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 163		
SVRSLSLSL		9
SEQ ID NO: 164	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 164		
TPRSPPLGL		9
SEQ ID NO: 165	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 165		
TPRSPPLGLI		10
SEQ ID NO: 166	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	7	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 166		
TQSSGKSSV		9
SEQ ID NO: 167	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 167		
VPKSPAFAL		9

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SEQ ID NO: 168	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 168		
VPTSPKSSL		9
SEQ ID NO: 169	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 169		
VPVSPGQQL		9
SEQ ID NO: 170	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	7	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 170		
YPSFRRSSL		9
SEQ ID NO: 171	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 171		
YPSSPRKAL		9
SEQ ID NO: 172	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
MOD_RES	4	
	note = Phosphorylated residue	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 172		
DRVYIHPF		8
SEQ ID NO: 173	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
MOD_RES	8	
	note = Phosphorylated residue	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 173		
RPFARSHSF		9
SEQ ID NO: 174	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
MOD_RES	6	
	note = Phosphorylated residue	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 174		
RPYSPSQYAL		10

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SEQ ID NO: 175	moltype = AA length = 10
FEATURE	Location/Qualifiers
MOD_RES	5
	note = Phosphorylated residue
source	1..10
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 175	
SPVSTRPLEP	10

1. An isolated phosphopeptide of 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 amino acids comprising a sequence selected from the group consisting of SEQ ID NOs: 70-171 or a sequence at least 90% identical thereto.
2. The isolated phosphopeptide of claim 1, wherein said sequence is selected from group consisting of SEQ ID NOs: 84, 87, 96, 102, 118, 121, 125, 126, 128, 132, 138, 145, 155, 164, and 165 or a sequence of at least 90% identical thereto.
3. The isolated phosphopeptide of claim 1, wherein said sequence is selected from the group consisting of SEQ ID NOs: 118, 121, 132, 145, 164, and 165 or a sequence of at least 90% identical thereto.
4. A composition comprising one or more phosphopeptides of claim 1 and a pharmaceutically acceptable carrier wherein the number is selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 and 30.
5. The composition of claim 4, wherein said composition has the ability to stimulate a T cell mediated immune response to at least one of said phosphopeptides.
6. The composition of claim 4, comprising a peptide capable of binding to the HLA-B*0702 allele on the WIC class I molecule.
7. The composition of claim 4, wherein the composition is capable of increasing the 5-year survival rate of breast cancer patients treated with the composition relative to average 5-year survival rates that could have been expected without treatment with the composition.
8. The composition of claim 1, wherein said composition comprises one or more phosphopeptides comprising a sequence selected from the group consisting of SEQ ID NOs: 84, 87, 96, 102, 118, 121, 125, 126-, 128, 132, 138, 145, 155, 164, and 165 and a pharmaceutical carrier.
9. An in vitro population of dendritic cells comprising the composition of claim 4.
10. An antibody or antibody-like molecule that specifically binds to a phosphopeptide comprising the sequence selected from the group consisting of SEQ ID NOs: 70-171.

11. The antibody or antibody-like molecule of claim 10, wherein the phosphopeptide comprises a sequence selected from the group consisting of SEQ ID NOs: 84, 87, 96, 102, 118, 121, 125, 126, 128, 132, 138, 145, 155, 164, and 165.
12. The antibody or antibody-like molecule of claim 10, wherein the antibody or antibody-like molecule is polyclonal, monoclonal, chimeric antibody, Fab fragments, or fragments produced by a Fab expression library or a T-cell receptor.
13. A composition comprising the antibody or antibody-like molecule of claim 10, further comprising a pharmaceutically acceptable carrier.
14. The composition of claim 13, further comprising an adjuvant.
15. A method of inducing an immunogenic response comprising administering to a patient in need thereof a dose of the composition of claim 4.
16. A method of treating or preventing cancer comprising administering to a patient in need thereof a dose of the composition of claim 4.
17. A method of treating or preventing breast cancer comprising administering to a patient in need thereof a dose of a composition comprising an isolated phosphopeptide comprising a sequence selected from the group consisting of SEQ ID NOs:70-171 in combination with a pharmaceutically acceptable carrier.
18. The method of claim 17, wherein the isolated phosphopeptide comprises a sequence selected from the group consisting of SEQ ID NO: 84, 87, 96, 102, 118, 121, 125, 126, 128, 132, 138, 145, 155, 164, and 165.
19. A method of treating or preventing breast cancer comprising administering to a patient in need thereof the population of the dendritic cells of claim 9 in combination with a pharmaceutically acceptable carrier.
20. A population of T-cells specific for a phosphopeptide of claim 1.

* * * * *