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SONG et al.(10) **Pub. No.: US 2023/0046543 A1**(43) **Pub. Date: Feb. 16, 2023**(54) **NOVEL PEPTIDES AND COMBINATION OF
PEPTIDES FOR USE IN IMMUNOTHERAPY
AGAINST LUNG CANCER, INCLUDING
NSCLC, SCLC AND OTHER CANCERS**(71) Applicant: **Immatics Biotechnologies GmbH**,
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Harpreet SINGH, Tuebingen (DE)(21) Appl. No.: **17/934,673**(22) Filed: **Sep. 23, 2022****Related U.S. Application Data**(63) Continuation of application No. 17/929,347, filed on
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No. 17/877,515, filed on Jul. 29, 2022, which is a
continuation of application No. 17/860,600, filed on
Jul. 8, 2022, which is a continuation of application
No. 17/371,755, filed on Jul. 9, 2021, which is a
continuation of application No. 17/227,885, filed on
Apr. 12, 2021, now Pat. No. 11,168,122, which is a
continuation of application No. 16/913,788, filed on
Jun. 26, 2020, now Pat. No. 11,001,616, which is a
continuation of application No. 16/026,707, filed on
Jul. 3, 2018, now Pat. No. 10,800,823.(60) Provisional application No. 62/529,758, filed on Jul.
7, 2017.(30) **Foreign Application Priority Data**

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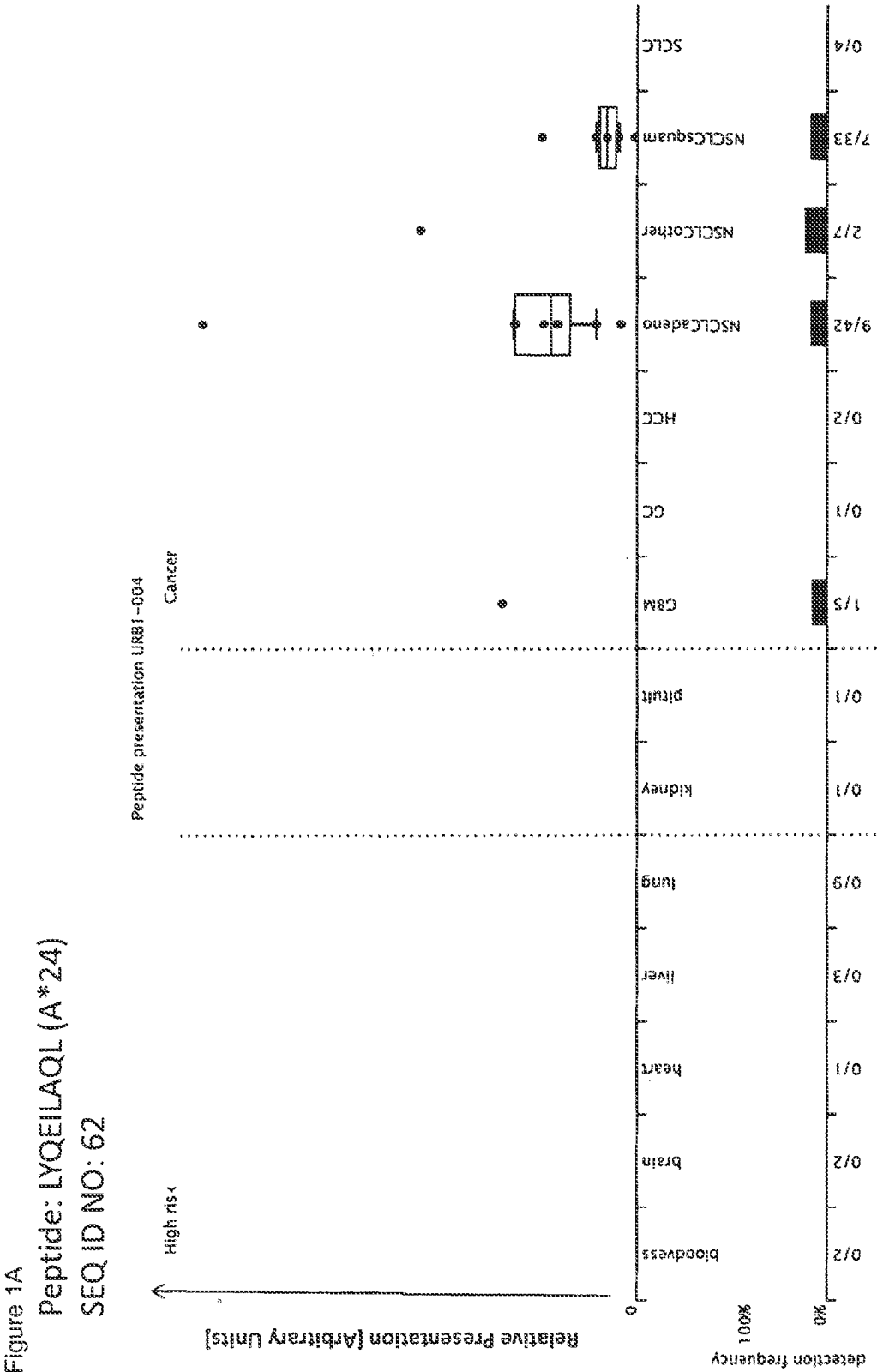
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C07K 7/06 (2006.01)
A61K 35/17 (2006.01)
C07K 14/74 (2006.01)
C12N 15/10 (2006.01)**C07K 16/28** (2006.01)**G01N 33/574** (2006.01)**C07K 16/30** (2006.01)**C07K 14/54** (2006.01)**C12N 15/115** (2006.01)**C07K 14/725** (2006.01)**C12N 5/0783** (2006.01)**A61K 39/00** (2006.01)**A61P 35/00** (2006.01)(52) **U.S. Cl.**CPC **C07K 14/4748** (2013.01); **C07K 7/06**
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(2013.01); **C07K 16/30** (2013.01); **C07K**
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C07K 2319/00 (2013.01); **A61K 2039/572**
(2013.01); **C12N 2501/50** (2013.01); **A61K**
38/00 (2013.01)

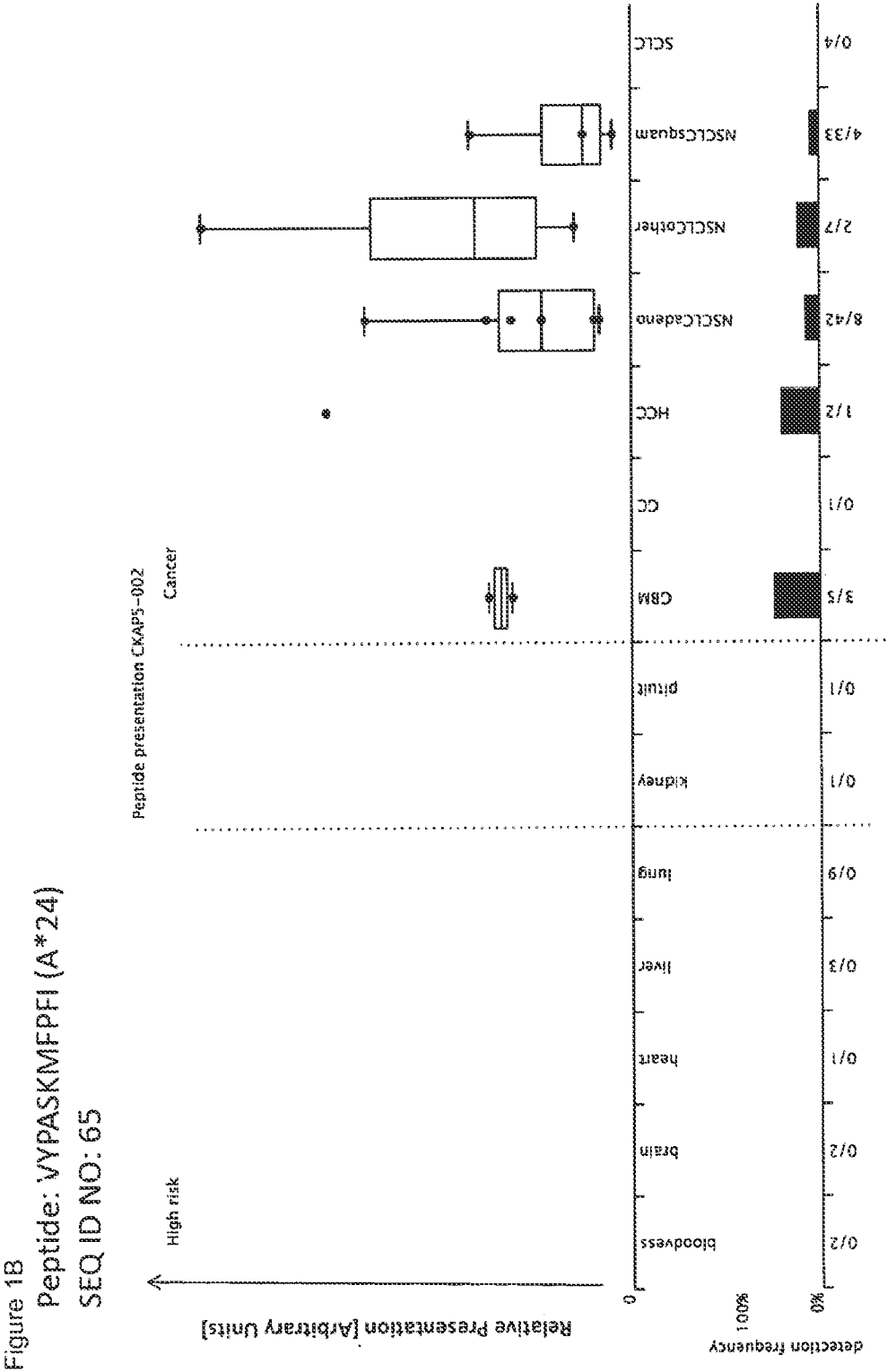
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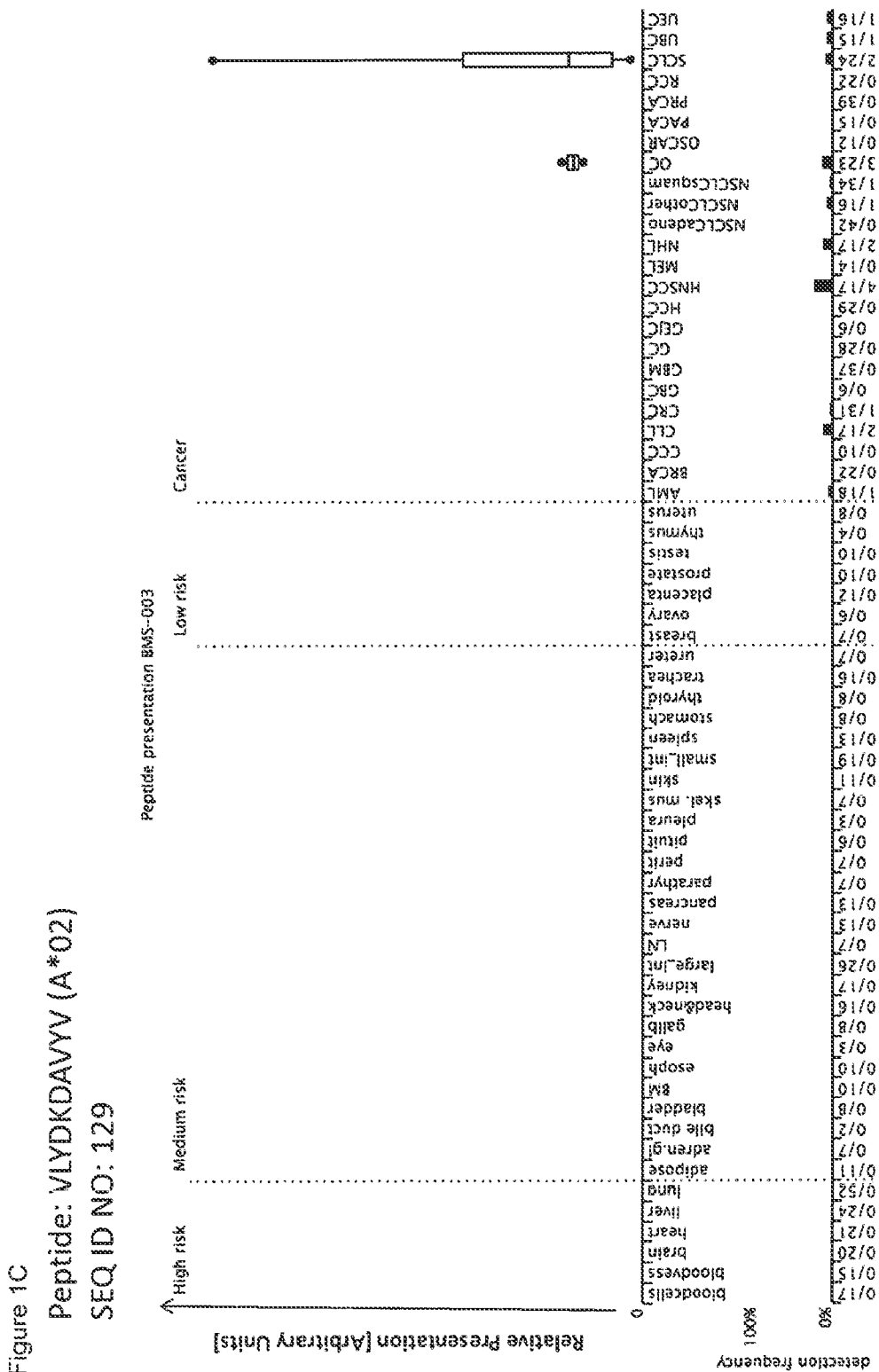
ABSTRACT

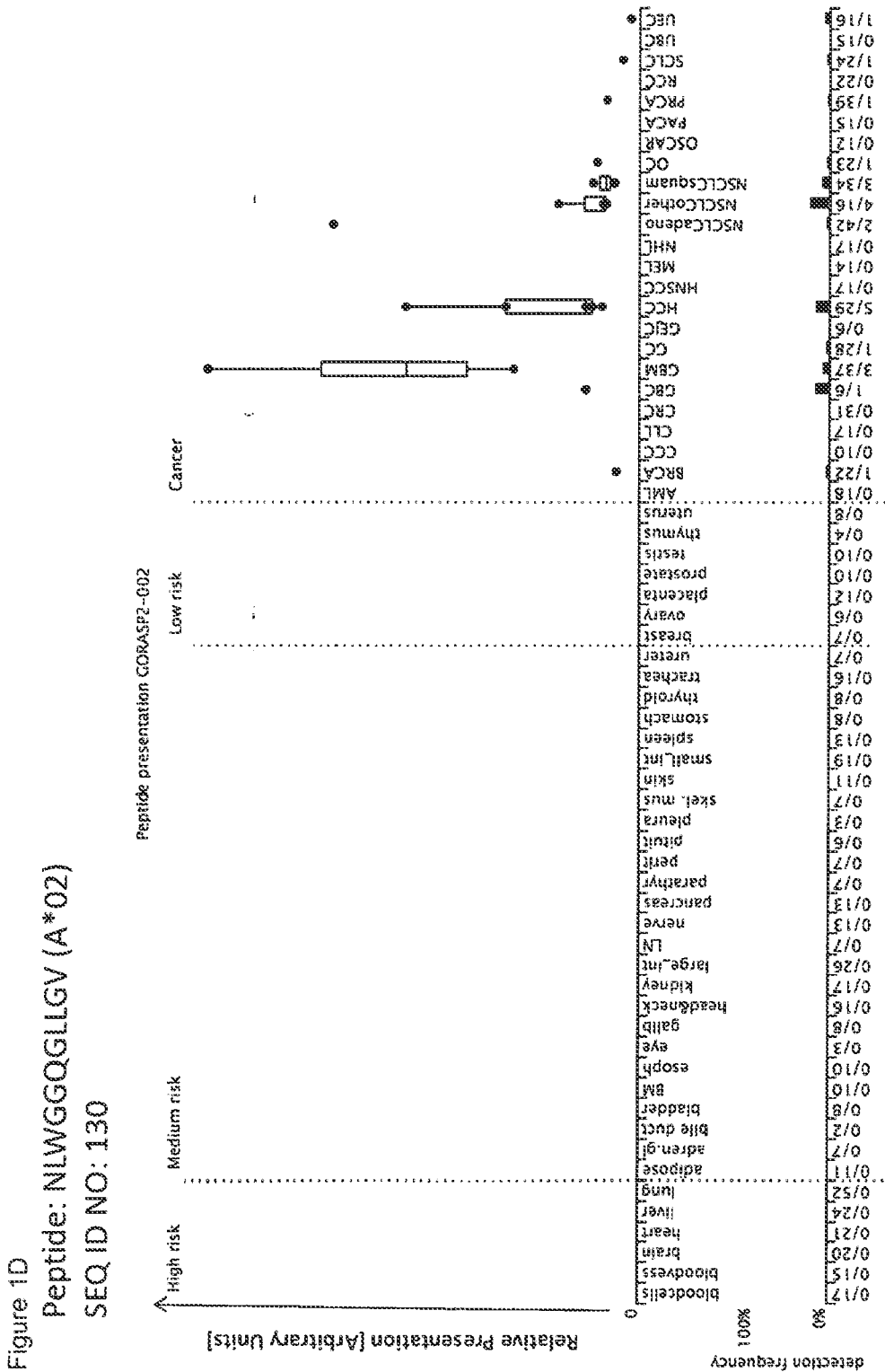
The present invention relates to peptides, proteins, nucleic acids and cells for use in immunotherapeutic methods. In particular, the present invention relates to the immunotherapy of cancer. The present invention furthermore relates to tumor-associated T-cell peptide epitopes, alone or in combination with other tumor-associated peptides that can for example serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses, or to stimulate T cells ex vivo and transfer into patients. Peptides bound to molecules of the major histocompatibility complex (MHC), or peptides as such, can also be targets of antibodies, soluble T-cell receptors, and other binding molecules.

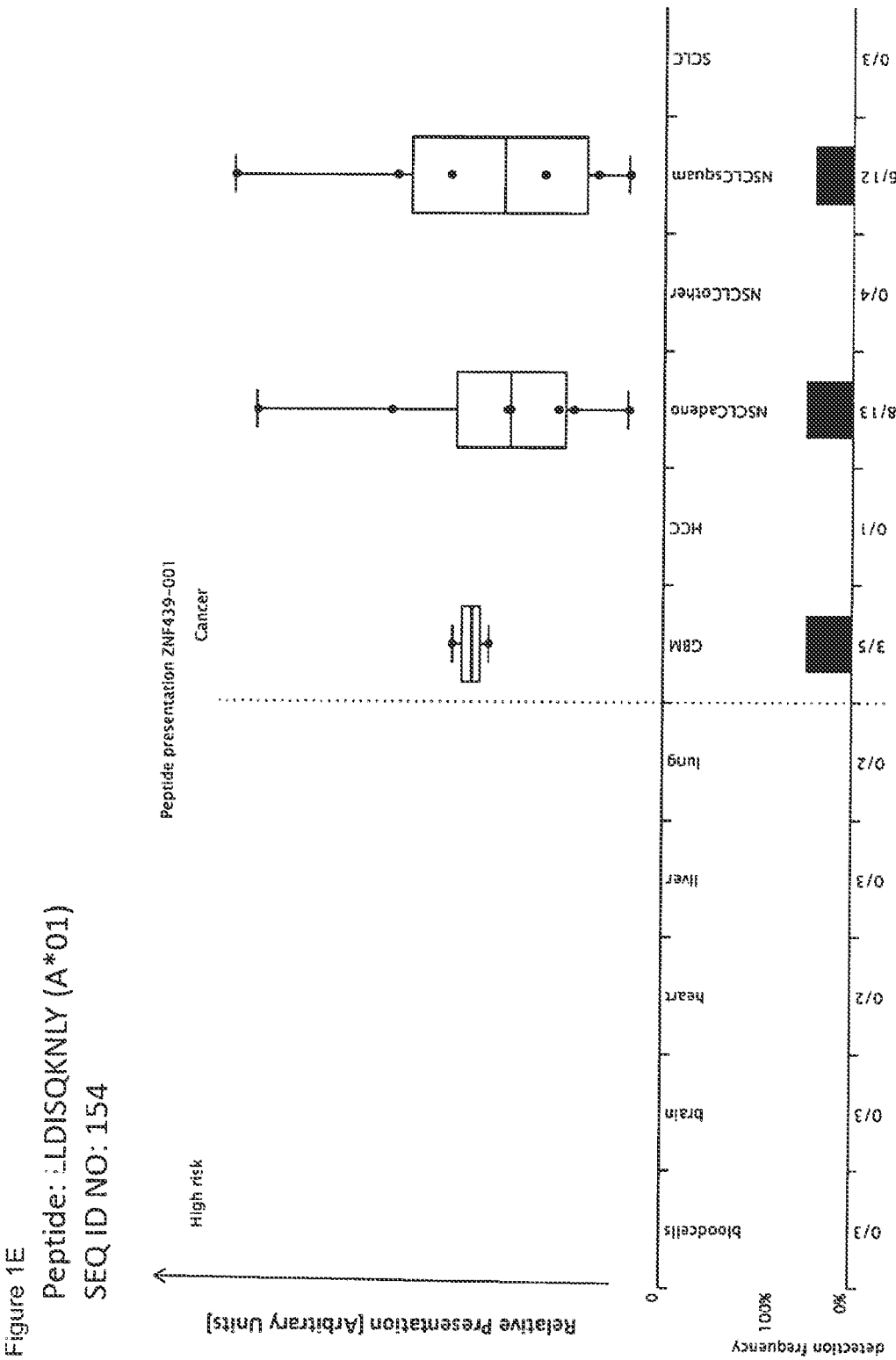
Specification includes a Sequence Listing.











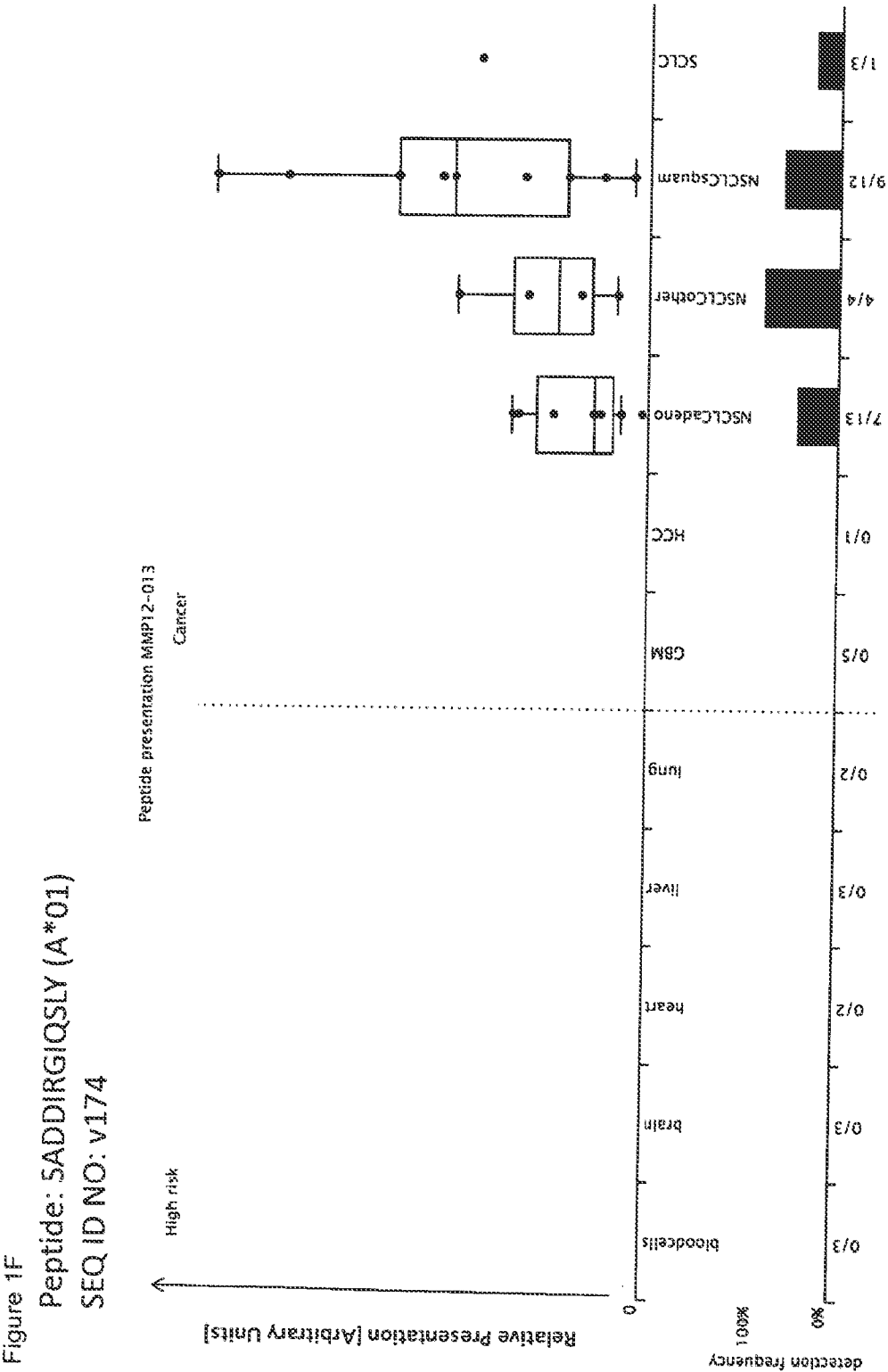
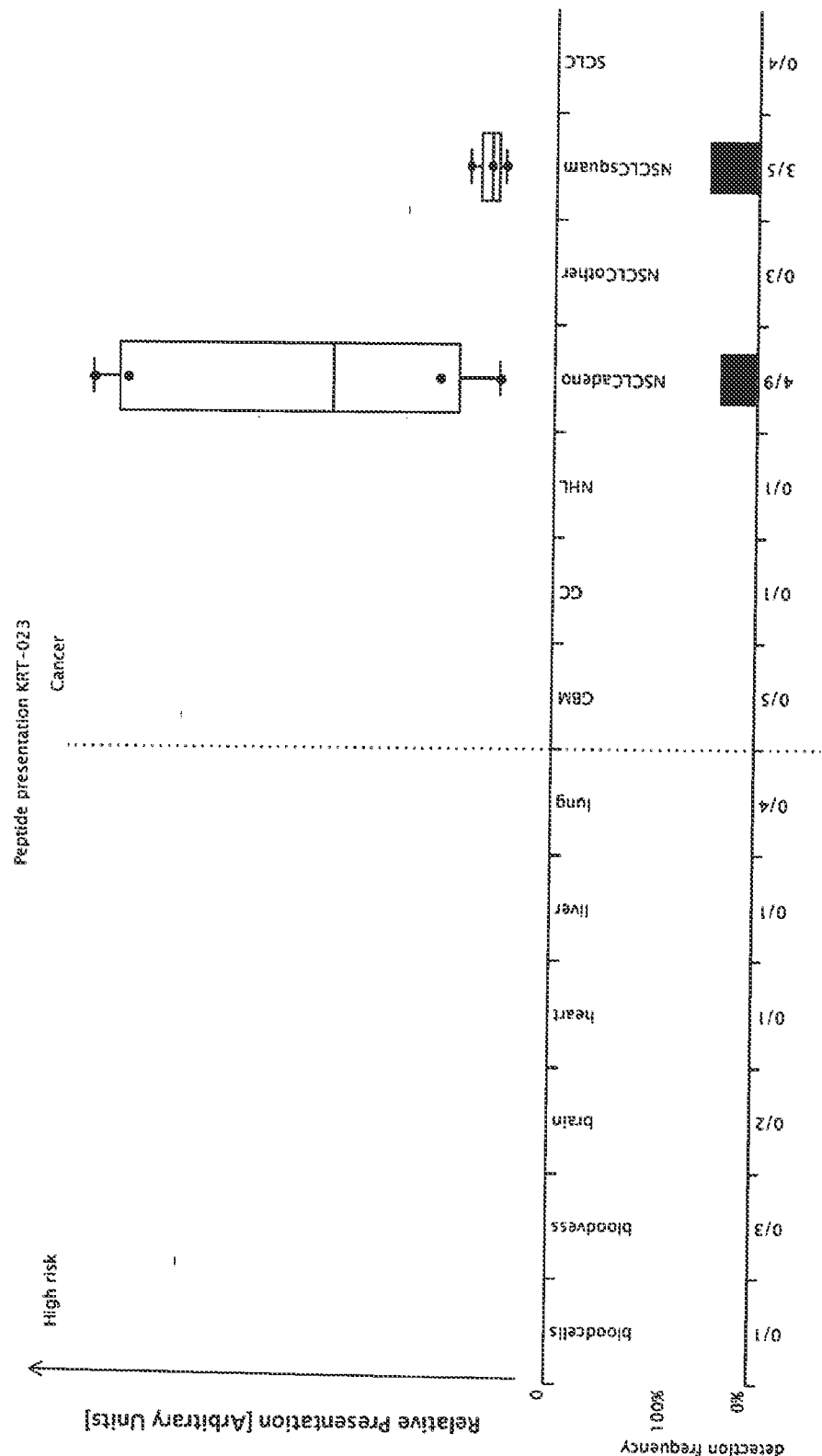
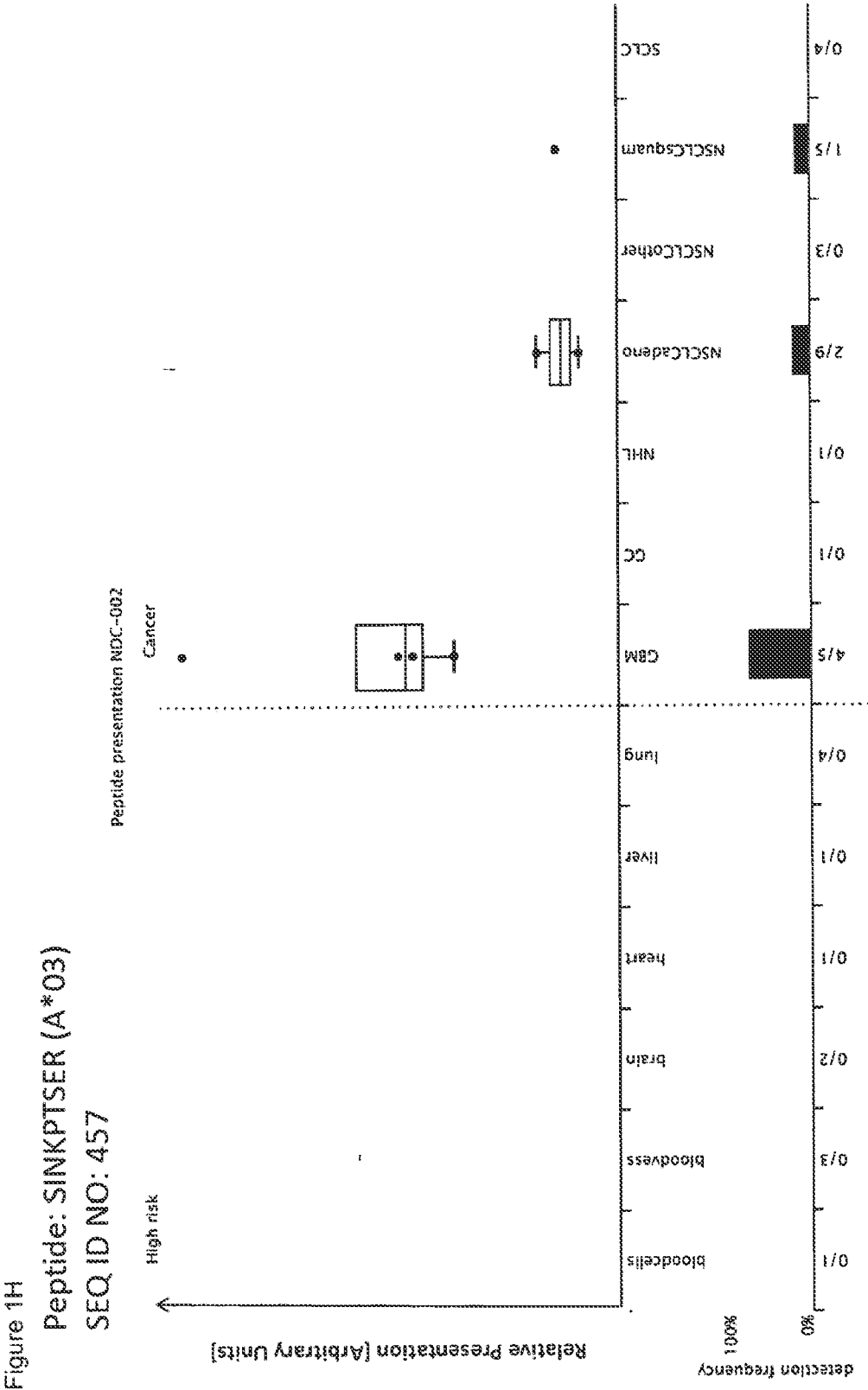
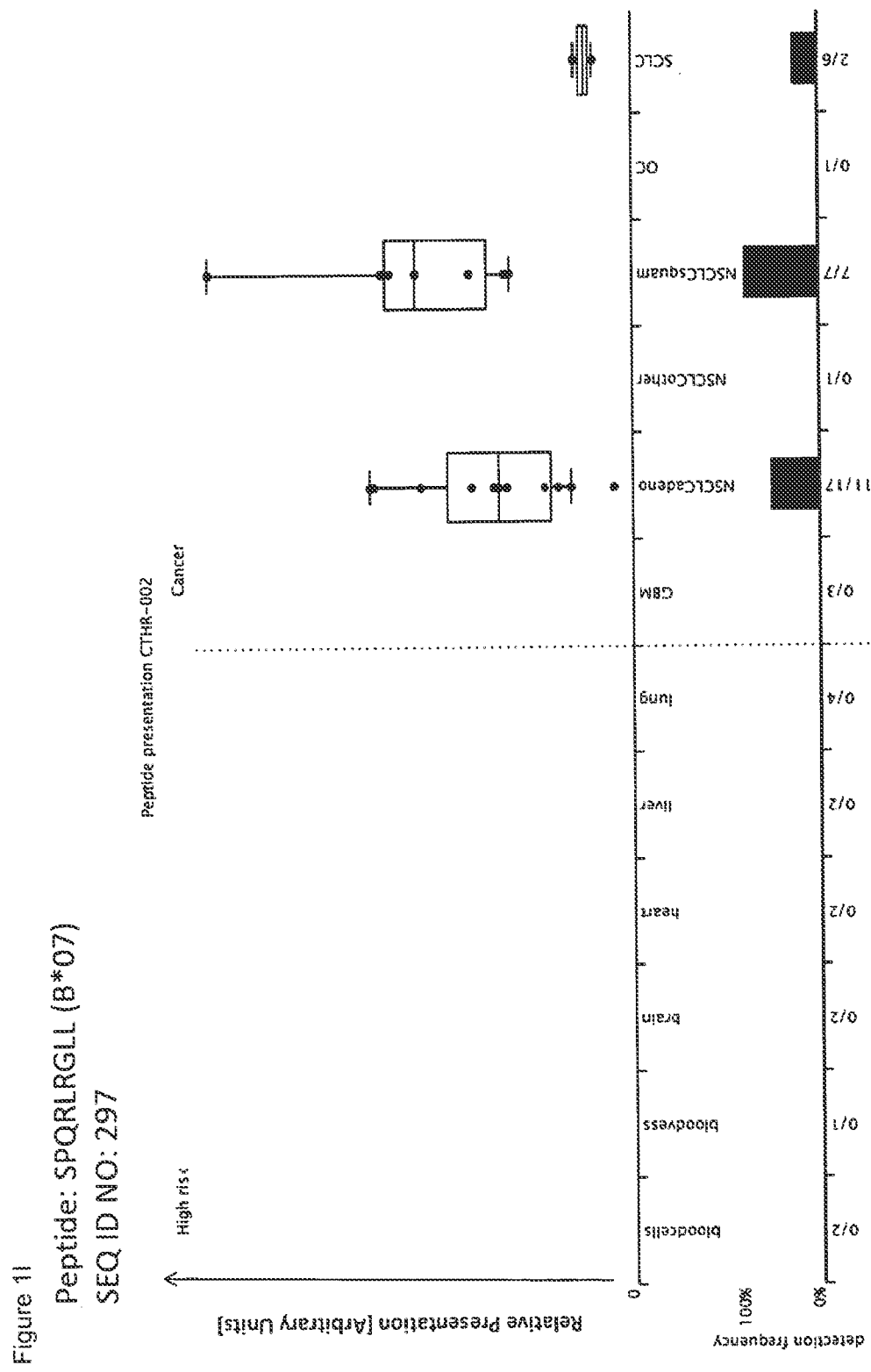
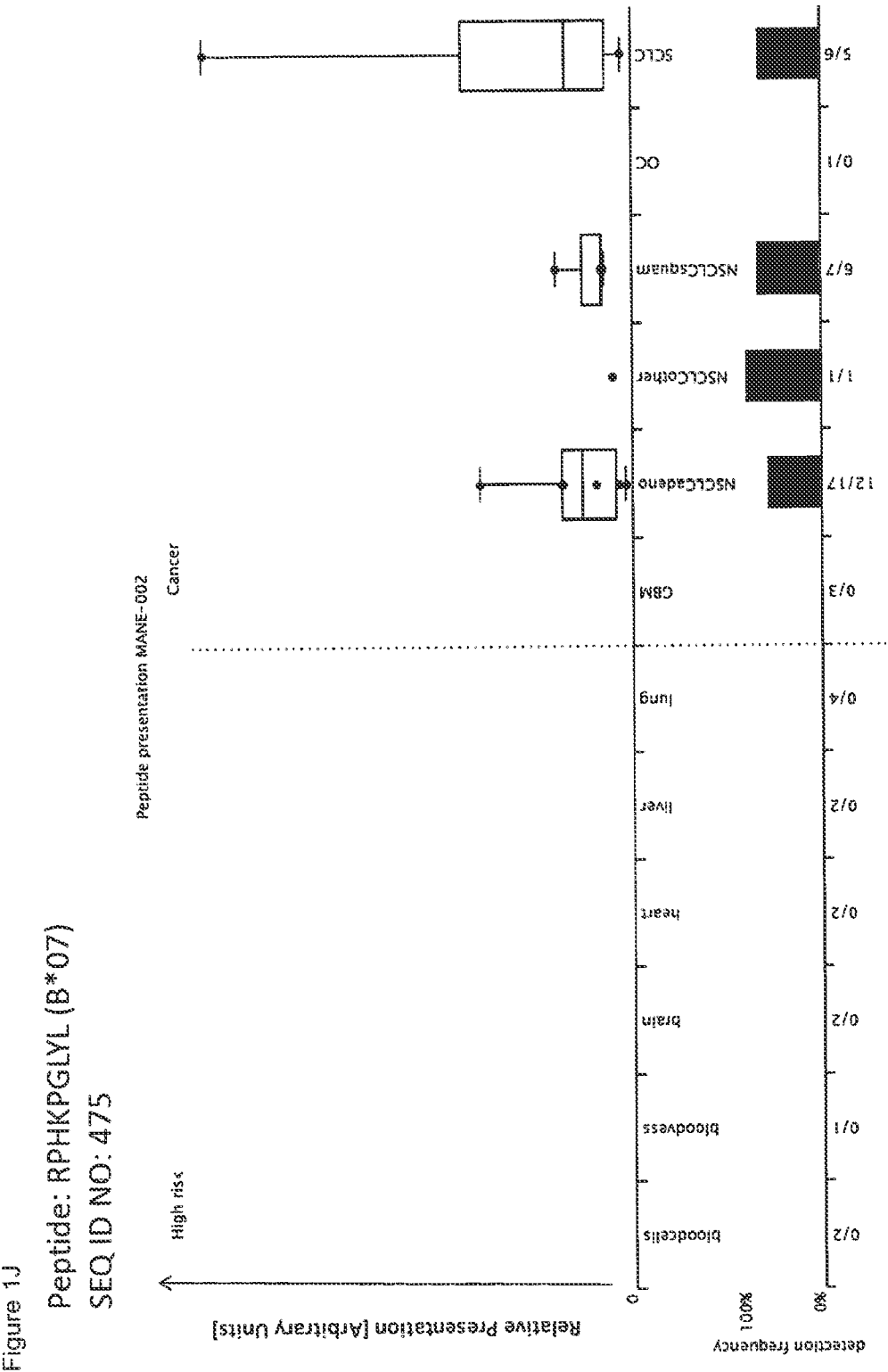


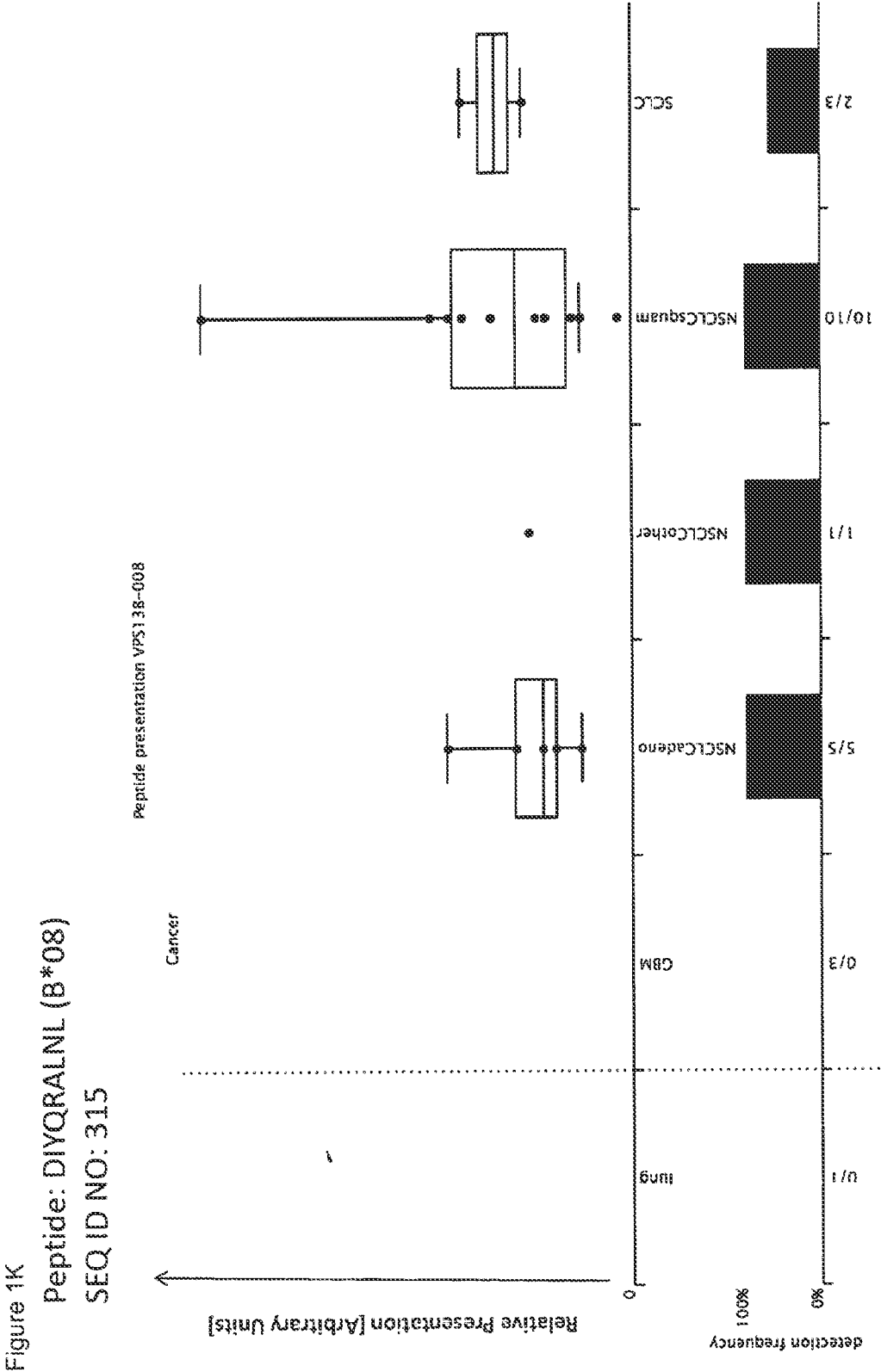
Figure 1G
Peptide: KLALEGALQK (A*03)
SEQ ID NO: 202

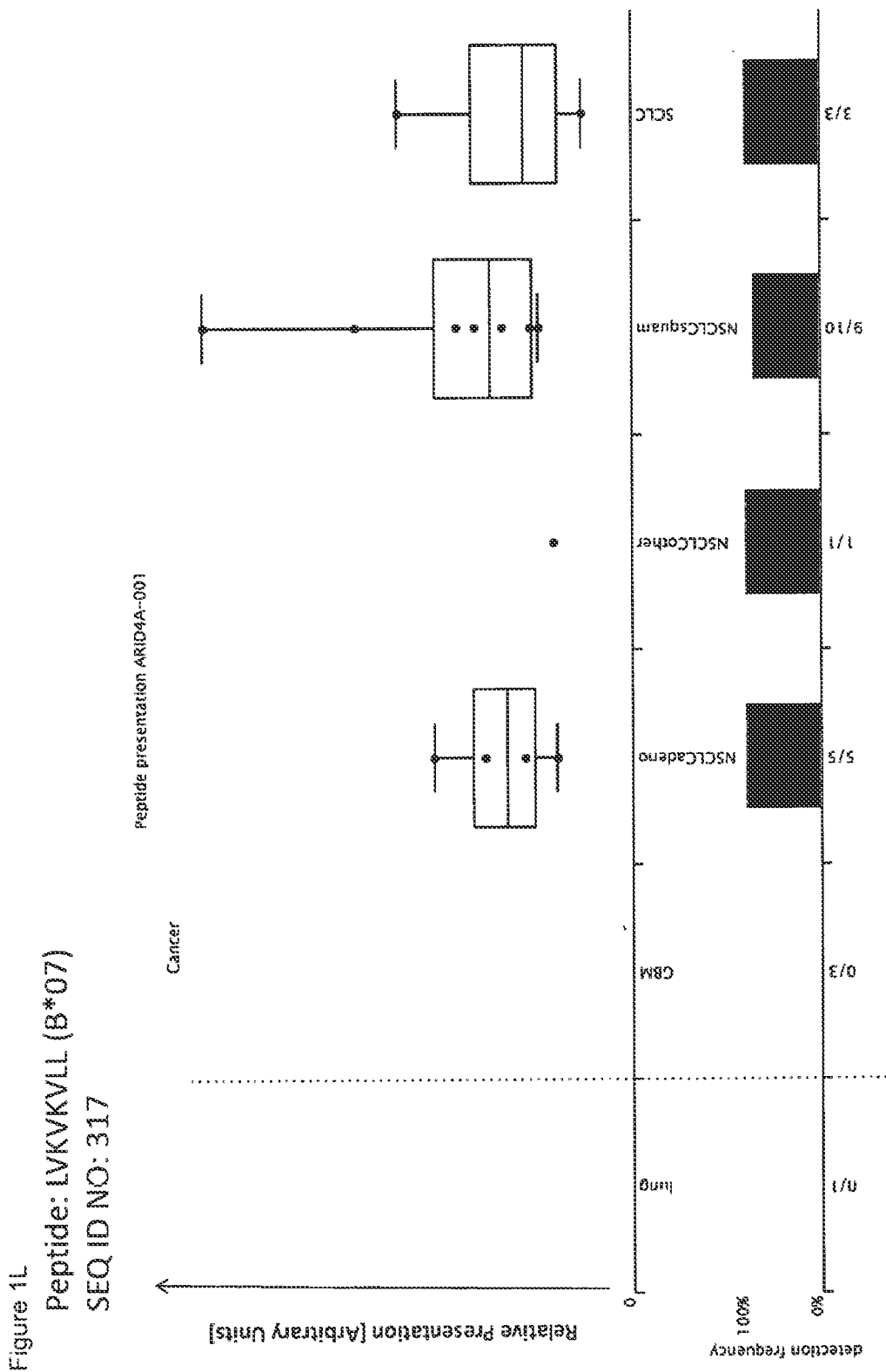


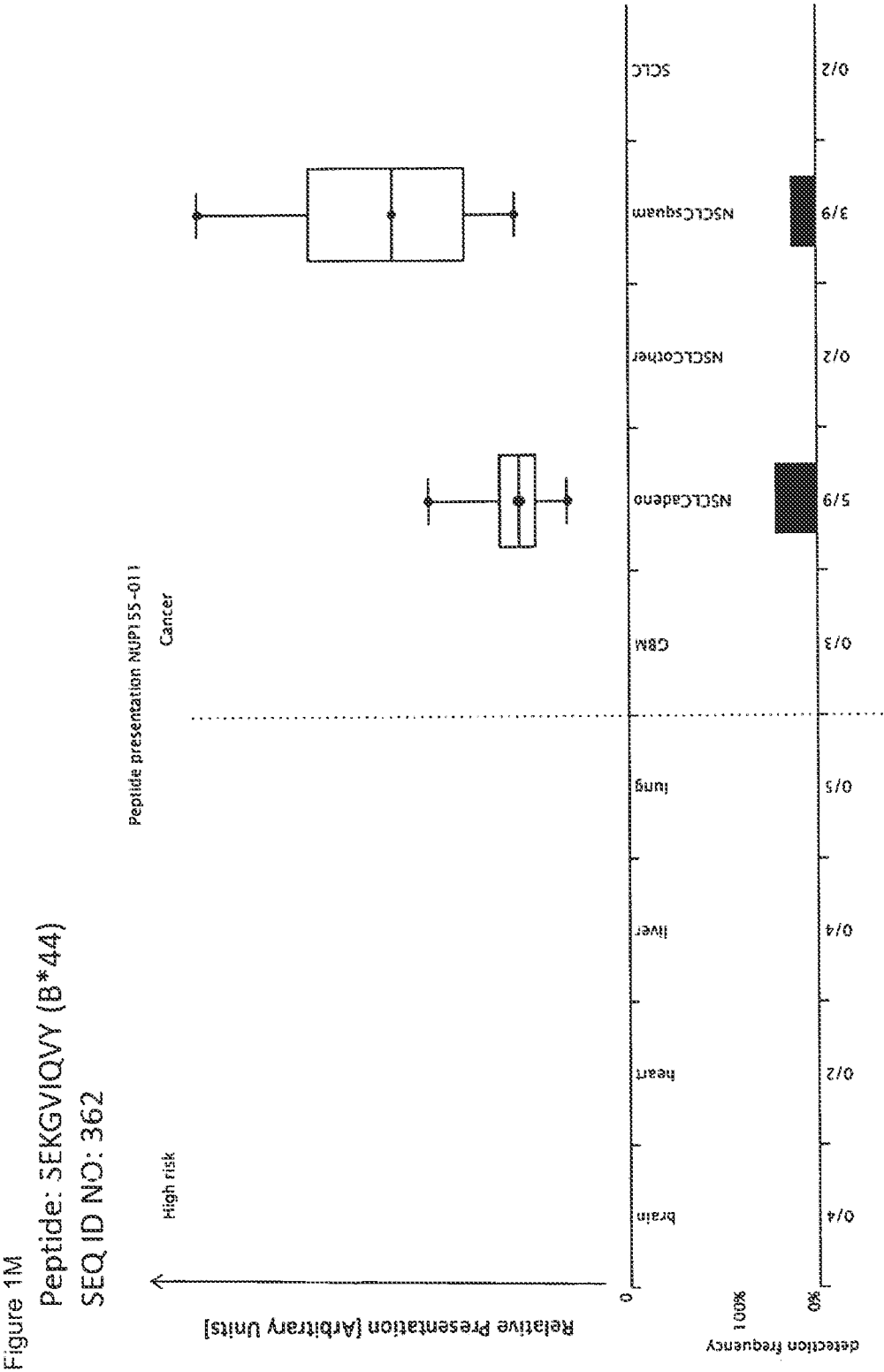












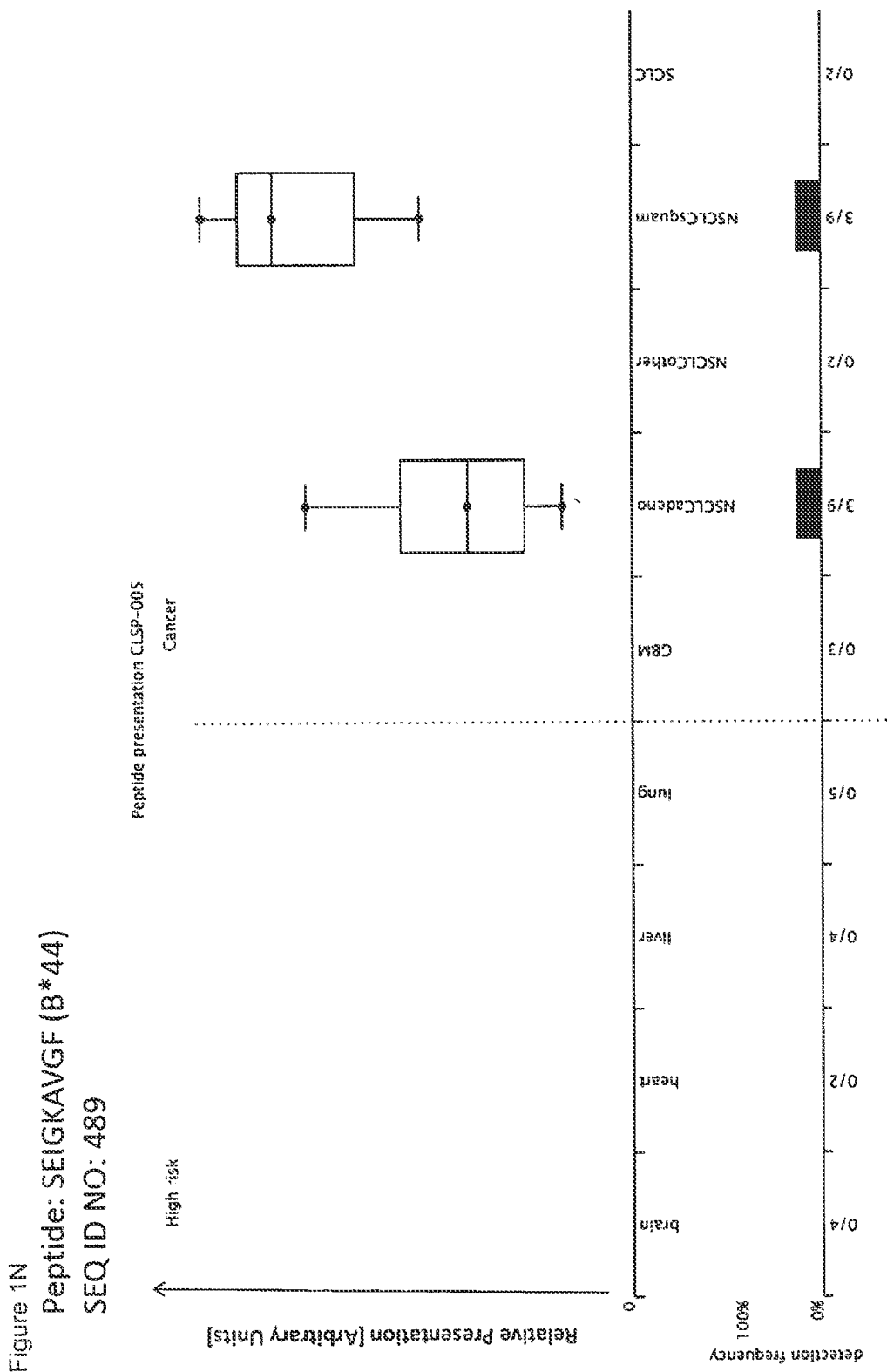


Figure 2A

Gene: ADAMTS12
Peptide: QYDPTPLTW
SEQ ID NO: 1

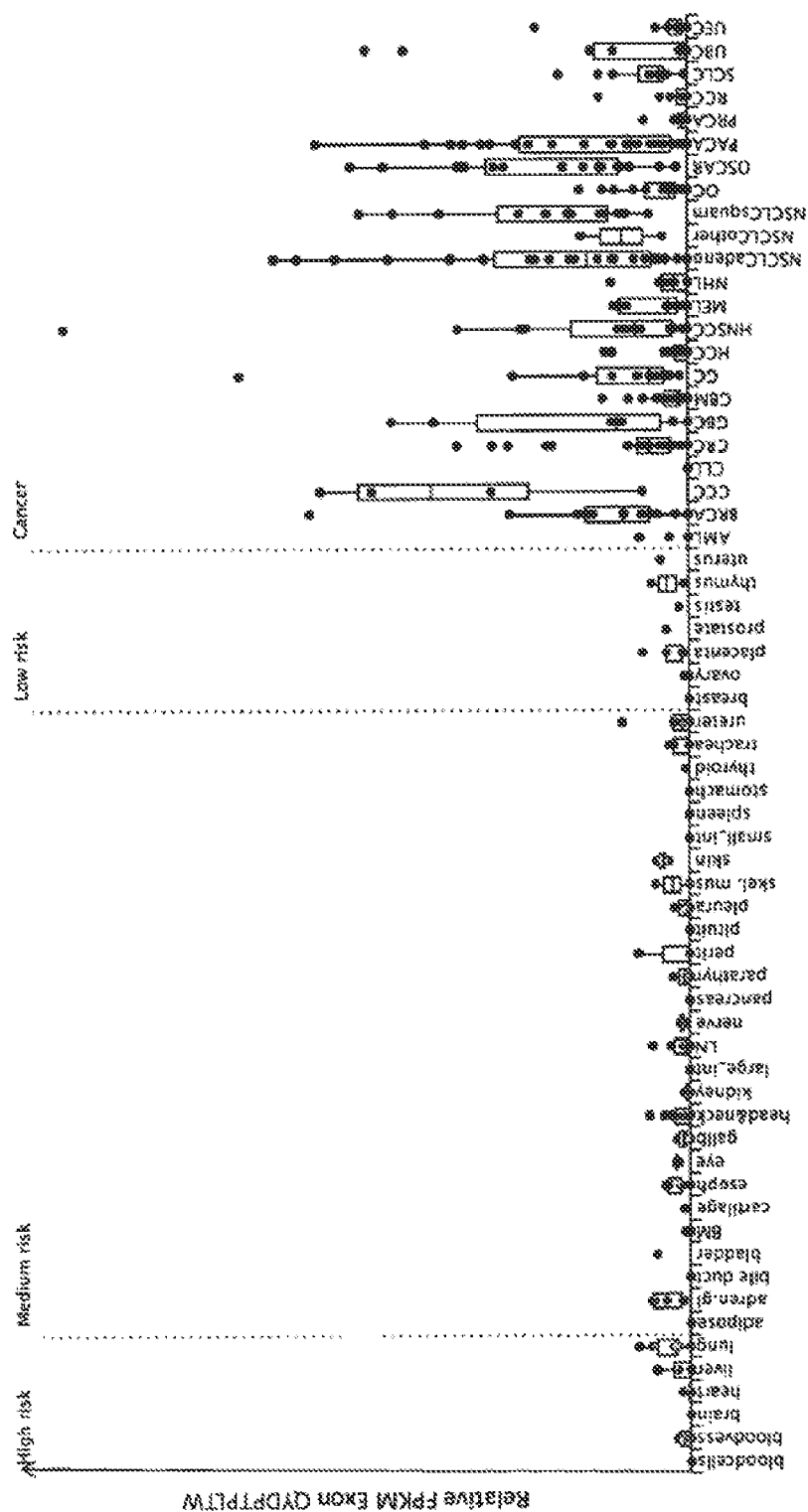


Figure 2B
Gene: MMP12
Peptide: VWSNVTPLKF
SEQ ID NO: 2

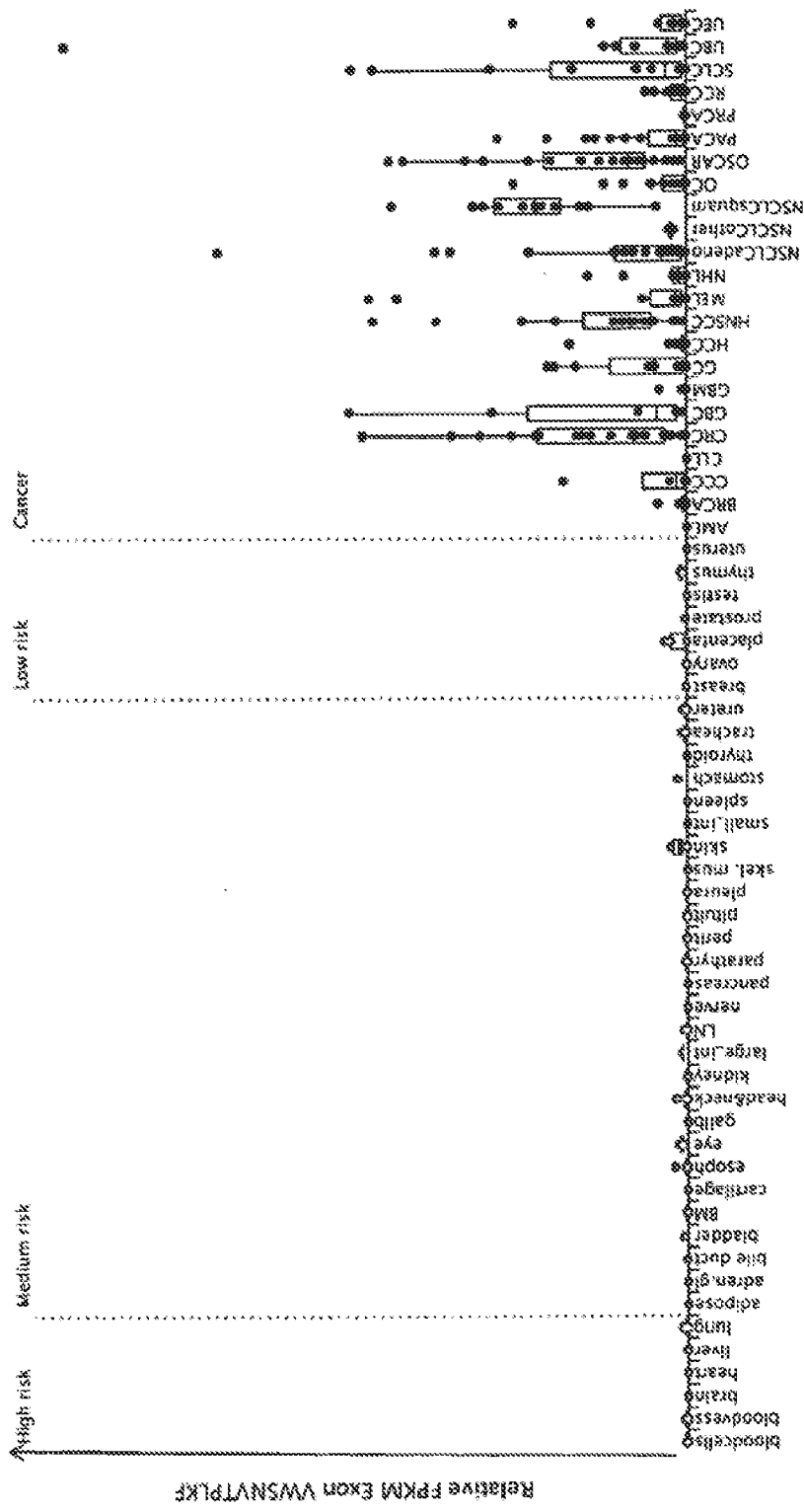


Figure 2C
Gene: MMP12
Peptide: YVDINTFRL
SEQ ID NO: 84

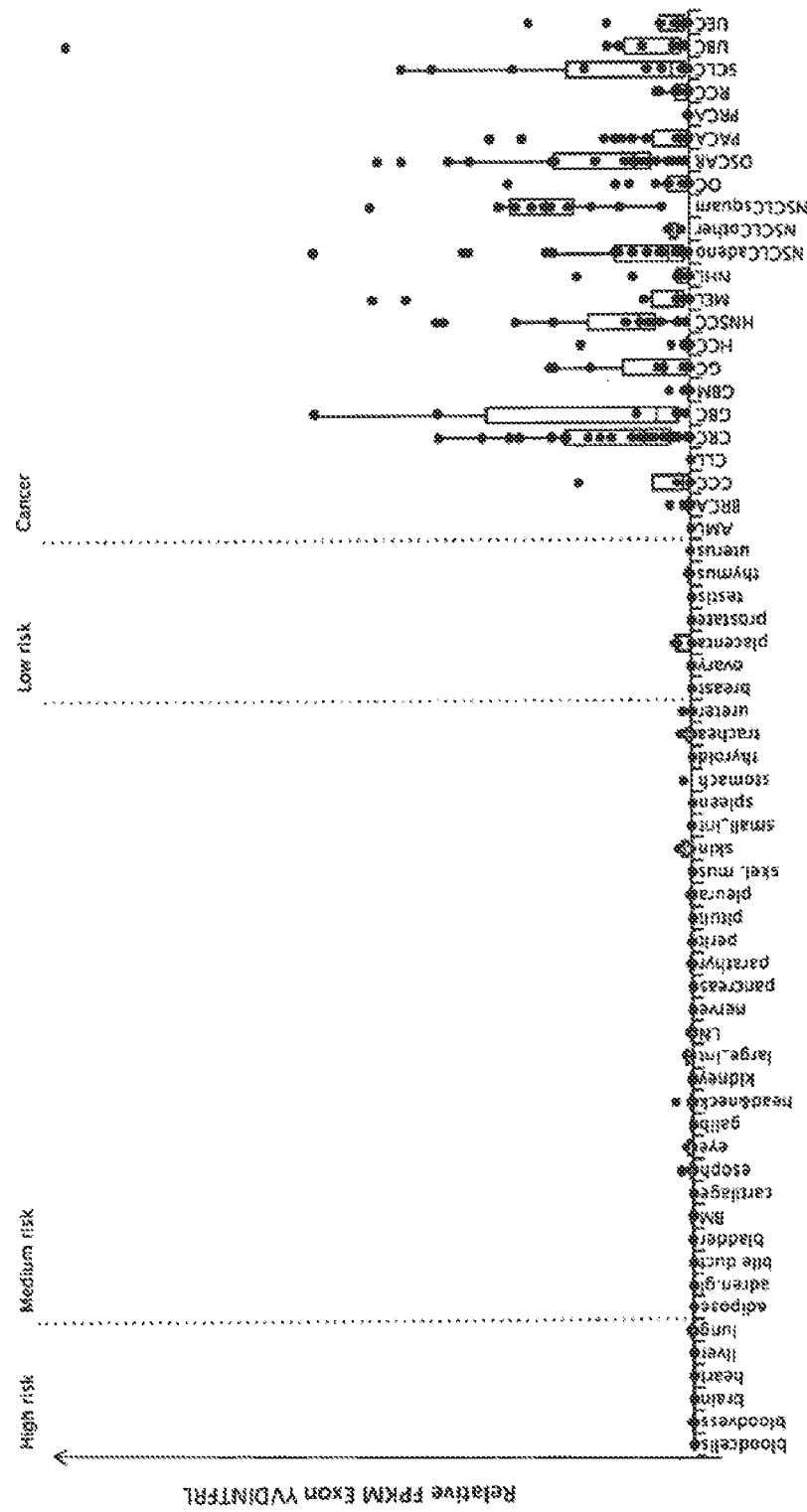


Figure 2D
Gene: KIF26B
Peptide: TLPPYQISQL
SEQ ID NO: 87

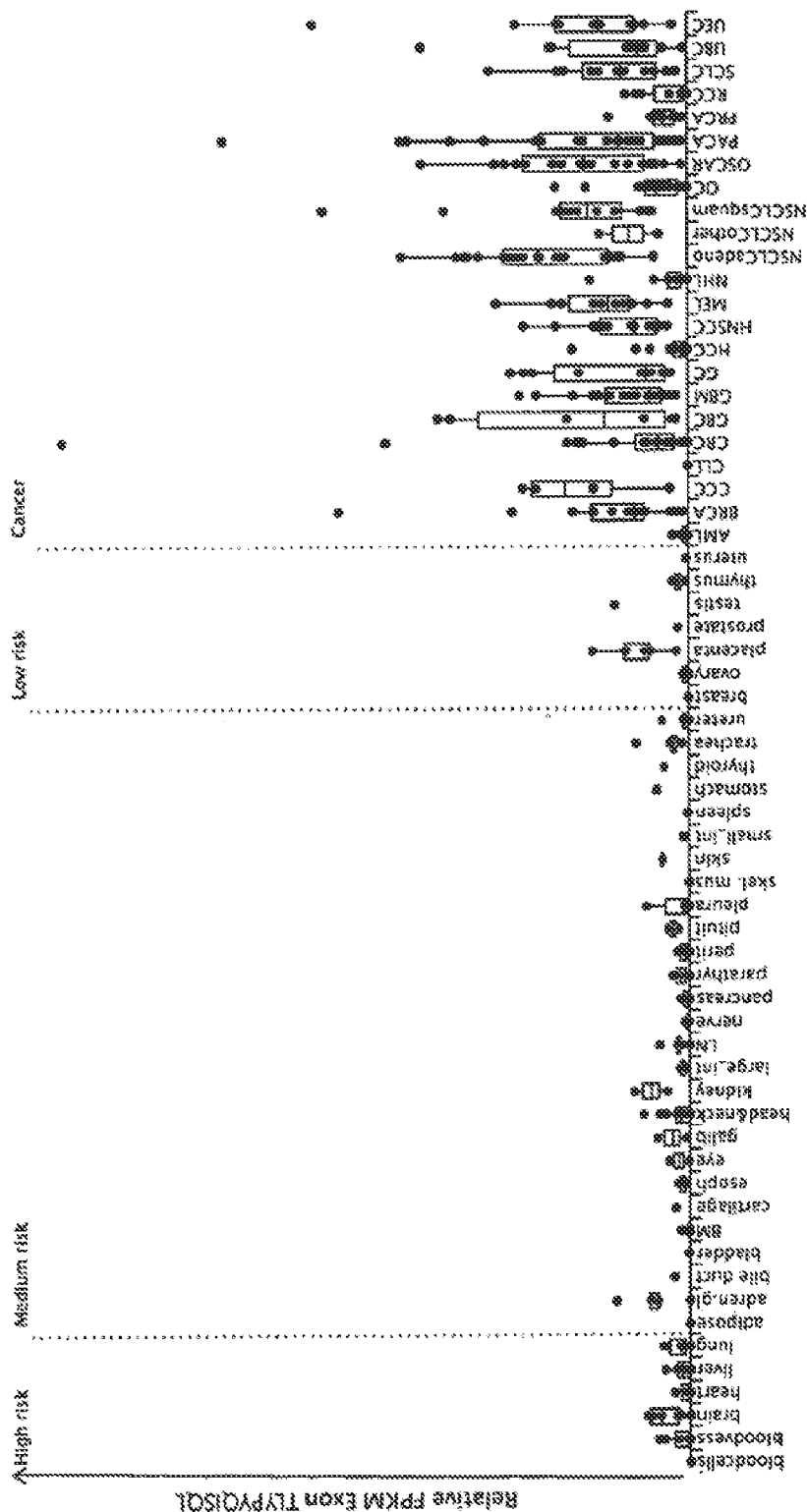
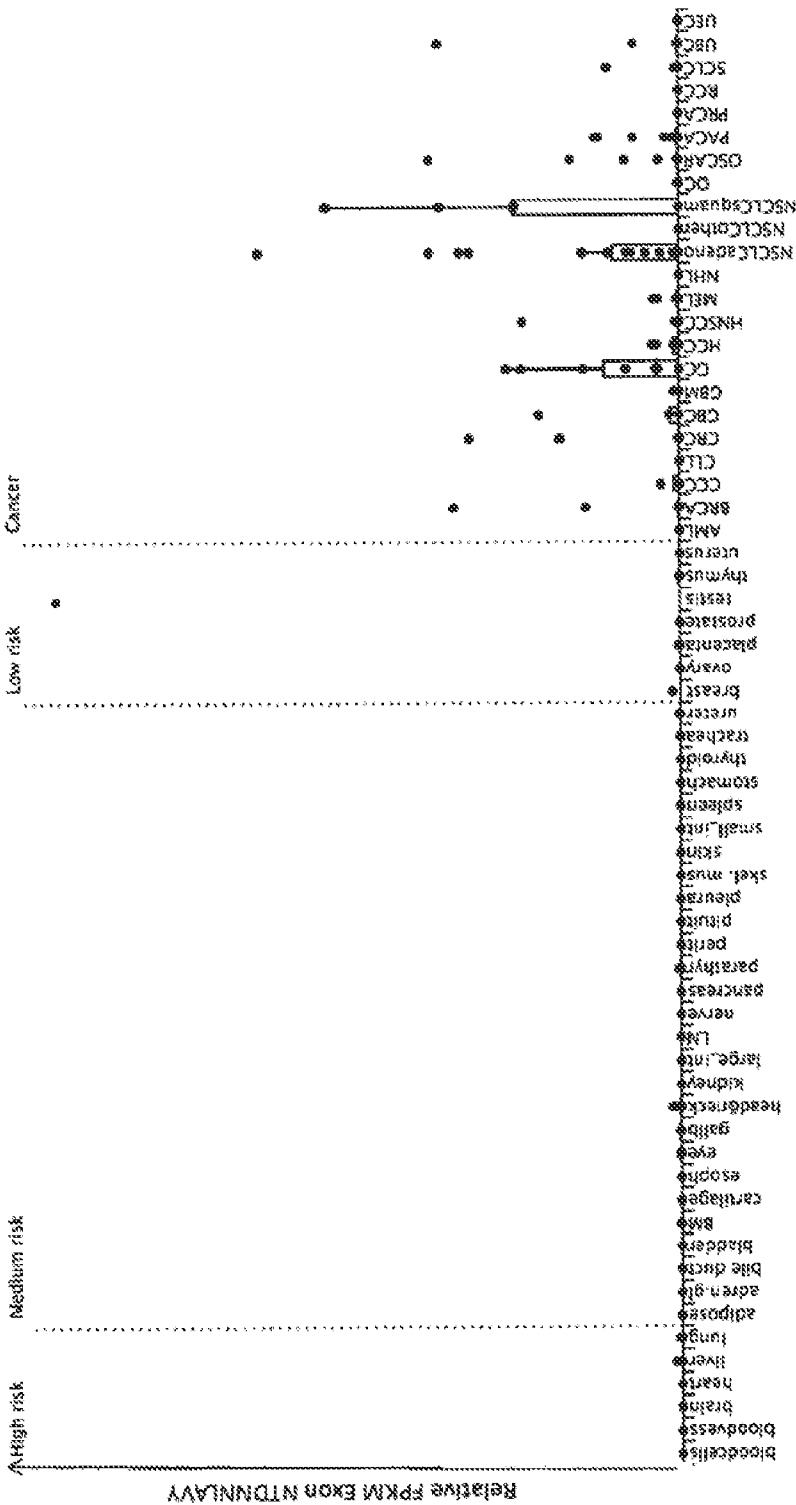


Figure 2E

Gene: CT83

Peptide: NTDNNLAVY

SEQ ID NO: 164



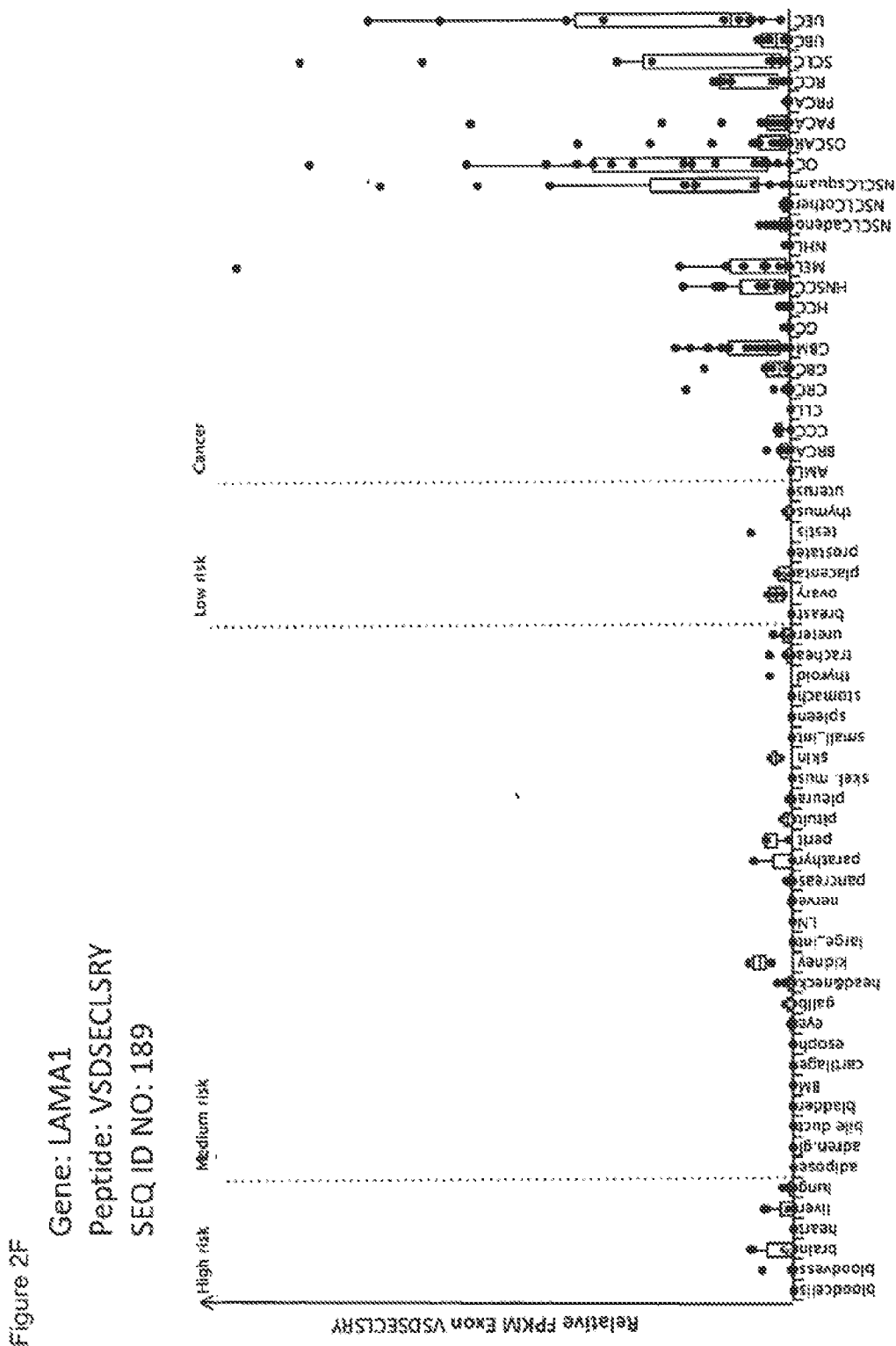
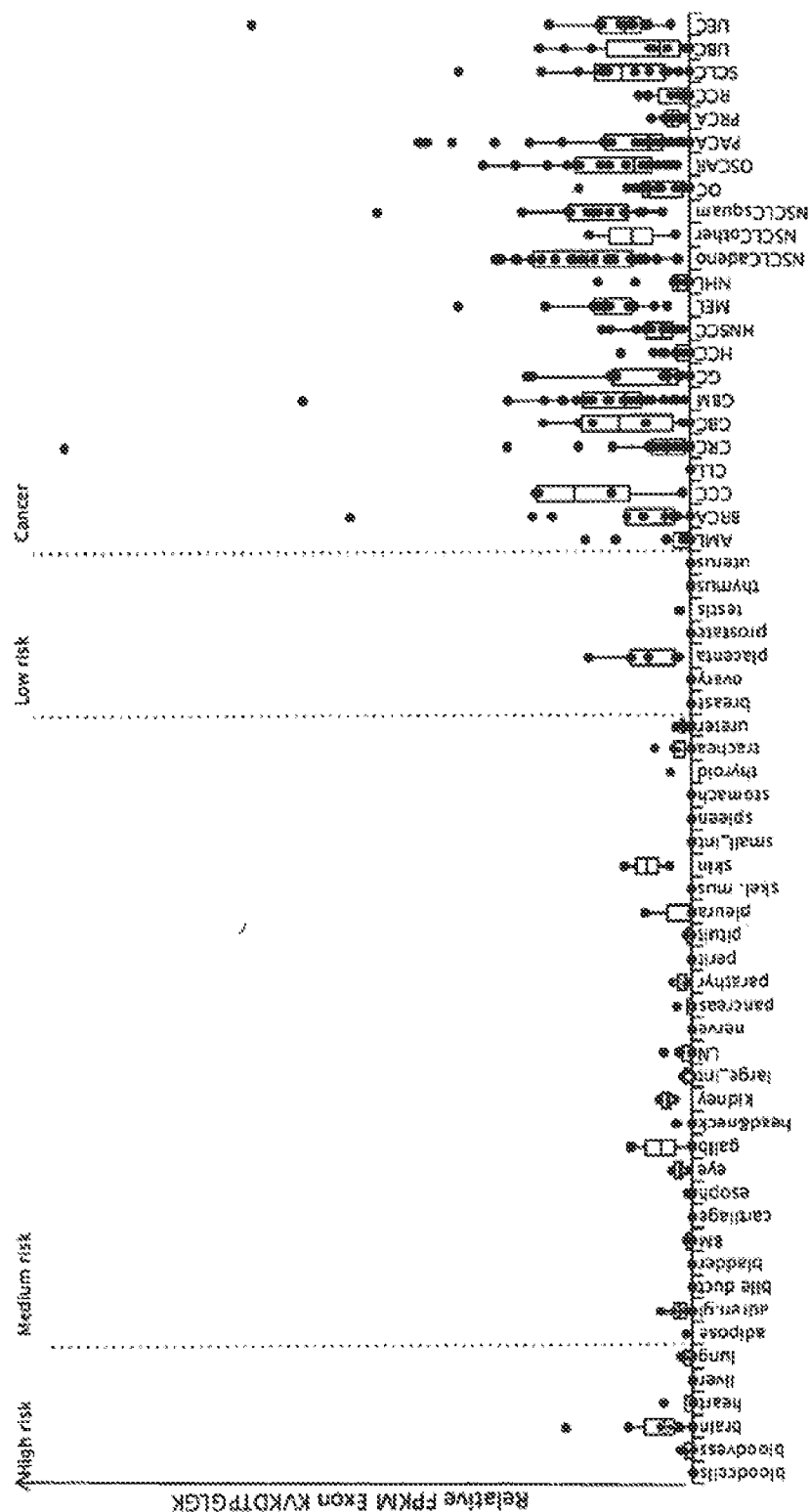


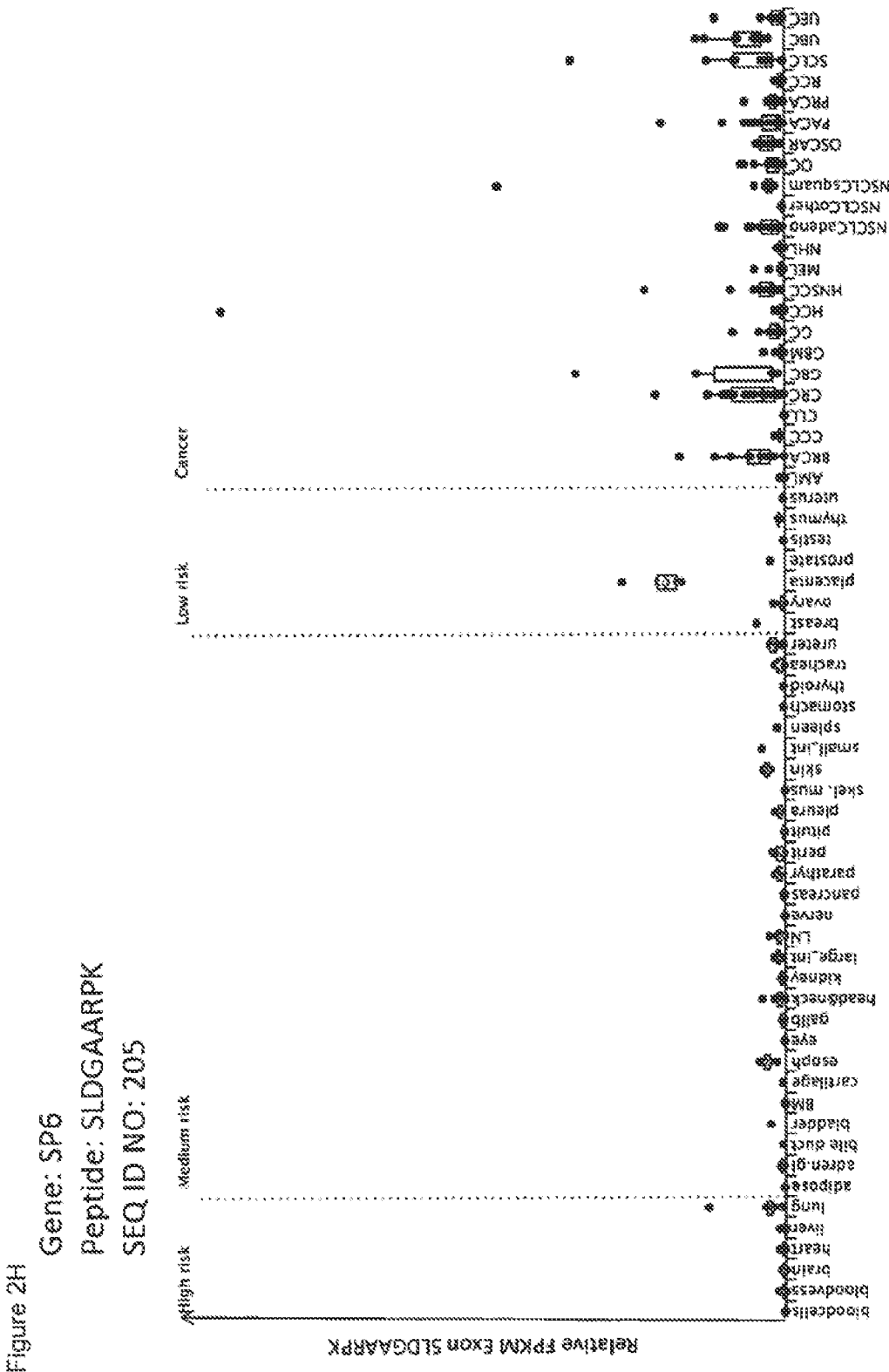
Figure 29

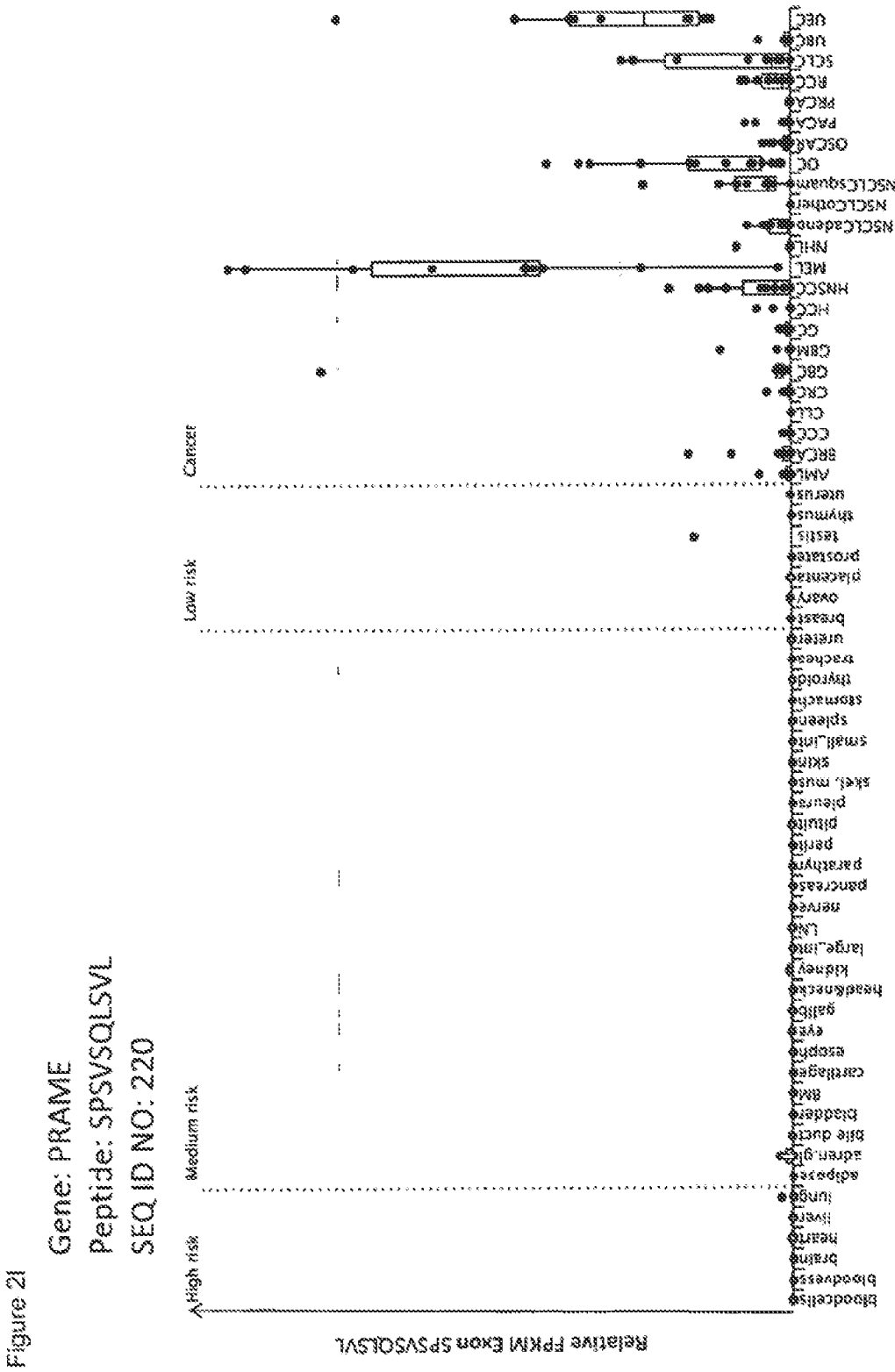
Gene: KF268

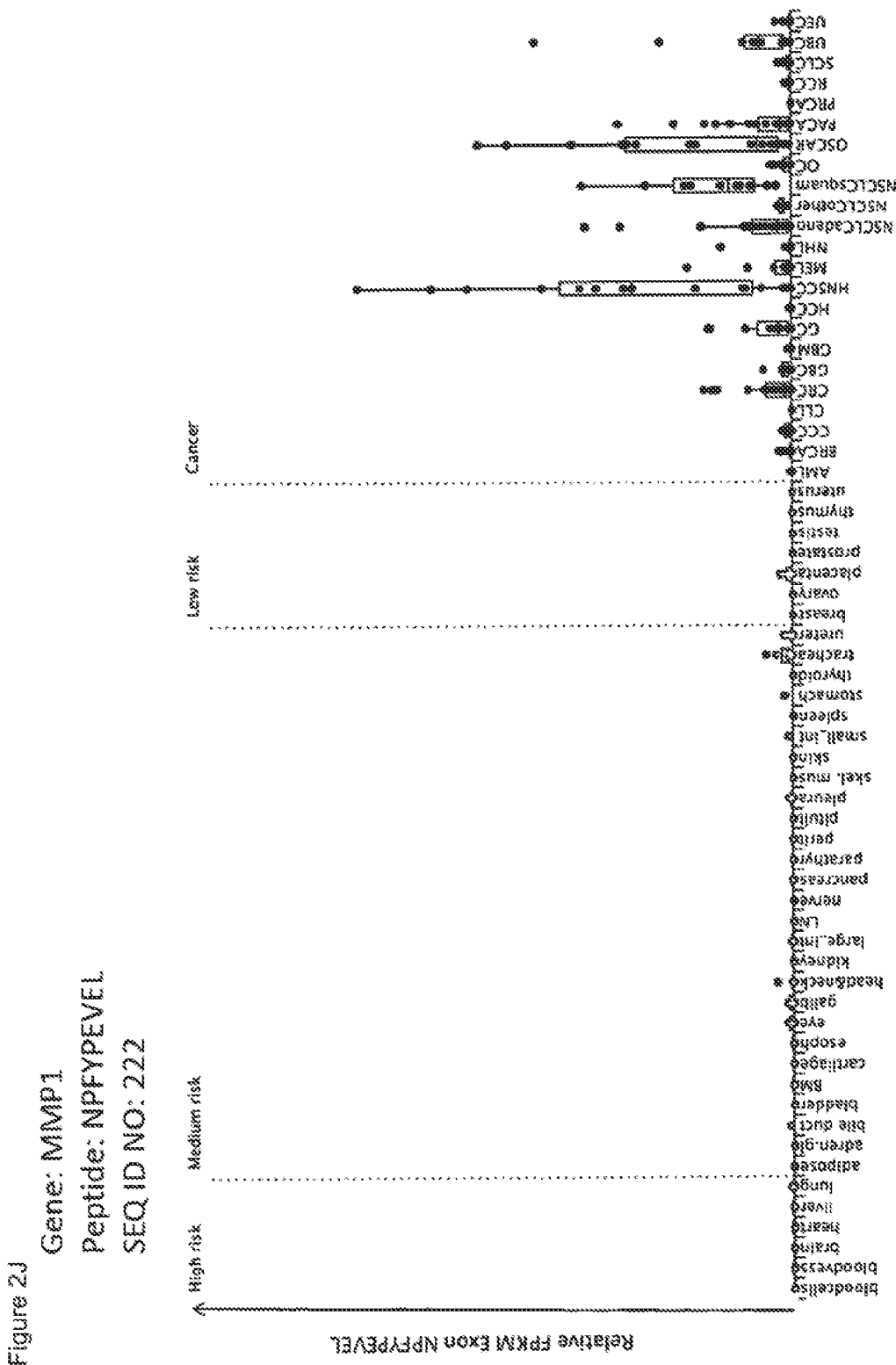
Peptide Vaccine

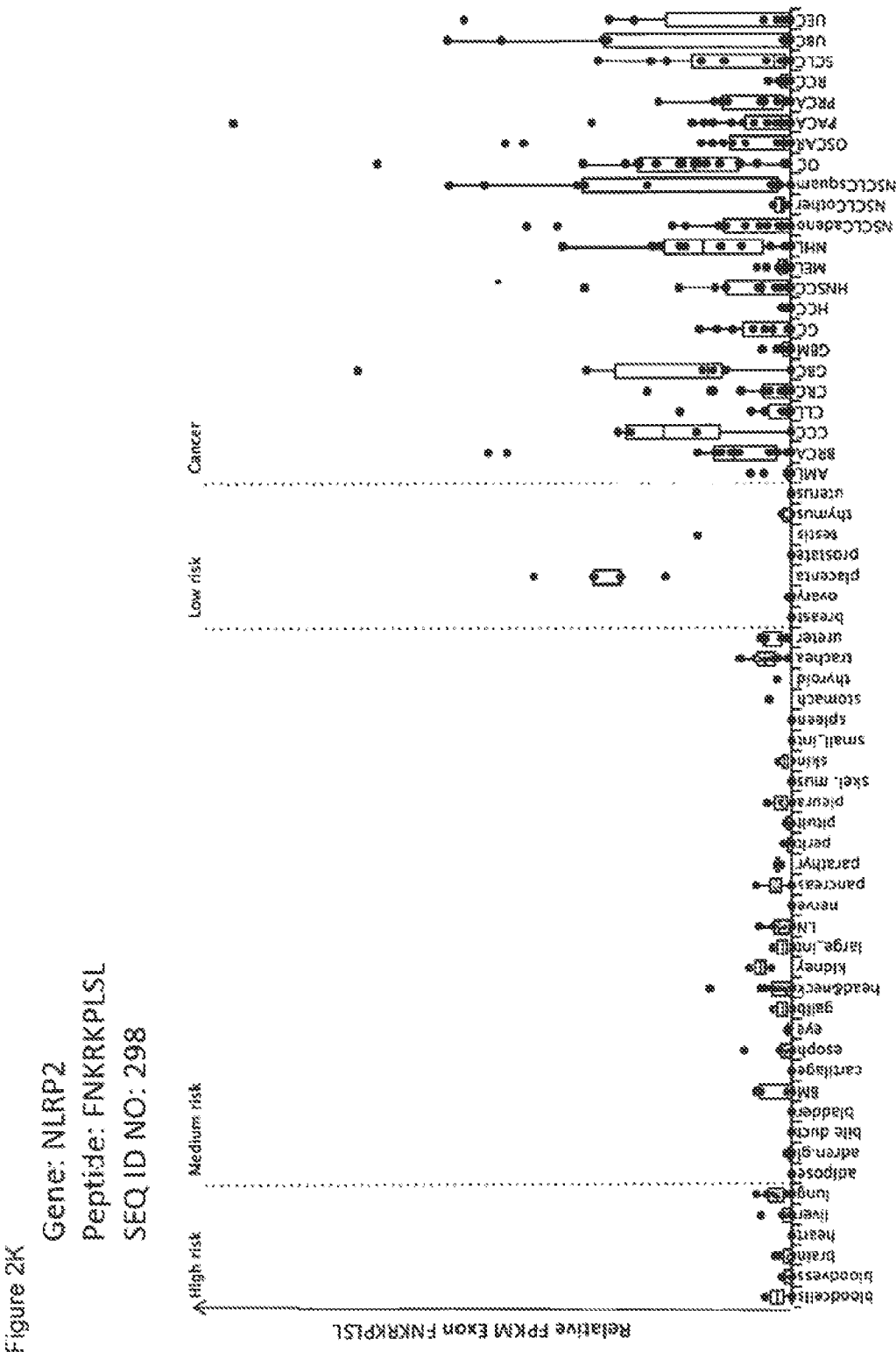
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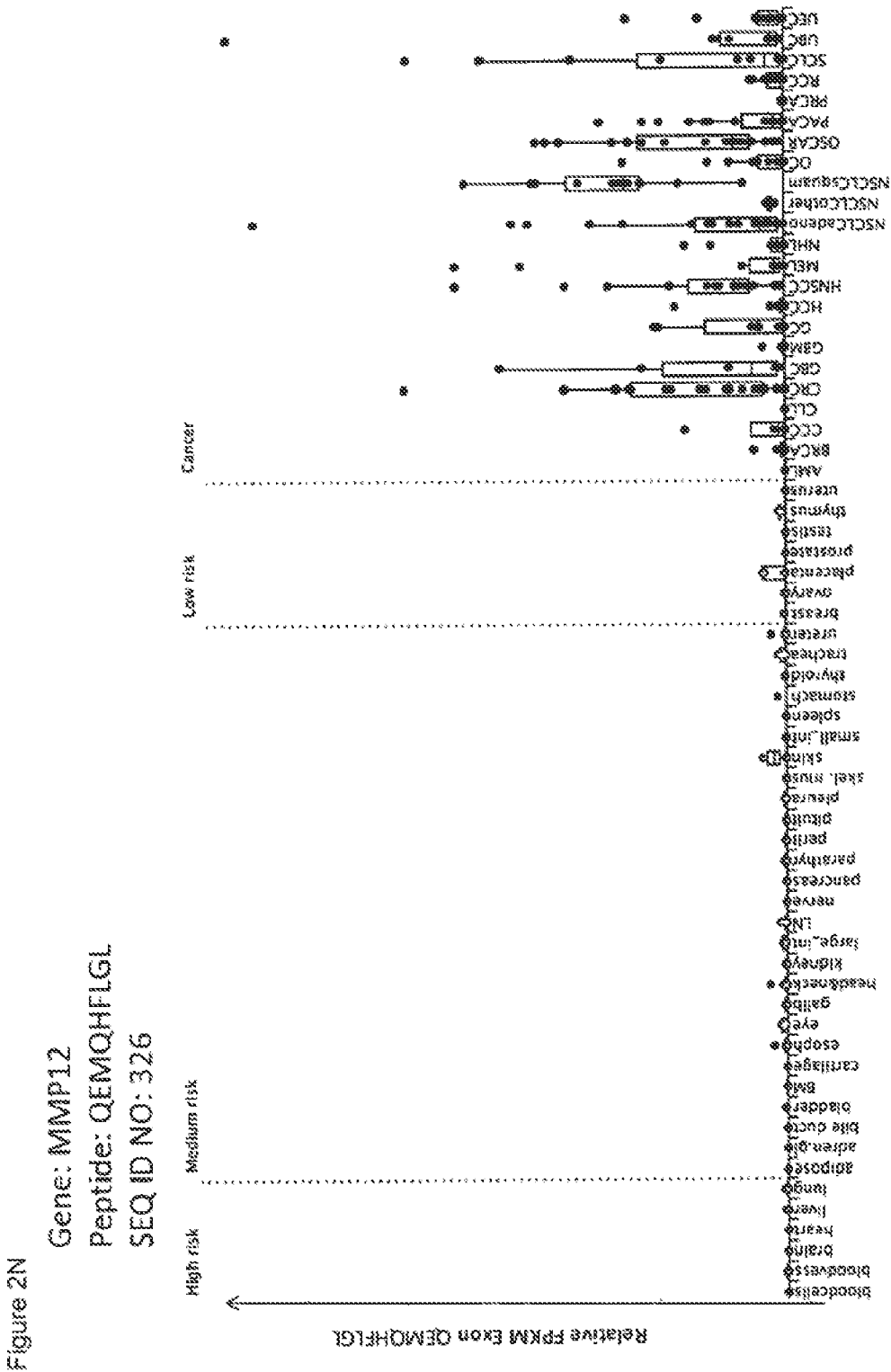


Figure 3A

Figure 3B

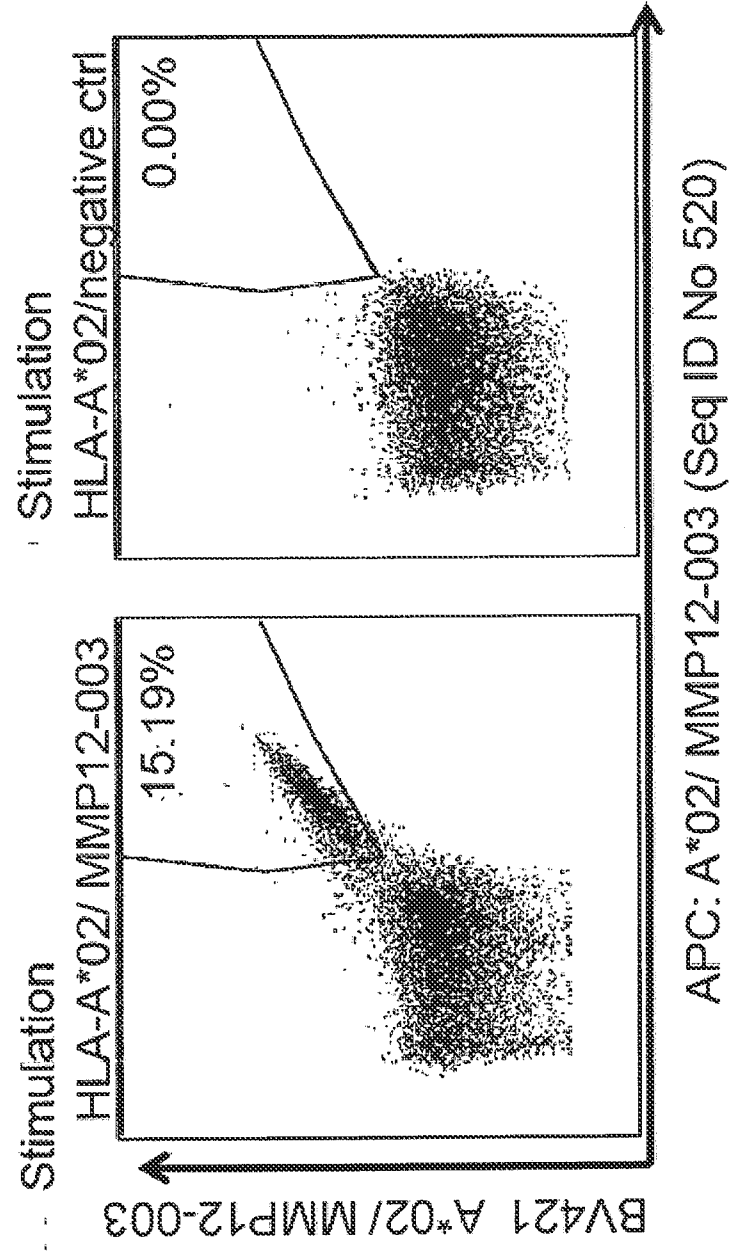


Figure 4B

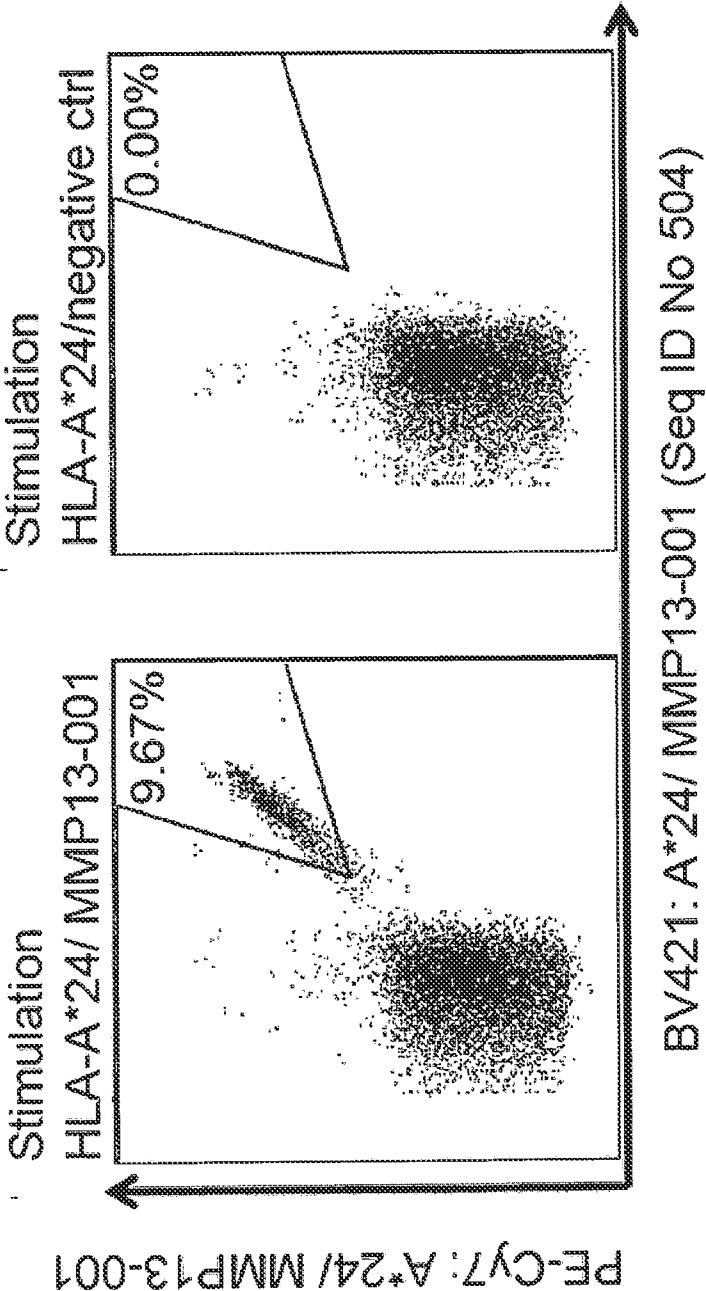


Figure 4A

Figure 5A

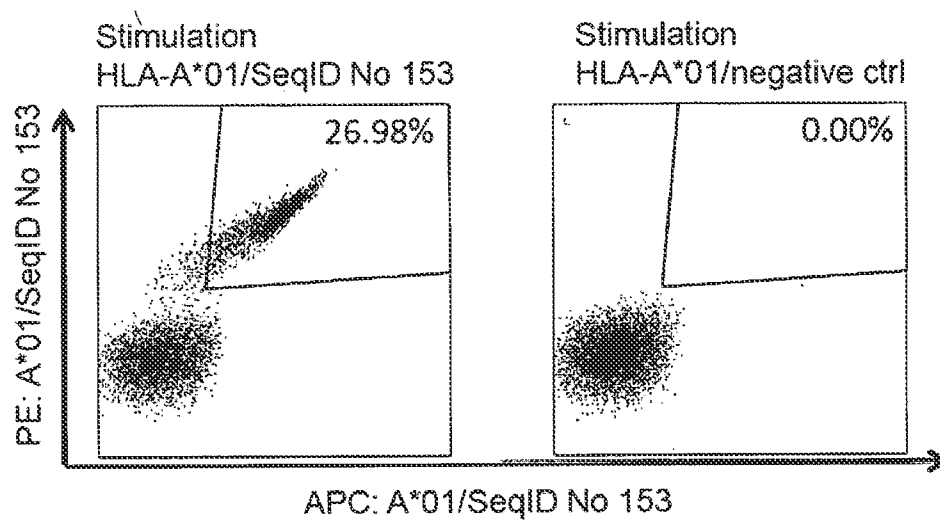


Figure 5B

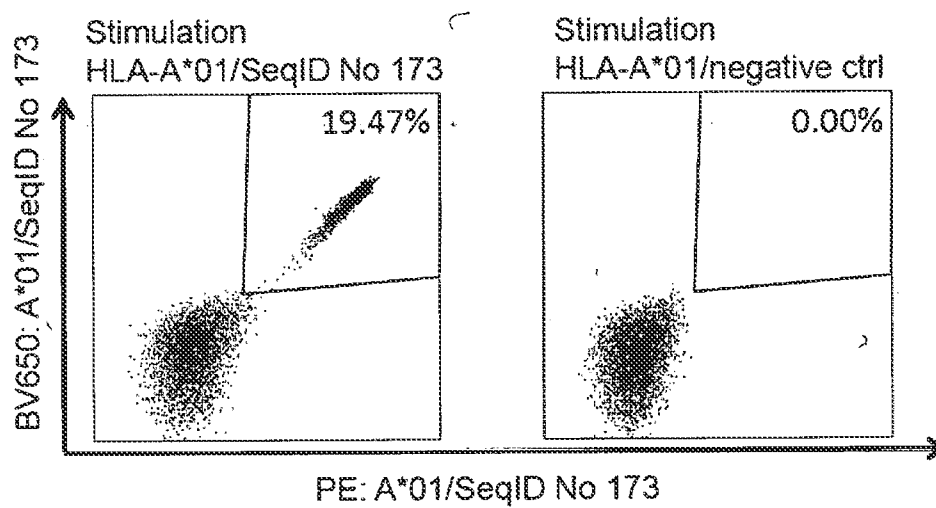


Figure 6A

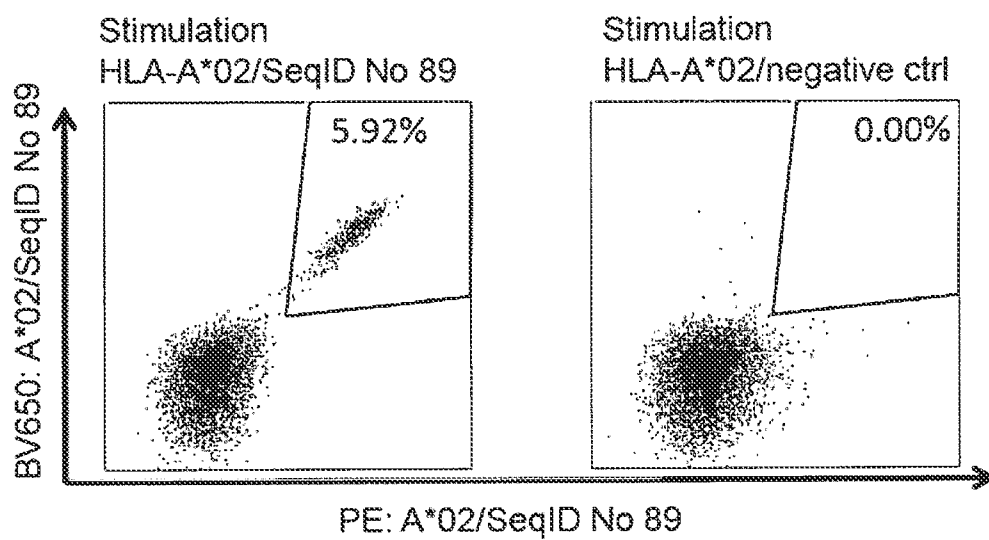


Figure 6B

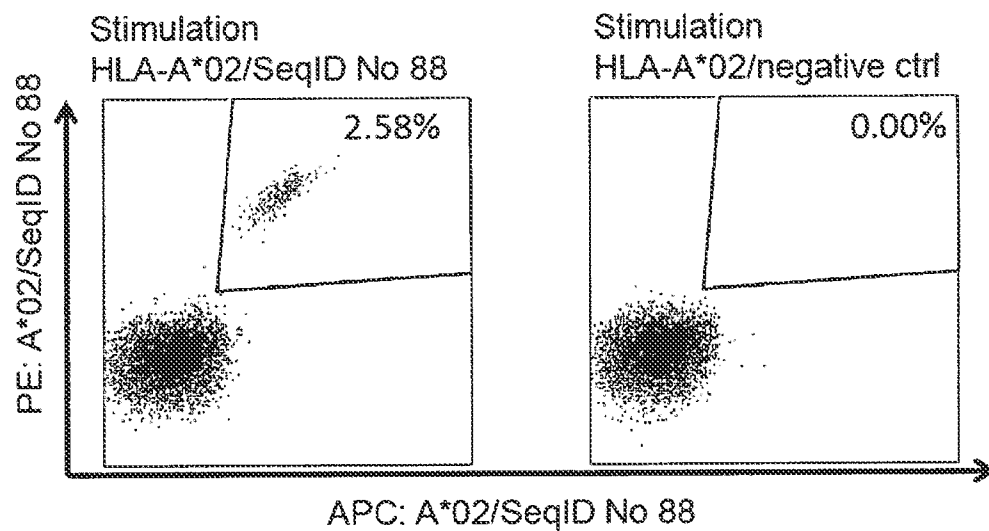


Figure 7A

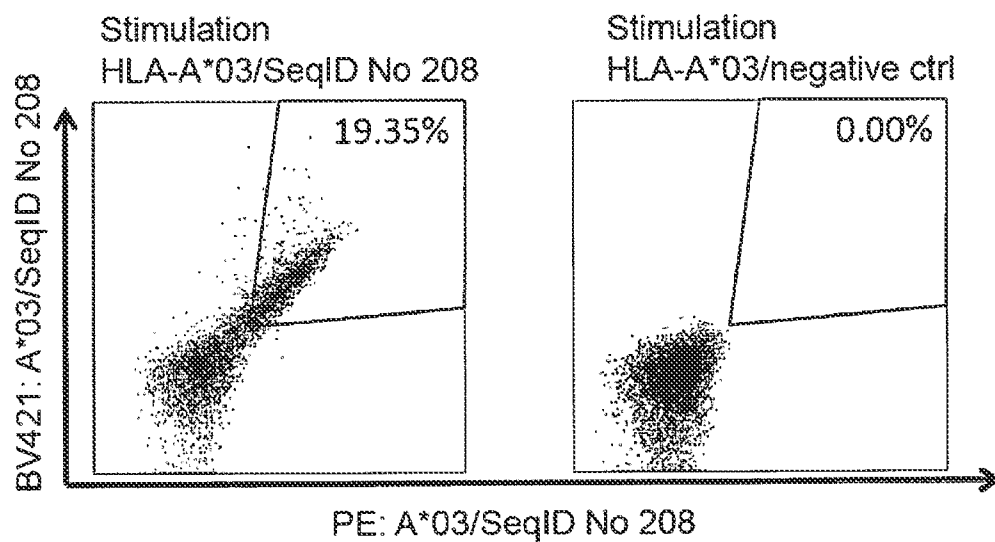


Figure 7B

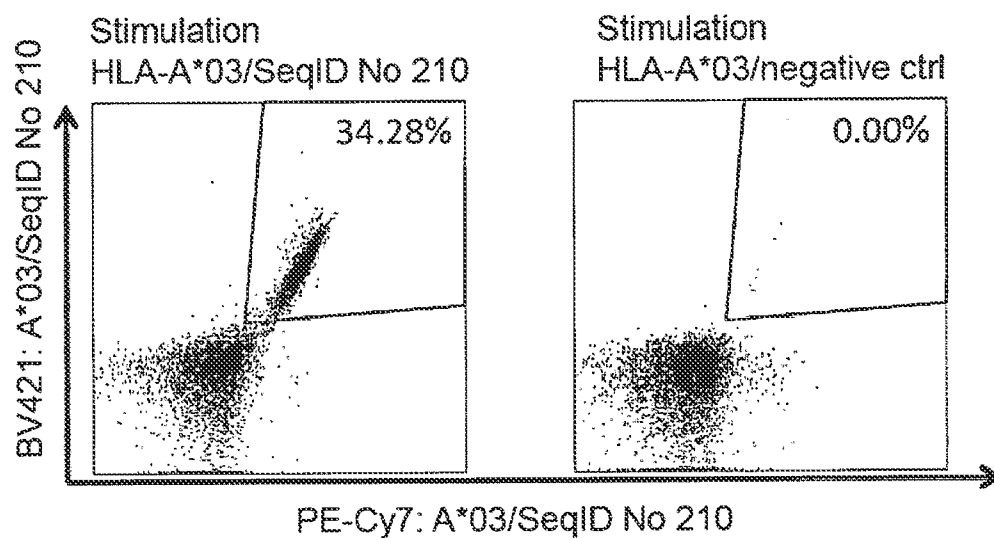


Figure 8A

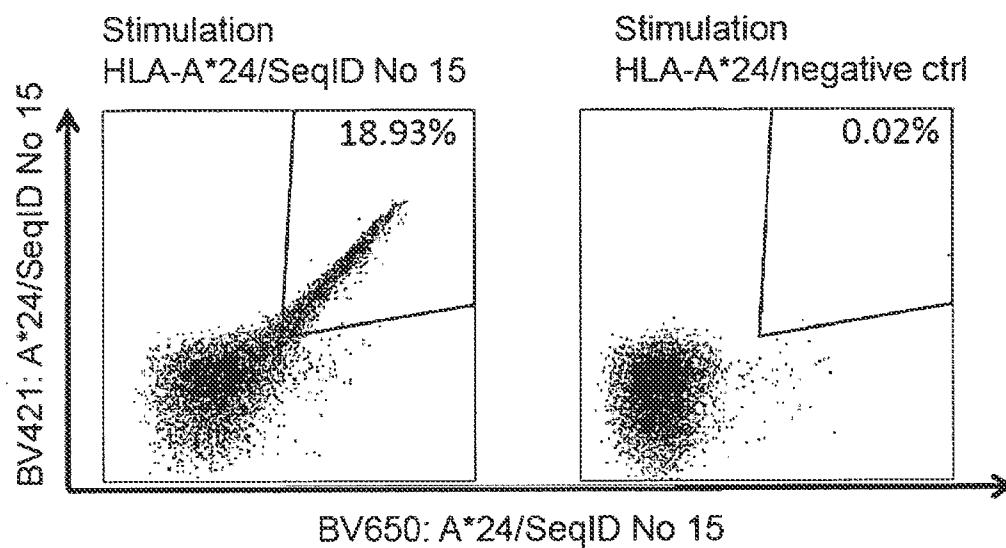


Figure 8B

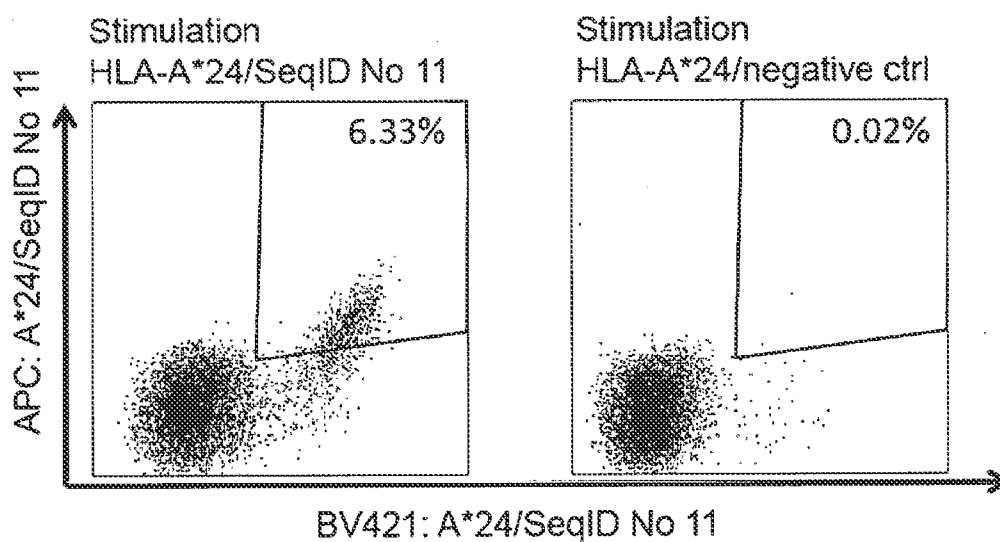


Figure 9A

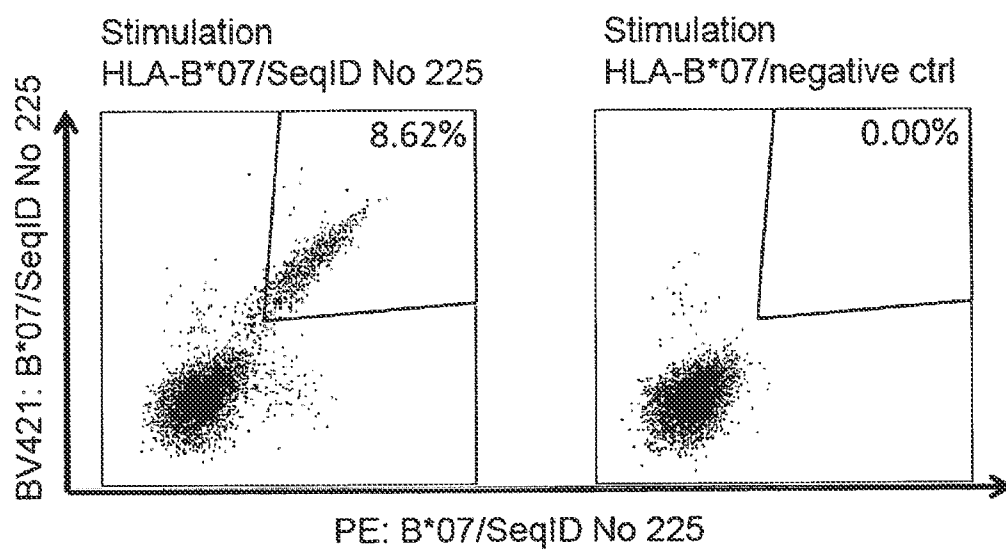


Figure 9B

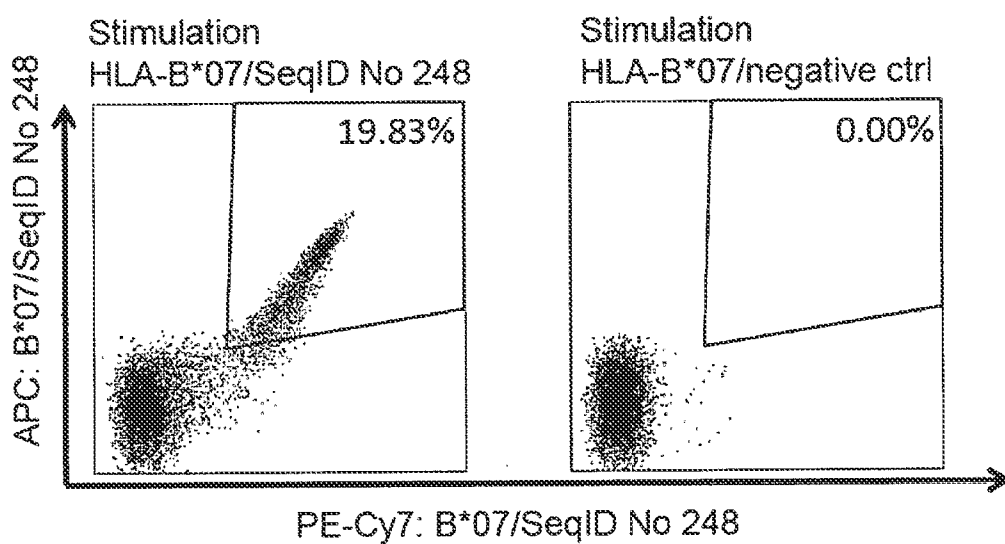


Figure 10A

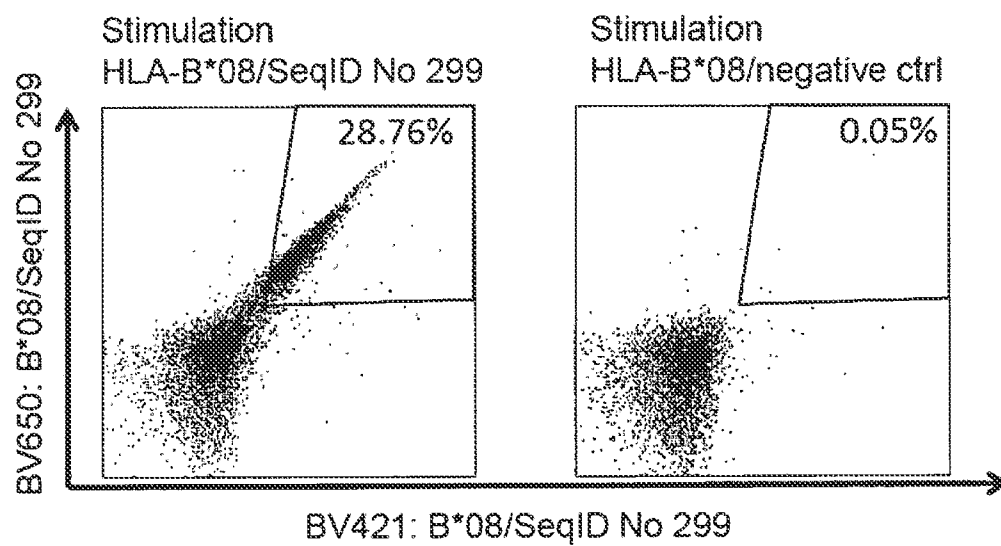


Figure 10B

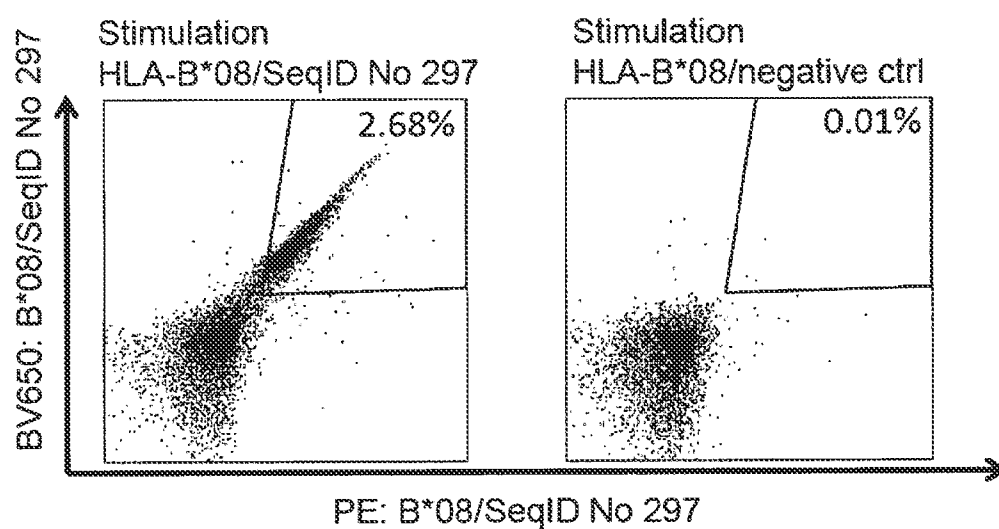


Figure 11A

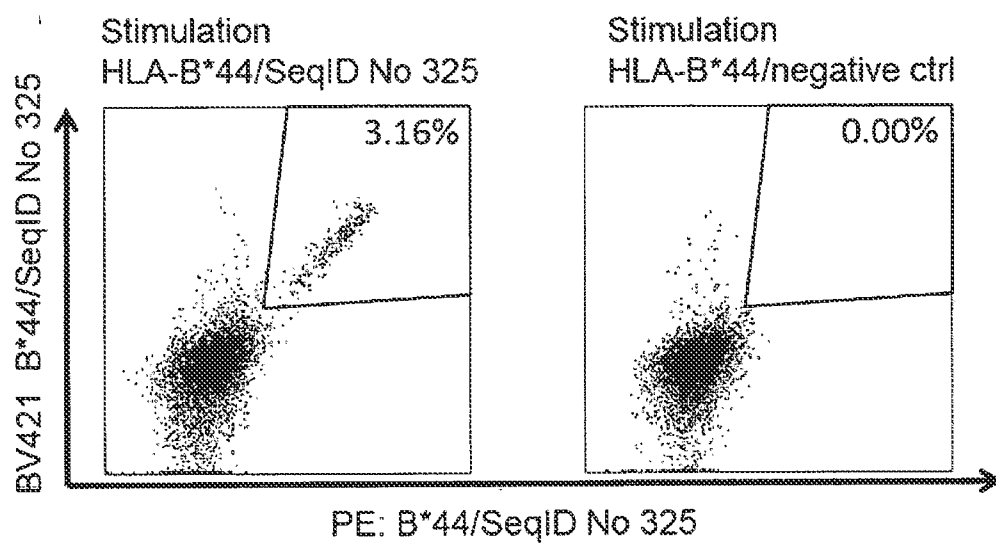
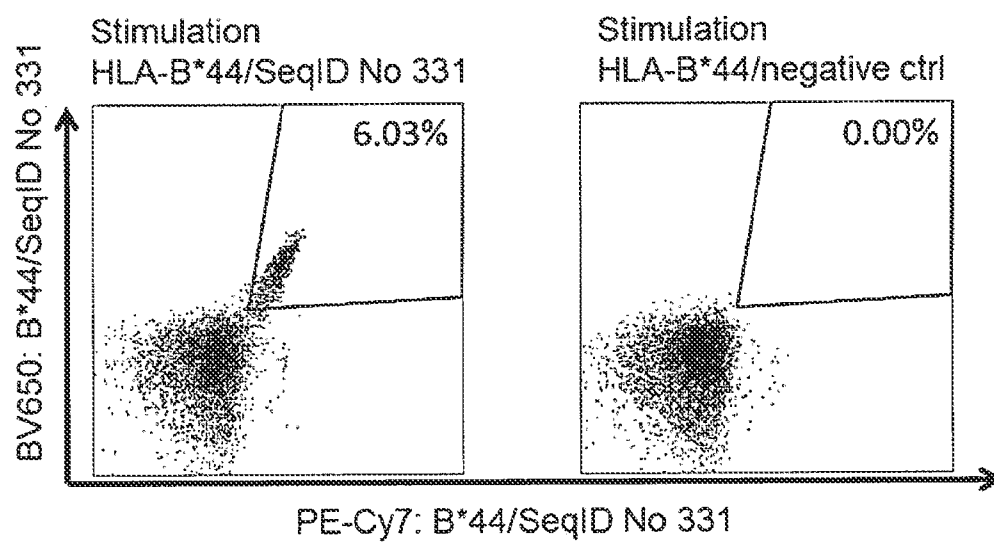


Figure 11B



**NOVEL PEPTIDES AND COMBINATION OF
PEPTIDES FOR USE IN IMMUNOTHERAPY
AGAINST LUNG CANCER, INCLUDING
NSCLC, SCLC AND OTHER CANCERS**

**CROSS REFERENCE TO RELATED
APPLICATIONS**

[0001] This application is a continuation of U.S. patent application Ser. No. 17/929,347, filed Sep. 2, 2022, which is a continuation of U.S. patent application Ser. No. 17/877,515, filed Jul. 29, 2022, which is a continuation of U.S. patent application Ser. No. 17/860,600, filed 8 Jul. 2022, which is a continuation of U.S. patent application Ser. No. 17/371,755, filed 9 Jul. 2021, which is a continuation of U.S. patent application Ser. No. 17/227,885, filed 12 Apr. 2021, now U.S. Pat. No. 11,168,122, issued 9 Nov. 2021, which is a continuation of U.S. patent application Ser. No. 16/913,788, filed 26 Jun. 2020, now U.S. Pat. No. 11,001,616, issued 11 May 2021, which is a continuation of U.S. patent application Ser. No. 16/026,707, filed 3 Jul. 2018, now U.S. Pat. No. 10,800,823, issued 13 Oct. 2020, which claims priority to U.S. Provisional Application No. 62/529,758, filed 7 Jul. 2017, and German Patent Application Number 102017115301.2, filed 7 Jul. 2017. The content of each of these applications is herein incorporated by reference in their entirety.

[0002] This application is also related to PCT/EP2018/067979, filed 3 Jul. 2018, the content of which is incorporated herein by reference in its entirety.

**REFERENCE TO SEQUENCE LISTING
SUBMITTED AS A COMPLIANT ASCII TEXT
FILE (.xml)**

[0003] Pursuant to the EFS-Web legal framework and 37 CFR §§ 1.821-825 (see MPEP § 2442.03 (a)), a Sequence Listing in the form of an ASCII-compliant text file (entitled "Sequence_Listing_2912919-089058_ST26.xml" created on 22 Sep. 2022, and 458,914 bytes in size) is submitted concurrently with the instant application, and the entire contents of the Sequence Listing are incorporated herein by reference.

BACKGROUND

[0004] The present invention relates to peptides, proteins, nucleic acids and cells for use in immunotherapeutic methods. In particular, the present invention relates to the immunotherapy of cancer. The present invention furthermore relates to tumor-associated T-cell peptide epitopes, alone or in combination with other tumor-associated peptides that can for example serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses, or to stimulate T cells ex vivo and transfer into patients. Peptides bound to molecules of the major histocompatibility complex (MHC), or peptides as such, can also be targets of antibodies, soluble T-cell receptors, and other binding molecules.

[0005] The present invention relates to several novel peptide sequences and their variants derived from HLA class I molecules of human tumor cells that can be used in vaccine compositions for eliciting anti-tumor immune responses, or as targets for the development of pharmaceutically/immunologically active compounds and cells.

DESCRIPTION OF RELATED ART

[0006] Lung cancer accounts for the most cancer-related deaths in both men and women. Worldwide, lung cancer is the most common cancer in terms of both incidence and mortality. In 2012, there were more than 1.8 million new cases (13% of total cancer incidence), and 1.6 million deaths (20% of total cancer mortality) due to lung cancer. Lung cancer is the leading cause of cancer death in men in 87 countries and in women in 26 countries. More than one third of all newly diagnosed cases occurred in China. The highest rates are in North America, Europe, and East Asia (World Cancer Report, 2014).

[0007] Since 1987, more women have died each year from lung cancer than from breast cancer. Death rates have continued to decline significantly in men from 1991-2003 by about 1.9% per year. Female lung cancer death rates are approaching a plateau after continuously increasing for several decades. These trends in lung cancer mortality reflect the decrease in smoking rates over the past 30 years.

[0008] An estimated 230,000 new cases of lung cancer and 160,000 deaths due to lung cancer are expected in 2013 in the USA according to the national cancer institute (NCI).

[0009] Historically, small cell lung carcinoma (SCLC) has been distinguished from non-small cell lung carcinoma (NSCLC), which includes the histological types of adenocarcinoma, squamous cell carcinoma, and large cell carcinoma. However, in the past decade, the distinction between adenocarcinoma and squamous cell carcinoma has been increasingly recognized because of major differences in genetics and also in responses to specific therapies. Therefore, lung cancers are increasingly classified according to molecular subtypes, predicated on particular genetic alterations that drive and maintain lung tumorigenesis (Travis et al., 2013).

[0010] Prognosis is generally poor. Of all people with lung cancer, 10-15% survive for five years after diagnosis. Poor survival of lung cancer patients is due, at least in part, to 80% of patients being diagnosed with metastatic disease and more than half of patients having distant metastases (SEER Stat facts, 2014). At presentation, 30-40% of cases of NSCLC are stage IV, and 60% of SCLC are stage IV.

[0011] The 1-year relative survival for lung cancer has slightly increased from 35% in 1975-1979 to 44% in 2010, largely due to improvements in surgical techniques and combined therapies. However, the 5-year survival rate for all stages combined is only 17%. The survival rate is 54% for cases detected when the disease is still localized; however, only 16% of lung cancers are diagnosed at this early stage (SEER Stat facts, 2014).

[0012] Treatment options are determined by the type (small cell or non-small cell) and stage of cancer and include surgery, radiation therapy, chemotherapy, and targeted biological therapies such as bevacizumab (AVASTIN®) and erlotinib (TARCEVA®). For localized cancers, surgery is usually the treatment of choice. Recent studies indicate that survival with early-stage, non-small cell lung cancer is improved by chemotherapy following surgery. Because the disease has usually spread by the time it is discovered, radiation therapy and chemotherapy are often used, sometimes in combination with surgery. Chemotherapy alone or combined with radiation is the usual treatment of choice for small cell lung cancer; on this regimen, a large percentage of patients experience remission, which is long lasting in some cases surgery (S3-Leitlinie Lungenkarzinom, 2011).

[0013] Advanced lung cancer has also been resistant to traditional chemotherapy. However, recent advances have led to exciting progress in therapies that are dependent on histology and genetics. The level of scrutiny is exemplified by trials of adjuvant chemotherapy designed to differentiate not only between mutations in codons 12 and 13 of KRAS, but also between different amino acid substitutions as determined by particular mutations at codon 12 (Shepherd et al., 2013).

[0014] To expand the therapeutic options for NSCLC, different immunotherapeutic approaches have been studied or are still under investigation. While vaccination with L-BLP25 or MAGEA3 failed to demonstrate a vaccine-mediated survival advantage in NSCLC patients, an allogeneic cell line-derived vaccine showed promising results in clinical studies. Additionally, further vaccination trials targeting gangliosides, the epidermal growth factor receptor and several other antigens are currently ongoing. An alternative strategy to enhance the patient's anti-tumor T cell response consists of blocking inhibitory T cell receptors or their ligands with specific antibodies. The therapeutic potential of several of these antibodies, including ipilimumab, nivolumab, pembrolizumab, MPDL3280A and MEDI-4736, in NSCLC is currently evaluated in clinical trials (Reinmuth et al., 2015).

[0015] Considering the severe side-effects and expense associated with treating cancer, there is a need to identify factors that can be used in the treatment of cancer in general and lung cancer (including NSCLC and SCLC) in particular. There is also a need to identify factors representing biomarkers for cancer in general and lung cancer (including NSCLC and SCLC), leading to better diagnosis of cancer, assessment of prognosis, and prediction of treatment success.

[0016] Immunotherapy of cancer represents an option of specific targeting of cancer cells while minimizing side effects. Cancer immunotherapy makes use of the existence of tumor associated antigens.

[0017] The current classification of tumor associated antigens (TAAs) comprises the following major groups:

[0018] a) Cancer-testis antigens: The first TAAs ever identified that can be recognized by T cells belong to this class, which was originally called cancer-testis (CT) antigens because of the expression of its members in histologically different human tumors and, among normal tissues, only in spermatocytes/spermatogonia of testis and, occasionally, in placenta. Since the cells of testis do not express class I and II HLA molecules, these antigens cannot be recognized by T cells in normal tissues and can therefore be considered as immunologically tumor-specific. Well-known examples for CT antigens are the MAGE family members and NY-ESO-1.

[0019] b) Differentiation antigens: These TAAs are shared between tumors and the normal tissue from which the tumor arose. Most of the known differentiation antigens are found in melanomas and normal melanocytes. Many of these melanocyte lineage-related proteins are involved in biosynthesis of melanin and are therefore not tumor specific but nevertheless are widely used for cancer immunotherapy. Examples include, but are not limited to, tyrosinase and Melan-A/MART-1 for melanoma or PSA for prostate cancer.

[0020] c) Over-expressed TAAs: Genes encoding widely expressed TAAs have been detected in histologically different types of tumors as well as in many normal tissues,

generally with lower expression levels. It is possible that many of the epitopes processed and potentially presented by normal tissues are below the threshold level for T-cell recognition, while their over-expression in tumor cells can trigger an anticancer response by breaking previously established tolerance. Prominent examples for this class of TAAs are Her-2/neu, survivin, telomerase, or WT1.

[0021] d) Tumor-specific antigens: These unique TAAs arise from mutations of normal genes (such as β -catenin, CDK4, etc.). Some of these molecular changes are associated with neoplastic transformation and/or progression. Tumor-specific antigens are generally able to induce strong immune responses without bearing the risk for autoimmune reactions against normal tissues. On the other hand, these TAAs are in most cases only relevant to the exact tumor on which they were identified and are usually not shared between many individual tumors. Tumor-specificity (or -association) of a peptide may also arise if the peptide originates from a tumor-(-associated) exon in case of proteins with tumor-specific (-associated) isoforms.

[0022] e) TAAs arising from abnormal post-translational modifications: Such TAAs may arise from proteins which are neither specific nor overexpressed in tumors but nevertheless become tumor associated by posttranslational processes primarily active in tumors. Examples for this class arise from altered glycosylation patterns leading to novel epitopes in tumors as for MUC1 or events like protein splicing during degradation which may or may not be tumor specific.

[0023] f) Oncoviral proteins: These TAAs are viral proteins that may play a critical role in the oncogenic process and, because they are foreign (not of human origin), they can evoke a T-cell response. Examples of such proteins are the human papilloma type 16 virus proteins, E6 and E7, which are expressed in cervical carcinoma.

[0024] T-cell based immunotherapy targets peptide epitopes derived from tumor-associated or tumor-specific proteins, which are presented by molecules of the major histocompatibility complex (MHC). The antigens that are recognized by the tumor specific T lymphocytes, that is, the epitopes thereof, can be molecules derived from all protein classes, such as enzymes, receptors, transcription factors, etc. which are expressed and, as compared to unaltered cells of the same origin, usually up-regulated in cells of the respective tumor.

[0025] There are two classes of MHC-molecules, MHC class I and MHC class II. MHC class I molecules are composed of an alpha heavy chain and beta-2-microglobulin, MHC class II molecules of an alpha and a beta chain. Their three-dimensional conformation results in a binding groove, which is used for non-covalent interaction with peptides.

[0026] MHC class I molecules can be found on most nucleated cells. They present peptides that result from proteolytic cleavage of predominantly endogenous proteins, defective ribosomal products (DRIPs) and larger peptides. However, peptides derived from endosomal compartments or exogenous sources are also frequently found on MHC class I molecules. This non-classical way of class I presentation is referred to as cross-presentation in the literature (Brossart and Bevan, 1997; Rock et al., 1990). MHC class II molecules can be found predominantly on professional antigen presenting cells (APCs), and primarily present peptides of exogenous or transmembrane proteins that are taken

up by APCs e.g. during endocytosis, and are subsequently processed. Complexes of peptide and MHC class I are recognized by CD8-positive T cells bearing the appropriate T-cell receptor (TCR), whereas complexes of peptide and MHC class II molecules are recognized by CD4-positive-helper-T cells bearing the appropriate TCR. It is well known that the TCR, the peptide and the MHC are thereby present in a stoichiometric amount of 1:1:1.

[0027] CD4-positive helper T cells play an important role in inducing and sustaining effective responses by CD8-positive cytotoxic T cells. The identification of CD4-positive T-cell epitopes derived from tumor associated antigens (TAA) is of great importance for the development of pharmaceutical products for triggering anti-tumor immune responses (Gnjatic et al., 2003). At the tumor site, T helper cells, support a cytotoxic T cell- (CTL-) friendly cytokine milieu (Mortara et al., 2006) and attract effector cells, e.g. CTLs, natural killer (NK) cells, macrophages, and granulocytes (Hwang et al., 2007).

[0028] In the absence of inflammation, expression of MHC class II molecules is mainly restricted to cells of the immune system, especially professional antigen-presenting cells (APC), e.g., monocytes, monocyte-derived cells, macrophages, dendritic cells. In cancer patients, cells of the tumor have been found to express MHC class II molecules (Dengjel et al., 2006).

[0029] Elongated (longer) peptides of the invention can act as MHC class II active epitopes.

[0030] T-helper cells, activated by MHC class II epitopes, play an important role in orchestrating the effector function of CTLs in anti-tumor immunity. T-helper cell epitopes that trigger a T-helper cell response of the TH1 type support effector functions of CD8-positive killer T cells, which include cytotoxic functions directed against tumor cells displaying tumor-associated peptide/MHC complexes on their cell surfaces. In this way tumor-associated T-helper cell peptide epitopes, alone or in combination with other tumor-associated peptides, can serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses.

[0031] It was shown in mammalian animal models, e.g., mice, that even in the absence of CD8-positive T lymphocytes, CD4-positive T cells are sufficient for inhibiting manifestation of tumors via inhibition of angiogenesis by secretion of interferon-gamma (IFN γ) (Beatty and Paterson, 2001; Mumberg et al., 1999). There is evidence for CD4 T cells as direct anti-tumor effectors (Braumuller et al., 2013; Tran et al., 2014).

[0032] Since the constitutive expression of HLA class II molecules is usually limited to immune cells, the possibility of isolating class II peptides directly from primary tumors was previously not considered possible. However, Dengjel et al. were successful in identifying a number of MHC Class II epitopes directly from tumors (WO 2007/028574, EP 1 760 088 B1).

[0033] Since both types of response, CD8 and CD4 dependent, contribute jointly and synergistically to the anti-tumor effect, the identification and characterization of tumor-associated antigens recognized by either CD8+ T cells (ligand: MHC class I molecule+peptide epitope) or by CD4-positive T-helper cells (ligand: MHC class II molecule+peptide epitope) is important in the development of tumor vaccines.

[0034] For an MHC class I peptide to trigger (elicit) a cellular immune response, it also must bind to an MHC-

molecule. This process is dependent on the allele of the MHC-molecule and specific polymorphisms of the amino acid sequence of the peptide. MHC-class-I-binding peptides are usually 8-12 amino acid residues in length and usually contain two conserved residues ("anchors") in their sequence that interact with the corresponding binding groove of the MHC-molecule. In this way, each MHC allele has a "binding motif" determining which peptides can bind specifically to the binding groove.

[0035] In the MHC class I dependent immune reaction, peptides not only have to be able to bind to certain MHC class I molecules expressed by tumor cells, they subsequently also have to be recognized by T cells bearing specific T cell receptors (TCR).

[0036] For proteins to be recognized by T-lymphocytes as tumor-specific or -associated antigens, and to be used in a therapy, prerequisites must be fulfilled. The antigen should be expressed mainly by tumor cells and not, or in comparably small amounts, by normal healthy tissues. In a preferred embodiment, the peptide should be over-presented by tumor cells as compared to normal healthy tissues. It is furthermore desirable that the respective antigen is not only present in a type of tumor, but also in high concentrations (i.e. copy numbers of the respective peptide per cell). Tumor-specific and tumor-associated antigens are often derived from proteins directly involved in transformation of a normal cell to a tumor cell due to their function, e.g. in cell cycle control or suppression of apoptosis. Additionally, downstream targets of the proteins directly causative for a transformation may be up-regulated and thus may be indirectly tumor-associated. Such indirect tumor-associated antigens may also be targets of a vaccination approach (Singh-Jasuja et al., 2004). It is essential that epitopes are present in the amino acid sequence of the antigen, in order to ensure that such a peptide ("immunogenic peptide"), being derived from a tumor associated antigen, leads to an in vitro or in vivo T-cell-response.

[0037] Basically, any peptide able to bind an MHC molecule may function as a T-cell epitope. A prerequisite for the induction of an in vitro or in vivo T-cell-response is the presence of a T cell having a corresponding TCR and the absence of immunological tolerance for this particular epitope.

[0038] Therefore, TAAs are a starting point for the development of a T cell based therapy including but not limited to tumor vaccines. The methods for identifying and characterizing the TAAs are usually based on the use of T-cells that can be isolated from patients or healthy subjects, or they are based on the generation of differential transcription profiles or differential peptide expression patterns between tumors and normal tissues. However, the identification of genes over-expressed in tumor tissues or human tumor cell lines, or selectively expressed in such tissues or cell lines, does not provide precise information as to the use of the antigens being transcribed from these genes in an immune therapy. This is because only an individual subpopulation of epitopes of these antigens are suitable for such an application since a T cell with a corresponding TCR has to be present and the immunological tolerance for this particular epitope needs to be absent or minimal. In a very preferred embodiment of the invention it is therefore important to select only those over- or selectively presented peptides against which a functional and/or a proliferating T cell can be found. Such a functional T cell is defined as a T cell, which upon stimulation with a

specific antigen can be clonally expanded and is able to execute effector functions (“effector T cell”).

[0039] In case of targeting peptide-MHC by specific TCRs (e.g. soluble TCRs) and antibodies or other binding molecules (scaffolds) according to the invention, the immunogenicity of the underlying peptides is secondary. In these cases, the presentation is the determining factor.

SUMMARY

[0040] In a first aspect of the present invention, the present invention relates to a peptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 489 or a variant sequence thereof which is at least 77%, preferably at least 88%, homologous (preferably at least 77% or at least 88% identical) to SEQ ID NO: 1 to SEQ ID NO: 489, wherein said variant binds to MHC and/or induces T cells cross-reacting with said peptide, or a pharmaceutical acceptable salt thereof, wherein said peptide is not the underlying full-length polypeptide.

[0041] The present invention further relates to a peptide of the present invention comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 489 or a variant thereof, which is at least 77%, preferably at least 88%, homologous (preferably at least 77% or at least 88% identical) to SEQ ID NO: 1 to SEQ ID NO: 489, wherein said peptide or variant thereof has an overall length of between 8 and 100, preferably between 8 and 30, and most preferred of between 8 and 14 amino acids.

[0042] The following tables show the peptides according to the present invention, their respective SEQ ID NOs, and the prospective source (underlying) genes for these peptides. In Table 1, peptides with SEQ ID NO: 1 to SEQ ID NO: 83 bind to HLA-A*24, peptides with SEQ ID NO: 84 to SEQ ID NO: 133 bind to HLA-A*02, peptides with SEQ ID NO: 134 to SEQ ID NO: 201 bind to HLA-A*01, peptides with SEQ ID NO: 202 to SEQ ID NO: 219 bind to HLA-A*03, peptides with SEQ ID NO: 220 to SEQ ID NO: 295 bind to HLA-B*07, peptides with SEQ ID NO: 296 to SEQ ID NO: 318 bind to HLA-B*08, peptides with SEQ ID NO: 319 to SEQ ID NO: 374 bind to HLA-B*44. The peptides in Table 2 have been disclosed before in large listings as results of high-throughput screenings with high error rates or calculated using algorithms, but have not been associated with cancer at all before. In Table 2, peptides with SEQ ID NO: 375 to SEQ ID NO: 387 bind to HLA-A*24, peptides with SEQ ID NO: 388 to SEQ ID NO: 393 bind to HLA-A*02, peptides with SEQ ID NO: 394 to SEQ ID NO: 452 bind to HLA-A*01, peptides with SEQ ID NO: 453 to SEQ ID NO: 458 bind to HLA-A*03, peptides with SEQ ID NO: 459 to SEQ ID NO: 475 bind to HLA-B*07, peptides with SEQ ID NO: 476 to SEQ ID NO: 489 bind to HLA-B*44. The peptides in Table 3 are additional peptides that may be useful in combination with the other peptides of the invention. In Table 3, peptides with SEQ ID NO: 490 to SEQ ID NO: 508 bind to HLA-A*24, peptides with SEQ ID NO: 509 to SEQ ID NO: 528 bind to HLA-A*02, peptides with SEQ ID NO: 529 to SEQ ID NO: 530 bind to HLA-B*07, peptide with SEQ ID NO: 531 binds to HLA-B*44.

TABLE 1

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
1	QYDPTPLTW	ADAMTS12	A*24
2	VWSNVTPLEKF	MMP12	A*24
3	YLEKFYGL	MMP12	A*24
4	SYEKVINYL	MAGEA9, MAGEA9B	A*24
5	RYMKKDYL	SLC35D3	A*24
6	KYKDYFPVI	MAGEC2, LOC392555	A*24
7	VQQWSVAVF	PTHLH	A*24/B*15
8	PFLPPAACFF	ASCL1	A*24
9	RILRFPWQL	MMP11	A*24/A*32
10	VWSDVTPLNF	MMP13	A*24
11	YYSKSVGFMQW	FAM111B	A*24
12	STIRGELFFF	MMP11	A*24/B*57
13	HYTYILEVF	SLC7A11	A*24
14	SYSSCYSF	KRT13, KRT17	A*24
15	KYALLQDL	PLEKHG4B	A*24
16	TYNPDFSSL	SP9	A*24
17	YYADKKTFIVL	SCN9A	A*24

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
18	DYIGSVEKW	HS6ST2	A*24
19	ILKEDPFLF	MACC1	A*24
20	EFTTVLYNF	TP63	A*24
21	SYEVRSTF	TAS2R38	A*24
22	TQPGDWTLF	POSTN	A*24/B*15
23	KFIISDWRF	FAM83A	A*24
24	MYPDLSELLM	NUP155	A*24
25	SYNGYVFYL	ROS1	A*24
26	KTPTNYLFL	NMUR2	A*24/B*35
27	NYTLYPITF	GXYLT1	A*24
28	YYSIISHTL	ROS1	A*24
29	VYPLLSRLYW	ROS1	A*24
30	QYLPGWTVLFL	SLC22A31	A*24
31	QYQNVLTW	DST	A*24
32	SLPDLTPTF	LAMB3	A*24
33	KSSVIASLLF	TMTC3	A*24/B*57
34	MQPRMFPLF	FGD6	A*24
35	KYLEESVWL	GPR98	A*24
36	KQMEDGHTLF	UHRF1	A*24/B*15
37	QWPWQASLQF	TMPRSS3	A*24
38	KYTNWKAFI	MBTD1	A*24
39	LIFMLANVF	GABRP	A*24/A*32
40	QYEPPSAPSTTF	DROSHA	A*24
41	VIYFMGAIF	OR7E24	A*24/B*15
42	TLPNTIYRF	ROS1	A*24
43	IQMDEPMAF	CDC7	A*24/B*15
44	AYLSAVGTF	ABCC1	A*24
45	KYFVPPQLF	B3GNT6	A*24
46	AFPVTSIFHTF	KCNG1, KCNG2	A*24
47	KYADYFLEV	CCNJ	A*24
48	VFIDHPVHLKF	TENM4	A*24
49	LYISEVRNI	DST	A*24
50	SYPELVKMVW	C5orf34	A*24
51	KYALLQEL	PLEKHG4	A*24
52	KYMKIFHKF	ZNF681	A*24
53	KYITNLEDL	TXNDC16	A*24

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
54	LLIKLLQTF	PRKDC	A*24/B*15
55	RWMDQRLVF	GABRP	A*24
56	VYMIEPLEL	ADAM23	A*24
57	YPSHQEF	POLA1	A*24
58	QFAAPLRGIYF	C1QTNF6	A*24
59	KYSTTFFMV	XPR1	A*24
60	TYLSIFDQL	SF3A3	A*24
61	NYAENILTL	FIGNL1	A*24
62	LYQEILAQL	URB1	A*24
63	VMPSDSFFF	GAL3ST4	A*24
64	NYAIFDEGHML	SMARCAD1	A*24
65	VYPASKMFPFI	CKAP5	A*24
66	IYFRDSSFL	TEP1	A*24
67	RYPGKFYRV	ZAK	A*24
68	IYQQIIQTY	NCAPG2	A*24
69	IMPEKFEFW	CHD2	A*24
70	PYTNVTFDF	CNOT6, CNOT6L, CNOT6LP1	A*24
71	SYMVLAPVF	SPIN1, SPNS1	A*24
72	RYEGILYTI	LSM14A, LSM14B	A*24
73	SYIGLPLTL	NPC1	A*24
74	VYDQYFITL	ATP8B2	A*24
75	NYIYSISVF	PLAA	A*24
76	WYGWHFPEL	NOP58	A*24
77	AYTLLGHEFV	CDC27	A*24
78	TWFPKTPMLF	KBTBD2	A*24
79	RYLADLPTL	CEP85	A*24
80	YYSPLRDLL	Rasa3	A*24
81	LYPEGLRLL	ATP6V0D2	A*24
82	RFLPSPVVI	CUL3	A*24
83	TYCQNIKEF	EIF3H	A*24
84	YVDINTFRL	MMP12	A*02
85	YIDEFQSLV	RTL1	A*02
86	FVIDGFDEL	NLRP2	A*02
87	TLYPYQISQL	KIF26B	A*02
88	VQMVITEAQKV	LAMC2	A*02
89	ILSTTMVTV	KIF26B	A*02

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
90	FLLMHPSI	NDST4	A*02
91	FALPGLLHA	LAMB3	A*02
92	NLRDLLSEV	KIF26B	A*02
93	TLQEKILQV	MYO3A	A*02
94	VLPDIETLIGV	TET1	A*02
95	ITIGVLARV	CEACAM6	A*02
96	HLVGGLHTV	DACH1, DACH2	A*02
97	VLALVNSTV	CBFA2T2	A*02
98	LQSSGLTLLL	MSLN1	A*02/B*13
99	FLKEKVPGL	CDKAL1	A*02
100	RQYPTPFQL	ZNF280C	A*02/B*48
101	FIISDWRFVL	FAM83A	A*02
102	SLLEQAIAL	ST18	A*02
103	FLYYPDPVL	PLXNA1	A*02
104	GMLDIFWGV	RASSF6	A*02
105	SLLTHIPTA	PLEKHG4	A*02
106	FIIDTTYPAYV	FAP	A*02
107	LLQGAIESV	PLEKHG4	A*02
108	MIIALSLYI	GPR33	A*02
109	LLGSIGLLGV	OPN3	A*02
110	LLADFQALL	CCDC87	A*02
111	ALCLLLHLL	MRGPRE	A*02
112	SVSDGIHSV	CELSR1	A*02
113	AVLTGLVEV	LRBA	A*02
114	ILDERQVLL	ITGAE	A*02
115	MLLETQDALYV	ADORA2B	A*02
116	VLMEENSKL	HAP1	A*02
117	FLDPNARPLV	CAD	A*02
118	ALSSVLHSI	FGD6	A*02
119	RTADITVTV	ITGAE	A*02
120	ALLANLPAV	SLC26A9	A*02
121	ALVDTLTGI	IPO9	A*02
122	ALLEMFPEITV	TXNDC16	A*02
123	LMAFFLAVV	OR6C75	A*02
124	SVASVLLYL	PRKDC	A*02
125	VLQPFLPSI	IPO9	A*02

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
126	FLSTVTSV	SOGA2	A*02
127	GLDGSLVFL	MARCH6	A*02
128	FLGTTPTL	SF3B3	A*02
129	VLVDKDAVYV	BMS1	A*02
130	NLWGGQGLLGV	GORASP2	A*02
131	LLKEFVQRV	COL6A3	A*02
132	ALWLVDPLTV	SLC33A1	A*02
133	MTLPVDAVISV	UFSP2	A*02
134	AAEIGDKSWLY	PLA2G7	A*01
135	ASEDSVLLY	CHAF1B	A*01
136	ATDLVVLDY	DICER1	A*01
137	ATSKFMEFY	EDNRA	A*01
138	DSDSCHFNY	DCBLD2	A*01
139	ECDMAFHIY	UHRF1, LOC728688	A*01
140	ESDREELNY	CBFA2T2	A*01
141	ESDVGVVY	DDX60L	A*01
142	EVAEPSVLFDLY	C9orf114	A*01
143	FIDYPKKEDY	PLAU	A*01
144	FLDSQNLSAY	BBS1, DPP3	A*01
145	FVDKPVAY	TAF1B	A*01
146	GLNTGSALSY	COL6A3	A*01/B*15
147	GSSDSSTLPKL	TDRD5	A*01
148	GTEFTTILY	TP73	A*01
149	GTEFTTVLY	TP63	A*01
150	GTELLSLVY	PRKDC	A*01
151	HSDLKVGEY	DICER1	A*01
152	HTDSLHLI	ANKRD52, FLJ25613	A*01
153	KLDRSVFTAY	FAM111B	A*01
154	LLDISQKNLY	ZNF439	A*01
155	LLDPNPHMY	RGS17	A*01
156	LLDSLREQY	SESTD1	A*01
157	LMDRPIFY	GALNS	A*01
158	LSDLKQGY	PKD2L1	A*01
159	LSDTSVIQFY	C16orf62	A*01
160	LTEAVLNRY	KIF26B	A*01
161	LVDDGTHGQY	TRPM2	A*01

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
162	LVDNSIRELQY	CARD8	A*01
163	NSDSSLTLREFY	FSTL4	A*01
164	NTDNNLAVY	CXorf61	A*01
165	NTDPTAPPY	CDH3	A*01
166	NTQITDIGRY	HMCN1	A*01
167	QSDPGTSVLGY	SEZ6	A*01
168	QTDHPQPILDRY	ITGAE	A*01
169	RLDTPLYFSY	LEPRE1	A*01
170	RSDDTAVYY	IGHA1, IGHA2, IGHD, IGHG3, IGHV1-18, IGHV1-2, IGHV4-31	A*01
171	RSDPVTNLNLY	CEACAM6, PSG1, PSG2, PSG4, PSG5, PSG7, PSG8	A*01
172	RTDSCSSAQAY	DCBLD2	A*01
173	RTEFNLNQY	COL12A1	A*01
174	SADDIRGIQSLY	MMP12	A*01
175	SDVTPLTF	MMP11	A*01
176	SRTINVSPLY	LAMA1	A*01
177	SSDEVNFLVY	TBL1XR1	A*01
178	SSDSSTLPKL	TDRD5	A*01/C*12
179	STAKSATWTY	TP63, TP73	A*01
180	STDPWQMAY	KDM1B	A*01
181	TADGKTYYY	TCERG1	A*01
182	TDYHVRVY	FNDC3B	A*01
183	TLEDIATSHLY	CBFA2T2	A*01
184	TSAHPEDSSFY	LOC731467, TRBV20-1	A*01
185	TSDSNLNKY	KCNH7	A*01
186	TTDIEKY	DDX60L	A*01
187	VADLHLYLY	GARS	A*01
188	VSDAKLDKY	RCOR2, LOC441644	A*01
189	VSDSECLSRV	LAMA1	A*01
190	VTGGINPLIDRY	FREM2	A*01
191	VTGGSLEYGVAY	DSE	A*01
192	VTEESFDSKFY	CDKAL1	A*01
193	VTEFSLNTY	COL6A3	A*01
194	VVADTKMIEY	ADAMTS12	A*01
195	VVDSVGGYLY	ROS1	A*01

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
196	WMFFVINY	TMEM217	A*01
197	YADTVRPEFY	COL6A3	A*01
198	YLDPVQRDLV	ZNF655	A*01
199	YLPQHTIETY	TP63	A*01/B*15
200	YSDDEVTKY	SDK2	A*01
201	YVGKEHMFY	MAGEA9, MAGEA9B	A*01
202	KLAELEGALQK	KRT81, KRT121P, KRT83, KRT85, KRT86	A*03
203	KVKDTPGLGK	KIF26B	A*03
204	AVFDKFIRY	BTBD17	A*03
205	SLDGAARPK	SP6	A*03
206	KLIDLSQVMY	MACC1	A*03/B*15
207	RSFNGLLTMY	LAMB3	A*03/B*15
208	GLASRILDAK	LAMB3	A*03
209	RTQIPMSEK	RASSF6	A*03
210	ATSGVPVYK	SLC44A5	A*03
211	TVNPVAIHK	GLI2	A*03
212	KAYEQVMHY	FOXA2	A*03
213	LNINMTSPMGTK	PCSK2	A*03
214	RTMSEAALVRK	RASSF6	A*03
215	MMFSGPQILKL	ABCC1	A*03/A*32
216	KLYAWELAF	ABCC1	A*03/A*32
217	RILNQILYY	FGD6	A*03
218	KTLVAELLILK	POLQ	A*03
219	RLRSSLVFK	FAM83B	A*03
220	SPSVSQLSVL	PRAME	B*07
221	VPDVAQFVL	MMP1	B*07
222	NPFYPEVEL	MMP1	B*07
223	YPKDIYSSF	MMP1	B*07
224	GPQFWHAAL	MMP11	B*07
225	LPFDGPGGIL	MMP11	B*07
226	SPRMSGLLSQT	DLL3	B*07
227	YPRGNHWAVGH	GRP	B*07
228	YPRGNHWAVGHL	GRP	B*07
229	VPLPAGGGTV	GRP	B*07
230	VPLPAGGGTVL	GRP	B*07
231	RPRALRDLQL	NLRP7	B*07

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
232	RPRALRDLQLL	NLRP7	B*07
233	KPYQGNPTF	DNAH17	B*07
234	RAKNAGVTI	LAMC2	B*07
235	MPLKHYLLL	LRRC15	B*07
236	RVRGGEDGDRAI	INSM1	B*07
237	RPAATAVISL	SLC7A11	B*07
238	KPGPPWAAF	DCBLD2	B*07
239	YVPSASLFML	E2F7	B*07
240	SPREVTTVL	DCBLD2	B*07
241	SARLATDAL	FAM83A	B*07
242	SPRWLPVSL	BTBD17	B*07
243	RPIENRILIL	PSG1, PSG3, PSG4, PSG5, PSG6, PSG7, PSG8, PSG9	B*07
244	FPYVRDFVM	COL6A3	B*07/B*35
245	RIREHVPQL	COL6A3	B*07
246	TPLPAVIVL	SLC7A11	B*07
247	RALLARLLL	PLAU	B*07
248	IPNWARQDL	NLRP7	B*07
249	VPSSRILQL	THEG	B*07
250	SPRDFLSGL	ABCA2, TPH1	B*07
251	VPRSSGQTV	SP6	B*07
252	SPDIRNTTV	DCBLD2	B*07
253	RVIDAVRFTL	TP63	B*07
254	NPFPHLITL	ROS1	B*07
255	MPLLENLYL	MXRA5	B*07
256	SPRVPSIEL	COL7A1	B*07
257	LPRIPFADV	ROS1	B*07
258	LPRGPLASL	CDH3	B*07
259	RPPAAGLRGISL	SEZ6L	B*07
260	YPQHPLNA	SOX2	B*07
261	APSARVGVC	KRT86	B*07
262	SAYPQRLEI	CYP24A1	B*07/B*51
263	HPAPYGDLL	GLI2	B*07
264	RPILIIITL	TP73	B*07
265	SPRQPPRLV	CYP24A1	B*07
266	HAYPPGPGL	MMP10	B*07/C*03

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
267	HPELVNHIVF	GALNT5	B*07/B*35
268	YPLFRGINL	COL5A1	B*07
269	APRAPRLML	ITGA3	B*07
270	APGPRFLVT	CD109	B*07
271	MPLPWSLALP	EGFL6	B*07/B*35
272	MPLPWSLALPL	EGFL6	B*07
273	MPLLWLRGF	INHBA	B*07/B*35
274	TPYQEHVAL	ZNF618	B*07/B*35
275	APHPPLSVV	IQGAP3	B*07
276	LPRAGGAPL	LAMB3	B*07
277	MPLFEPRVF	PTK7	B*07/B*35
278	HPMIDINGIIVF	COL5A1	B*07/B*35
279	SPARASPAL	TMPRSS13	B*07
280	VPISEEGTPVL	KIAA0754	B*07
281	RPRAPVTPA	HES6	B*07
282	MPQIETRVIL	ECT2	B*07
283	RPHSLSSEL	ITGAE	B*07
284	FPVTSIFHTF	KCNGL1, KCNG2	B*07/B*35
285	FPSFLTNSL	CEP192	B*07/B*35
286	VPTLRSEL	DST, MACF1	B*07
287	APREEQQRSL	KIAA1211	B*07
288	FPQKFIDLL	SASS6	B*07
289	VPENHSVAL	FAM83B	B*07
290	APYRPPDISL	TANC2	B*07
291	SPQRLRGLL	CTHRC1	B*07
292	SPQRLRGLLL	CTHRC1	B*07
293	RPRSALPRLLLP	FZD2	B*07
294	GPTPNTGAAL	COL6A3	B*07
295	KPEGTRIAV	COL6A3	B*07
296	MPMQDIKM	PRAME	B*08
297	RAQLKLVAL	KLHDC7B	B*08
298	FNKRKPLSL	NLRP2	B*08
299	MAQFKEISL	NLRP2	B*08
300	VASPKHCVL	KIF26B	B*08
301	YMHKLLVL	PTH2	B*08/B*35
302	HLQKQTSI	TP63	B*08

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
303	LPFPKFTV	GALNT5	B*08
304	ELKKLYCQI	TP63	B*08
305	ALKLRVAVL	C16orf59	B*08
306	ILKVKVGL	POSTN	B*08
307	ILLPRTVSL	MXRA5	B*08
308	MLKQKVEEL	DST	B*08
309	DAIQRKYSC	DST	B*08
310	LPPKKFVL	NUP155	B*08
311	EIRIRVVQM	PRKDC	B*08
312	EAMLRNKEL	CENPF	B*08
313	ELKKKEYEEL	CENPF	B*08
314	AIISRLVAL	TANC2	B*08
315	DIYQRALNL	VPS13B	B*08
316	VIKEKALTL	USP9X, USP9Y	B*08
317	LVKVKVLL	ARID4A	B*08
318	EAARSVEL	DSCR3	B*08
319	AEMLERVIKNI	MAGEA4	B*44
320	MEVDPIGHVYIF	MAGEA3, MAGEA6	B*44
321	AEMLESVIKNI	MAGEA1, MAGEA8, MAGEA9, MAGEA9B	B*44
322	KEVDPAGHSY	MAGEA8, MAGEA9, MAGEA9B	B*44
323	SEFMQVIF	MAGEA9, MAGEA9B	B*44
324	TDSIHAWTF	SLC35D3	B*44/B*18
325	QEQDVLVQKY	MMP1	B*44
326	QEMQHFLGL	MMP12	B*44
327	YEIEARNQVF	MMP12	B*44/B*18
328	FEYDFLLQRI	MMP12	B*44
329	NEHPSNNW	LAMC2	B*44
330	KEGDLGGKQW	ADAMTS12	B*44
331	EDAQGHIW	MMP11	B*44
332	MEVPVIKI	ECT2	B*44
333	AETLSTIQI	KIF26B	B*44
334	AEDEPAAHL	KIF26B	B*44
335	KELEATKQY	KIF26B	B*44
336	ASSSGPMRWW	LAMB3	B*44/B*57
337	TENRYCVQL	JUP, KRT13, KRT17	B*44

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
338	SEGSEPALLHSW	FAM83A	B*44
339	SEPALLHSW	FAM83A	B*44
340	TEFSLNTY	COL6A3	B*44
341	EEIEGKGSFTYF	POSTN	B*44
342	HEFSSPSHL	TP63	B*44
343	TEFTTVLY	TP63	B*44
344	EEATGQFHVY	CEACAM1, CEACAM3, CEACAM6	B*44
345	IEFIHPQAF	MXRA5	B*44
346	VEAPGPVHVYW	PTK7	B*44
347	ALNPYQYQY	DLX5	B*44/A*29
348	AEIQGNINHV	IQGAP3	B*44
349	AEQDMRELT	DST	B*44
350	GECDVFKEIL	DCBLD2	B*44
351	EEVNYINTF	CCNE2	B*44
352	NEVLTYIKF	ABCC5	B*44
353	GEIIMQNNW	SERTAD4	B*44
354	TEDPTILRI	PLXNA1	B*44
355	SDMVRFHLE	SGK196	B*44
356	EEGRVYLF	ITGA2	B*44
357	RELENCFQIQ	DNAH14	B*44
358	KEADIHFLI	COL6A5	B*44
359	DELFSLALY	NUP155	B*44
360	AEVPTGVII	ITGA2	B*44
361	SENLFASF	ITGA2	B*44
362	SEKGVIVQY	NUP155	B*44
363	AELDKLTSV	CENPF	B*44
364	AETPIQNV	MET	B*44
365	SEMNVNMKY	MET	B*44
366	AENLFRAF	PRKDC	B*44
367	GEVHPSEMI	PRKDC	B*44
368	GEFPVRVQV	YEATS2	B*44
369	EEIERFFKL	NUP155	B*44
370	YEDLSQKY	CENPF	B*44
371	GELALKKKI	PRKDC	B*44

TABLE 1-continued

Peptides according to the present invention.			
Seq ID No	Sequence	Gene(s)	HLA allotype
372	TEGIIMKDF	MET	B*44
373	MEMQKSPVF	FSTL4, GRM7, LOC440173, LOC644919, LOC728755, SLC44A5	B*44
374	DEVNFLVY	TBL1X, TBL1XR1, TBL1Y	B*44/B*18

TABLE 2

Additional peptides according to the present invention with no prior known cancer association.			
Seq ID No	Sequence	Gene(s)	HLA allotype
375	VYSDLHAFYY	MANEAL	A*24
376	KYVKDFHKF	ZNF724P	A*24
377	VYVGAVNRI	PLXNA1	A*24
378	KFLGPAEHLTF	PROM2	A*24
379	NYIVPDQKQIF	POLA1	A*24
380	VFQEKHHVI	MOXD1	A*24
381	TYSKKHFRI	CHEK2	A*24
382	IYHSHHPTL	OPA1	A*24
383	RYKQDVERF	SMC5	A*24
384	KYVKVFDKF	ZNF107	A*24
385	MYINEVERL	PTPN14	A*24
386	VYNDHSIYVW	MAPKBP1	A*24
387	RWLPQKNAAQF	DOCK5, PPP2R2A	A*24
388	FSIPEGALVAV	ABCC1	A*02
389	TLMEQPLTTL	TXNDC16	A*02
390	HIMPTVHTV	ADNP2	A*02
391	SLIDMRGIETV	SMC6	A*02
392	SLFKDQMEL	IPO8	A*02
393	ILLPYLQTL	TIPARP	A*02
394	ASEAEMRLFY	DHX37	A*01
395	ASEASRLAHY	HIST1H2BA, HIST1H2BL, HIST3H2BB	A*01
396	ASEFGNHLYL	SF3B3	A*01
397	ASEITSKGASLY	CLUAP1	A*01
398	ASEQQALHTVQY	NUP188	A*01
399	ATDIPCLLY	RINT1	A*01

TABLE 2-continued

Additional peptides according to the present invention with no prior known cancer association.			
Seq ID No	Sequence	Gene(s)	HLA allotype
400	ATDISRQNEY	PDE7A	A*01
401	DSDESYMEKSLY	CLSPN	A*01
402	DTDSQRLAY	E2F1	A*01
403	ELDSKVEVLTY	SNX7	A*01
404	ETARKFLYY	GPD2	A*01
405	ETEEGIYWRY	KREMEN2	A*01
406	ETEQTKEWDY	FUT11	A*01
407	FSDNDKLYLY	RFX5	A*01
408	FTEQWTDGY	TLK2	A*01
409	FVDPLVTNY	TRIT1	A*01
410	GSDHQSPSSSSY	ZBTB43	A*01
411	GTVYEDLRY	UBE2C	A*01
412	ILDEVIMGY	KIF11	A*01
413	ISDRYYTALY	CEBPZ	A*01
414	KTDESLTKY	CHD8	A*01
415	LLDPRSHTY	DOCK8	A*01
416	LLDTAQKNLY	ZNF614	A*01
417	LLEDKHFQSY	WDR6	A*01
418	LSDPSGPKSY	RPS6KC1	A*01
419	LSELKPMSY	TMTC3	A*01
420	LTEDEKTLQY	TUBGCP2	A*01
421	LTELLERAAFY	SLC15A4	A*01
422	MIDVTKSY	DCTN5	A*01
423	NLDAVHDITVAY	LCLAT1	A*01
424	NLDEEKQLLY	FRMD6	A*01

TABLE 2-continued

Additional peptides according to the present invention with no prior known cancer association.			
Seq ID No	Sequence	Gene(s)	HLA allotype
425	NLDIIQQEY	WDR75	A*01
426	NLDQATRVAY	SMC4	A*01
427	NSDEQKITEMVY	LRBA	A*01
428	NSELSCQLY	TYMS	A*01
429	NTEDSSMSGYLY	FGD6	A*01
430	NTEGLHHLY	SMEK2, SMEK3P	A*01
431	NTSDMMGRMSY	ARID1A	A*01
432	NVDPVQHTY	AGRN	A*01
433	QIDTGENLY	ZNF267	A*01
434	QTDCAPNNGY	NOMO1, NOMO2, NOMO3	A*01
435	QTDDTWRTY	ZMYM2	A*01
436	QTETGTPYMLY	RRM1	A*01
437	STDGKHWWEY	CCNT1, CCNT2	A*01
438	STDNFNCKY	FGD6	A*01
439	TLDAGKFQIY	DHX15	A*01
440	TLDENPGVRY	STXBP3	A*01
441	TLDSALNAASY	TCTN3	A*01
442	TSDFSFRFTNY	CCNE2	A*01
443	TTDFPSESSFY	CXorf21	A*01
444	TTDTVIRSY	SETD4	A*01
445	VLDQKGKITEY	ABCB10	A*01
446	VTAQVVGTERY	PLD2	A*01
447	VVDEDEHLY	CHST11	A*01
448	YLDIPNPRY	CIT	A*01
449	YLDRTGNVSFY	TRIM4	A*01
450	YSDDGQKWTVY	DCBLD2	A*01
451	YSDSLVQKGY	MSH6	A*01
452	YVDAVLGKGHQY	NUP160	A*01
453	AINTSIKNK	TRPM8	A*03
454	KVYTPSISK	CDKAL1	A*03
455	RIADIFVKK	FGD6	A*03
456	SMFTAILKK	LRBA	A*03
457	SINKPTSER	NDC80	A*03
458	GIADFVLKY	RNFT2	A*03

TABLE 2-continued

Additional peptides according to the present invention with no prior known cancer association.			
Seq ID No	Sequence	Gene(s)	HLA allotype
459	RPMQQARAQL	KLHDC7B	B*07
460	MPMAGDMNGL	TP63	B*07
461	RPILIIIVTL	TP63	B*07
462	RPFHTRATV	KIF26B	B*07
463	TPKAGPTL	KIF26B	B*07
464	YPRPGTPAA	CDKAL1	B*07
465	VPRPIFSQL	GREB1, GREB1L	B*07
466	APYKSVTSL	FGD6	B*07
467	KPFSSFTSM	RASSF6	B*07
468	SPMYGQAGL	FOXA2	B*07
469	YPENGVVQM	UHRF1	B*07
470	SPNSYFRVL	PCDHB13, PCDHB8	B*07
471	KPRPDVTNEL	CDCA7	B*07
472	NPRATDAQL	LRBA	B*07
473	LPRALLSSL	IL4I1	B*07
474	LPRLLPAL	HEATR2	B*07
475	RPHKPGLYL	MANEA	B*07
476	AEEEIMKKI	IGF2BP3	B*44
477	QENSYQSRL	LAMC2	B*44
478	SEIEQEIGSL	LAMC2	B*44
479	AEIQPQTQV	PTK7	B*44
480	GEVSGLTADF	CDKAL1	B*44
481	RELQHEHSL	FAT1	B*44
482	TEREWADEW	CBFA2T2	B*44
483	EENDQSTHKW	YEATS2	B*44
484	AEVGFVRFF	MSH2	B*44
485	SEIEDSTKQVF	BRCA2	B*44
486	SEDDPILQI	NUP155	B*44
487	AEDQLHHSF	GXYLT1	B*44
488	TEFPPIIKMY	TXNDC16	B*44
489	SEIGKAVGF	CLSPN	B*44

TABLE 3

Peptides according to the present invention useful for e.g. personalized cancer therapies.			
Seq ID No	Sequence	Gene(s)	HLA allotype
490	SYVKVLHHL	MAGEA12, LOC101060230	A*24
491	KYLEKYNNL	MMP1	A*24
492	NYEDHFPLL	MAGEA10	A*24
493	TYKYVDINTF	MMP12	A*24
494	RYLEKPYGL	MMP12	A*24
495	SYNDALLTF	TRPM8	A*24
496	VFMKDGFFYF	MMP1	A*24
497	NYPKSIHSF	MMP12	A*24
498	EYIRALQQL	ASCL1	A*24
499	VYFVAPAKF	LAMC2	A*24
500	VWSDVTPLTF	MMP11	A*24
501	GYIDNVTLI	LAMC2	A*24
502	SVHKITSTF	LAMC2	A*24
503	VHFEDTGKTLF	MMP13	A*24
504	VYEKNGYIYF	MMP13	A*24
505	AYISGLDVF	DNAH17	A*24
506	RYVFPLPYL	SOX14	A*24
507	VYIAELEKI	SMC1B	A*24
508	IYVTGGHLF	KLHDC7B	A*24
509	ALLEEEEGV	MAGEA4	A*02
510	KVLEHVVRV	MAGEA4, MAGEA8	A*02
511	KIWEELSVLEV	MAGEA3, MAGEA6	A*02
512	VLGEEQEGV	MAGEA9, MAGEA9B	A*02
513	KLVELEHTL	CXorf61	A*02
514	VQLDSIEDLEV	PRAME	A*02
515	KIFEMLEGV	CT45A1, CT45A2, CT45A3, CT45A4, CT45A5, CT45A6, LOC101060208, LOC101060210, LOC101060211	A*02
516	YTFSGDVQL	MMP1	A*02
517	TLYNPERTITV	IGF2BP1, IGF2BP3	A*02
518	GLLEDERALQL	MEX3A	A*02
519	KIQEILTQV	IGF2BP3	A*02
520	KIQEMQHFL	MMP12	A*02
521	FVYGEPREL	MAGEC2, LOC392555	A*02

TABLE 3-continued

Peptides according to the present invention useful for e.g. personalized cancer therapies.			
Seq ID No	Sequence	Gene(s)	HLA allotype
522	TLDEKVAEL	MAGEC2	A*02
523	HLIAEIHTA	PTHLH	A*02
524	KVWSDVTPL	MMP11, MMP13	A*02
525	RLDDLKMTV	LAMC2	A*02
526	VLSFFILTL	KLHDC7B	A*02
527	LLDSVSRL	LAMC2	A*02
528	RLLDSVSRL	LAMC2	A*02
529	HPSAHDVIL	LAMC2	B*07
530	APAAWLRSAA	MMP11	B*07
531	AEIEADRSY	LAMC2	B*44

[0043] The present invention furthermore generally relates to the peptides according to the present invention for use in the treatment of proliferative diseases, such as, for example, acute myeloid leukemia, breast cancer, bile duct cancer, brain cancer, chronic lymphocytic leukemia, colorectal carcinoma, esophageal cancer, gallbladder cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular cancer, melanoma, non-Hodgkin lymphoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer, urinary bladder cancer, uterine cancer.

[0044] Particularly preferred are the peptides—alone or in combination—according to the present invention selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 489. More preferred are the peptides—alone or in combination—selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 374 (see Table 1), and their uses in the immunotherapy of lung cancer (including NSCLC and SCLC), acute myeloid leukemia, breast cancer, bile duct cancer, brain cancer, chronic lymphocytic leukemia, colorectal carcinoma, esophageal cancer, gallbladder cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular cancer, melanoma, non-Hodgkin lymphoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer, urinary bladder cancer, uterine cancer, and preferably lung cancer (including NSCLC and SCLC).

[0045] Thus, another aspect of the present invention relates to the use of the peptides according to the present invention for the—preferably combined—treatment of a proliferative disease selected from the group of lung cancer (including NSCLC and SCLC), acute myeloid leukemia, breast cancer, bile duct cancer, brain cancer, chronic lymphocytic leukemia, colorectal carcinoma, esophageal cancer, gallbladder cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular cancer, melanoma, non-Hodgkin lymphoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer, urinary bladder cancer, uterine cancer.

[0046] The present invention furthermore relates to peptides according to the present invention that have the ability to bind to a molecule of the human major histocompatibility

complex (MHC) class-I or—in an elongated form, such as a length-variant—MHC class-II.

[0047] The present invention further relates to the peptides according to the present invention wherein said peptides (each) consist or consist essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 489.

[0048] The present invention further relates to the peptides according to the present invention, wherein said peptide is modified and/or includes non-peptide bonds.

[0049] The present invention further relates to the peptides according to the present invention, wherein said peptide is part of a fusion protein, in particular fused to the N-terminal amino acids of the HLA-DR antigen-associated invariant chain (Ii), or fused to (or into the sequence of) an antibody, such as, for example, an antibody that is specific for dendritic cells.

[0050] The present invention further relates to a nucleic acid, encoding the peptides according to the present invention. The present invention further relates to the nucleic acid according to the present invention that is DNA, cDNA, PNA, RNA or combinations thereof.

[0051] The present invention further relates to an expression vector capable of expressing and/or expressing a nucleic acid according to the present invention.

[0052] The present invention further relates to a peptide according to the present invention, a nucleic acid according to the present invention or an expression vector according to the present invention for use in the treatment of diseases and in medicine, in particular in the treatment of cancer.

[0053] The present invention further relates to antibodies that are specific against the peptides according to the present invention or complexes of said peptides according to the present invention with MHC, and methods of making these.

[0054] The present invention further relates to T-cell receptors (TCRs), in particular soluble TCR (sTCRs) and cloned TCRs engineered into autologous or allogeneic T cells, and methods of making these, as well as NK cells or other cells bearing said TCR or cross-reacting with said TCRs.

[0055] The antibodies and TCRs are additional embodiments of the immunotherapeutic use of the peptides according to the invention at hand.

[0056] The present invention further relates to a host cell comprising a nucleic acid according to the present invention or an expression vector as described before. The present invention further relates to the host cell according to the present invention that is an antigen presenting cell, and preferably is a dendritic cell.

[0057] The present invention further relates to a method for producing a peptide according to the present invention, said method comprising culturing the host cell according to the present invention, and isolating the peptide from said host cell or its culture medium.

[0058] The present invention further relates to said method according to the present invention, wherein the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell or artificial antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell.

[0059] The present invention further relates to the method according to the present invention, wherein the antigen-presenting cell comprises an expression vector capable of expressing or expressing said peptide containing SEQ ID

No. 1 to SEQ ID No. 489, preferably containing SEQ ID No. 1 to SEQ ID No. 374, or a variant amino acid sequence.

[0060] The present invention further relates to activated T cells, produced by the method according to the present invention, wherein said T cell selectively recognizes a cell which expresses a polypeptide comprising an amino acid sequence according to the present invention.

[0061] The present invention further relates to a method of killing target cells in a patient which target cells aberrantly express a polypeptide comprising any amino acid sequence according to the present invention, the method comprising administering to the patient an effective number of T cells as produced according to the present invention.

[0062] The present invention further relates to the use of any peptide as described, the nucleic acid according to the present invention, the expression vector according to the present invention, the cell according to the present invention, the activated T lymphocyte, the T cell receptor or the antibody or other peptide- and/or peptide-MHC-binding molecules according to the present invention as a medicament or in the manufacture of a medicament. Preferably, said medicament is active against cancer.

[0063] Preferably, said medicament is a cellular therapy, a vaccine or a protein based on a soluble TCR or antibody.

[0064] The present invention further relates to a use according to the present invention, wherein said cancer cells are lung cancer (including NSCLC and SCLC), acute myeloid leukemia, breast cancer, bile duct cancer, brain cancer, chronic lymphocytic leukemia, colorectal carcinoma, esophageal cancer, gallbladder cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular cancer, melanoma, non-Hodgkin lymphoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer, urinary bladder cancer, uterine cancer, and preferably lung cancer (including NSCLC and SCLC) cells.

[0065] The present invention further relates to biomarkers based on the peptides according to the present invention, herein called “targets” that can be used in the diagnosis of cancer, preferably lung cancer (including NSCLC and SCLC). The marker can be over-presentation of the peptide (s) themselves, or over-expression of the corresponding gene(s). The markers may also be used to predict the probability of success of a treatment, preferably an immunotherapy, and most preferred an immunotherapy targeting the same target that is identified by the biomarker. For example, an antibody or soluble TCR can be used to stain sections of the tumor to detect the presence of a peptide of interest in complex with MHC.

[0066] Optionally the antibody carries a further effector function such as an immune stimulating domain or toxin.

[0067] The present invention also relates to the use of these novel targets in the context of cancer treatment.

DETAILED DESCRIPTION OF A PREFERRED EMBODIMENT

[0068] Stimulation of an immune response is dependent upon the presence of antigens recognized as foreign by the host immune system. The discovery of the existence of tumor associated antigens has raised the possibility of using a host's immune system to intervene in tumor growth. Various mechanisms of harnessing both the humoral and cellular arms of the immune system are currently being explored for cancer immunotherapy.

[0069] Specific elements of the cellular immune response are capable of specifically recognizing and destroying tumor cells. The isolation of T-cells from tumor-infiltrating cell populations or from peripheral blood suggests that such cells play an important role in natural immune defense against cancer. CD8-positive T-cells, which recognize class I molecules of the major histocompatibility complex (MHC)-bearing peptides of usually 8 to 10 amino acid residues derived from proteins or defect ribosomal products (DRIPS) located in the cytosol, play an important role in this response. The MHC-molecules of the human are also designated as human leukocyte-antigens (HLA).

[0070] As used herein and except as noted otherwise all terms are defined as given below.

[0071] The term “T-cell response” means the specific proliferation and activation of effector functions induced by a peptide in vitro or in vivo. For MHC class I restricted cytotoxic T cells, effector functions may be lysis of peptide-pulsed, peptide-precursor pulsed or naturally peptide-presenting target cells, secretion of cytokines, preferably Interferon-gamma, TNF-alpha, or IL-2 induced by peptide, secretion of effector molecules, preferably granzymes or perforins induced by peptide, or degranulation.

[0072] The term “peptide” is used herein to designate a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The peptides are preferably 9 amino acids in length, but can be as short as 8 amino acids in length, and as long as 10, 11, or 12 or longer, and in case of MHC class II peptides (elongated variants of the peptides of the invention) they can be as long as 13, 14, 15, 16, 17, 18, 19 or 20 or more amino acids in length.

[0073] Furthermore, the term “peptide” shall include salts of a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. Preferably, the salts are pharmaceutical acceptable salts of the peptides, such as, for example, the chloride or acetate (trifluoroacetate) salts. It has to be noted that the salts of the peptides according to the present invention differ substantially from the peptides in their state(s) in vivo, as the peptides are not salts in vivo.

[0074] The term “peptide” shall also include “oligopeptide”. The term “oligopeptide” is used herein to designate a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The length of the oligopeptide is not critical to the invention, as long as the correct epitope or epitopes are maintained therein. The oligopeptides are typically less than about 30 amino acid residues in length, and greater than about 15 amino acids in length.

[0075] The term “polypeptide” designates a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The length of the polypeptide is not critical to the invention as long as the correct epitopes are maintained. In contrast to the terms peptide or oligopeptide, the term polypeptide is meant to refer to molecules containing more than about 30 amino acid residues.

[0076] A peptide, oligopeptide, protein or polynucleotide coding for such a molecule is “immunogenic” (and thus is an “immunogen” within the present invention), if it is capable

of inducing an immune response. In the case of the present invention, immunogenicity is more specifically defined as the ability to induce a T-cell response. Thus, an “immunogen” would be a molecule that is capable of inducing an immune response, and in the case of the present invention, a molecule capable of inducing a T-cell response. In another aspect, the immunogen can be the peptide, the complex of the peptide with MHC, oligopeptide, and/or protein that is used to raise specific antibodies or TCRs against it.

[0077] A class I T cell “epitope” requires a short peptide that is bound to a class I MHC receptor, forming a ternary complex (MHC class I alpha chain, beta-2-microglobulin, and peptide) that can be recognized by a T cell bearing a matching T-cell receptor binding to the MHC/peptide complex with appropriate affinity. Peptides binding to MHC class I molecules are typically 8-14 amino acids in length, and most typically 9 amino acids in length.

[0078] In humans, there are three different genetic loci that encode MHC class I molecules (the MHC-molecules of the human are also designated human leukocyte antigens (HLA)): HLA-A, HLA-B, and HLA-C. HLA-A*01, HLA-A*02, and HLA-B*07 are examples of different MHC class I alleles that can be expressed from these loci.

TABLE 4

Expression frequencies F of HLA-A*02, HLA-A*01, HLA-A*03, HLA-A*24, HLA-B*07, HLA-B*08 and HLA-B*44 serotypes. Haplotype frequencies Gf are derived from a study which used HLA-typing data from a registry of more than 6.5 million volunteer donors in the U.S. (Gragert et al., 2013). The haplotype frequency is the frequency of a distinct allele on an individual chromosome. Due to the diploid set of chromosomes within mammalian cells, the frequency of genotypic occurrence of this allele is higher and can be calculated employing the Hardy-Weinberg principle ($F = 1 - (1 - Gf)^2$).		
Allele	Population	Calculated phenotype from allele frequency (F)
A*02	African (N = 28557)	32.3%
	European Caucasian (N = 1242890)	49.3%
	Japanese (N = 24582)	42.7%
	Hispanic, S + Cent Amer. (N = 146714)	46.1%
	Southeast Asian (N = 27978)	30.4%
A*01	African (N = 28557)	10.2%
	European Caucasian (N = 1242890)	30.2%
	Japanese (N = 24582)	1.8%
	Hispanic, S + Cent Amer. (N = 146714)	14.0%
	Southeast Asian (N = 27978)	21.0%
A*03	African (N = 28557)	14.8%
	European Caucasian (N = 1242890)	26.4%
	Japanese (N = 24582)	1.8%
	Hispanic, S + Cent Amer. (N = 146714)	14.4%
	Southeast Asian (N = 27978)	10.6%
A*24	African (N = 28557)	2.0%
	European Caucasian (N = 1242890)	8.6%
	Japanese (N = 24582)	35.5%
	Hispanic, S + Cent Amer. (N = 146714)	13.6%
	Southeast Asian (N = 27978)	16.9%

TABLE 4-continued

Expression frequencies F of HLA-A*02, HLA-A*01, HLA-A*03, HLA-A*24, HLA-B*07, HLA-B*08 and HLA-B*44 serotypes. Haplotype frequencies Gf are derived from a study which used HLA-typing data from a registry of more than 6.5 million volunteer donors in the U.S. (Gragert et al., 2013). The haplotype frequency is the frequency of a distinct allele on an individual chromosome. Due to the diploid set of chromosomes within mammalian cells, the frequency of genotypic occurrence of this allele is higher and can be calculated employing the Hardy-Weinberg principle ($F = 1 - (1 - Gf)^2$).		
Allele	Population	Calculated phenotype from allele frequency (F)
B*07	African (N = 28557)	14.7%
	European Caucasian (N = 1242890)	25.0%
	Japanese(N = 24582)	11.4%
	Hispanic, S + Cent Amer. (N = 146714)	12.2%
	Southeast Asian (N = 27978)	10.4%
B*08	African (N = 28557)	6.0%
	European Caucasian (N = 1242890)	21.6%
	Japanese(N = 24582)	1.0%
	Hispanic, S + Cent Amer. (N = 146714)	7.6%
	Southeast Asian (N = 27978)	6.2%
B*44	African (N = 28557)	10.6%
	European Caucasian (N = 1242890)	26.9%
	Japanese(N = 24582)	13.0%
	Hispanic, S + Cent Amer. (N = 146714)	18.2%
	Southeast Asian (N = 27978)	13.1%

[0079] The peptides of the invention, preferably when included into a vaccine of the invention as described herein bind to A*02, A*01, A*03, A*24, B*07, B*08 or B*44. A vaccine may also include pan-binding MHC class II peptides. Therefore, the vaccine of the invention can be used to treat cancer in patients that are A*02-, A*01-, A*03-, A*24-, B*07-, B*08- or B*44-positive, whereas no selection for MHC class II allotypes is necessary due to the pan-binding nature of these peptides.

[0080] If A*02 peptides of the invention are combined with peptides binding to another allele, for example A*24, a higher percentage of any patient population can be treated compared with addressing either MHC class I allele alone. While in most populations less than 50% of patients could be addressed by either allele alone, a vaccine comprising HLA-A*24 and HLA-A*02 epitopes can treat at least 60% of patients in any relevant population. Specifically, the following percentages of patients will be positive for at least one of these alleles in various regions: USA 61%, Western Europe 62%, China 75%, South Korea 77%, Japan 86% (calculated from www.allelefrequencies.net).

TABLE 5

HLA alleles coverage in European Caucasian population (calculated from (Gragert et al., 2013)).				
	coverage (at least one A-allele)	combined with B*07	combined with B*44	combined with B*07 and B*44
A*02/A*01	70%	78%	78%	84%
A*02/A*03	68%	76%	76%	83%
A*02/A*24	61%	71%	71%	80%
A*01/A*03	52%	64%	65%	75%
A*01/A*24	44%	58%	59%	71%
A*03/A*24	40%	55%	56%	69%
A*02/A*01/A*03	84%	88%	88%	91%
A*02/A*01/A*24	79%	84%	84%	89%
A*02/A*03/A*24	77%	82%	83%	88%
A*01/A*03/A*24	63%	72%	73%	81%
A*02/A*01/A*03/A*24	90%	92%	93%	95%

[0081] In a preferred embodiment, the term “nucleotide sequence” refers to a heteropolymer of deoxyribonucleotides.

[0082] The nucleotide sequence coding for a particular peptide, oligopeptide, or polypeptide may be naturally occurring or they may be synthetically constructed. Generally, DNA segments encoding the peptides, polypeptides, and proteins of this invention are assembled from cDNA fragments and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene that is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

[0083] As used herein the term “a nucleotide coding for (or encoding) a peptide” refers to a nucleotide sequence coding for the peptide including artificial (man-made) start and stop codons compatible for the biological system the sequence is to be expressed by, for example, a dendritic cell or another cell system useful for the production of TCRs.

[0084] As used herein, reference to a nucleic acid sequence includes both single stranded and double stranded nucleic acid. Thus, for example for DNA, the specific sequence, unless the context indicates otherwise, refers to the single strand DNA of such sequence, the duplex of such sequence with its complement (double stranded DNA) and the complement of such sequence.

[0085] The term “coding region” refers to that portion of a gene which either naturally or normally codes for the expression product of that gene in its natural genomic environment, i.e., the region coding in vivo for the native expression product of the gene.

[0086] The coding region can be derived from a non-mutated (“normal”), mutated or altered gene, or can even be derived from a DNA sequence, or gene, wholly synthesized in the laboratory using methods well known to those of skill in the art of DNA synthesis.

[0087] The term “expression product” means the polypeptide or protein that is the natural translation product of the gene and any nucleic acid sequence coding equivalents resulting from genetic code degeneracy and thus coding for the same amino acid(s).

[0088] The term “fragment”, when referring to a coding sequence, means a portion of DNA comprising less than the complete coding region, whose expression product retains

essentially the same biological function or activity as the expression product of the complete coding region.

[0089] The term “DNA segment” refers to a DNA polymer, in the form of a separate fragment or as a component of a larger DNA construct, which has been derived from DNA isolated at least once in substantially pure form, i.e., free of contaminating endogenous materials and in a quantity or concentration enabling identification, manipulation, and recovery of the segment and its component nucleotide sequences by standard biochemical methods, for example, by using a cloning vector. Such segments are provided in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns, which are typically present in eukaryotic genes. Sequences of non-translated DNA may be present downstream from the open reading frame, where the same do not interfere with manipulation or expression of the coding regions.

[0090] The term “primer” means a short nucleic acid sequence that can be paired with one strand of DNA and provides a free 3'-OH end at which a DNA polymerase starts synthesis of a deoxyribonucleotide chain.

[0091] The term “promoter” means a region of DNA involved in binding of RNA polymerase to initiate transcription.

[0092] The term “isolated” means that the material is removed from its original environment (e.g., the natural environment, if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

[0093] The polynucleotides, and recombinant or immunogenic polypeptides, disclosed in accordance with the present invention may also be in “purified” form. The term “purified” does not require absolute purity; rather, it is intended as a relative definition, and can include preparations that are highly purified or preparations that are only partially purified, as those terms are understood by those of skill in the relevant art. For example, individual clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. Furthermore, a claimed polypeptide which has a purity of preferably 99.999%, or at least 99.99% or 99.9%; and even desirably 99% by weight or greater is expressly encompassed.

[0094] The nucleic acids and polypeptide expression products disclosed according to the present invention, as well as expression vectors containing such nucleic acids and/or such polypeptides, may be in “enriched form”. As used herein, the term “enriched” means that the concentration of the material is at least about 2, 5, 10, 100, or 1000 times its natural concentration (for example), advantageously 0.01%, by weight, preferably at least about 0.1% by weight. Enriched preparations of about 0.5%, 1%, 5%, 10%, and 20% by weight are also contemplated. The sequences, constructs, vectors, clones, and other materials comprising the present invention can advantageously be in enriched or isolated form. The term “active fragment” means a fragment, usually

of a peptide, polypeptide or nucleic acid sequence, that generates an immune response (i.e., has immunogenic activity) when administered, alone or optionally with a suitable adjuvant or in a vector, to an animal, such as a mammal, for example, a rabbit or a mouse, and also including a human, such immune response taking the form of stimulating a T-cell response within the recipient animal, such as a human. Alternatively, the “active fragment” may also be used to induce a T-cell response in vitro.

[0095] As used herein, the terms “portion”, “segment” and “fragment”, when used in relation to polypeptides, refer to a continuous sequence of residues, such as amino acid residues, which sequence forms a subset of a larger sequence. For example, if a polypeptide were subjected to treatment with any of the common endopeptidases, such as trypsin or chymotrypsin, the oligopeptides resulting from such treatment would represent portions, segments or fragments of the starting polypeptide. When used in relation to polynucleotides, these terms refer to the products produced by treatment of said polynucleotides with any of the endonucleases.

[0096] In accordance with the present invention, the term “percent identity” or “percent identical”, when referring to a sequence, means that a sequence is compared to a claimed or described sequence after alignment of the sequence to be compared (the “Compared Sequence”) with the described or claimed sequence (the “Reference Sequence”). The percent identity is then determined according to the following formula:

$$\text{percent identity} = 100[1 - (C/R)]$$

wherein C is the number of differences between the Reference Sequence and the Compared Sequence over the length of alignment between the Reference Sequence and the Compared Sequence, wherein

[0097] (i) each base or amino acid in the Reference Sequence that does not have a corresponding aligned base or amino acid in the Compared Sequence and

[0098] (ii) each gap in the Reference Sequence and

[0099] (iii) each aligned base or amino acid in the Reference Sequence that is different from an aligned base or amino acid in the Compared Sequence, constitutes a difference and

[0100] (iiii) the alignment has to start at position 1 of the aligned sequences;

[0101] and R is the number of bases or amino acids in the Reference Sequence over the length of the alignment with the Compared Sequence with any gap created in the Reference Sequence also being counted as a base or amino acid.

[0102] If an alignment exists between the Compared Sequence and the Reference Sequence for which the percent identity as calculated above is about equal to or greater than a specified minimum Percent Identity then the Compared Sequence has the specified minimum percent identity to the Reference Sequence even though alignments may exist in which the herein above calculated percent identity is less than the specified percent identity.

[0103] As mentioned above, the present invention thus provides a peptide comprising a sequence that is selected from the group of consisting of SEQ ID NO: 1 to SEQ ID NO: 489 or a variant thereof which is 88% homologous to SEQ ID NO: 1 to SEQ ID NO: 489, or a variant thereof that will induce T cells cross-reacting with said peptide. The peptides of the invention have the ability to bind to a

molecule of the human major histocompatibility complex (MHC) class-I or elongated versions of said peptides to class II.

[0104] In the present invention, the term “homologous” refers to the degree of identity (see percent identity above) between sequences of two amino acid sequences, i.e. peptide or polypeptide sequences. The aforementioned “homology” is determined by comparing two sequences aligned under optimal conditions over the sequences to be compared. Such a sequence homology can be calculated by creating an alignment using, for example, the ClustalW algorithm. Commonly available sequence analysis software, more specifically, Vector NTI, GENETYX or other tools are provided by public databases.

[0105] A person skilled in the art will be able to assess, whether T cells induced by a variant of a specific peptide will be able to cross-react with the peptide itself (Appay et al., 2006; Colombetti et al., 2006; Fong et al., 2001; Zaremba et al., 1997).

[0106] By a “variant” of the given amino acid sequence the inventors mean that the side chains of, for example, one or two of the amino acid residues are altered (for example by replacing them with the side chain of another naturally occurring amino acid residue or some other side chain) such that the peptide is still able to bind to an HLA molecule in substantially the same way as a peptide consisting of the given amino acid sequence in consisting of SEQ ID NO: 1 to SEQ ID NO: 489. For example, a peptide may be modified so that it at least maintains, if not improves, the ability to interact with and bind to the binding groove of a suitable MHC molecule, such as HLA-A*02 or -DR, and in that way, it at least maintains, if not improves, the ability to bind to the TCR of activated T cells.

[0107] These T cells can subsequently cross-react with cells and kill cells that express a polypeptide that contains the natural amino acid sequence of the cognate peptide as defined in the aspects of the invention. As can be derived from the scientific literature and databases (Rammensee et al., 1999; Godkin et al., 1997), certain positions of HLA binding peptides are typically anchor residues forming a core sequence fitting to the binding motif of the HLA receptor, which is defined by polar, electrophysical, hydrophobic and spatial properties of the polypeptide chains constituting the binding groove. Thus, one skilled in the art would be able to modify the amino acid sequences set forth in SEQ ID NO: 1 to SEQ ID NO 489, by maintaining the known anchor residues, and would be able to determine whether such variants maintain the ability to bind MHC class I or II molecules. The variants of the present invention retain the ability to bind to the TCR of activated T cells, which can subsequently cross-react with and kill cells that express a polypeptide containing the natural amino acid sequence of the cognate peptide as defined in the aspects of the invention.

[0108] The original (unmodified) peptides as disclosed herein can be modified by the substitution of one or more residues at different, possibly selective, sites within the peptide chain, if not otherwise stated. Preferably those substitutions are located at the end of the amino acid chain. Such substitutions may be of a conservative nature, for example, where one amino acid is replaced by an amino acid of similar structure and characteristics, such as where a hydrophobic amino acid is replaced by another hydrophobic amino acid. Even more conservative would be replacement

of amino acids of the same or similar size and chemical nature, such as where leucine is replaced by isoleucine. In studies of sequence variations in families of naturally occurring homologous proteins, certain amino acid substitutions are more often tolerated than others, and these are often show correlation with similarities in size, charge, polarity, and hydrophobicity between the original amino acid and its replacement, and such is the basis for defining “conservative substitutions.”

[0109] Conservative substitutions are herein defined as exchanges within one of the following five groups: Group 1-small aliphatic, nonpolar or slightly polar residues (Ala, Ser, Thr, Pro, Gly); Group 2-polar, negatively charged residues and their amides (Asp, Asn, Glu, Gln); Group 3-polar, positively charged residues (His, Arg, Lys); Group 4-large, aliphatic, nonpolar residues (Met, Leu, Ile, Val, Cys); and Group 5-large, aromatic residues (Phe, Tyr, Trp).

[0110] Less conservative substitutions might involve the replacement of one amino acid by another that has similar characteristics but is somewhat different in size, such as replacement of an alanine by an isoleucine residue. Highly non-conservative replacements might involve substituting an acidic amino acid for one that is polar, or even for one that is basic in character. Such “radical” substitutions cannot, however, be dismissed as potentially ineffective since chemical effects are not totally predictable and radical substitutions might well give rise to serendipitous effects not otherwise predictable from simple chemical principles.

[0111] Of course, such substitutions may involve structures other than the common L-amino acids. Thus, D-amino acids might be substituted for the L-amino acids commonly found in the antigenic peptides of the invention and yet still be encompassed by the disclosure herein. In addition, non-standard amino acids (i.e., other than the common naturally occurring proteinogenic amino acids) may also be used for substitution purposes to produce immunogens and immunogenic polypeptides according to the present invention.

[0112] If substitutions at more than one position are found to result in a peptide with substantially equivalent or greater antigenic activity as defined below, then combinations of those substitutions will be tested to determine if the combined substitutions result in additive or synergistic effects on the antigenicity of the peptide. At most, no more than 4 positions within the peptide would be simultaneously substituted.

[0113] A peptide consisting essentially of the amino acid sequence as indicated herein can have one or two non-anchor amino acids (see below regarding the anchor motif) exchanged without that the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or —II is substantially changed or is negatively affected, when compared to the non-modified peptide. In another embodiment, in a peptide consisting essentially of the amino acid sequence as indicated herein, one or two amino acids can be exchanged with their conservative exchange partners (see herein below) without that the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or —II is substantially changed, or is negatively affected, when compared to the non-modified peptide.

[0114] The amino acid residues that do not substantially contribute to interactions with the T-cell receptor can be modified by replacement with other amino acid whose incorporation does not substantially affect T-cell reactivity and does not eliminate binding to the relevant MHC. Thus,

apart from the proviso given, the peptide of the invention may be any peptide (by which term the inventors include oligopeptide or polypeptide), which includes the amino acid sequences or a portion or variant thereof as given.

TABLE 6

Variants and motif of the peptides according to SEQ ID NO: 4, 13, 90, 93, 138, 171, 202, 204, 224, 294, 306, 316, 322 and 327.									
Position	1	2	3	4	5	6	7	8	9
SEQ ID No 4	S	Y	E	K	V	I	N	Y	L
Variant		F							I
		F							F
		F							F
Position	1	2	3	4	5	6	7	8	9
SEQ ID No 13	H	Y	T	Y	I	L	E	V	F
Variant		F							L
		F							I
		F							L
Position	1	2	3	4	5	6	7	8	
SEQ ID No 90	F	L	L	M	H	P	S	I	
Variant								V	
								L	
								A	
								V	
		M							
		M						L	
		M						A	
		A						V	
		A							
		A						L	
		A						A	
		V						V	
		V							
		V						L	
		V						A	
		T						V	
		T							
		T						L	
		T						A	
		Q						V	
		Q							
		Q						L	
		Q						A	
Position	1	2	3	4	5	6	7	8	9
SEQ ID No 93	T	L	Q	E	K	I	L	Q	V
Variant									I
									L
									A
		M							
		M							I
		M							L
		M							A
		A							
		A							I
		A							L
		A							A
		V							
		V							I
		V							L
		V							A
		T							
		T							I
		T							L
		T							A
		Q							

TABLE 6-continued

Variants and motif of the peptides according to SEQ ID NO: 4, 13, 90, 93, 138, 171, 202, 204, 224, 294, 306, 316, 322 and 327.											
			Q						I		
			Q						L		
			Q						A		
Position	1	2	3	4	5	6	7	8	9		
SEQ ID No 138	D	S	D	S	C	H	F	N	Y		
Variant			E						A		
			E								
		T							A		
		T									
		T	E						A		
		T	E						A		
Position	1	2	3	4	5	6	7	8	9	10	11
SEQ ID No 171	R	S	D	P	V	T	L	N	V	L	Y
Variant			E								A
			E								A
		T									A
		T									A
		T	E								A
		T	E								A
Position	1	2	3	4	5	6	7	8	9	10	11
SEQ ID No 202	K	L	A	E	L	E	G	A	L	Q	K
Variant											Y
											R
											F
		I									
		I									Y
		I									R
		I									F
		M									
		M									Y
		M									R
		M									F
		V									
		V									Y
		V									R
		V									F
		T									
		T									Y
		T									R
		T									F
Position	1	2	3	4	5	6	7	8	9		
SEQ ID No 204	A	V	F	D	K	F	I	R	Y		
Variant		L							K		
		L									
		L							R		
		L							F		
		I							K		
		I									
		I							R		
		I							F		
		M							K		
		M									
		M							R		
		M							F		
									K		
									R		
									F		
									K		
		T									
		T									
		T							R		
		T							F		

TABLE 6-continued

Variants and motif of the peptides according to SEQ ID NO: 4, 13, 90, 93, 138, 171, 202, 204, 224, 294, 306, 316, 322 and 327.									
Position	1	2	3	4	5	6	7	8	9
SEQ ID No 224 Variant	G	P	Q	P	W	H	A	A	L F V M A I

Position	1	2	3	4	5	6	7	8	9	10
SEQ ID No 294 Variant	G	P	T	P	N	T	G	A	A	L F V M A I

Position	1	2	3	4	5	6	7	8
SEQ ID No 306 Variant	I	L	K	V	K	V	G	L V I M F R R R R R H H H H H R

TABLE 6-continued

Variants and motif of the peptides according to SEQ ID NO: 4, 13, 90, 93, 138, 171, 202, 204, 224, 294, 306, 316, 322 and 327.									
								R	
								R	V
								R	I
								R	M
								R	F
								H	
								H	V
								H	I
								H	M
								H	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I
								R	M
								R	F
								R	
								R	V
								R	I

[0116] The peptides of the invention can be elongated by up to four amino acids, that is 1, 2, 3 or 4 amino acids can be added to either end in any combination between 4:0 and 0:4. Combinations of the elongations according to the invention can be found in Table 7.

TABLE 7

Combinations of the elongations of peptides of the invention	
C-terminus	N-terminus
4	0
3	0 or 1
2	0 or 1 or 2
1	0 or 1 or 2 or 3
0	0 or 1 or 2 or 3 or 4
N-terminus	C-terminus
4	0
3	0 or 1
2	0 or 1 or 2
1	0 or 1 or 2 or 3
0	0 or 1 or 2 or 3 or 4

[0117] The amino acids for the elongation/extension can be the peptides of the original sequence of the protein or any other amino acid(s). The elongation can be used to enhance the stability or solubility of the peptides.

[0118] Thus, the epitopes of the present invention may be identical to naturally occurring tumor-associated or tumor-specific epitopes or may include epitopes that differ by no more than four residues from the reference peptide, as long as they have substantially identical antigenic activity.

[0119] In an alternative embodiment, the peptide is elongated on either or both sides by more than 4 amino acids, preferably to a total length of up to 30 amino acids. This may lead to MHC class II binding peptides. Binding to MHC class II can be tested by methods known in the art.

[0120] Accordingly, the present invention provides peptides and variants of MHC class I epitopes, wherein the peptide or variant has an overall length of from 8 and 100, from 9 and 100, from 10 and 100, from 11 and 100, from 12 and 100, preferably from 8 and 30, and from 9 and 30, from 10 and 30, from 11 and 30, from 12 and 30, most preferred from 8 and 14, from 9 and 14, from 10 and 14, from 11 and 14, from 12 and 14. The present invention further provides peptides and variants of MHC class I epitopes, wherein the peptide or variant has an overall length of namely 8, 9, 10, 11, 12, 13, or 14 amino acids, in case of the elongated class II binding peptides the length can also be 15, 16, 17, 18, 19, 20, 21 or 22 amino acids.

[0121] Of course, the peptide or variant according to the present invention will have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class I or II. Binding of a peptide or a variant to a MHC complex may be tested by methods known in the art.

[0122] Preferably, when the T cells specific for a peptide according to the present invention are tested against the substituted peptides, the peptide concentration at which the substituted peptides achieve half the maximal increase in lysis relative to background is no more than about 1 mM, preferably no more than about 1 μ M, more preferably no more than about 1 nM, and still more preferably no more than about 100 μ M, and most preferably no more than about 10 μ M. It is also preferred that the substituted peptide be recognized by T cells from more than one individual, at least two, and more preferably three individuals.

[0123] In a particularly preferred embodiment of the invention the peptide consists or consists essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 489.

[0124] "Consisting essentially of" shall mean that a peptide according to the present invention, in addition to the sequence according to any of SEQ ID NO: 1 to SEQ ID NO 489 or a variant thereof contains additional N- and/or C-terminally located stretches of amino acids that are not necessarily forming part of the peptide that functions as an epitope for MHC molecules epitope.

[0125] Nevertheless, these stretches can be important to provide an efficient introduction of the peptide according to the present invention into the cells. In one embodiment of the present invention, the peptide is part of a fusion protein which comprises, for example, the 80 N-terminal amino acids of the HLA-DR antigen-associated invariant chain (p33, in the following "Ii") as derived from the NCBI, GenBank Accession number X00497. In other fusions, the peptides of the present invention can be fused to an antibody as described herein, or a functional part thereof, in particular into a sequence of an antibody, so as to be specifically targeted by said antibody, or, for example, to or into an antibody that is specific for dendritic cells as described herein.

[0126] In addition, the peptide or variant may be modified further to improve stability and/or binding to MHC molecules in order to elicit a stronger immune response. Methods for such an optimization of a peptide sequence are well known in the art and include, for example, the introduction of reverse peptide bonds or non-peptide bonds.

[0127] In a reverse peptide bond, amino acid residues are not joined by peptide ($-\text{CO}-\text{NH}-$) linkages but the peptide bond is reversed. Such retro-inverso peptidomimetics may be made using methods known in the art, for example such as those described in Meziere et al (1997) (Meziere et al., 1997), incorporated herein by reference. This approach involves making pseudopeptides containing changes involving the backbone, and not the orientation of side chains. Meziere et al. (Meziere et al., 1997) show that for MHC binding and T helper cell responses, these pseudopeptides are useful. Retro-inverse peptides, which contain $\text{NH}-\text{CO}$ bonds instead of $\text{CO}-\text{NH}$ peptide bonds, are much more resistant to proteolysis.

[0128] A non-peptide bond is, for example, $-\text{CH}_2-\text{NH}$, $-\text{CH}_2\text{S}-$, $-\text{CH}_2\text{CH}_2-$, $-\text{CH}=\text{CH}-$, $-\text{COCH}_2-$, $-\text{CH}(\text{OH})\text{CH}_2-$, and $-\text{CH}_2\text{SO}-$. U.S. Pat. No. 4,897, 445 provides a method for the solid phase synthesis of non-peptide bonds ($-\text{CH}_2-\text{NH}$) in polypeptide chains which involves polypeptides synthesized by standard procedures and the non-peptide bond synthesized by reacting an amino aldehyde and an amino acid in the presence of NaCNBH_3 .

[0129] Peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, to enhance the stability, bioavailability, and/or affinity of the peptides. For example, hydrophobic groups such as carbobenzoxy, dansyl, or t-butyloxycarbonyl groups may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxy-carbonyl group may be placed at the peptides' amino termini. Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini.

[0130] Further, the peptides of the invention may be synthesized to alter their steric configuration. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer. Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well-known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or binding action of the peptides of the invention.

[0131] Similarly, a peptide or variant of the invention may be modified chemically by reacting specific amino acids either before or after synthesis of the peptide. Examples for such modifications are well known in the art and are summarized e.g. in R. Lundblad, *Chemical Reagents for Protein Modification*, 3rd ed. CRC Press, 2004 (Lundblad, 2004), which is incorporated herein by reference. Chemical modification of amino acids includes but is not limited to, modification by acylation, amidination, pyridoxylation of lysine, reductive alkylation, trinitrobenzylation of amino groups with 2,4,6-trinitrobenzene sulphonic acid (TNBS), amide modification of carboxyl groups and sulphhydryl modification by performic acid oxidation of cysteine to cysteic acid, formation of mercurial derivatives, formation of mixed disulphides with other thiol compounds, reaction with maleimide, carboxymethylation with iodoacetic acid or iodoacetamide and carbamoylation with cyanate at alkaline pH, although without limitation thereto. In this regard, the skilled person is referred to Chapter 15 of *Current Protocols In Protein Science*, Eds. Coligan et al. (John Wiley and Sons NY 1995-2000) (Coligan et al., 1995) for more extensive methodology relating to chemical modification of proteins.

[0132] Briefly, modification of e.g. arginyl residues in proteins is often based on the reaction of vicinal dicarbonyl compounds such as phenylglyoxal, 2,3-butanedione, and 1,2-cyclohexanedione to form an adduct. Another example is the reaction of methylglyoxal with arginine residues. Cysteine can be modified without concomitant modification of other nucleophilic sites such as lysine and histidine. As a result, a large number of reagents are available for the modification of cysteine. The websites of companies such as Sigma-Aldrich (www.sigma-aldrich.com) provide information on specific reagents.

[0133] Selective reduction of disulfide bonds in proteins is also common. Disulfide bonds can be formed and oxidized during the heat treatment of biopharmaceuticals. Woodward's Reagent K may be used to modify specific glutamic acid residues. N-(3-(dimethylamino)propyl)-N'-ethylcarbodiimide can be used to form intra-molecular crosslinks between a lysine residue and a glutamic acid residue. For example, diethylpyrocarbonate is a reagent for the modification of histidyl residues in proteins. Histidine can also be modified using 4-hydroxy-2-nonenal. The reaction of lysine residues and other α -amino groups is, for example, useful in binding of peptides to surfaces or the cross-linking of proteins/peptides. Lysine is the site of attachment of poly(ethylene)glycol and the major site of modification in the glycosylation of proteins. Methionine residues in proteins can be modified with e.g. iodoacetamide, bromoethylamine, and chloramine T.

[0134] Tetranitromethane and N-acetylimidazole can be used for the modification of tyrosyl residues. Cross-linking via the formation of dityrosine can be accomplished with hydrogen peroxide/copper ions.

[0135] Recent studies on the modification of tryptophan have used N-bromosuccinimide, 2-hydroxy-5-nitrobenzyl bromide or 3-bromo-3-methyl-2-(2-nitrophenylmercapto)-3H-indole (BPNS-skatole).

[0136] Successful modification of therapeutic proteins and peptides with PEG is often associated with an extension of circulatory half-life while cross-linking of proteins with glutaraldehyde, polyethylene glycol diacrylate and formaldehyde is used for the preparation of hydrogels. Chemical modification of allergens for immunotherapy is often achieved by carbamylation with potassium cyanate.

[0137] A peptide or variant, wherein the peptide is modified or includes non-peptide bonds is a preferred embodiment of the invention.

[0138] Another embodiment of the present invention relates to a non-naturally occurring peptide wherein said peptide consists or consists essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 489 and has been synthetically produced (e.g. synthesized) as a pharmaceutically acceptable salt. Methods to synthetically produce peptides are well known in the art. The salts of the peptides according to the present invention differ substantially from the peptides in their state(s) in vivo, as the peptides as generated in vivo are no salts. The non-natural salt form of the peptide mediates the solubility of the peptide, in particular in the context of pharmaceutical compositions comprising the peptides, e.g. the peptide vaccines as disclosed herein. A sufficient and at least substantial solubility of the peptide(s) is required in order to efficiently provide the peptides to the subject to be treated. Preferably, the salts are pharmaceutically acceptable salts of the peptides. These salts according to the invention include alkaline and earth alkaline salts such as salts of the Hofmeister series comprising as anions PO_4^{3-} , SO_4^{2-} , CH_3COO^- , Cl^- , Br^- , NO_3^- , ClO_4^- , SCN^- and as cations NH_4^+ , Rb^+ , K^+ , Na^+ , Cs^+ , Li^+ , Zn^{2+} , Mg^{2+} , Ca^{2+} , Mn^{2+} , Cu^{2+} and Ba^{2+} . Particularly salts are selected from $(\text{NH}_4)_3\text{PO}_4$, $(\text{NH}_4)_2\text{HPO}_4$, $(\text{NH}_4)_2\text{H}_2\text{PO}_4$, $(\text{NH}_4)_2\text{SO}_4$, $\text{NH}_4\text{CH}_3\text{COO}$, NH_4Cl , NH_4Br , NH_4NO_3 , NH_4ClO_4 , NH_4I , NH_4SCN , Rb_3PO_4 , Rb_2HPO_4 , RbH_2PO_4 , Rb_2SO_4 , $\text{Rb}_4\text{CH}_3\text{COO}$, Rb_4Cl , Rb_4Br , Rb_4NO_3 , Rb_4ClO_4 , Rb_4I , Rb_4SCN , K_3PO_4 , K_2HPO_4 , KH_2PO_4 , K_2SO_4 , KCH_3COO , KCl , KBr , KNO_3 , KClO_4 , KI , KSCN , Na_3PO_4 , Na_2HPO_4 , NaH_2PO_4 , Na_2SO_4 , NaCH_3COO , NaCl , NaBr , NaNO_3 , NaClO_4 , NaI , NaSCN , ZnCl_2 , Cs_3PO_4 , Cs_2HPO_4 , CsH_2PO_4 , Cs_2SO_4 , CsCH_3COO , CsCl , CsBr , CsNO_3 , CsClO_4 , CsI , CsSCN , Li_3PO_4 , Li_2HPO_4 , LiH_2PO_4 , Li_2SO_4 , LiCH_3COO , LiCl , LiBr , LiNO_3 , LiClO_4 , LiI , LiSCN , Cu_2SO_4 , $\text{Mg}_3(\text{PO}_4)_2$, Mg_2HPO_4 , $\text{Mg}(\text{H}_2\text{PO}_4)_2$, Mg_2SO_4 , $\text{Mg}(\text{CH}_3\text{COO})_2$, MgCl_2 , MgBr_2 , $\text{Mg}(\text{NO}_3)_2$, $\text{Mg}(\text{ClO}_4)_2$, MgI_2 , $\text{Mg}(\text{SCN})_2$, MnCl_2 , $\text{Ca}_3(\text{PO}_4)_2$, Ca_2HPO_4 , $\text{Ca}(\text{H}_2\text{PO}_4)_2$, CaSO_4 , $\text{Ca}(\text{CH}_3\text{COO})_2$, CaCl_2 , CaBr_2 , $\text{Ca}(\text{NO}_3)_2$, $\text{Ca}(\text{ClO}_4)_2$, CaI_2 , $\text{Ca}(\text{SCN})_2$, $\text{Ba}_3(\text{PO}_4)_2$, Ba_2HPO_4 , $\text{Ba}(\text{H}_2\text{PO}_4)_2$, BaSO_4 , $\text{Ba}(\text{CH}_3\text{COO})_2$, BaCl_2 , BaBr_2 , $\text{Ba}(\text{NO}_3)_2$, $\text{Ba}(\text{ClO}_4)_2$, BaI_2 , and $\text{Ba}(\text{SCN})_2$. Particularly preferred are NH acetate, MgCl_2 , KH_2PO_4 , Na_2SO_4 , KCl , NaCl , and CaCl_2 , such as, for example, the chloride or acetate (trifluoroacetate) salts.

[0139] Generally, peptides and variants (at least those containing peptide linkages between amino acid residues) may be synthesized by the Fmoc-polyamide mode of solid-phase peptide synthesis as disclosed by Lukas et al. (Lukas et al., 1981) and by references as cited therein. Temporary N-amino group protection is afforded by the 9-fluorenylmethoxycarbonyl (Fmoc) group. Repetitive cleavage of this

highly base-labile protecting group is done using 20% piperidine in N, N-dimethylformamide. Side-chain functionalities may be protected as their butyl ethers (in the case of serine threonine and tyrosine), butyl esters (in the case of glutamic acid and aspartic acid), butyloxycarbonyl derivative (in the case of lysine and histidine), trityl derivative (in the case of cysteine) and 4-methoxy-2,3,6-trimethylbenzenesulphonyl derivative (in the case of arginine). Where glutamine or asparagine are C-terminal residues, use is made of the 4,4'-dimethoxybenzhydryl group for protection of the side chain amido functionalities. The solid-phase support is based on a polydimethyl-acrylamide polymer constituted from the three monomers dimethylacrylamide (backbone-monomer), bisacryloylethylene diamine (cross linker) and acryloylsarcosine methyl ester (functionalizing agent). The peptide-to-resin cleavable linked agent used is the acid-labile 4-hydroxymethyl-phenoxyacetic acid derivative. All amino acid derivatives are added as their preformed symmetrical anhydride derivatives with the exception of asparagine and glutamine, which are added using a reversed N, N-dicyclohexyl-carbodiimide/1-hydroxybenzotriazole mediated coupling procedure. All coupling and deprotection reactions are monitored using ninhydrin, trinitrobenzene sulphonic acid or isotin test procedures. Upon completion of synthesis, peptides are cleaved from the resin support with concomitant removal of side-chain protecting groups by treatment with 95% trifluoroacetic acid containing a 50% scavenger mix. Scavengers commonly used include ethanedithiol, phenol, anisole and water, the exact choice depending on the constituent amino acids of the peptide being synthesized. Also a combination of solid phase and solution phase methodologies for the synthesis of peptides is possible (see, for example, (Bruckdorfer et al., 2004), and the references as cited therein).

[0140] Trifluoroacetic acid is removed by evaporation in vacuo, with subsequent trituration with diethyl ether affording the crude peptide. Any scavengers present are removed by a simple extraction procedure which on lyophilization of the aqueous phase affords the crude peptide free of scavengers. Reagents for peptide synthesis are generally available from e.g. Calbiochem-Novabiochem (Nottingham, UK).

[0141] Purification may be performed by any one, or a combination of, techniques such as re-crystallization, size exclusion chromatography, ion-exchange chromatography, hydrophobic interaction chromatography and (usually) reverse-phase high performance liquid chromatography using e.g. acetonitrile/water gradient separation.

[0142] Analysis of peptides may be carried out using thin layer chromatography, electrophoresis, in particular capillary electrophoresis, solid phase extraction (CSPE), reverse-phase high performance liquid chromatography, amino-acid analysis after acid hydrolysis and by fast atom bombardment (FAB) mass spectrometric analysis, as well as MALDI and ESI-Q-TOF mass spectrometric analysis.

[0143] In order to select over-presented peptides, a presentation profile is calculated showing the median sample presentation as well as replicate variation. The profile juxtaposes samples of the tumor entity of interest to a baseline of normal tissue samples. Each of these profiles can then be consolidated into an over-presentation score by calculating the p-value of a Linear Mixed-Effects Model (Pinheiro et al., 2015) adjusting for multiple testing by False Discovery Rate (Benjamini and Hochberg, 1995) (cf. Example 1, FIGS. 1A through 1N).

[0144] For the identification and relative quantitation of HLA ligands by mass spectrometry, HLA molecules from shock-frozen tissue samples were purified and HLA-associated peptides were isolated. The isolated peptides were separated and sequences were identified by online nano-electrospray-ionization (nanoESI) liquid chromatography-mass spectrometry (LC-MS) experiments. The resulting peptide sequences were verified by comparison of the fragmentation pattern of natural tumor-associated peptides (TUMAPs) recorded from lung cancer (including NSCLC and SCLC) samples (N=201 samples) with the fragmentation patterns of corresponding synthetic reference peptides of identical sequences. Since the peptides were directly identified as ligands of HLA molecules of primary tumors, these results provide direct evidence for the natural processing and presentation of the identified peptides on primary cancer tissue obtained from 201 lung cancer (including NSCLC and SCLC) patients.

[0145] The discovery pipeline XPRESIDENT® v2.1 (see, for example, US 2013-0096016, which is hereby incorporated by reference in its entirety) allows the identification and selection of relevant over-presented peptide vaccine candidates based on direct relative quantitation of HLA-restricted peptide levels on cancer tissues in comparison to several different non-cancerous tissues and organs. This was achieved by the development of label-free differential quantitation using the acquired LC-MS data processed by a proprietary data analysis pipeline, combining algorithms for sequence identification, spectral clustering, ion counting, retention time alignment, charge state deconvolution and normalization.

[0146] Presentation levels including error estimates for each peptide and sample were established. Peptides exclusively presented on tumor tissue and peptides over-presented in tumor versus non-cancerous tissues and organs have been identified.

[0147] HLA-peptide complexes from lung cancer (including NSCLC and SCLC) tissue samples were purified and HLA-associated peptides were isolated and analyzed by LC-MS (see example 1). All TUMAPs contained in the present application were identified with this approach on lung cancer (including NSCLC and SCLC) samples confirming their presentation on lung cancer (including NSCLC and SCLC).

[0148] TUMAPs identified on multiple lung cancer (including NSCLC and SCLC) and normal tissues were quantified using ion-counting of label-free LC-MS data. The method assumes that LC-MS signal areas of a peptide correlate with its abundance in the sample. All quantitative signals of a peptide in various LC-MS experiments were normalized based on central tendency, averaged per sample and merged into a bar plot, called presentation profile. The presentation profile consolidates different analysis methods like protein database search, spectral clustering, charge state deconvolution (decharging) and retention time alignment and normalization.

[0149] Besides over-presentation of the peptide, mRNA expression of the underlying gene was tested. mRNA data were obtained via RNASeq analyses of normal tissues and cancer tissues (cf. Example 2, FIGS. 2A through 2N). An additional source of normal tissue data was a database of publicly available RNA expression data from around 3000 normal tissue samples (Lonsdale, 2013). Peptides which are derived from proteins whose coding mRNA is highly

expressed in cancer tissue, but very low or absent in vital normal tissues, were preferably included in the present invention.

[0150] The present invention provides peptides that are useful in treating cancers/tumors, preferably lung cancer (including NSCLC and SCLC) that over- or exclusively present the peptides of the invention. These peptides were shown by mass spectrometry to be naturally presented by HLA molecules on primary human lung cancer (including NSCLC and SCLC) samples.

[0151] Many of the source gene/proteins (also designated “full-length proteins” or “underlying proteins”) from which the peptides are derived were shown to be highly over-expressed in cancer compared with normal tissues—“normal tissues” in relation to this invention shall mean either healthy lung cells or other normal tissue cells, demonstrating a high degree of tumor association of the source genes (see Example 2). Moreover, the peptides themselves are strongly over-presented on tumor tissue—“tumor tissue” in relation to this invention shall mean a sample from a patient suffering from lung cancer (including NSCLC and SCLC), but not on normal tissues (see Example 1).

[0152] HLA-bound peptides can be recognized by the immune system, specifically T lymphocytes. T cells can destroy the cells presenting the recognized HLA/peptide complex, e.g. lung cancer (including NSCLC and SCLC) cells presenting the derived peptides.

[0153] The peptides of the present invention have been shown to be capable of stimulating T cell responses and/or are over-presented and thus can be used for the production of antibodies and/or TCRs, such as soluble TCRs, according to the present invention (see Example 3, Example 4). Furthermore, the peptides when complexed with the respective MHC can be used for the production of antibodies and/or TCRs, in particular sTCRs, according to the present invention, as well. Respective methods are well known to the person of skill, and can be found in the respective literature as well (see also below). Thus, the peptides of the present invention are useful for generating an immune response in a patient by which tumor cells can be destroyed. An immune response in a patient can be induced by direct administration of the described peptides or suitable precursor substances (e.g. elongated peptides, proteins, or nucleic acids encoding these peptides) to the patient, ideally in combination with an agent enhancing the immunogenicity (i.e. an adjuvant). The immune response originating from such a therapeutic vaccination can be expected to be highly specific against tumor cells because the target peptides of the present invention are not presented on normal tissues in comparable copy numbers, preventing the risk of undesired autoimmune reactions against normal cells in the patient.

[0154] The present description further relates to T-cell receptors (TCRs) comprising an alpha chain and a beta chain (“alpha/beta TCRs”). Also provided are peptides according to the invention capable of binding to TCRs and antibodies when presented by an MHC molecule.

[0155] The present description also relates to fragments of the TCRs according to the invention that are capable of binding to a peptide antigen according to the present invention when presented by an HLA molecule. The term particularly relates to soluble TCR fragments, for example TCRs missing the transmembrane parts and/or constant regions, single chain TCRs, and fusions thereof to, for example, with Ig.

[0156] The present description also relates to nucleic acids, vectors and host cells for expressing TCRs and peptides of the present description; and methods of using the same.

[0157] The term “T-cell receptor” (abbreviated TCR) refers to a heterodimeric molecule comprising an alpha polypeptide chain (alpha chain) and a beta polypeptide chain (beta chain), wherein the heterodimeric receptor is capable of binding to a peptide antigen presented by an HLA molecule. The term also includes so-called gamma/delta TCRs.

[0158] In one embodiment the disembodiment, provides a method of producing a TCR as described herein, the method comprising culturing a host cell capable of expressing the TCR under conditions suitable to promote expression of the TCR.

[0159] The description in another aspect relates to methods according to the description, wherein the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell or artificial antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell or the antigen is loaded onto class I or II MHC tetramers by tetramerizing the antigen/class I or II MHC complex monomers.

[0160] The alpha and beta chains of alpha/beta TCR’s, and the gamma and delta chains of gamma/delta TCRs, are generally regarded as each having two “domains”, namely variable and constant domains. The variable domain consists of a concatenation of variable region (V), and joining region (J). The variable domain may also include a leader region (L). Beta and delta chains may also include a diversity region (D). The alpha and beta constant domains may also include C-terminal transmembrane (TM) domains that anchor the alpha and beta chains to the cell membrane.

[0161] With respect to gamma/delta TCRs, the term “TCR gamma variable domain” as used herein refers to the concatenation of the TCR gamma V (TRGV) region without leader region (L), and the TCR gamma J (TRGJ) region, and the term TCR gamma constant domain refers to the extracellular TRGC region, or to a C-terminal truncated TRGC sequence. Likewise, the term “TCR delta variable domain” refers to the concatenation of the TCR delta V (TRDV) region without leader region (L) and the TCR delta D/J (TRDD/TRDJ) region, and the term “TCR delta constant domain” refers to the extracellular TRDC region, or to a C-terminal truncated TRDC sequence.

[0162] TCRs of the present description preferably bind to a peptide-HLA molecule complex with a binding affinity (KD) of about 100 μ M or less, about 50 μ M or less, about 25 μ M or less, or about 10 μ M or less. More preferred are high affinity TCRs having binding affinities of about 1 μ M or less, about 100 nM or less, about 50 nM or less, about 25 nM or less. Non-limiting examples of preferred binding affinity ranges for TCRs of the present invention include about 1 nM to about 10 nM; about 10 nM to about 20 nM; about 20 nM to about 30 nM; about 30 nM to about 40 nM; about 40 nM to about 50 nM; about 50 nM to about 60 nM; about 60 nM to about 70 nM; about 70 nM to about 80 nM; about 80 nM to about 90 nM; and about 90 nM to about 100 nM.

[0163] As used herein in connect with TCRs of the present description, “specific binding” and grammatical variants

thereof are used to mean a TCR having a binding affinity (KD) for a peptide-HLA molecule complex of 100 μ M or less.

[0164] Alpha/beta heterodimeric TCRs of the present description may have an introduced disulfide bond between their constant domains. Preferred TCRs of this type include those which have a TRAC constant domain sequence and a TRBC1 or TRBC2 constant domain sequence except that Thr 48 of TRAC and Ser 57 of TRBC1 or TRBC2 are replaced by cysteine residues, the said cysteines forming a disulfide bond between the TRAC constant domain sequence and the TRBC1 or TRBC2 constant domain sequence of the TCR.

[0165] With or without the introduced inter-chain bond mentioned above, alpha/beta heterodimeric TCRs of the present description may have a TRAC constant domain sequence and a TRBC1 or TRBC2 constant domain sequence, and the TRAC constant domain sequence and the TRBC1 or TRBC2 constant domain sequence of the TCR may be linked by the native disulfide bond between Cys4 of exon 2 of TRAC and Cys2 of exon 2 of TRBC1 or TRBC2.

[0166] TCRs of the present description may comprise a detectable label selected from the group consisting of a radionuclide, a fluorophore and biotin. TCRs of the present description may be conjugated to a therapeutically active agent, such as a radionuclide, a chemotherapeutic agent, or a toxin.

[0167] In an embodiment, a TCR of the present description having at least one mutation in the alpha chain and/or having at least one mutation in the beta chain has modified glycosylation compared to the unmutated TCR.

[0168] In an embodiment, a TCR comprising at least one mutation in the TCR alpha chain and/or TCR beta chain has a binding affinity for, and/or a binding half-life for, a peptide-HLA molecule complex, which is at least double that of a TCR comprising the unmutated TCR alpha chain and/or unmutated TCR beta chain. Affinity-enhancement of tumor-specific TCRs, and its exploitation, relies on the existence of a window for optimal TCR affinities. The existence of such a window is based on observations that TCRs specific for HLA-A2-restricted pathogens have KD values that are generally about 10-fold lower when compared to TCRs specific for HLA-A2-restricted tumor-associated self-antigens. For TCRs specific for pathogens restricted to other alleles compared to tumor-associated self-antigens the KD values might be in a slightly different range, but there are no general differences between the different alleles with respect to the possibility of creating TCRs. It is now known, although tumor antigens have the potential to be immunogenic, because tumors arise from the individual's own cells only mutated proteins or proteins with altered translational processing will be seen as foreign by the immune system. Antigens that are upregulated or overexpressed (so called self-antigens) will not necessarily induce a functional immune response against the tumor: T-cells expressing TCRs that are highly reactive to these antigens will have been negatively selected within the thymus in a process known as central tolerance, meaning that only T-cells with low-affinity TCRs for self-antigens remain. Therefore, affinity of TCRs or variants of the present description to peptides can be enhanced by methods well known in the art.

[0169] The present description further relates to a method of identifying and isolating a TCR according to the present

description, said method comprising incubating PBMCs from healthy donors negative with respect to the allele at hand with the HLA/peptide monomers, incubating the PBMCs with tetramer-phycoerythrin (PE) and isolating the high avidity T-cells by fluorescence activated cell sorting (FACS)—Calibur analysis.

[0170] The present description further relates to a method of identifying and isolating a TCR according to the present description, said method comprising obtaining a transgenic mouse with the entire human TCR $\alpha\beta$ gene loci (1.1 and 0.7 Mb), whose T-cells express a diverse human TCR repertoire that compensates for mouse TCR deficiency, immunizing the mouse with a peptide, incubating PBMCs obtained from the transgenic mice with tetramer-phycoerythrin (PE), and isolating the high avidity T-cells by fluorescence activated cell sorting (FACS)—Calibur analysis.

[0171] In one aspect, to obtain T-cells expressing TCRs of the present description, nucleic acids encoding TCR-alpha and/or TCR-beta chains of the present description are cloned into expression vectors, such as gamma retrovirus or lentivirus. The recombinant viruses are generated and then tested for functionality, such as antigen specificity and functional avidity. An aliquot of the final product is then used to transduce the target T-cell population (generally purified from patient PBMCs), which is expanded before infusion into the patient.

[0172] In another aspect, to obtain T-cells expressing TCRs of the present description, TCR RNAs are synthesized by techniques known in the art, e.g., in vitro transcription systems. The in vitro-synthesized TCR RNAs are then introduced into primary CD8+ T-cells obtained from healthy donors by electroporation to re-express tumor specific TCR-alpha and/or TCR-beta chains.

[0173] To increase the expression, nucleic acids encoding TCRs of the present description may be operably linked to strong promoters, such as retroviral long terminal repeats (LTRs), cytomegalovirus (CMV), murine stem cell virus (MSCV) U3, phosphoglycerate kinase (PGK), β -actin, ubiquitin, and a simian virus 40 (SV40)/CD43 composite promoter, elongation factor (EF)-1a and the spleen focus-forming virus (SFFV) promoter. In a preferred embodiment, the promoter is heterologous to the nucleic acid being expressed.

[0174] In addition to strong promoters, TCR expression cassettes of the present description may contain additional elements that can enhance transgene expression, including a central polypurine tract (cPPT), which promotes the nuclear translocation of lentiviral constructs (Follenzi et al., 2000), and the woodchuck hepatitis virus posttranscriptional regulatory element (wPRE), which increases the level of transgene expression by increasing RNA stability (Zufferey et al., 1999).

[0175] The alpha and beta chains of a TCR of the present invention may be encoded by nucleic acids located in separate vectors, or may be encoded by polynucleotides located in the same vector.

[0176] Achieving high-level TCR surface expression requires that both the TCR-alpha and TCR-beta chains of the introduced TCR be transcribed at high levels. To do so, the TCR-alpha and TCR-beta chains of the present description may be cloned into bi-cistronic constructs in a single vector, which has been shown to be capable of over-coming this obstacle. The use of a viral intraribosomal entry site (IRES) between the TCR-alpha and TCR-beta chains results in the

coordinated expression of both chains, because the TCR-alpha and TCR-beta chains are generated from a single transcript that is broken into two proteins during translation, ensuring that an equal molar ratio of TCR-alpha and TCR-beta chains are produced (Schmitt et al., 2009).

[0177] Nucleic acids encoding TCRs of the present description may be codon optimized to increase expression from a host cell. Redundancy in the genetic code allows some amino acids to be encoded by more than one codon, but certain codons are less “op-timal” than others because of the relative availability of matching tRNAs as well as other factors (Gustafsson et al., 2004). Modifying the TCR-alpha and TCR-beta gene sequences such that each amino acid is encoded by the optimal codon for mammalian gene expression, as well as eliminating mRNA instability motifs or cryptic splice sites, has been shown to significantly enhance TCR-alpha and TCR-beta gene expression (Scholten et al., 2006).

[0178] Furthermore, mispairing between the introduced and endogenous TCR chains may result in the acquisition of specificities that pose a significant risk for autoimmunity. For example, the formation of mixed TCR dimers may reduce the number of CD3 molecules available to form properly paired TCR complexes, and therefore can significantly decrease the functional avidity of the cells expressing the introduced TCR (Kuball et al., 2007).

[0179] To reduce mispairing, the C-terminus domain of the introduced TCR chains of the present description may be modified in order to promote interchain affinity, while decreasing the ability of the introduced chains to pair with the endogenous TCR. These strategies may include replacing the human TCR-alpha and TCR-beta C-terminus domains with their murine counterparts (murinized C-terminus domain); generating a second interchain disulfide bond in the C-terminus domain by introducing a second cysteine residue into both the TCR-alpha and TCR-beta chains of the introduced TCR (cysteine modification); swapping interacting residues in the TCR-alpha and TCR-beta chain C-terminus domains (“knob-in-hole”); and fusing the variable domains of the TCR-alpha and TCR-beta chains directly to CD3 (CD3 fusion) (Schmitt et al., 2009).

[0180] In an embodiment, a host cell is engineered to express a TCR of the present description. In preferred embodiments, the host cell is a human T-cell or T-cell progenitor. In some embodiments, the T-cell or T-cell progenitor is obtained from a cancer patient. In other embodiments, the T-cell or T-cell progenitor is obtained from a healthy donor. Host cells of the present description can be allogeneic or autologous with respect to a patient to be treated. In one embodiment, the host is a gamma/delta T-cell transformed to express an alpha/beta TCR.

[0181] A “pharmaceutical composition” is a composition suitable for administration to a human being in a medical setting. Preferably, a pharmaceutical composition is sterile and produced according to GMP guidelines.

[0182] The pharmaceutical compositions comprise the peptides either in the free form or in the form of a pharmaceutically acceptable salt (see also above). In an aspect, a peptide described herein is in the form of a pharmaceutically acceptable salt. In another aspect, a peptide in the form of a pharmaceutical salt is in crystalline form.

[0183] In an aspect, a pharmaceutically acceptable salt described herein refers to salts which possess toxicity profiles within a range that is acceptable for pharmaceutical applications.

[0184] As used herein, “a pharmaceutically acceptable salt” refers to a derivative of the disclosed peptides wherein the peptide is modified by making acid or base salts of the agent. For example, acid salts are prepared from the free base (typically wherein the neutral form of the drug has a neutral —NH_2 group) involving reaction with a suitable acid. Suitable acids for preparing acid salts include both organic acids, e.g., acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, malic acid, malonic acid, succinic acid, maleic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methane sulfonic acid, ethane sulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like, as well as inorganic acids, e.g., hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid phosphoric acid and the like. Conversely, preparation of basic salts of acid moieties which may be present on a peptide are prepared using a pharmaceutically acceptable base such as sodium hydroxide, potassium hydroxide, ammonium hydroxide, calcium hydroxide, trimethylamine or the like.

[0185] In an aspect, pharmaceutically acceptable salts may increase the solubility and/or stability of peptides of described herein. In another aspect, pharmaceutical salts described herein may be prepared by conventional means from the corresponding carrier peptide or complex by reacting, for example, the appropriate acid or base with peptides or complexes as described herein. In another aspect, the pharmaceutically acceptable salts are in crystalline form or semi-crystalline form. In yet another aspect, pharmaceutically acceptable salts may include, for example, those described in Handbook of Pharmaceutical Salts: Properties, Selection, and Use By P. H. Stahl and C. G. Wermuth (Wiley-VCH 2002) and L. D. Bighley, S. M. Berge, D. C. Monkhouse, in “Encyclopedia of Pharmaceutical Technology”. Eds. J. Swarbrick and J. C. Boylan, Vol. 13, Marcel Dekker, Inc., New York, Basel, Hong Kong 1995, pp. 453-499, each of these references is herein incorporated by reference in their entirety.

[0186] In an especially preferred embodiment, the pharmaceutical compositions comprise the peptides as salts of acetic acid (acetates), trifluoro acetates or hydrochloric acid (chlorides).

[0187] Preferably, the medicament of the present invention is an immunotherapeutic such as a vaccine. It may be administered directly into the patient, into the affected organ or systemically i.d., i.m., s.c., i.p. and i.v., or applied ex vivo to cells derived from the patient or a human cell line which are subsequently administered to the patient, or used in vitro to select a subpopulation of immune cells derived from the patient, which are then re-administered to the patient. If the nucleic acid is administered to cells in vitro, it may be useful for the cells to be transfected so as to co-express immune-stimulating cytokines, such as interleukin-2. The peptide may be substantially pure, or combined with an immune-stimulating adjuvant (see below) or used in combination with immune-stimulatory cytokines, or be administered with a suitable delivery system, for example liposomes. The peptide may also be conjugated to a suitable carrier such as keyhole limpet haemocyanin (KLH) or mannan (see WO 95/18145 and (Longenecker et al., 1993)). The peptide may

also be tagged, may be a fusion protein, or may be a hybrid molecule. The peptides whose sequence is given in the present invention are expected to stimulate CD4 or CD8 T cells. However, stimulation of CD8 T cells is more efficient in the presence of help provided by CD4 T-helper cells. Thus, for MHC Class I epitopes that stimulate CD8 T cells the fusion partner or sections of a hybrid molecule suitably provide epitopes which stimulate CD4-positive T cells. CD4- and CD8-stimulating epitopes are well known in the art and include those identified in the present invention.

[0188] In one aspect, the vaccine comprises at least one peptide having the amino acid sequence set forth SEQ ID No. 1 to SEQ ID No. 489, and at least one additional peptide, preferably two to 50, more preferably two to 25, even more preferably two to 20 and most preferably two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen or eighteen peptides. The peptide(s) may be derived from one or more specific TAAs and may bind to MHC class I molecules.

[0189] A further aspect of the invention provides a nucleic acid (for example a polynucleotide) encoding a peptide or peptide variant of the invention. The polynucleotide may be, for example, DNA, cDNA, PNA, RNA or combinations thereof, either single- and/or double-stranded, or native or stabilized forms of polynucleotides, such as, for example, polynucleotides with a phosphorothioate backbone and it may or may not contain introns so long as it codes for the peptide. Of course, only peptides that contain naturally occurring amino acid residues joined by naturally occurring peptide bonds are encodable by a polynucleotide. A still further aspect of the invention provides an expression vector capable of expressing a polypeptide according to the invention.

[0190] A variety of methods have been developed to link polynucleotides, especially DNA, to vectors for example via complementary cohesive termini. For instance, complementary homopolymer tracts can be added to the DNA segment to be inserted to the vector DNA. The vector and DNA segment are then joined by hydrogen bonding between the complementary homopolymeric tails to form recombinant DNA molecules.

[0191] Synthetic linkers containing one or more restriction sites provide an alternative method of joining the DNA segment to vectors. Synthetic linkers containing a variety of restriction endonuclease sites are commercially available from a number of sources including International Biotechnologies Inc. New Haven, Conn., USA.

[0192] A desirable method of modifying the DNA encoding the polypeptide of the invention employs the polymerase chain reaction as disclosed by Saiki R K, et al. (Saiki et al., 1988). This method may be used for introducing the DNA into a suitable vector, for example by engineering in suitable restriction sites, or it may be used to modify the DNA in other useful ways as is known in the art. If viral vectors are used, pox- or adenovirus vectors are preferred.

[0193] The DNA (or in the case of retroviral vectors, RNA) may then be expressed in a suitable host to produce a polypeptide comprising the peptide or variant of the invention. Thus, the DNA encoding the peptide or variant of the invention may be used in accordance with known techniques, appropriately modified in view of the teachings contained herein, to construct an expression vector, which is then used to transform an appropriate host cell for the expression and production of the polypeptide of the inven-

tion. Such techniques include those disclosed, for example, in U.S. Pat. Nos. 4,440,859, 4,530,901, 4,582,800, 4,677,063, 4,678,751, 4,704,362, 4,710,463, 4,757,006, 4,766,075, and 4,810,648.

[0194] The DNA (or in the case of retroviral vectors, RNA) encoding the polypeptide constituting the compound of the invention may be joined to a wide variety of other DNA sequences for introduction into an appropriate host. The companion DNA will depend upon the nature of the host, the manner of the introduction of the DNA into the host, and whether episomal maintenance or integration is desired.

[0195] Generally, the DNA is inserted into an expression vector, such as a plasmid, in proper orientation and correct reading frame for expression. If necessary, the DNA may be linked to the appropriate transcriptional and translational regulatory control nucleotide sequences recognized by the desired host, although such controls are generally available in the expression vector. The vector is then introduced into the host through standard techniques. Generally, not all of the hosts will be transformed by the vector. Therefore, it will be necessary to select for transformed host cells. One selection technique involves incorporating into the expression vector a DNA sequence, with any necessary control elements, that codes for a selectable trait in the transformed cell, such as antibiotic resistance.

[0196] Alternatively, the gene for such selectable trait can be on another vector, which is used to co-transform the desired host cell.

[0197] Host cells that have been transformed by the recombinant DNA of the invention are then cultured for a sufficient time and under appropriate conditions known to those skilled in the art in view of the teachings disclosed herein to permit the expression of the polypeptide, which can then be recovered.

[0198] Many expression systems are known, including bacteria (for example *E. coli* and *Bacillus subtilis*), yeasts (for example *Saccharomyces cerevisiae*), filamentous fungi (for example *Aspergillus* spec.), plant cells, animal cells and insect cells. Preferably, the system can be mammalian cells such as CHO cells available from the ATCC Cell Biology Collection.

[0199] A typical mammalian cell vector plasmid for constitutive expression comprises the CMV or SV40 promoter with a suitable poly A tail and a resistance marker, such as neomycin. One example is pSVL available from Pharmacia, Piscataway, N.J., USA. An example of an inducible mammalian expression vector is pMSG, also available from Pharmacia. Useful yeast plasmid vectors are pRS403-406 and pRS413-416 and are generally available from Stratagene Cloning Systems, La Jolla, Calif. 92037, USA. Plasmids pRS403, pRS404, pRS405 and pRS406 are Yeast Integrating plasmids (YIps) and incorporate the yeast selectable markers HIS3, TRP1, LEU2 and URA3. Plasmids pRS413-416 are Yeast Centromere plasmids (Ycps). CMV promoter-based vectors (for example from Sigma-Aldrich) provide transient or stable expression, cytoplasmic expression or secretion, and N-terminal or C-terminal tagging in various combinations of FLAG, 3×FLAG, c-myc or MAT. These fusion proteins allow for detection, purification and analysis of recombinant protein. Dual-tagged fusions provide flexibility in detection.

[0200] The strong human cytomegalovirus (CMV) promoter regulatory region drives constitutive protein expres-

sion levels as high as 1 mg/L in COS cells. For less potent cell lines, protein levels are typically ~0.1 mg/L. The presence of the SV40 replication origin will result in high levels of DNA replication in SV40 replication permissive COS cells. CMV vectors, for example, can contain the pMB1 (derivative of pBR322) origin for replication in bacterial cells, the b-lactamase gene for ampicillin resistance selection in bacteria, hGH polyA, and the fl origin. Vectors containing the pre-pro-trypsin leader (PPT) sequence can direct the secretion of FLAG fusion proteins into the culture medium for purification using ANTI-FLAG antibodies, resins, and plates. Other vectors and expression systems are well known in the art for use with a variety of host cells.

[0201] In another embodiment two or more peptides or peptide variants of the invention are encoded and thus expressed in a successive order (similar to “beads on a string” constructs). In doing so, the peptides or peptide variants may be linked or fused together by stretches of linker amino acids, such as for example LLLLLL, or may be linked without any additional peptide(s) between them. These constructs can also be used for cancer therapy, and may induce immune responses both involving MHC I and MHC II.

[0202] The present invention also relates to a host cell transformed with a polynucleotide vector construct of the present invention. The host cell can be either prokaryotic or eukaryotic. Bacterial cells may be preferred prokaryotic host cells in some circumstances and typically are a strain of *E. coli* such as, for example, the *E. coli* strains DH5 available from Bethesda Research Laboratories Inc., Bethesda, Md., USA, and RR1 available from the American Type Culture Collection (ATCC) of Rockville, Md., USA (No ATCC 31343). Preferred eukaryotic host cells include yeast, insect and mammalian cells, preferably vertebrate cells such as those from a mouse, rat, monkey or human fibroblastic and colon cell lines. Yeast host cells include YPH499, YPH500 and YPH501, which are generally available from Stratagene Cloning Systems, La Jolla, Calif. 92037, USA. Preferred mammalian host cells include Chinese hamster ovary (CHO) cells available from the ATCC as CCL61, NIH Swiss mouse embryo cells NIH/3T3 available from the ATCC as CRL 1658, monkey kidney-derived COS-1 cells available from the ATCC as CRL 1650 and 293 cells which are human embryonic kidney cells. Preferred insect cells are Sf9 cells which can be transfected with baculovirus expression vectors. An overview regarding the choice of suitable host cells for expression can be found in, for example, the textbook of Paulina Balbás and Argelia Lorence “Methods in Molecular Biology Recombinant Gene Expression, Reviews and Protocols,” Part One, Second Edition, ISBN 978-1-58829-262-9, and other literature known to the person of skill.

[0203] Transformation of appropriate cell hosts with a DNA construct of the present invention is accomplished by well-known methods that typically depend on the type of vector used. With regard to transformation of prokaryotic host cells, see, for example, Cohen et al. (Cohen et al., 1972) and (Green and Sambrook, 2012). Transformation of yeast cells is described in Sherman et al. (Sherman et al., 1986). The method of Beggs (Beggs, 1978) is also useful. With regard to vertebrate cells, reagents useful in transfecting such cells, for example calcium phosphate and DEAE-dextran or liposome formulations, are available from Stratagene Cloning Systems, or Life Technologies Inc., Gaithersburg, Md. 20877, USA. Electroporation is also useful for

transforming and/or transfecting cells and is well known in the art for transforming yeast cell, bacterial cells, insect cells and vertebrate cells.

[0204] Successfully transformed cells, i.e. cells that contain a DNA construct of the present invention, can be identified by well-known techniques such as PCR. Alternatively, the presence of the protein in the supernatant can be detected using antibodies.

[0205] It will be appreciated that certain host cells of the invention are useful in the preparation of the peptides of the invention, for example bacterial, yeast and insect cells. However, other host cells may be useful in certain therapeutic methods. For example, antigen-presenting cells, such as dendritic cells, may usefully be used to express the peptides of the invention such that they may be loaded into appropriate MHC molecules. Thus, the current invention provides a host cell comprising a nucleic acid or an expression vector according to the invention.

[0206] In a preferred embodiment, the host cell is an antigen presenting cell, in particular a dendritic cell or antigen presenting cell. APCs loaded with a recombinant fusion protein containing prostatic acid phosphatase (PAP) were approved by the U.S. Food and Drug Administration (FDA) on Apr. 29, 2010, to treat asymptomatic or minimally symptomatic metastatic HRPc (Sipuleucel-T) (Rini et al., 2006; Small et al., 2006).

[0207] A further aspect of the invention provides a method of producing a peptide or its variant, the method comprising culturing a host cell and isolating the peptide from the host cell or its culture medium.

[0208] In another embodiment, the peptide, the nucleic acid or the expression vector of the invention are used in medicine. For example, the peptide or its variant may be prepared for intravenous (i.v.) injection, sub-cutaneous (s.c.) injection, intradermal (i.d.) injection, intraperitoneal (i.p.) injection, intramuscular (i.m.) injection. Preferred methods of peptide injection include s.c., i.d., i.p., i.m., and i.v. Preferred methods of DNA injection include i.d., i.m., s.c., i.p. and i.v. Doses of e.g. between 50 µg and 1.5 mg, preferably 125 µg to 500 µg, of peptide or DNA may be given and will depend on the respective peptide or DNA. Dosages of this range were successfully used in previous trials (Walter et al., 2012).

[0209] The polynucleotide used for active vaccination may be substantially pure, or contained in a suitable vector or delivery system. The nucleic acid may be DNA, cDNA, PNA, RNA or a combination thereof. Methods for designing and introducing such a nucleic acid are well known in the art. An overview is provided by e.g. Teufel et al. (Teufel et al., 2005). Polynucleotide vaccines are easy to prepare, but the mode of action of these vectors in inducing an immune response is not fully understood. Suitable vectors and delivery systems include viral DNA and/or RNA, such as systems based on adenovirus, vaccinia virus, retroviruses, herpes virus, adeno-associated virus or hybrids containing elements of more than one virus. Non-viral delivery systems include cationic lipids and cationic polymers and are well known in the art of DNA delivery. Physical delivery, such as via a “gene-gun” may also be used. The peptide or peptides encoded by the nucleic acid may be a fusion protein, for example with an epitope that stimulates T cells for the respective opposite CDR as noted above.

[0210] The medicament of the invention may also include one or more adjuvants. Adjuvants are substances that non-

specifically enhance or potentiate the immune response (e.g., immune responses mediated by CD8-positive T cells and helper-T (TH) cells to an antigen, and would thus be considered useful in the medicament of the present invention. Suitable adjuvants include, but are not limited to, 1018 ISS, aluminum salts, AMPLIVAX®, AS15, BCG, CP-870, 893, CpG7909, CyaA, dSLIM, flagellin or TLR5 ligands derived from flagellin, FLT3 ligand, GM-CSF, IC30, IC31, Imiquimod (ALDARA®), resiquimod, ImuFact IMP321, Interleukins as IL-2, IL-13, IL-21, Interferon-alpha or -beta, or pegylated derivatives thereof, IS Patch, ISS, ISCOMA-TRIX, ISCOMs, JuvImmune®, LipoVac, MALP2, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, water-in-oil and oil-in-water emulsions, OK-432, OM-174, OM-197-MP-EC, ONTAK, OspA, PepTel® vector system, poly(lactid co-glycolid) [PLG]-based and dextran microparticles, talactoferrin SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Aquila's QS21 stimulon, which is derived from saponin, mycobacterial extracts and synthetic bacterial cell wall mimics, and other proprietary adjuvants such as Ribi's Detox, Quil, or Superfos. Adjuvants such as Freund's or GM-CSF are preferred. Several immunological adjuvants (e.g., MF59) specific for dendritic cells and their preparation have been described previously (Allison and Krummel, 1995). Also, cytokines may be used. Several cytokines have been directly linked to influencing dendritic cell migration to lymphoid tissues (e.g., TNF-), accelerating the maturation of dendritic cells into efficient antigen-presenting cells for T-lymphocytes (e.g., GM-CSF, IL-1 and IL-4) (U.S. Pat. No. 5,849,589, specifically incorporated herein by reference in its entirety) and acting as immunoadjuvants (e.g., IL-12, IL-15, IL-23, IL-7, IFN-alpha, IFN-beta) (Gabrilovich et al., 1996).

[0211] CpG immunostimulatory oligonucleotides have also been reported to enhance the effects of adjuvants in a vaccine setting. Without being bound by theory, CpG oligonucleotides act by activating the innate (non-adaptive) immune system via Toll-like receptors (TLR), mainly TLR9. CpG triggered TLR9 activation enhances antigen-specific humoral and cellular responses to a wide variety of antigens, including peptide or protein antigens, live or killed viruses, dendritic cell vaccines, autologous cellular vaccines and polysaccharide conjugates in both prophylactic and therapeutic vaccines. More importantly it enhances dendritic cell maturation and differentiation, resulting in enhanced activation of TH1 cells and strong cytotoxic T-lymphocyte (CTL) generation, even in the absence of CD4 T cell help. The TH1 bias induced by TLR9 stimulation is maintained even in the presence of vaccine adjuvants such as alum or incomplete Freund's adjuvant (IFA) that normally promote a TH2 bias. CpG oligonucleotides show even greater adjuvant activity when formulated or co-administered with other adjuvants or in formulations such as microparticles, nanoparticles, lipid emulsions or similar formulations, which are especially necessary for inducing a strong response when the antigen is relatively weak. They also accelerate the immune response and enable the antigen doses to be reduced by approximately two orders of magnitude, with comparable antibody responses to the full-dose vaccine without CpG in some experiments (Krieg, 2006). U.S. Pat. No. 6,406,705 B1 describes the combined use of CpG oligonucleotides, non-nucleic acid adjuvants and an antigen to induce an antigen-

specific immune response. A CpG TLR9 antagonist is dSLIM (double Stem Loop Immunomodulator) by Mologen (Berlin, Germany) which is a preferred component of the pharmaceutical composition of the present invention. Other TLR binding molecules such as RNA binding TLR 7, TLR 8 and/or TLR 9 may also be used.

[0212] Other examples for useful adjuvants include, but are not limited to chemically modified CpGs (e.g. CpR, Idera), dsRNA analogues such as Poly(I:C) and derivatives thereof (e.g. AmpliGen®, Hiltonol®, poly-(ICLC), poly(IC-R), poly(I:C12U), non-CpG bacterial DNA or RNA as well as immunoactive small molecules and antibodies such as cyclophosphamide, sunitinib, Bevacizumab®, celebrex, NCX-4016, sildenafil, tadalafil, vardenafil, sorafenib, temozolomide, temsirolimus, XL-999, CP-547632, pazopanib, VEGF Trap, ZD2171, AZD2171, anti-CTLA4, other antibodies targeting key structures of the immune system (e.g. anti-CD40, anti-TGFbeta, anti-TNFalpha receptor) and SC58175, which may act therapeutically and/or as an adjuvant. The amounts and concentrations of adjuvants and additives useful in the context of the present invention can readily be determined by the skilled artisan without undue experimentation.

[0213] Preferred adjuvants are anti-CD40, imiquimod, resiquimod, GM-CSF, cyclophosphamide, sunitinib, bevacizumab, interferon-alpha, CpG oligonucleotides and derivatives, poly-(I:C) and derivatives, RNA, sildenafil, and particulate formulations with PLG or virosomes.

[0214] In a preferred embodiment, the pharmaceutical composition according to the invention the adjuvant is selected from the group consisting of colony-stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim), cyclophosphamide, imiquimod, resiquimod, and interferon-alpha.

[0215] In a preferred embodiment, the pharmaceutical composition according to the invention the adjuvant is selected from the group consisting of colony-stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim), cyclophosphamide, imiquimod and resiquimod. In a preferred embodiment of the pharmaceutical composition according to the invention, the adjuvant is cyclophosphamide, imiquimod or resiquimod. Even more preferred adjuvants are Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, poly-ICLC (Hiltonol®) and anti-CD40 mAB, or combinations thereof.

[0216] This composition is used for parenteral administration, such as subcutaneous, intradermal, intramuscular or oral administration. For this, the peptides and optionally other molecules are dissolved or suspended in a pharmaceutically acceptable, preferably aqueous carrier. In addition, the composition can contain excipients, such as buffers, binding agents, blasting agents, diluents, flavors, lubricants, etc. The peptides can also be administered together with immune stimulating substances, such as cytokines. An extensive listing of excipients that can be used in such a composition, can be, for example, taken from A. Kibbe, Handbook of Pharmaceutical Excipients (Kibbe, 2000). The composition can be used for a prevention, prophylaxis and/or therapy of adenomatous or cancerous diseases. Exemplary formulations can be found in, for example, EP2112253.

[0217] In an aspect, peptides or other molecules described herein may be combined with an aqueous carrier. In an

aspect, the aqueous carrier is selected from ion exchangers, alumina, aluminum stearate, magnesium stearate, lecithin, serum proteins, such as human serum albumin, buffer substances such as phosphates, glycine, sorbic acid, potassium sorbate, partial glyceride mixtures of saturated vegetable fatty acids, salts or electrolytes, such as protamine sulfate, disodium hydrogen phosphate, dicalcium phosphate, potassium hydrogen phosphate, sodium chloride, zinc salts, colloidal silica, magnesium trisilicate, polyvinyl pyrrolidone, polyvinylpyrrolidone-vinyl acetate, cellulose-based substances (e.g., microcrystalline cellulose, hydroxypropyl methylcellulose, hydroxypropyl methylcellulose acetate succinate, hydroxypropyl methylcellulose Phthalate), starch, lactose monohydrate, mannitol, trehalose sodium lauryl sulfate, and crosscarmellose sodium, polyethylene glycol, sodium carboxymethylcellulose, polyacrylates, polymethacrylate, waxes, polyethylene-polyoxypropylene-block polymers, polyethylene glycol and wool fat.

[0218] In an aspect, the aqueous carrier contains multiple components, such as water together with a non-water carrier component, such as those components described herein. In another aspect, the aqueous carrier is capable of imparting improved properties when combined with a peptide or other molecule described herein, for example, improved solubility, efficacy, and/or improved immunotherapy. In addition, the composition can contain excipients, such as buffers, binding agents, blasting agents, diluents, flavors, lubricants, etc. A “pharmaceutically acceptable diluent,” for example, may include solvents, bulking agents, stabilizing agents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like which are physiologically compatible. Examples of pharmaceutically acceptable diluents include one or more of saline, phosphate buffered saline, dextrose, glycerol, ethanol, and the like as well as combinations thereof. In many cases it will be preferable to include one or more isotonic agents, for example, sugars such as trehalose and sucrose, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Pharmaceutically acceptable substances such as wetting or minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, are also within the scope of the present invention. In addition, the composition can contain excipients, such as buffers, binding agents, blasting agents, diluents, flavors, and lubricants.

[0219] It is important to realize that the immune response triggered by the vaccine according to the invention attacks the cancer in different cell-stages and different stages of development. Furthermore, different cancer associated signaling pathways are attacked. This is an advantage over vaccines that address only one or few targets, which may cause the tumor to easily adapt to the attack (tumor escape). Furthermore, not all individual tumors express the same pattern of antigens. Therefore, a combination of several tumor-associated peptides ensures that every single tumor bears at least some of the targets. The composition is designed in such a way that each tumor is expected to express several of the antigens and cover several independent pathways necessary for tumor growth and maintenance. Thus, the vaccine can easily be used “off-the-shelf” for a larger patient population. This means that a pre-selection of patients to be treated with the vaccine can be restricted to HLA typing, does not require any additional biomarker assessments for antigen expression, but it is still ensured that

several targets are simultaneously attacked by the induced immune response, which is important for efficacy (Banchereau et al., 2001; Walter et al., 2012).

[0220] As used herein, the term “scaffold” refers to a molecule that specifically binds to an (e.g. antigenic) determinant. In one embodiment, a scaffold is able to direct the entity to which it is attached (e.g. a (second) antigen binding moiety) to a target site, for example to a specific type of tumor cell or tumor stroma bearing the antigenic determinant (e.g. the complex of a peptide with MHC, according to the application at hand). In another embodiment, a scaffold is able to activate signaling through its target antigen, for example a T cell receptor complex antigen. Scaffolds include but are not limited to antibodies and fragments thereof, antigen binding domains of an antibody, comprising an antibody heavy chain variable region and an antibody light chain variable region, binding proteins comprising at least one ankyrin repeat motif and single domain antigen binding (SDAB) molecules, aptamers, (soluble) TCRs and (modified) cells such as allogenic or autologous T cells. To assess whether a molecule is a scaffold binding to a target, binding assays can be performed.

[0221] “Specific” binding means that the scaffold binds the peptide-MHC-complex of interest better than other naturally occurring peptide-MHC-complexes, to an extent that a scaffold armed with an active molecule that is able to kill a cell bearing the specific target is not able to kill another cell without the specific target but presenting other peptide-MHC complex(es). Binding to other peptide-MHC complexes is irrelevant if the peptide of the cross-reactive peptide-MHC is not naturally occurring, i.e. not derived from the human HLA-peptidome. Tests to assess target cell killing are well known in the art. They should be performed using target cells (primary cells or cell lines) with unaltered peptide-MHC presentation, or cells loaded with peptides such that naturally occurring peptide-MHC levels are reached.

[0222] Each scaffold can comprise a labelling which provides that the bound scaffold can be detected by determining the presence or absence of a signal provided by the label. For example, the scaffold can be labelled with a fluorescent dye or any other applicable cellular marker molecule. Such marker molecules are well known in the art. For example, a fluorescence-labelling, for example provided by a fluorescence dye, can provide a visualization of the bound aptamer by fluorescence or laser scanning microscopy or flow cytometry.

[0223] Each scaffold can be conjugated with a second active molecule such as for example IL-21, anti-CD3, and anti-CD28.

[0224] For further information on polypeptide scaffolds see for example the background section of WO 2014/071978A1 and the references cited therein.

[0225] The present invention further relates to aptamers. Aptamers (see for example WO 2014/191359 and the literature as cited therein) are short single-stranded nucleic acid molecules, which can fold into defined three-dimensional structures and recognize specific target structures. They have appeared to be suitable alternatives for developing targeted therapies. Aptamers have been shown to selectively bind to a variety of complex targets with high affinity and specificity.

[0226] Aptamers recognizing cell surface located molecules have been identified within the past decade and

provide means for developing diagnostic and therapeutic approaches. Since aptamers have been shown to possess almost no toxicity and immunogenicity they are promising candidates for biomedical applications. Indeed aptamers, for example prostate-specific membrane-antigen recognizing aptamers, have been successfully employed for targeted therapies and shown to be functional in xenograft in vivo models. Furthermore, aptamers recognizing specific tumor cell lines have been identified.

[0227] DNA aptamers can be selected to reveal broad-spectrum recognition properties for various cancer cells, and particularly those derived from solid tumors, while non-tumorigenic and primary healthy cells are not recognized. If the identified aptamers recognize not only a specific tumor sub-type but rather interact with a series of tumors, this renders the aptamers applicable as so-called broad-spectrum diagnostics and therapeutics.

[0228] Further, investigation of cell-binding behavior with flow cytometry showed that the aptamers revealed very good apparent affinities that are within the nanomolar range.

[0229] Aptamers are useful for diagnostic and therapeutic purposes. Further, it could be shown that some of the aptamers are taken up by tumor cells and thus can function as molecular vehicles for the targeted delivery of anti-cancer agents such as siRNA into tumor cells.

[0230] Aptamers can be selected against complex targets such as cells and tissues and complexes of the peptides comprising, preferably consisting of, a sequence according to any of SEQ ID NO 1 to SEQ ID NO 489, according to the present invention with the MHC molecule, using the cell-SELEX (Systematic Evolution of Ligands by Exponential enrichment) technique.

[0231] The peptides of the present invention can be used to generate and develop specific antibodies against MHC/peptide complexes. These can be used for therapy, targeting toxins or radioactive substances to the diseased tissue. Another use of these antibodies can be targeting radionuclides to the diseased tissue for imaging purposes such as PET. This use can help to detect small metastases or to determine the size and precise localization of diseased tissues.

[0232] Therefore, it is a further aspect of the invention to provide a method for producing a recombinant antibody specifically binding to a human major histocompatibility complex (MHC) class I or II being complexed with a HLA-restricted antigen (preferably a peptide according to the present invention), the method comprising: immunizing a genetically engineered non-human mammal comprising cells expressing said human major histocompatibility complex (MHC) class I or II with a soluble form of a MHC class I or II molecule being complexed with said HLA-restricted antigen; isolating mRNA molecules from antibody producing cells of said non-human mammal; producing a phage display library displaying protein molecules encoded by said mRNA molecules; and isolating at least one phage from said phage display library, said at least one phage displaying said antibody specifically binding to said human major histocompatibility complex (MHC) class I or II being complexed with said HLA-restricted antigen.

[0233] It is thus a further aspect of the invention to provide an antibody that specifically binds to a human major histocompatibility complex (MHC) class I or II being complexed with a HLA-restricted antigen, wherein the antibody pref-

erably is a polyclonal antibody, monoclonal antibody, bispecific antibody and/or a chimeric antibody.

[0234] Respective methods for producing such antibodies and single chain class I major histocompatibility complexes, as well as other tools for the production of these antibodies are disclosed in WO 03/068201, WO 2004/084798, WO 01/72768, WO 03/070752, and in publications (Cohen et al., 2003a; Cohen et al., 2003b; Denkberg et al., 2003), which for the purposes of the present invention are all explicitly incorporated by reference in their entireties.

[0235] Preferably, the antibody is binding with a binding affinity of below 20 nanomolar, preferably of below 10 nanomolar, to the complex, which is also regarded as "specific" in the context of the present invention.

[0236] The present invention relates to a peptide comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 489, or a variant thereof which is at least 88% homologous (preferably identical) to SEQ ID NO: 1 to SEQ ID NO: 489 or a variant thereof that induces T cells cross-reacting with said peptide, wherein said peptide is not the underlying full-length polypeptide.

[0237] The present invention further relates to a peptide comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 489 or a variant thereof which is at least 88% homologous (preferably identical) to SEQ ID NO: 1 to SEQ ID NO: 489, wherein said peptide or variant has an overall length of between 8 and 100, preferably between 8 and 30, and most preferred between 8 and 14 amino acids.

[0238] The present invention further relates to the peptides according to the invention that have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or -II.

[0239] The present invention further relates to the peptides according to the invention wherein the peptide consists or consists essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 489.

[0240] The present invention further relates to the peptides according to the invention, wherein the peptide is (chemically) modified and/or includes non-peptide bonds.

[0241] The present invention further relates to the peptides according to the invention, wherein the peptide is part of a fusion protein, in particular comprising N-terminal amino acids of the HLA-DR antigen-associated invariant chain (Ii), or wherein the peptide is fused to (or into) an antibody, such as, for example, an antibody that is specific for dendritic cells.

[0242] The present invention further relates to a nucleic acid, encoding the peptides according to the invention, provided that the peptide is not the complete (full) human protein.

[0243] The present invention further relates to the nucleic acid according to the invention that is DNA, cDNA, PNA, RNA or combinations thereof.

[0244] The present invention further relates to an expression vector capable of expressing a nucleic acid according to the present invention.

[0245] The present invention further relates to a peptide according to the present invention, a nucleic acid according to the present invention or an expression vector according to the present invention for use in medicine, in particular in the treatment of lung cancer (including NSCLC and SCLC).

[0246] The present invention further relates to a host cell comprising a nucleic acid according to the present invention or an expression vector according to the present invention.

[0247] The present invention further relates to the host cell according to the present invention that is an antigen presenting cell, and preferably a dendritic cell.

[0248] The present invention further relates to a method of producing a peptide according to the present invention, said method comprising culturing the host cell according to the present invention, and isolating the peptide from said host cell or its culture medium.

[0249] The present invention further relates to the method according to the present invention, where-in the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell.

[0250] The present invention further relates to the method according to the invention, wherein the antigen-presenting cell comprises an expression vector capable of expressing said peptide containing SEQ ID NO: 1 to SEQ ID NO: 489 or said variant amino acid sequence.

[0251] The present invention further relates to activated T cells, produced by the method according to the present invention, wherein said T cells selectively recognizes a cell which aberrantly expresses a polypeptide comprising an amino acid sequence according to the present invention.

[0252] The present invention further relates to a method of killing target cells in a patient which target cells aberrantly express a polypeptide comprising any amino acid sequence according to the present invention, the method comprising administering to the patient an effective number of T cells as according to the present invention.

[0253] The present invention further relates to the use of any peptide described, a nucleic acid according to the present invention, an expression vector according to the present invention, a cell according to the present invention, or an activated cytotoxic T lymphocyte according to the present invention as a medicament or in the manufacture of a medicament. The present invention further relates to a use according to the present invention, wherein the medicament is active against cancer.

[0254] The present invention further relates to a use according to the invention, wherein the medicament is a vaccine. The present invention further relates to a use according to the invention, wherein the medicament is active against cancer.

[0255] The present invention further relates to a use according to the invention, wherein said cancer cells are lung cancer (including NSCLC and SCLC) cells or other solid or hematological tumor cells such as acute myeloid leukemia, breast cancer, bile duct cancer, brain cancer, chronic lymphocytic leukemia, colorectal carcinoma, esophageal cancer, gallbladder cancer, gastric cancer, head and neck squamous cell carcinoma, hepatocellular cancer, melanoma, non-Hodgkin lymphoma, ovarian cancer, pancreatic cancer, prostate cancer, renal cell cancer, urinary bladder cancer, uterine cancer.

[0256] The present invention further relates to particular marker proteins and biomarkers based on the peptides according to the present invention, herein called "targets" that can be used in the diagnosis and/or prognosis of lung

cancer (including NSCLC and SCLC). The present invention also relates to the use of these novel targets for cancer treatment.

[0257] The term "antibody" or "antibodies" is used herein in a broad sense and includes both polyclonal and monoclonal antibodies. In addition to intact or "full" immunoglobulin molecules, also included in the term "antibodies" are fragments (e.g. CDRs, Fv, Fab and Fc fragments) or polymers of those immunoglobulin molecules and humanized versions of immunoglobulin molecules, as long as they exhibit any of the desired properties (e.g., specific binding of a lung cancer (including NSCLC and SCLC) marker (poly) peptide, delivery of a toxin to a lung cancer (including NSCLC and SCLC) cell expressing a cancer marker gene at an increased level, and/or inhibiting the activity of a lung cancer (including NSCLC and SCLC) marker polypeptide) according to the invention.

[0258] Whenever possible, the antibodies of the invention may be purchased from commercial sources. The antibodies of the invention may also be generated using well-known methods. The skilled artisan will understand that either full length lung cancer (including NSCLC and SCLC) marker polypeptides or fragments thereof may be used to generate the antibodies of the invention. A polypeptide to be used for generating an antibody of the invention may be partially or fully purified from a natural source, or may be produced using recombinant DNA techniques.

[0259] For example, a cDNA encoding a peptide according to the present invention, such as a peptide according to SEQ ID NO: 1 to SEQ ID NO: 489 polypeptide, or a variant or fragment thereof, can be expressed in prokaryotic cells (e.g., bacteria) or eukaryotic cells (e.g., yeast, insect, or mammalian cells), after which the recombinant protein can be purified and used to generate a monoclonal or polyclonal antibody preparation that specifically bind the lung cancer (including NSCLC and SCLC) marker polypeptide used to generate the antibody according to the invention.

[0260] One of skill in the art will realize that the generation of two or more different sets of monoclonal or polyclonal antibodies maximizes the likelihood of obtaining an antibody with the specificity and affinity required for its intended use (e.g., ELISA, immunohistochemistry, in vivo imaging, immunotoxin therapy). The antibodies are tested for their desired activity by known methods, in accordance with the purpose for which the antibodies are to be used (e.g., ELISA, immunohistochemistry, immunotherapy, etc.; for further guidance on the generation and testing of antibodies, see, e.g., Greenfield, 2014 (Greenfield, 2014)). For example, the antibodies may be tested in ELISA assays or, Western blots, immunohistochemical staining of formalin-fixed cancers or frozen tissue sections. After their initial in vitro characterization, antibodies intended for therapeutic or in vivo diagnostic use are tested according to known clinical testing methods.

[0261] The term "monoclonal antibody" as used herein refers to an antibody obtained from a substantially homogeneous population of antibodies, i.e.; the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. The monoclonal antibodies herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class

or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired antagonistic activity (U.S. Pat. No. 4,816,567, which is hereby incorporated in its entirety).

[0262] Monoclonal antibodies of the invention may be prepared using hybridoma methods. In a hybridoma method, a mouse or other appropriate host animal is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro.

[0263] The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Pat. No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies).

[0264] In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly Fab fragments, can be accomplished using routine techniques known in the art. For instance, digestion can be performed using papain. Examples of papain digestion are described in WO 94/29348 and U.S. Pat. No. 4,342,566. Papain digestion of antibodies typically produces two identical antigen binding fragments, called Fab fragments, each with a single antigen binding site, and a residual Fc fragment. Pepsin treatment yields a F(ab')₂ fragment and a pFc' fragment.

[0265] The antibody fragments, whether attached to other sequences or not, can also include insertions, deletions, substitutions, or other selected modifications of particular regions or specific amino acids residues, provided the activity of the fragment is not significantly altered or impaired compared to the non-modified antibody or antibody fragment. These modifications can provide for some additional property, such as to remove/add amino acids capable of disulfide bonding, to increase its bio-longevity, to alter its secretory characteristics, etc. In any case, the antibody fragment must possess a bioactive property, such as binding activity, regulation of binding at the binding domain, etc. Functional or active regions of the antibody may be identified by mutagenesis of a specific region of the protein, followed by expression and testing of the expressed polypeptide. Such methods are readily apparent to a skilled practitioner in the art and can include site-specific mutagenesis of the nucleic acid encoding the antibody fragment.

[0266] The antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab' or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework (FR) residues of the human immunoglobulin are

replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin.

[0267] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[0268] Transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production can be employed. For example, it has been described that the homozygous deletion of the antibody heavy chain joining region gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. Human antibodies can also be produced in phage display libraries.

[0269] Antibodies of the invention are preferably administered to a subject in a pharmaceutically acceptable carrier. Typically, an appropriate amount of a pharmaceutically-acceptable salt is used in the formulation to render the formulation isotonic. Examples of the pharmaceutically-acceptable carrier include saline, Ringer's solution and dextrose solution. The pH of the solution is preferably from about 5 to about 8, and more preferably from about 7 to about 7.5. Further carriers include sustained release preparations such as semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, liposomes or microparticles. It will be apparent to those persons skilled in the art that certain carriers may be more preferable depending upon, for instance, the route of administration and concentration of antibody being administered.

[0270] The antibodies can be administered to the subject, patient, or cell by injection (e.g., intravenous, intraperitoneal, subcutaneous, intramuscular), or by other methods such as infusion that ensure its delivery to the bloodstream in an effective form. The antibodies may also be administered by intratumoral or peritumoral routes, to exert local as well as systemic therapeutic effects. Local or intravenous injection is preferred.

[0271] Effective dosages and schedules for administering the antibodies may be determined empirically, and making such determinations is within the skill in the art. Those skilled in the art will understand that the dosage of antibodies that must be administered will vary depending on, for example, the subject that will receive the antibody, the route of administration, the particular type of antibody used and other drugs being administered. A typical daily dosage of the antibody used alone might range from about 1 ($\mu\text{g/kg}$ to up to 100 mg/kg of body weight or more per day, depending on the factors mentioned above. Following administration of an antibody, preferably for treating lung cancer (including NSCLC and SCLC), the efficacy of the therapeutic antibody can be assessed in various ways well known to the skilled practitioner. For instance, the size, number, and/or distribution of cancer in a subject receiving treatment may be monitored using standard tumor imaging techniques. A therapeutically-administered antibody that arrests tumor growth, results in tumor shrinkage, and/or prevents the development of new tumors, compared to the disease course that would occur in the absence of antibody administration, is an efficacious antibody for treatment of cancer.

[0272] It is a further aspect of the invention to provide a method for producing a soluble T-cell receptor (sTCR) recognizing a specific peptide-MHC complex. Such soluble T-cell receptors can be generated from specific T-cell clones, and their affinity can be increased by mutagenesis targeting the complementarity-determining regions. For the purpose of T-cell receptor selection, phage display can be used (US 2010/0113300, (Liddy et al., 2012)). For the purpose of stabilization of T-cell receptors during phage display and in case of practical use as drug, alpha and beta chain can be linked e.g. by non-native disulfide bonds, other covalent bonds (single-chain T-cell receptor), or by dimerization domains (Boulter et al., 2003; Card et al., 2004; Willcox et al., 1999). The T-cell receptor can be linked to toxins, drugs, cytokines (see, for example, US 2013/0115191), and domains recruiting effector cells such as an anti-CD3 domain, etc., in order to execute particular functions on target cells. Moreover, it could be expressed in T cells used for adoptive transfer. Further information can be found in WO 2004/033685A1 and WO 2004/074322A1. A combination of sTCRs is described in WO 2012/056407A1. Further methods for the production are disclosed in WO 2013/057586A1.

[0273] In addition, the peptides and/or the TCRs or antibodies or other binding molecules of the present invention can be used to verify a pathologist's diagnosis of a cancer based on a biopsied sample.

[0274] The antibodies or TCRs may also be used for in vivo diagnostic assays. Generally, the antibody is labeled with a radionucleotide (such as ^{111}In , ^{99}Tc , ^{14}C , ^{131}I , ^3H , ^{32}P or ^{35}S) so that the tumor can be localized using immunoscintigraphy. In one embodiment, antibodies or fragments thereof bind to the extracellular domains of two or more targets of a protein selected from the group consisting of the above-mentioned proteins, and the affinity value (K_d) is less than $1 \times 10^{-6} \text{ M}$.

[0275] Antibodies for diagnostic use may be labeled with probes suitable for detection by various imaging methods. Methods for detection of probes include, but are not limited to, fluorescence, light, confocal and electron microscopy; magnetic resonance imaging and spectroscopy; fluoroscopy, computed tomography and positron emission tomography.

Suitable probes include, but are not limited to, fluorescein, rhodamine, eosin and other fluorophores, radioisotopes, gold, gadolinium and other lanthanides, paramagnetic iron, fluorine-18 and other positron-emitting radionuclides. Additionally, probes may be bi- or multi-functional and be detectable by more than one of the methods listed. These antibodies may be directly or indirectly labeled with said probes. Attachment of probes to the antibodies includes covalent attachment of the probe, incorporation of the probe into the antibody, and the covalent attachment of a chelating compound for binding of probe, amongst others well recognized in the art. For immunohistochemistry, the disease tissue sample may be fresh or frozen or may be embedded in paraffin and fixed with a preservative such as formalin. The fixed or embedded section contains the sample are contacted with a labeled primary antibody and secondary antibody, wherein the antibody is used to detect the expression of the proteins in situ.

[0276] Another aspect of the present invention includes an in vitro method for producing activated T cells, the method comprising contacting in vitro T cells with antigen loaded human MHC molecules expressed on the surface of a suitable antigen-presenting cell for a period of time sufficient to activate the T cell in an antigen specific manner, wherein the antigen is a peptide according to the invention. Preferably a sufficient amount of the antigen is used with an antigen-presenting cell.

[0277] Preferably the mammalian cell lacks or has a reduced level or function of the TAP peptide transporter. Suitable cells that lack the TAP peptide transporter include T2, RMA-S and *Drosophila* cells. TAP is the transporter associated with antigen processing.

[0278] The human peptide loading deficient cell line T2 is available from the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Md. 20852, USA under Catalogue No CRL 1992; the *Drosophila* cell line Schneider line 2 is available from the ATCC under Catalogue No CRL 19863; the mouse RMA-S cell line is described in Ljunggren et al. (Ljunggren and Karre, 1985).

[0279] Preferably, before transfection the host cell expresses substantially no MHC class I molecules. It is also preferred that the stimulator cell expresses a molecule important for providing a co-stimulatory signal for T-cells such as any of B7.1, B7.2, ICAM-1 and LFA 3. The nucleic acid sequences of numerous MHC class I molecules and of the co-stimulator molecules are publicly available from the GenBank and EMBL databases.

[0280] In case of a MHC class I epitope being used as an antigen, the T cells are CD8-positive T cells.

[0281] If an antigen-presenting cell is transfected to express such an epitope, preferably the cell comprises an expression vector capable of expressing a peptide containing SEQ ID NO: 1 to SEQ ID NO: 489, or a variant amino acid sequence thereof.

[0282] A number of other methods may be used for generating T cells in vitro. For example, autologous tumor-infiltrating lymphocytes can be used in the generation of CTL. Plebanski et al. (Plebanski et al., 1995) made use of autologous peripheral blood lymphocytes (PLBs) in the preparation of T cells. Furthermore, the production of autologous T cells by pulsing dendritic cells with peptide or polypeptide, or via infection with recombinant virus is possible. Also, B cells can be used in the production of autologous T cells. In addition, macrophages pulsed with

peptide or polypeptide, or infected with recombinant virus, may be used in the preparation of autologous T cells. S. Walter et al. (Walter et al., 2003) describe the in vitro priming of T cells by using artificial antigen presenting cells (aAPCs), which is also a suitable way for generating T cells against the peptide of choice. In the present invention, aAPCs were generated by the coupling of preformed MHC: peptide complexes to the surface of polystyrene particles (microbeads) by biotin:streptavidin biochemistry. This system permits the exact control of the MHC density on aAPCs, which allows to selectively elicit high- or low-avidity antigen-specific T cell responses with high efficiency from blood samples. Apart from MHC:peptide complexes, aAPCs should carry other proteins with co-stimulatory activity like anti-CD28 antibodies coupled to their surface. Furthermore, such aAPC-based systems often require the addition of appropriate soluble factors, e. g. cytokines, like interleukin-12.

[0283] Allogeneic cells may also be used in the preparation of T cells and a method is described in detail in WO 97/26328, incorporated herein by reference. For example, in addition to *Drosophila* cells and T2 cells, other cells may be used to present antigens such as CHO cells, baculovirus-infected insect cells, bacteria, yeast, and vaccinia-infected target cells. In addition, plant viruses may be used (see, for example, Porta et al. (Porta et al., 1994) which describes the development of cowpea mosaic virus as a high-yielding system for the presentation of foreign peptides.

[0284] The activated T cells that are directed against the peptides of the invention are useful in therapy. Thus, a further aspect of the invention provides activated T cells obtainable by the foregoing methods of the invention.

[0285] Activated T cells, which are produced by the above method, will selectively recognize a cell that aberrantly expresses a polypeptide that comprises an amino acid sequence of SEQ ID NO: 1 to SEQ ID NO 489.

[0286] Preferably, the T cell recognizes the cell by interacting through its TCR with the HLA/peptide-complex (for example, binding). The T cells are useful in a method of killing target cells in a patient whose target cells aberrantly express a polypeptide comprising an amino acid sequence of the invention wherein the patient is administered an effective number of the activated T cells. The T cells that are administered to the patient may be derived from the patient and activated as described above (i.e. they are autologous T cells). Alternatively, the T cells are not from the patient but are from another individual. Of course, it is preferred if the individual is a healthy individual. By "healthy individual" the inventors mean that the individual is generally in good health, preferably has a competent immune system and, more preferably, is not suffering from any disease that can be readily tested for, and detected.

[0287] In vivo, the target cells for the CD8-positive T cells according to the present invention can be cells of the tumor (which sometimes express MHC class II) and/or stromal cells surrounding the tumor (tumor cells) (which sometimes also express MHC class II; (Dengjel et al., 2006)).

[0288] The T cells of the present invention may be used as active ingredients of a therapeutic composition. Thus, the invention also provides a method of killing target cells in a patient whose target cells aberrantly express a polypeptide comprising an amino acid sequence of the invention, the method comprising administering to the patient an effective number of T cells as defined above.

[0289] By "aberrantly expressed" the inventors also mean that the polypeptide is over-expressed compared to levels of expression in normal tissues or that the gene is silent in the tissue from which the tumor is derived but in the tumor it is expressed. By "over-expressed" the inventors mean that the polypeptide is present at a level at least 1.2-fold of that present in normal tissue; preferably at least 2-fold, and more preferably at least 4-fold or 6-fold the level present in normal tissue.

[0290] T cells may be obtained by methods known in the art, e.g. those described above.

[0291] Protocols for this so-called adoptive transfer of T cells are well known in the art. Reviews can be found in: Gattioni et al. and Morgan et al. (Gattioni et al., 2006; Morgan et al., 2006).

[0292] Another aspect of the present invention includes the use of the peptides complexed with MHC to generate a T-cell receptor whose nucleic acid is cloned and is introduced into a host cell, preferably a T cell. This engineered T cell can then be transferred to a patient for therapy of cancer.

[0293] Any molecule of the invention, i.e. the peptide, nucleic acid, antibody, expression vector, cell, activated T cell, T-cell receptor or the nucleic acid encoding it, is useful for the treatment of disorders, characterized by cells escaping an immune response. Therefore, any molecule of the present invention may be used as medicament or in the manufacture of a medicament. The molecule may be used by itself or combined with other molecule(s) of the invention or (a) known molecule(s).

[0294] The present invention is further directed at a kit comprising:

[0295] (a) a container containing a pharmaceutical composition as described above, in solution or in lyophilized form;

[0296] (b) optionally a second container containing a diluent or reconstituting solution for the lyophilized formulation; and

[0297] (c) optionally, instructions for (i) use of the solution or (ii) reconstitution and/or use of the lyophilized formulation.

[0298] The kit may further comprise one or more of (iii) a buffer, (iv) a diluent, (v) a filter, (vi) a needle, or (v) a syringe. The container is preferably a bottle, a vial, a syringe or test tube; and it may be a multi-use container. The pharmaceutical composition is preferably lyophilized.

[0299] Kits of the present invention preferably comprise a lyophilized formulation of the present invention in a suitable container and instructions for its reconstitution and/or use. Suitable containers include, for example, bottles, vials (e.g. dual chamber vials), syringes (such as dual chamber syringes) and test tubes. The container may be formed from a variety of materials such as glass or plastic. Preferably the kit and/or container contain/s instructions on or associated with the container that indicates directions for reconstitution and/or use. For example, the label may indicate that the lyophilized formulation is to be reconstituted to peptide concentrations as described above. The label may further indicate that the formulation is useful or intended for subcutaneous administration.

[0300] The container holding the formulation may be a multi-use vial, which allows for repeat administrations (e.g., from 2-6 administrations) of the reconstituted formulation.

The kit may further comprise a second container comprising a suitable diluent (e.g., sodium bicarbonate solution).

[0301] Upon mixing of the diluent and the lyophilized formulation, the final peptide concentration in the reconstituted formulation is preferably at least 0.15 mg/mL/peptide (=75 µg) and preferably not more than 3 mg/mL/peptide (=1500 µg). The kit may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

[0302] Kits of the present invention may have a single container that contains the formulation of the pharmaceutical compositions according to the present invention with or without other components (e.g., other compounds or pharmaceutical compositions of these other compounds) or may have distinct container for each component.

[0303] Preferably, kits of the invention include a formulation of the invention packaged for use in combination with the co-administration of a second compound (such as adjuvants (e.g. GM-CSF), a chemotherapeutic agent, a natural product, a hormone or antagonist, an anti-angiogenesis agent or inhibitor, an apoptosis-inducing agent or a chelator) or a pharmaceutical composition thereof. The components of the kit may be pre-complexed or each component may be in a separate distinct container prior to administration to a patient. The components of the kit may be provided in one or more liquid solutions, preferably, an aqueous solution, more preferably, a sterile aqueous solution. The components of the kit may also be provided as solids, which may be converted into liquids by addition of suitable solvents, which are preferably provided in another distinct container.

[0304] The container of a therapeutic kit may be a vial, test tube, flask, bottle, syringe, or any other means of enclosing a solid or liquid. Usually, when there is more than one component, the kit will contain a second vial or other container, which allows for separate dosing. The kit may also contain another container for a pharmaceutically acceptable liquid. Preferably, a therapeutic kit will contain an apparatus (e.g., one or more needles, syringes, eye droppers, pipette, etc.), which enables administration of the agents of the invention that are components of the present kit.

[0305] The present formulation is one that is suitable for administration of the peptides by any acceptable route such as oral (enteral), nasal, ophthalmic, subcutaneous, intradermal, intramuscular, intravenous or transdermal. Preferably, the administration is s.c., and most preferably i.d. administration may be by infusion pump.

[0306] Since the peptides of the invention were isolated from lung cancer (including NSCLC and SCLC), the medicament of the invention is preferably used to treat lung cancer (including NSCLC and SCLC).

[0307] The present invention further relates to a method for producing a personalized pharmaceutical for an individual patient comprising manufacturing a pharmaceutical composition comprising at least one peptide selected from a warehouse of pre-screened TUMAPs, wherein the at least one peptide used in the pharmaceutical composition is selected for suitability in the individual patient. In one embodiment, the pharmaceutical composition is a vaccine. The method could also be adapted to produce T cell clones for down-stream applications, such as TCR isolations, or soluble antibodies, and other treatment options.

[0308] A “personalized pharmaceutical” shall mean specifically tailored therapies for one individual patient that will only be used for therapy in such individual patient, including actively personalized cancer vaccines and adoptive cellular therapies using autologous patient tissue.

[0309] As used herein, the term “warehouse” shall refer to a group or set of peptides that have been pre-screened for immunogenicity and/or over-presentation in a particular tumor type. The term “warehouse” is not intended to imply that the particular peptides included in the vaccine have been pre-manufactured and stored in a physical facility, although that possibility is contemplated. It is expressly contemplated that the peptides may be manufactured de novo for each individualized vaccine produced, or may be pre-manufactured and stored. The warehouse (e.g. in the form of a database) is composed of tumor-associated peptides which were highly overexpressed in the tumor tissue of lung cancer (including NSCLC and SCLC) patients with various HLA-A HLA-B and HLA-C alleles. It may contain MHC class I and MHC class II peptides or elongated MHC class I peptides. In addition to the tumor associated peptides collected from several lung cancers (including NSCLC and SCLC) tissues, the warehouse may contain HLA-A*02, HLA-A*01, HLA-A*03, HLA-A*24, HLA-B*07, HLA-B*08 and HLA-B*44 marker peptides. These peptides allow comparison of the magnitude of T-cell immunity induced by TUMAPs in a quantitative manner and hence allow important conclusion to be drawn on the capacity of the vaccine to elicit anti-tumor responses. Secondly, they function as important positive control peptides derived from a “non-self” antigen in the case that any vaccine-induced T-cell responses to TUMAPs derived from “self” antigens in a patient are not observed. And thirdly, it may allow conclusions to be drawn, regarding the status of immunocompetence of the patient.

[0310] TUMAPs for the warehouse are identified by using an integrated functional genomics approach combining gene expression analysis, mass spectrometry, and T-cell immunology (XPresident®). The approach assures that only TUMAPs truly present on a high percentage of tumors but not or only minimally expressed on normal tissue, are chosen for further analysis. For initial peptide selection, lung cancer (including NSCLC and SCLC) samples from patients and blood from healthy donors were analyzed in a stepwise approach:

[0311] 1. HLA ligands from the malignant material were identified by mass spectrometry

[0312] 2. Genome-wide messenger ribonucleic acid (mRNA) expression analysis was used to identify genes over-expressed in the malignant tissue (lung cancer (including NSCLC and SCLC)) compared with a range of normal organs and tissues

[0313] 3. Identified HLA ligands were compared to gene expression data. Peptides over-presented or selectively presented on tumor tissue, preferably encoded by selectively expressed or over-expressed genes as detected in step 2 were considered suitable TUMAP candidates for a multi-peptide vaccine.

[0314] 4. Literature research was performed in order to identify additional evidence supporting the relevance of the identified peptides as TUMAPs

[0315] 5. The relevance of over-expression at the mRNA level was confirmed by redetection of selected TUMAPs from step 3 on tumor tissue and lack of (or infrequent) detection on healthy tissues.

[0316] 6. In order to assess, whether an induction of in vivo T-cell responses by the selected peptides may be feasible, in vitro immunogenicity assays were performed using human T cells from healthy donors as well as from lung cancer (including NSCLC and SCLC) patients.

[0317] In an aspect, the peptides are pre-screened for immunogenicity before being included in the warehouse. By way of example, and not limitation, the immunogenicity of the peptides included in the warehouse is determined by a method comprising in vitro T-cell priming through repeated stimulations of CD8+ T cells from healthy donors with artificial antigen presenting cells loaded with peptide/MHC complexes and anti-CD28 antibody.

[0318] This method is preferred for rare cancers and patients with a rare expression profile. In contrast to multi-peptide cocktails with a fixed composition as currently developed, the warehouse allows a significantly higher matching of the actual expression of antigens in the tumor with the vaccine. Selected single or combinations of several “off-the-shelf” peptides will be used for each patient in a multitarget approach. In theory, an approach based on selection of e.g. 5 different antigenic peptides from a library of 50 would already lead to approximately 17 million possible drug product (DP) compositions.

[0319] In an aspect, the peptides are selected for inclusion in the vaccine based on their suitability for the individual patient based on the method according to the present invention as described herein, or as below.

[0320] The HLA phenotype, transcriptomic and peptidomic data is gathered from the patient’s tumor material, and blood samples to identify the most suitable peptides for each patient containing “warehouse” and patient-unique (i.e. mutated) TUMAPs. Those peptides will be chosen, which are selectively or over-expressed in the patients’ tumor and, where possible, show strong in vitro immunogenicity if tested with the patients’ individual PBMCs.

[0321] Preferably, the peptides included in the vaccine are identified by a method comprising: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient; (b) comparing the peptides identified in (a) with a warehouse (database) of peptides as described above; and (c) selecting at least one peptide from the warehouse (database) that correlates with a tumor-associated peptide identified in the patient. For example, the TUMAPs presented by the tumor sample are identified by: (a1) comparing expression data from the tumor sample to expression data from a sample of normal tissue corresponding to the tissue type of the tumor sample to identify proteins that are over-expressed or aberrantly expressed in the tumor sample; and (a2) correlating the expression data with sequences of MHC ligands bound to MHC class I and/or class II molecules in the tumor sample to identify MHC ligands derived from proteins over-expressed or aberrantly expressed by the tumor. Preferably, the sequences of MHC ligands are identified by eluting bound peptides from MHC molecules isolated from the tumor sample, and sequencing the eluted ligands. Preferably, the tumor sample and the normal tissue are obtained from the same patient.

[0322] In addition to, or as an alternative to, selecting peptides using a warehousing (database) model, TUMAPs may be identified in the patient de novo, and then included in the vaccine. As one example, candidate TUMAPs may be identified in the patient by (a1) comparing expression data from the tumor sample to expression data from a sample of

normal tissue corresponding to the tissue type of the tumor sample to identify proteins that are over-expressed or aberrantly expressed in the tumor sample; and (a2) correlating the expression data with sequences of MHC ligands bound to MHC class I and/or class II molecules in the tumor sample to identify MHC ligands derived from proteins over-expressed or aberrantly expressed by the tumor. As another example, proteins may be identified containing mutations that are unique to the tumor sample relative to normal corresponding tissue from the individual patient, and TUMAPs can be identified that specifically target the mutation. For example, the genome of the tumor and of corresponding normal tissue can be sequenced by whole genome sequencing: For discovery of non-synonymous mutations in the protein-coding regions of genes, genomic DNA and RNA are extracted from tumor tissues and normal non-mutated genomic germline DNA is extracted from peripheral blood mononuclear cells (PBMCs). The applied NGS approach is confined to the re-sequencing of protein coding regions (exome re-sequencing). For this purpose, exonic DNA from human samples is captured using vendor-supplied target enrichment kits, followed by sequencing with e.g. a HiSeq2000 (Illumina). Additionally, tumor mRNA is sequenced for direct quantification of gene expression and validation that mutated genes are expressed in the patients’ tumors. The resultant millions of sequence reads are processed through software algorithms. The output list contains mutations and gene expression. Tumor-specific somatic mutations are determined by comparison with the PBMC-derived germline variations and prioritized. The de novo identified peptides can then be tested for immunogenicity as described above for the warehouse, and candidate TUMAPs possessing suitable immunogenicity are selected for inclusion in the vaccine.

[0323] In one exemplary embodiment, the peptides included in the vaccine are identified by: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient by the method as described above; (b) comparing the peptides identified in (a) with a warehouse of peptides that have been prescreened for immunogenicity and overrepresentation in tumors as compared to corresponding normal tissue; (c) selecting at least one peptide from the warehouse that correlates with a tumor-associated peptide identified in the patient; and (d) optionally, selecting at least one peptide identified de novo in (a) confirming its immunogenicity.

[0324] In one exemplary embodiment, the peptides included in the vaccine are identified by: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient; and (b) selecting at least one peptide identified de novo in (a) and confirming its immunogenicity.

[0325] Once the peptides for a personalized peptide based vaccine are selected, the vaccine is produced. The vaccine preferably is a liquid formulation consisting of the individual peptides dissolved in between 20-40% DMSO, preferably about 30-35% DMSO, such as about 33% DMSO.

[0326] Each peptide to be included into a product is dissolved in DMSO. The concentration of the single peptide solution has to be chosen depending on the number of peptides to be included into the product. The single peptide-DMSO solutions are mixed in equal parts to achieve a solution containing all peptides to be included in the product with a concentration of ~2.5 mg/ml per peptide. The mixed

solution is then diluted 1:3 with water for injection to achieve a concentration of 0.826 mg/ml per peptide in 33% DMSO. The diluted solution is filtered through a 0.22 μ m sterile filter. The final bulk solution is obtained.

[0327] Final bulk solution is filled into vials and stored at -20° C. until use. One vial contains 700 μ L solution, containing 0.578 mg of each peptide. Of this, 500 μ L (approx. 400 μ g per peptide) will be applied for intradermal injection.

[0328] In addition to being useful for treating cancer, the peptides of the present invention are also useful as diagnostics. Since the peptides were generated from lung cancer (including NSCLC and SCLC) cells and since it was determined that these peptides are not or at lower levels present in normal tissues, these peptides can be used to diagnose the presence of a cancer.

[0329] The presence of claimed peptides on tissue biopsies in blood samples can assist a pathologist in diagnosis of cancer. Detection of certain peptides by means of antibodies, mass spectrometry or other methods known in the art can tell the pathologist that the tissue sample is malignant or inflamed or generally diseased, or can be used as a biomarker for lung cancer (including NSCLC and SCLC). Presence of groups of peptides can enable classification or sub-classification of diseased tissues.

[0330] The detection of peptides on diseased tissue specimen can enable the decision about the benefit of therapies involving the immune system, especially if T-lymphocytes are known or expected to be involved in the mechanism of action. Loss of MHC expression is a well described mechanism by which infected or malignant cells escape immunosurveillance. Thus, presence of peptides shows that this mechanism is not exploited by the analyzed cells.

[0331] The peptides of the present invention might be used to analyze lymphocyte responses against those peptides such as T cell responses or antibody responses against the peptide or the peptide complexed to MHC molecules. These lymphocyte responses can be used as prognostic markers for decision on further therapy steps. These responses can also be used as surrogate response markers in immunotherapy approaches aiming to induce lymphocyte responses by different means, e.g. vaccination of protein, nucleic acids, autologous materials, adoptive transfer of lymphocytes. In gene therapy settings, lymphocyte responses against peptides can be considered in the assessment of side effects. Monitoring of lymphocyte responses might also be a valuable tool for follow-up examinations of transplantation therapies, e.g. for the detection of graft versus host and host versus graft diseases.

[0332] The present invention will now be described in the following examples which describe preferred embodiments thereof, and with reference to the accompanying figures, nevertheless, without being limited thereto. For the purposes of the present invention, all references as cited herein are incorporated by reference in their entireties.

FIGURES

[0333] FIGS. 1A through 1N show the over-presentation of various peptides in different cancer tissues (black dots). Upper part: Median MS signal intensities from technical replicate measurements are plotted as dots for single positive normal (grey dots) and tumor samples (black dots) on which the peptide was detected. Tumor and normal samples are grouped according to organ of origin, and box-and-whisker

plots represent median, 25th and 75th percentile (box), and minimum and maximum (whiskers) of normalized signal intensities over multiple samples. Normal organs are ordered according to risk categories (blood cells, blood vessels, brain, liver, lung: high risk, grey dots; reproductive organs, breast, prostate: low risk, grey dots; all other organs: medium risk; grey dots). Lower part: The relative peptide detection frequency in every organ is shown as spine plot. Numbers below the panel indicate number of samples on which the peptide was detected out of the total number of samples analyzed for each organ. If the peptide has been detected on a sample but could not be quantified for technical reasons, the sample is included in this representation of detection frequency, but no dot is shown in the upper part of the figure. FIGS. 1A to 1B show the over-presentation of various peptides in HLA-A*24 cancer tissues compared to a panel of HLA-A*24 normal samples (N=19 for normal samples, N=94 for tumor samples). Tissues (from left to right): Normal samples: bloodvess (blood vessels); brain; heart; liver; lung; kidney; pituit (pituitary). Tumor samples: GBM: glioblastoma; GC: gastric cancer; HCC: hepatocellular carcinoma; NSCLCaden (non-small cell lung cancer adenocarcinoma); NSCLCother (non-small cell lung cancer); NSCLCsquam (non-small cell lung cancer squamous cell); SCLC: small cell lung cancer. FIG. 1A) Gene symbol: URB1, Peptide: LYQEIL AQL (SEQ ID NO.: 62), FIG. 1B) Gene symbol: CKAP5, Peptide: VYPASKMF PFI (SEQ ID NO.: 65). FIGS. 1C to 1D show the over-presentation of various peptides in HLA-A*02 cancer tissues compared to a panel of HLA-A*02 normal samples (N=469 for normal samples, N=528 for tumor samples). Tissues (from left to right): Normal samples: blood cells; bloodvess (blood vessels); brain; heart; liver; lung; adipose (adipose tissue); adren. gl. (adrenal gland); bile duct; bladder; BM (bone marrow); esoph (esophagus); eye; gallb (gallbladder); head&neck; kidney; large_int (large intestine); LN (lymph node); nerve; pancreas; parathyr (parathyroid gland); perit (peritoneum); pituit (pituitary); pleura; skel. mus (skeletal muscle); skin; small_int (small intestine); spleen; stomach; thyroid; trachea; ureter; breast; ovary; placenta; prostate; testis; thymus; uterus. Tumor samples: AML: acute myeloid leukemia; BRCA: breast cancer; CCC: cholangiocellular carcinoma; CLL: chronic lymphocytic leukemia; CRC: colorectal cancer; GBC: gallbladder cancer; GBM: glioblastoma; GC: gastric cancer; GEJC: stomach cardia esophagus, cancer; HCC: hepatocellular carcinoma; HNSCC: head-and-neck cancer; MEL: melanoma; NHL: non-hodgkin lymphoma; NSCLCaden (non-small cell lung cancer adenocarcinoma); NSCLCother (non-small cell lung cancer); NSCLCsquam (non-small cell lung cancer squamous cell); OC: ovarian cancer; OSCAR: esophageal cancer; PACA: pancreatic cancer; PRCA: prostate cancer; RCC: renal cell carcinoma; SCLC: small cell lung cancer; UBC: urinary bladder carcinoma; UEC: uterine and endometrial cancer. FIG. 1C) Gene symbol: BMS1, Peptide: VLYDKDAVYV (SEQ ID NO.: 129), FIG. 1D) Gene symbol: GORASP2, Peptide: NLWGGQGLLG V (SEQ ID NO.: 130). FIGS. 1E to 1F show the over-presentation of various peptides in HLA-A*01 cancer tissues compared to a panel of HLA-A*01 normal samples (N=13 for normal samples, N=40 for tumor samples). Tissues (from left to right): Normal samples: blood cells; brain; heart; liver; lung. Tumor samples: GBM: glioblastoma; HCC: hepatocellular carcinoma; NSCLCaden (non-small cell lung cancer adenocar-

cinoma); NSCLCother (non-small cell lung cancer); NSCLCsquam (non-small cell lung cancer squamous cell); SCLC: small cell lung cancer. FIG. 1E) Gene symbol: ZNF439, Peptide: LLDISQKNLY (SEQ ID NO.: 154), FIG. 1F) Gene symbol: MMP12, Peptide: SADDIRGIQSLY (SEQ ID NO.: 174). FIGS. 1G to 1H show the over-presentation of various peptides in HLA-A*03 cancer tissues compared to a panel of HLA-A*03 normal samples (N=12 for normal samples, N=28 for tumor samples). Tissues (from left to right): Normal samples: blood cells; bloodvess (blood vessels); brain; heart; liver; lung. Tumor samples: GBM: glioblastoma; GC: gastric cancer; NHL: non-hodgkin lymphoma; NSCLCadeno (non-small cell lung cancer adenocarcinoma); NSCLCother (non-small cell lung cancer); NSCLCsquam (non-small cell lung cancer squamous cell); SCLC: small cell lung cancer. FIG. 1G) Gene symbols: KRT81, KRT121P, KRT83, KRT85, KRT86, Peptide: KLALEGALQK (SEQ ID NO.: 202), FIG. 1H) Gene symbol: NDC80, Peptide: SINKPTSER (SEQ ID NO.: 457). FIGS. 1I to 1J show the over-presentation of various peptides in HLA-B*07 cancer tissues compared to a panel of HLA-B*07 normal samples (N=13 for normal samples, N=36 for tumor samples). Tissues (from left to right): Normal samples: blood cells; bloodvess (blood vessels); brain; heart; liver; lung. Tumor samples: GBM: glioblastoma; NSCLCadeno (non-small cell lung cancer adenocarcinoma); NSCLCother (non-small cell lung cancer); NSCLCsquam (non-small cell lung cancer squamous cell); OC: ovarian cancer; SCLC: small cell lung cancer. FIG. 1I) Gene symbol: CTHRC1, Peptide: SPQRLRGLL (SEQ ID NO.: 291), FIG. 1J) Gene symbol: MANEA, Peptide: RPHKPGLYL (SEQ ID NO.: 475). FIGS. 1K to 1L show the over-presentation of various peptides in HLA-B*08 cancer tissues compared to a panel of HLA-B*08 normal samples (N=1 for normal samples, N=22 for tumor samples). Tissues (from left to right): Normal samples: lung. Tumor samples: GBM: glioblastoma; NSCLCadeno (non-small cell lung cancer adenocarcinoma); NSCLCother (non-small cell lung cancer); NSCLCsquam (non-small cell lung cancer squamous cell); SCLC: small cell lung cancer. FIG. 1K) Gene symbol: VPS13B, Peptide: DIYQRALNL (SEQ ID NO.: 315), FIG. 1L) Gene symbol: ARID4A, Peptide: LVKVKVLL (SEQ ID NO.: 317). FIGS. 1M to 1N show the over-presentation of various peptides in HLA-B*44 cancer tissues compared to a panel of HLA-B*44 normal samples (N=15 for normal samples, N=25 for tumor samples). Tissues (from left to right): Normal samples: brain; heart; liver; lung. Tumor samples: GBM: glioblastoma; NSCLCadeno (non-small cell lung cancer adenocarcinoma); NSCLCother (non-small cell lung cancer); NSCLCsquam (non-small cell lung cancer squamous cell); SCLC: small cell lung cancer. FIG. 1M) Gene symbol: NUP155, Peptide: SEKGVIQVY (SEQ ID NO.: 362), FIG. 1N) Gene symbol: CLSPN, Peptide: SEIGKAVGF (SEQ ID NO.: 489).

[0334] FIGS. 2A through 2N show exemplary exon expression profile of source genes of the present invention that are over-expressed in different cancer samples. Tumor (black dots) and normal (grey dots) samples are grouped according to organ of origin, and box-and-whisker plots represent median, 25th and 75th percentile (box), and minimum and maximum (whiskers) RPKM values. Normal organs are ordered according to risk categories. FPKM=fragments per kilobase per million mapped reads. Normal samples: blood cells; bloodvess: blood vessel; brain;

heart; liver; lung; adipose: adipose tissue; adren. gl.: adrenal gland; bile duct; bladder; BM: bone marrow; cartilage; esoph: esophagus; eye; gallb: gallbladder; head and neck; kidney; large_int: large intestine; LN: lymph node; nerve; pancreas; parathyr: parathyroid; perit: peritoneum; pituit: pituitary; pleura; skel. mus: skeletal muscle; skin; small_int: small intestine; spleen; stomach; thyroid; trachea; ureter; breast; ovary; placenta; prostate; testis; thymus; uterus. Tumor samples: AML: acute myeloid leukemia; BRCA: breast cancer; CCC: cholangiocellular carcinoma; CLL: chronic lymphocytic leukemia; CRC: colorectal cancer; GBC: gallbladder cancer; GBM: glioblastoma; GC: gastric cancer; HCC: hepatocellular carcinoma; HNSCC: head-and-neck cancer; MEL: melanoma; NHL: non-hodgkin lymphoma; NSCLCadeno: non-small cell lung cancer adenocarcinoma; NSCLCother: non-small cell lung cancer; NSCLCsquam: non-small cell lung cancer squamous cell; OC: ovarian cancer; OSCAR: esophageal cancer; PACA: pancreatic cancer; PRCA: prostate cancer; RCC: renal cell carcinoma; SCLC: small cell lung cancer; UBC: urinary bladder carcinoma; UEC: uterine and endometrial cancer. FIG. 2A) Gene symbol: ADAMTS12, Peptide: QYDPTPLTW (SEQ ID No. 1), FIG. 2B) Gene symbol: MMP12, Peptide: VWSNVTPLKF (SEQ ID No. 2), FIG. 2C) Gene symbol: MMP12, Peptide: YVDINTFRL (SEQ ID No. 84), FIG. 2D) Gene symbol: KIF26B, Peptide: TLY-PYQISQL (SEQ ID No. 87), FIG. 2E) Gene symbol: CT83, Peptide: NTDNNLAVY (SEQ ID No. 164), FIG. 2F) Gene symbol: LAMA1, Peptide: VSDSECLSRV (SEQ ID No. 189), FIG. 2G) Gene symbol: KIF26B, Peptide: KVKDTPGLGK (SEQ ID No. 203), FIG. 2H) Gene symbol: SP6, Peptide: SLDGAARPK (SEQ ID No. 205), FIG. 2I) Gene symbol: PRAME, Peptide: SPSVSQSLVL (SEQ ID No. 220), FIG. 2J) Gene symbol: MMP1, Peptide: NPFYPEVEL (SEQ ID No. 222), FIG. 2K) Gene symbol: NLRP2, Peptide: FNKRKPLSL (SEQ ID No. 298), FIG. 2L) Gene symbol: KIF26B, Peptide: VASPKHCVL (SEQ ID No. 300), FIG. 2M) Gene symbols: MAGEA3, MAGEA6, Peptide: MEVDPIGHVYIF (SEQ ID No. 320), FIG. 2N) Gene symbol: MMP12, Peptide: QEMQHFLGL (SEQ ID No. 326).

[0335] FIG. 3A and FIG. 3B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-A*02+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*02 in complex with SeqID No 520 peptide (KIQEMQHFL, Seq ID NO: 520) (FIG. 3A, left panel). After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*02/SeqID 520 (FIG. 3A). Right panel (FIG. 3B) show control staining of cells stimulated with irrelevant A*02/peptide complexes. Viable singlet cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

[0336] FIG. 4A and FIG. 4B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-A*24+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*24 in complex with SeqID No 504 peptide (FIG. 4A, left panel). After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*24/SeqID No 504 (VYEKNGYIYF, Seq ID NO: 504)

(FIG. 4A). Right panel (FIG. 4B) shows control staining of cells stimulated with irrelevant A*24/peptide complexes. Viable singlet cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

[0337] FIG. 5A and FIG. 5B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-A*01+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*01 in complex with SeqID No 153 peptide (KLDRSVFTAY, Seq ID NO: 153) (FIG. 5A, left panel) and SeqID No 173 peptide (RTEFNLNQY, Seq ID NO: 173) (FIG. 5B, left panel), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*01/SeqID No 153 (FIG. 5A) or A*01/SeqID No 173. Right panels (FIGS. 5A and 5B) show control staining of cells stimulated with irrelevant A*01/peptide complexes. Viable single cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

[0338] FIG. 6A and FIG. 6B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-A*02+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*02 in complex with SeqID No 89 peptide (ILSTMVTV, Seq ID NO: 89) (FIG. 6A, left panel) and SeqID No 88 peptide (VQMVITEAQKV, Seq ID NO: 88) (FIG. 6B, left panel), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*02/SeqID No 89 (FIG. 6A) or A*02/SeqID No 88 (FIG. 6B). Right panels (FIGS. 6A and 6B) show control staining of cells stimulated with irrelevant A*02/peptide complexes. Viable single cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

[0339] FIG. 7A and FIG. 7B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-A*03+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*03 in complex with SeqID No 208 peptide (GLASRILDAK, Seq ID NO: 208) (FIG. 7A, left panel) and SeqID No 210 peptide (ATSGVPVYK, Seq ID NO: 210) (FIG. 7B, left panel), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*03/SeqID No 208 (FIG. 7A) or A*03/SeqID No 210 (FIG. 7B). Right panels (FIGS. 7A and 7B) show control staining of cells stimulated with irrelevant A*03/peptide complexes. Viable single cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

[0340] FIG. 8A and FIG. 8B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-A*24+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*24 in complex with SeqID No 15 peptide (KYALLLQDL, Seq ID NO: 15) (FIG. 8A, left panel) and SeqID No 11 peptide

(YYSKSVGFMQW, Seq ID NO: 11) (FIG. 8B, left panel), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*24/SeqID No 15 (FIG. 8A) or A*24/SeqID No 11 (FIG. 8B). Right panels (FIGS. 8A and 8B) show control staining of cells stimulated with irrelevant A*24/peptide complexes. Viable single cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

[0341] FIG. 9A and FIG. 9B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-B*07+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-B*07 in complex with SeqID No 225 peptide (LPFDGPGGIL, Seq ID NO: 225) (FIG. 9A, left panel) and SeqID No 248 peptide (IPNWARQDL, Seq ID NO: 248) (FIG. 9B, left panel), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with B*07/SeqID No 225 (FIG. 9A) or B*07/SeqID No 248 (FIG. 9B). Right panels (FIGS. 9A and 9B) show control staining of cells stimulated with irrelevant B*07/peptide complexes. Viable single cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

[0342] FIG. 10A and FIG. 10B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-B*08+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-B*08 in complex with SeqID No 299 peptide (MAQFKEISL, Seq ID NO: 299) (FIG. 10A, left panel) and SeqID No 297 peptide (RAQLKLVAL, Seq ID NO: 297) (FIG. 10B, left panel), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with B*08/SeqID No 299 (FIG. 10A) or B*08/SeqID No 297 (FIG. 10B). Right panels (FIGS. 10A and 10B) show control staining of cells stimulated with irrelevant B*08/peptide complexes. Viable single cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

[0343] FIG. 11A and FIG. 11B show exemplary results of peptide-specific in vitro CD8+ T cell responses of a healthy HLA-B*44+ donor. CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-B*44 in complex with SeqID No 325 peptide (QEQDVLDVQKY, Seq ID NO: 325) (FIG. 11A, left panel) and SeqID No 331 peptide (EDAQGHIW, Seq ID NO: 331) (FIG. 11B, left panel), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining single cells were gated for CD8+ lymphocytes with B*44/SeqID No 325 (FIG. 11A) or B*44/SeqID No 331 (FIG. 11B). Right panels (FIGS. 11A and 11B) show control staining of cells stimulated with irrelevant B*44/peptide complexes. Viable single cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

EXAMPLES

Example 1

[0344] Identification and Quantitation of Tumor Associated Peptides Presented on the Cell Surface

[0345] Tissue Samples

[0346] Patients' tumor tissues were obtained from: Asterand (Detroit, Mich., USA & Royston, Herts, UK); Bio-Options Inc. (Brea, Calif., USA); Geneticist Inc. (Glendale, Calif., USA); University Hospital Heidelberg (Heidelberg, Germany); ProteoGenex Inc. (Culver City, Calif., USA); Tissue Solutions Ltd (Glasgow, UK); University Hospital Munich (Munich, Germany). Normal tissues were obtained from Asterand (Detroit, Mich., USA & Royston, Herts, UK); Bio-Options Inc. (Brea, Calif., USA); BioServe (Beltsville, Md., USA); Capital BioScience Inc. (Rockville, Md., USA); Centre for Clinical Transfusion Medicine Tuebingen (Tübingen, Germany); Geneticist Inc. (Glendale, Calif., USA); Kyoto Prefectural University of Medicine (KPUM) (Kyoto, Japan); Osaka City University (OCU) (Osaka, Japan); ProteoGenex Inc. (Culver City, Calif., USA); Tissue Solutions Ltd (Glasgow, UK); University Hospital Geneva (Geneva, Switzerland); University Hospital Heidelberg (Heidelberg, Germany); University Hospital Tübingen (Tübingen, Germany); University Hospital Munich (Munich, Germany). Written informed consents of all patients had been given before surgery or autopsy. Tissues were shock-frozen immediately after excision and stored until isolation of TUMAPs at -70°C . or below.

[0347] Isolation of HLA Peptides from Tissue Samples

[0348] HLA peptide pools from shock-frozen tissue samples were obtained by immune precipitation from solid tissues according to a slightly modified protocol (Falk et al., 1991; Seeger et al., 1999) using the HLA-A*02-specific antibody BB7.2, the HLA-A, —B, C-specific antibody W6/32, the HLA-DR specific antibody L243 and the HLA DP specific antibody B7/21, CNBr-activated sepharose, acid treatment, and ultrafiltration.

[0349] Mass Spectrometry Analyses

[0350] The HLA peptide pools as obtained were separated according to their hydrophobicity by reversed-phase chromatography (nanoAcquity UPLC system, Waters) and the eluting peptides were analyzed in LTQ-velos and fusion hybrid mass spectrometers (ThermoElectron) equipped with an ESI source. Peptide pools were loaded directly onto the analytical fused-silica micro-capillary column (75 μm i.d. $\times$ 250 mm) packed with 1.7 μm C18 reversed-phase material (Waters) applying a flow rate of 400 nL per minute. Subse-

quently, the peptides were separated using a two-step 180 minute-binary gradient from 10% to 33% B at a flow rate of 300 nL per minute. The gradient was composed of Solvent A (0.1% formic acid in water) and solvent B (0.1% formic acid in acetonitrile). A gold coated glass capillary (PicoTip, New Objective) was used for introduction into the nanoESI source. The LTQ-Orbitrap mass spectrometers were operated in the data-dependent mode using a TOPS strategy. In brief, a scan cycle was initiated with a full scan of high mass accuracy in the orbitrap ($R=30\,000$), which was followed by MS/MS scans also in the orbitrap ($R=7500$) on the 5 most abundant precursor ions with dynamic exclusion of previously selected ions. Tandem mass spectra were interpreted by SEQUEST at a fixed false discovery rate ($q\leq 0.05$) and additional manual control. In cases where the identified peptide sequence was uncertain it was additionally validated by comparison of the generated natural peptide fragmentation pattern with the fragmentation pattern of a synthetic sequence-identical reference peptide.

[0351] Label-free relative LC-MS quantitation was performed by ion counting i.e. by extraction and analysis of LC-MS features (Mueller et al., 2007). The method assumes that the peptide's LC-MS signal area correlates with its abundance in the sample. Extracted features were further processed by charge state deconvolution and retention time alignment (Mueller et al., 2008; Sturm et al., 2008). Finally, all LC-MS features were cross-referenced with the sequence identification results to combine quantitative data of different samples and tissues to peptide presentation profiles. The quantitative data were normalized in a two-tier fashion according to central tendency to account for variation within technical and biological replicates. Thus, each identified peptide can be associated with quantitative data allowing relative quantification between samples and tissues. In addition, all quantitative data acquired for peptide candidates was inspected manually to assure data consistency and to verify the accuracy of the automated analysis. For each peptide, a presentation profile was calculated showing the mean sample presentation as well as replicate variations. The profiles juxtapose cancer samples to a baseline of normal tissue samples. Presentation profiles of peptides exemplary over-presented or exclusively presented on tumors are shown in FIGS. 1A through 1N.

[0352] Table 8 shows the presentation on various cancer entities for selected peptides, and thus the particular relevance of the peptides as mentioned for the diagnosis and/or treatment of the cancers as indicated (e.g. peptide SEQ ID No. 3 for hepatocellular carcinoma, peptide SEQ ID No. 11 for melanoma, ovarian cancer and uterine cancer).

TABLE 8

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
3	YLEKFYGL	HCC
6	KYKDYPFVI	HCC
9	RILRFPWQL	MEL
11	YYSKSVGFMQW	MEL, OC, UEC

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
13	HYTYILEVF	GC, UEC
14	SYSSCYSF	GC
18	DYIGSVEKW	PRCA
19	ILKEDPFLF	OC, RCC
21	SYEVRSTF	CCC, OC, PRCA
22	TQPGDWTLF	MEL
23	KFIISDWRF	MEL
24	MYPDLSELLM	AML, GBM, OC, UEC
26	KTPTNYLFL	GC
28	YYSIISHTL	HCC
31	QYQNVLTWL	GBM, GC, HCC, MEL, NHL, PRCA, RCC, UEC
32	SLPDLTPTF	PRCA
33	KSSVIASLLF	GBM
34	MQPRMFFLF	AML, GBM, HCC, MEL, UEC
36	KQMEDGHTLF	AML, OC
37	QWPWQASLQF	GC
38	KYTNWKAFL	AML, HCC
41	VIYFMGAIF	HCC, PRCA, UEC
43	IQMDEPMAF	AML, MEL, OC
44	AYLSAVGTF	AML, GC, MEL
45	KYFVPPQLF	GC
47	KYADYFLEV	GBM, OC, UEC
48	VFIDHPVHLKF	UEC
50	SYPELVKMWV	AML, GC, HCC
51	KYALLLQEL	AML, CLL, GBM, GC, HCC, MEL, OC, PRCA, RCC, UEC
52	KYMKIFHKF	OC, UEC
53	KYITNLEDL	PRCA
54	LLIKLLQTF	AML, GBM, MEL, OC, PRCA, RCC
55	RWMDQRLVF	GC, HCC, MEL, UEC
56	VYMIEPLEL	GBM, NHL
57	YPSHQEF	GBM, RCC

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
58	QFAAPLRGIYF	GBM, HCC
59	KYSTTFFMV	GBM
60	TYLSIFDQL	AML, GC, HCC, OC
61	NYAENILTL	AML, GBM, GC, MEL
62	LYQEILAQQL	AML, GBM, GC, HCC, MEL, PRCA, RCC
63	VMPSDSFFF	MEL, NHL, OC, UEC
64	NYAIPDEGHML	GBM, GC
65	VYPASKMFPI	GBM, GC, HCC, MEL, NHL, OC, UEC
66	IYFRDSSFL	AML, GC, MEL
67	RYPGKFYRV	OC
68	IYQQIIQTY	GC, MEL, UEC
69	IMPEKFEFW	AML, GC, MEL, NHL, UEC
70	PYTNVTFDF	GC, MEL
71	SYMVLAPVF	MEL
72	RYEGILYTI	GC, HCC, NHL, PRCA
73	SYIGLPLTL	GC, HCC, RCC
74	VYDQYFITL	AML, PRCA
76	WYGWHFPEL	AML, GC, HCC, RCC, UEC
77	AYTLLGHEFV	GC, MEL, OC
78	TWFPKTPMLF	AML, GBM, GC, HCC, MEL, UEC
79	RYLADLPTL	GC, HCC, OC, UEC
80	YYSPLRDLL	MEL
82	RFLPSPVVI	AML, GC, HCC, MEL, PRCA, UEC
83	TYCQNIKEF	AML, OC, PRCA, UEC
84	YVDINTFRL	HCC
86	FVIDGFDEL	CRC, GC, NHL, OSCAR
87	TLYPYQISQL	HCC, OSCAR
90	FLLMHPSI	CLL, HCC, RCC
91	FALPGLLHA	GC, HCC, NHL, OSCAR, RCC
92	NLRDLLSEV	HCC
93	TLQEKILQV	CLL, GBM, NHL
95	ITIGVLARV	CRC, PACA

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
96	HLVGGGLHTV	AML, BRCA, CRC, GC, MEL, OC, PRCA
97	VLALVNSTV	CLL
98	LQSSGLTLLL	GBM, OC, PRCA
99	FLKEKVPGI	CLL, GC, MEL, NHL
100	RQYPTPFQL	AML, CLL, CRC, GBM, NHL, OC, RCC
101	FIISDWRPVL	HNSCC
102	SLLEQAIAL	GC, HCC, NHL, OC, UEC
103	FLYYDPDVL	GBC, HCC, MEL, NHL
105	SLLTHTIPTA	AML, CRC, HNSCC, MEL, OC, OSCAR, RCC, UBC, UEC
106	FIIDTTYPAYV	CRC, OC, OSCAR
107	LLQGAIESV	BRCA, CLL, CRC, HNSCC, MEL, NHL, UBC, UEC
108	MIIALSLYI	AML, BRCA
110	LLADFQALL	RCC
111	ALCLLLHLL	AML, GBC, HCC, HNSCC, RCC
113	AVLTGLVEV	BRCA, CLL, CRC, GC, HCC, NHL, OSCAR, RCC, UEC
114	ILDERQVLL	AML, BRCA, CRC, GBC, GC, HCC, HNSCC, MEL, NHL, OC, OSCAR, PACA, UBC, UEC
115	MLLETQDALYV	HNSCC
116	VLMEENSKL	GBM
117	FLDPNARPLV	NHL, OC
118	ALSSVLHSI	AML, BRCA, CRC, GBC, HCC, HNSCC, MEL, NHL, OC, OSCAR, PACA, RCC, UBC
119	RTADITVTV	AML, CRC, UBC
120	ALLANLPVAV	GBC, GC, OC, PACA
121	ALVDTLTGI	HNSCC, NHL, UEC
122	ALLEMFPEITV	BRCA, OC, PRCA
123	LMAFFLAVV	CCC, HCC, NHL, OSCAR, RCC
124	SVASVLLYL	AML, BRCA, CLL, HCC, HNSCC, NHL, OC
125	VLQPFPLPSI	AML, BRCA, CCC, CLL, CRC, HCC, HNSCC, MEL, NHL, OC, RCC
126	FLSTVTSV	CCC, GBM, HCC, HNSCC, MEL, NHL, OSCAR, PACA, RCC, UBC, UEC

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
127	GLDGSLVFL	AML, CLL, CRC, GBM, HCC, HNSCC, MEL, NHL, OC, OSCAR, UBC
128	FLGTTPTL	AML, CLL, GBM, HNSCC, NHL, OC, UBC, UEC
129	VLYDKDAVVV	AML, CLL, CRC, HNSCC, NHL, OC, UBC, UEC
130	NLWGGQGGLGV	BRCA, GBC, GBM, GC, HCC, OC, PRCA, UEC
131	LLKEFVQRV	BRCA, CRC, HCC, HNSCC, OC, OSCAR
132	ALWLVDPLTV	CLL, CRC, GBM, HCC
133	MTLPVDAVISV	CLL, CRC, HCC, HNSCC, NHL, PRCA, UEC
134	AAEIGDKSWLY	GC, MEL, NHL, UEC
135	ASEDSVLLY	GBM, GC, MEL, NHL, OSCAR, PRCA,
136	ATDLVVLDRY	GBM, GC, HCC, MEL, NHL, OSCAR, PRCA, UEC
137	ATSKFMEFY	GBM, MEL, OC, PRCA, UEC
139	ECDMAFHIY	MEL, OC
140	ESDREELNY	GC, PRCA
141	ESDVGVVVY	GBM, GC
142	EVAEPSVLFDLY	GC, MEL, NHL, OC, UEC
144	FLDSQNLSAY	GC
145	FVDKPVAY	GBM, GC, MEL
146	GLNTGSALSY	GC, OC
148	GTEFTTILY	GC, NHL, OSCAR, PRCA
149	GTEFTTVLY	GC, HNSCC, MEL, OSCAR, PRCA
150	GTELLSLVY	GC, MEL, NHL, OC, PRCA, UEC
152	HTDSLHLII	GC, MEL, OC
154	LLDISQKNLY	GBM, NHL, PRCA
155	LLDPNPHMY	PRCA
156	LLDSLREQY	GC, NHL, OSCAR
157	LMDRPIFY	GBM, GC, MEL, NHL
159	LSDTSVIQFY	GBM, GC, HCC, MEL, NHL, PRCA
160	LTEAVLNRY	OC
161	LVDDGTHGQY	GBM, GC, MEL
162	LVDNSIRELQY	GC, HCC, MEL, NHL, OC, UEC
163	NSDSSLTLREFY	HCC, PRCA

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
166	NTQITDIGRY	MEL
167	QSDPGTSLVGY	GBM
169	RLDTPLYFSY	MEL, OC
170	RSDDTAVYY	CLL, GC, HCC, NHL, PRCA, UEC
172	RTDSCSSAQAY	MEL
173	RTEFNLNQY	GBC, GC, MEL, UEC
177	SSDEVNFLVY	GC, MEL, OC, UEC
178	SSDSSTLPKL	GC, OC, PRCA
179	STAKSATWTY	PRCA
180	STDPWIQMAY	GBM, GC, MEL
181	TADGKTYYY	GBM, HCC, MEL, PRCA
182	TDYHVRVY	GBM, PRCA
184	TSAHPEDSSFY	GC, NHL, PRCA
186	TTDIEKY	GC, MEL,
187	VADLHLYLY	GC, MEL, OC, PRCA, RCC
190	VTGGINPLIDRY	MEL
191	VTDGSLYEGVAY	GC, MEL, UEC
192	VTEESFDSKFY	GC
193	VTEFSLNTY	GBC, GC, MEL, OC, OSCAR, UEC
196	WMFFVINY	UEC
197	YADTVRPEFY	OC
198	YLDPVQRDLY	GBM, GC, HCC, MEL, NHL, OC, UEC
202	KLAELEGALQK	MEL, OC, UEC
204	AVFDKFIRY	GBM
207	RSFNGLTMY	MEL, OC
210	ATSGVPVYK	UEC
211	TVNPVAIHK	GBM, NHL, OC, PRCA, UEC
212	KAYEQVMHY	UEC
213	LNINMTSPMGTK	GBM, GC, MEL, NHL, PACA
214	RTMSEALVRK	GC, NHL, OC, PRCA, UEC
215	MMFSGPQILKL	MEL
216	KLYAWELAF	AML, GBM, MEL, OC, PRCA

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
217	RILNQILYY	AML, GBM, GC, HCC, MEL, NHL, PRCA, UEC
218	KTLVAELLILK	AML, NHL, UEC
219	RLRSSLVFK	UEC
220	SPSVSQLSVL	UEC
235	MPLKHYLLL	MEL, NHL, OC, UEC
237	RPAATAVISL	GBM, NHL, OC
244	FPYVRDFVM	GBC, MEL, NHL, OC, UEC
247	RALLARLLL	NHL
251	VPRSSGQTV	BRCA, GBM, UEC
255	MPLLENLYL	OC, UEC
256	SPRVPSIEL	NHL
259	RPPAAGLRGISL	GBM
260	YPQHPGLNA	BRCA, GBM, GC, NHL
262	SAYPQRLEI	GC
263	HPAPYGDLL	UEC
271	MPLPWSLALP	MEL
273	MPLLWLRGF	UEC
274	TPYQEHVAL	OC
275	APHPPLSVV	AML, BRCA, MEL
276	LPRAGGAFI	NHL, OC, RCC, UEC
277	MPLFEPRVF	OC, UEC
278	HPMIDINGHVF	UEC
280	VPISEEGTPVL	MEL, OC, PRCA, UEC
281	RPRAPVTPA	GBM
282	MPQIETRVIL	UEC
283	RPHSLSSEL	AML, NHL
284	FPVTSIFHTF	MEL, OC, UEC
285	FPSFLTNSL	AML
286	VPTLRSEL	OC
288	FPQKFIDLL	UEC
289	VPENHSVAL	UEC
290	APYRPPDISL	BRCA

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
292	SPQRLRGLLL	NHL
293	RPRSALPRLLLP	NHL, UEC
295	KPEGTRIAV	NHL, UEC
296	MPMQDIKM	UEC
300	VASPKHCVL	OC
301	YMHKLLVL	AML, NHL, OC, PRCA, UEC
305	ALKLRVAVL	NHL
306	ILKVKVGL	MEL, OC
308	MLKQKVEEL	OSCAR
311	EIRIRVVQM	MEL, NHL, OC, PRCA
313	ELKKKEYEEL	NHL
314	AIISRLVAL	NHL, OSCAR, UBC
316	VIKEKALTL	NHL, OC, PRCA, RCC
318	EAAIRSVEL	GBM, MEL, NHL, OC
321	AEMLESVIKNY	NHL
322	KEVDPAGHSY	NHL
323	SEFMQVIF	NHL
328	FEYDFLLQRI	UEC
330	KEGDLGGKQW	NHL
335	KELEATKQY	MEL, NHL
337	TENRYCVQL	HCC
342	HEFSSPSHL	NHL
343	TEFTTVLY	GBM, NHL, PRCA
345	IEFIHPQAF	GBM, GC, NHL, PRCA
347	ALNPYQYQY	UEC
348	AEIQGNINHV	UEC
351	EEVNYINTF	AML, MEL, NHL, OC
354	TEDPTILRI	GC, HCC, OC, PRCA, UEC
356	EEGRVYLF	GBM, PRCA
357	RELENCFQIQ	UEC
359	DELFSIALLY	NHL
363	AELDKLTSV	GBM, UEC

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
366	AENLFRAP	GBM, NHL, OC
367	GEVHPSEMI	UEC
368	GEFPVRVQV	AML, GC, OC, UEC
370	YEDLSQKY	GBM, NHL, OC
371	GELALKKKI	UEC
372	TEGIIMKDF	OC, PRCA, RCC, UEC
373	MEMQKSPVF	NHL, OC
374	DEVNFLVY	CCC, GBC, GBM, NHL, OC, PRCA
375	VYSDLHAFYY	GBM, GC, HCC, MEL, PRCA
376	KYVKDFHKF	AML, OC, PRCA, UEC
377	VYVGAVNRI	GC, HCC, PRCA
378	KFLGPAEHLTF	OC
379	NYIVPDQKIF	GBM, GC, HCC, MEL, OC, PRCA
380	VFQEKHHVI	PRCA
381	TYSKKHFRI	MEL, OC
382	IYHSHHPTL	AML, MEL, NHL, OC, UEC
383	RYKQDVERF	AML, MEL, OC, PRCA, UEC
384	KYVKVFDKF	AML, UEC
385	MYINEVERL	GBM, MEL, OC, PRCA, UEC
386	VYNDHSIYVW	AML, GBM, HCC, MEL, NHL, PRCA, UEC
387	RWLPQKNAAQF	AML, GC, HCC, MEL, OC, RCC, UEC
388	FSIPEGALVAV	AML, CCC, CLL, CRC, GBC, GC, HCC, HNSCC, MEL, NHL, OC, OSCAR, PRCA, RCC, UBC, UEC
389	TLMEQPLTTL	AML, BRCA, CRC, HCC, HNSCC, NHL, OC, PRCA, UEC
390	HIMPTVHTV	BRCA, CLL, GBM, HCC, HNSCC, MEL, NHL, OC, OSCAR, UBC, UEC
391	SLIDMRGIETV	BRCA, CLL, GBM, HCC, HNSCC, OC, UBC
392	SLFKDQMEL	AML, BRCA, CLL, CRC, GBM, HCC, MEL, NHL, OC, PRCA, RCC, UBC, UEC
393	ILLPYLQTL	AML, BRCA, CLL, CRC, GBM, HCC, HNSCC, NHL, OC
394	ASEAEMRLFY	GBM, GC, MEL, NHL
395	ASEASRLAHY	GBM, GC, NHL, PRCA, UEC

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
396	ASEFGNHYLY	GBM, GC, MEL, UEC
397	ASEITSKGASLY	GBM, GC, HCC, MEL, OC, PRCA
398	ASEQQALHTVQY	GBM, GC, MEL, NHL, PRCA, UEC
399	ATDIPCLLY	MEL
400	ATDISRQNEY	GBM, GC, NHL, OC
401	DSDESYMEKSLY	GC
402	DTDSQRLAY	GBM, GC, MEL
403	ELDSKVEVLTY	GBM, GC, MEL, OC, PRCA
404	ETARKFLYY	GBM
405	ETEEGIYWRY	GC
406	ETEQTKEFDY	GBM, GC, MEL, OC, RCC, UEC
407	FSDNDKLYLY	GBM, GC, MEL, NHL, PRCA, UEC
408	FTEQWTDGY	GBM, GC, OC, OSCAR, PRCA,
409	FVDPLVTNY	GBM, GC, HCC, MEL, NHL, OC, OSCAR, PRCA, RCC
410	GSDHQSPSSSSY	GBM, GC, MEL, OC, PRCA,
411	GTVYEDLRY	GBM, GC, HCC, MEL, NHL, OC, OSCAR
412	ILDEVIMGY	GBM, GC, MEL, NHL, OC, OSCAR
413	ISDRYYTALY	GBM, GC, PRCA, UEC
414	KTDESLTKY	GC, NHL, PRCA
415	LLDPRSYHTY	GC, NHL
416	LLDTAQKNLY	GBM, NHL, PRCA
417	LLEDKHFQSY	GBM, GC, HCC, MEL, NHL, OC, PRCA, UEC
418	LSDPSPGPKSY	GBM, HCC, PRCA
419	LSELKPMSY	GBM, GC, HCC, MEL, OSCAR, PRCA, RCC, UEC
420	LTEDKETLQY	GC, HCC, MEL, NHL, PRCA
421	LTELLERAAFY	GC, MEL, NHL, UEC
422	MIDVTKSY	GBM, GC, MEL, NHL, OC, OSCAR, PRCA, UEC
423	NLDAVHDITVAY	GC, MEL, PRCA, UEC
424	NLDEEKQLLY	MEL, PRCA
425	NLDIIQQEY	GBM, GC, HCC, MEL, NHL, OC, OSCAR, PRCA, UEC

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
426	NLDQATRVAY	NHL
427	NSDEQKITEMVY	GC
428	NSELSCQLY	GBM, GC, MEL, RCC
429	NTEDSSMSGYLY	GC, MEL,
430	NTEGLHHLY	GBM, HCC, MEL, PRCA
431	NTSDMMGRMSY	GC, MEL, NHL, OC,
432	NVDPVQHTY	GBM, GC, HCC, HNSCC, MEL, NHL, OC, OSCAR, PRCA, RCC, UEC
433	QIDTGENLY	GC, MEL
434	QTDCAPNNGY	GBM, GC, MEL, PRCA
435	QTDDTWRTEY	GBM, GC, MEL, NHL, PRCA
436	QTETGTPYMLY	GBM, GC, MEL, NHL, OC, OSCAR, PRCA, UEC
437	STDGKHWEY	GC, MEL, NHL, PRCA
438	STDNFNCKY	GC, HCC, MEL
439	TLDAGKFQIY	GC, HCC, MEL, NHL, PRCA, UEC
440	TLDENPGVRY	GBM, GC, HCC, MEL, NHL, PRCA, UEC
441	TLDSALNAASY	GBM, GC, MEL, NHL, PRCA, RCC
442	TSDFSRTNY	GBM
443	TTDFPSESSFY	GC, MEL, NHL, OC, PRCA, UEC
444	TTDTVIRSY	GC, MEL, UEC
445	VLDQGKITEY	GBM, HCC
446	VTAQVVGTERY	GC, MEL
447	VVEDHELIY	GBM
448	YLDIPNPRY	GBM, MEL, RCC
449	YLDRTGNVSFY	GBM, GC, HCC, MEL, PRCA, RCC
450	YSDDGQKWTY	MEL
451	YDSLVLQKGY	GBM, GC, HCC, OC, PRCA, UEC
452	YVDAVLGKGHQY	GBM, GC, MEL, NHL, OC, PRCA, UEC
453	AINTSIKKN	PRCA
454	KVYTPSISK	GBM, HCC, MEL, UEC
455	RIADIFVKK	GC, MEL, NHL, OC, UEC
456	SMFTAILKK	AML, MEL, NHL, OC, UEC

TABLE 8-continued

Overview of presentation of selected tumor-associated peptides of the present invention across entities. AML = acute myeloid leukemia, BRCA = breast cancer, CCC = bile duct cancer, GBM = brain cancer, CLL = chronic lymphocytic leukemia, CRC = colorectal carcinoma, OSCAR = esophageal cancer, GBC = gallbladder adenocarcinoma, GC = gastric cancer, HNSCC = head and neck squamous cell carcinoma, HCC = hepatocellular carcinoma, MEL = melanoma, NHL = non-Hodgkin lymphoma, OC = ovarian cancer, PACA = pancreatic cancer, PRCA = prostate cancer and benign prostate hyperplasia, RCC = renal cell carcinoma, UBC = urinary bladder cancer, UEC = uterine cancer.		
SEQ ID No.	Sequence	Peptide Presentation on cancer entities
457	SINKPTSER	GBM
458	GIADFVLKY	AML, BRCA, GBM, MEL, NHL, UEC
461	RPILIIIVTL	NHL
464	YPRPGTPAA	AML, GC, MEL, NHL, OC, RCC
465	VPRPIFSQL	NHL
468	SPMYGQAGL	RCC
469	YPENGVVQM	AML, OC
470	SPNSYFRVL	RCC
471	KRPDPVTNEL	NHL
472	NPRATDAQL	AML
473	LPRALSSL	NHL, OC
474	LPRLLPAL	AML, NHL
476	AEEEIMKKI	NHL
477	QENSYQSRL	OC
479	AEIQPQTQV	UEC
480	GEVSGLTADF	MEL, NHL, OC
481	RELQHEHSL	OC
482	TEREWADEW	AML, MEL, NHL, OC, RCC
483	EENDQSTHKW	MEL, NHL, OC, RCC, UEC
484	AEVGFVRFF	AML, MEL, NHL, OC
485	SEIEDSTKQVF	MEL, NHL, OC
486	SEDDPILQI	NHL, OC, UEC
487	AEDQLHHSF	AML, NHL
488	TEFPIIKMY	AML, MEL, NHL, OC, PRCA

Example 2

[0353] Expression Profiling of Genes Encoding the Peptides of the Invention

[0354] Over-presentation or specific presentation of a peptide on tumor cells compared to normal cells is sufficient for its usefulness in immunotherapy, and some peptides are tumor-specific despite their source protein occurring also in normal tissues. Still, mRNA expression profiling adds an additional level of safety in selection of peptide targets for immunotherapies. Especially for therapeutic options with high safety risks, such as affinity-matured TCRs, the ideal

target peptide will be derived from a protein that is unique to the tumor and not found on normal tissues.

[0355] RNA Sources and Preparation

[0356] Surgically removed tissue specimens were provided as indicated above (see Example 1) after written informed consent had been obtained from each patient. Tumor tissue specimens were snap-frozen immediately after surgery and later homogenized with mortar and pestle under liquid nitrogen. Total RNA was prepared from these samples using TRI Reagent (Ambion, Darmstadt, Germany) fol-

lowed by a cleanup with RNeasy (QIAGEN, Hilden, Germany); both methods were performed according to the manufacturer's protocol.

[0357] Total RNA from healthy human tissues for RNASeq experiments was obtained from: Asterand (Detroit, Mich., USA & Royston, Herts, UK); Bio-Options Inc. (Brea, Calif., USA); BioCat GmbH (Heidelberg, Germany); Bio-Serve (Beltsville, Md., USA); Capital BioScience Inc. (Rockville, Md., USA); Geneticist Inc. (Glendale, Calif., USA); Heidelberg University Hospital (Thoraxklinik, Heidelberg, Germany); Istituto Nazionale Tumori "Pascali" (Naples, Italy); ProteoGenex Inc. (Culver City, Calif., USA).

[0358] Total RNA from tumor tissues for RNASeq experiments was obtained from: Asterand (Detroit, Mich., USA & Royston, Herts, UK); Geneticist Inc. (Glendale, Calif., USA); ProteoGenex Inc. (Culver City, Calif., USA); Tissue Solutions Ltd (Glasgow, UK); University Hospital Bonn (Bonn, Germany); University Hospital Tübingen (Tübingen, Germany).

[0359] Quality and quantity of all RNA samples were assessed on an Agilent 2100 Bioanalyzer (Agilent, Waldbronn, Germany) using the RNA 6000 Pico LabChip Kit (Agilent).

[0360] RNAseq Experiments

[0361] Gene expression analysis of—tumor and normal tissue RNA samples was performed by next generation sequencing (RNAseq) by CeGaT (Tübingen, Germany). Briefly, sequencing libraries are prepared using the Illumina HiSeq v4 reagent kit according to the provider's protocol (Illumina Inc., San Diego, Calif., USA), which includes RNA fragmentation, cDNA conversion and addition of sequencing adaptors. Libraries derived from multiple samples are mixed equimolar and sequenced on the Illumina HiSeq 2500 sequencer according to the manufacturer's instructions, generating 50 bp single end reads. Processed reads are mapped to the human genome (GRCh38) using the STAR software. Expression data are provided on transcript level as RPKM (Reads Per Kilobase per Million mapped reads, generated by the software Cufflinks) and on exon level (total reads, generated by the software Bedtools), based on annotations of the ensembl sequence database (Ensembl77). Exon reads are normalized for exon length and alignment size to obtain RPKM values.

[0362] Exemplary expression profiles of source genes of the present invention that are highly over-expressed or exclusively expressed in lung cancer (including NSCLC and SCLC) are shown in FIGS. 2A through 2N. Expression scores for further exemplary genes are shown in Table 9.

TABLE 9

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.					
SEQ ID		Gene Expression			
No	Sequence	NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
1	QYDPTPLTW	+++	+++	+	+
2	VWSNVTPCLKF	+++	+++	+	+++
3	YLEKFYGL	+++	+++		+++
4	SYEKVINYL		+++		+++
5	RYMKDYLI				+++
6	KYKDYFPVI	+	+++		++
7	VQQWSVAVF		+++		
8	PFLPPAACFF				+++
9	RILRFPWQL	+++	++		
10	VWSDVTPLNF	++	+++		
11	YYSKSVGFMQW				++
12	STIRGELFFF	++	++		
13	HYTYILEVF	++	++		
14	SYSSCYSF		++		

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID		Gene Expression			
No	Sequence	NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
15	KYALLLQDL		+		++
16	TYNPDFSSL				++
17	YYADKKTFFVL	+	++	+	
18	DYIGSVEKW	+	+		
19	ILKEDPFLF	+			
20	EFTTVLYNF		+		
21	SYEVRSTF	+	+		+
22	TQPGDWTLF	+			
23	KFIISDWRF	+			
24	MYPDLSELLM			+	+
25	SYNGYVFYL	+		+	
26	KTPNTNYLF		+		
27	NYTLYPITF				+
28	YYSIISHTL	+		+	
29	VYPLLSRLYW	+		+	
30	QYLPGWTVLF	+			
31	QYQNVLTW		+		
32	SLPDLTPTF	+	+		
33	KSSVIASLLF		+		
34	MQPRMFFLF	+	+		
35	KYLEESVWL				+
36	KQMEDGHTLF				+
37	QWPWQASLQF				+
38	KYTNWKAPL				+
39	LIFMLANVF		+		
40	QYEPPSAPSTTF				+
41	VIIYFMGAIF		+		
42	TLPNITIYRF	+		+	
43	IQMDEPMAF				+

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID		Gene Expression			
No	Sequence	NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
44	AYLSAVGTF		+		
45	KYFVPPQLF	+			
46	APPVTSIFHTF		+		+
47	KYADYFLEV				+
48	VFIDHPVHLKF				+
49	LYISEVRNI		+		
50	SYPELVKMWV				+
51	KYALLLQEL				+
52	KYMKIFHKF				+
53	KYITNLEDL				+
54	LLIKLLQTF				+
55	RWMDQRLVF		+		
56	VYMIPELEL		+		
57	YPSHQEF				+
84	YVDINTFRL	+++	+++	+	+++
85	YIDEFQSLV				++
86	FVIDGFDEL	++	++		++
87	TLYPYQISQL	++	++	+	++
88	VQMVITEAQKV	++	++		
89	ILSTTMVTV	++	++	+	+
90	FLLMHPSI				++
91	FALPGLLHA	++	++		
92	NLRDLLSEV	++	++	+	+
93	TLQEKILQV				++
94	VLPDIETLIGV		++		++
95	ITIGVLARV	++			
96	HLVGGLHTV				+
97	VLALVNSTV				+
98	LQSSGLTLLL	+	+		+

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID	Sequence	Gene Expression			
		NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
99	FLKEKVPGI				+
100	RQYPTPFQL		+		+
101	FIISDWRFVL	+			
102	SLLEQAIAL				+
103	FLYYPDPVL		+		
104	GMLDIFWGV				+
105	SLLTHIPTA				+
106	FIIDTTYPAYV	+			
107	LLQGAIESV				+
108	MIIALSLYI	+	+		
109	LLLGSIQLLGV	+			
110	LLADFQALL				+
111	ALCLLLHLL				+
112	SVSDGIHSV		+		
113	AVLTGLVEV				+
114	ILDERQVLL		+	+	
115	MLLETQDALYV	+	+		
116	VLMEENSKL		+		
117	FLDPNARPLV				+
118	ALSSVLHSI	+			
119	RTADITVTV		+	+	
120	ALLANLPAV	+		+	
121	ALVDTLTGI				+
122	ALLEMFPEITV				+
123	LMAFFLAVV				+
124	SVASVLLYL		+		
138	DSDSCHFNY	++			
139	ECDMAFHIY				+
140	ESDREELNY				+

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCothers = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID		Gene Expression			
No	Sequence	NSCLCadeno	NSCLCsquam	NSCLCothers	SCLC
143	FIDYPKKEDY	++	+		
146	GLNTGSALSY	++	+		
147	GSSDSSTLPKL		+		
148	GTEFTTILY				+
149	GTEFTTVLY		+		
150	GTELLSLVY		+		
153	KLDRSVFTAY				++
155	LLDPNPHMY	+			++
158	LSDLLKQGY			++	+
160	LTEAVLNRY	++	++	+	++
163	NSDSSLTLREFY	+			+
164	NTDNNLAVY	+++	+++		+
165	NTDPTAPPY	+	+		
166	NTQITDIGRY	+	+		
167	QSDPGTSVLGY				+
168	QTDHPQPILDY		+	++	
171	RSDPVTNLVLY	++			
172	RTDSCSSAQAQY	+			
174	SADDIRGIQSLY	+++	+++	+	+++
175	SDVTPLTF	+++	++		
176	SRTINVSPLY		+		+
177	SSDEVNFLVY		+	+	
178	SSDSSTLPKL		+		
179	STAKSATWTY		++		
183	TLEDIATSHLY				+
185	TSDSNLNKY				++
188	VSDAKLDKY				+
189	VSDSECLSRV		+++		+++
190	VTGGINPLIDY				++

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID	Sequence	Gene Expression			
		NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
192	VTEESFDSKIFY				+
193	VTEPSLNTY	++	+		
194	WADTKMIEY	++	+		
195	VVDSVGGLY	+		++	
199	YLPQHTIETY		+		
200	YSDEDVTKY		+		++
201	YVGKEHMFY		+++		+++
202	KLAELEGALQK	+++	+		
203	KVKDTPGLGK	++	++	+	+
204	AVFDKFIRY				++
205	SLDGAARPK	+	+		++
206	KLIDLSQVMY	+			
207	RSFNGLLTMY	+	+		
208	GLASRILDAK	+	+		
209	RTQIPMSEK				+
210	ATSGVPVYK	+			+
211	TVNPVAIHK		+		
212	KAYEQVMHY				+
213	LNINMTSPMGTK				+
214	RTMSEALVRK				+
215	MMFSGPQILKL		+		
216	KLYAWELAF		+		
217	RILNQILYY	+			
218	KTLVAELLILK		+		+
219	RLRSSLVFK		+		
220	SPSVSQLSVL	++	+++		+++
221	VPDVAQFVL	+++	+++		
222	NPFYPEVEL	+++	+++		
223	YPKDIYSSF	++	+++		

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID	Sequence	Gene Expression			
		NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
224	GPQPWHAAL	+++	++		+
225	LPPDGPGGIL	+++	++		
226	SPRMSGLLSQT				+++
227	YPRGNHWAVGH				+++
228	YPRGNHWAVGHL				+++
229	VPLPAGGGTV				+++
230	VPLPAGGGTVL				+++
231	RPRALRDLQL	+	++		+
232	RPRALRDLQLL	+	++		+
233	KPYQGNPTF		++		
234	RAKNAGVTI	++	++		
235	MPLKHYLLL	++			
236	RVRGGEDGDRAL				++
237	RPAATAVISL	++	++		
238	KPGPPWAAF	++			
239	YVPSASLFML		+		++
240	SPREVTTVL	++			
241	SARLATDAL	++			
242	SPRWLPVSL				++
243	RPIENRILIL	+	++		
244	FPYVRDFVM	++	+		
245	RIREHVPQL	++	+		
246	TPLPAVIVL	+	++		
247	RALLARLLL	++	+		
248	IPNWARQDL		++	+	
249	VPSSRILQL		++		+
250	SPRDFLSGL				++
251	VPRSSGQTV	+	+		++
252	SPDIRNTTV	++			

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID	Sequence	Gene Expression			
		NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
253	RVIDAVRFTL		++		
254	NPFPHLITL	+	+	+	
255	MPLLENLYL	+	+		
256	SPRVPSIEL		+		
257	LPRIPFADV	+	+	++	
258	LPRGPLASL	+	+		
259	RPPAAGLRGISL				+
260	YPQHPGLNA		+		+
261	APSARVGVC	+	+	+	
262	SAYPQRLEI	+			
263	HPAPYGDLL		+		+
264	RPILIHTL				+
265	SPRQPRLV	+			
266	HAYPPGPGL		+		
267	HPELVNHIVF	+			
268	YPLFRGINL	+	+		
269	APRAPRLML	+			
270	APGPRFLVT	+	+		
271	MPLPWSLALP		+		
272	MPLPWSLALPL		+		
273	MPLLWLRGF	+	+	+	
274	TPYQEHVAL				+
275	APHPPLSW				+
276	LPRAGGAFI	+	+		
277	MPLFEPRVF	+	+		+
278	HPMIDINGIIVF	+	+		
279	SPARASPAL	+			
280	VPISEEGTPVL				+
281	RPRAPVTPA				+

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID		Gene Expression			
No	Sequence	NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
282	MPQIETRVIL		+		+
283	RPHSLSSEL		+	+	
284	FPVTSIFHTF		+		+
285	FPSFLTNSL				+
286	VPTRLSEL		+		
287	APREEQQRSL				+
288	FPQKFIDLL				+
289	VPENHSVAL		+		
290	APYRPPDISL	+			
296	MPMQDIKM	+++	+++		+++
297	RAQLKLVAL		+++		
298	FNKRKPLSL	+	++		+
299	MAQFKEISL	+	++		+
300	VASPKHCVL	++	++	+	+
301	YMHKLLVL				++
302	HLLQKQTSI		++		
303	LPFPKFTV	++			
304	ELKKLYCQI		+		
305	ALKLRVAVL				+
306	ILKVKVGL	+			
307	ILLPRTVSL	+	+		
308	MLKQKVEEL		+		
309	DAIQRKYSC		+		
310	LPPKKFVL				+
311	EIRIRWQM		+		
312	EAMLRNKEL				+
313	ELKKKEYEEL				+
314	AIISRLVAL	+			
319	AEMLERVIKNY	++	+++		+++

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID		Gene Expression			
No	Sequence	NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
320	MEVDPIGHVYIF	+++	+++		+++
321	AEMLESVIKNY	+	+++		+++
322	KEVDPAGHSY		+++		+++
323	SEFMQVIF		+++		+++
324	TDSIHAWTF				+++
325	QEQDVLVQKY	+++	+++		
326	QEMQHFLGL	+++	+++		+++
327	YEIEARNQVF	+++	+++		+++
328	FEYDFLLQRI	++	+++		+++
329	NEHPSNNW	++	+++		
330	KEGDLGGKQW	++	++	+	+
331	EDAQGHIW	++	++		
332	MEVPVIKI	+	++	+	++
333	AETLSTIQI	++	++		+
334	AEDEPAAAH	++	++	+	+
335	KELEATKQY	++	++		+
336	ASSSGPMRWW	++	++		
337	TENRYCVQL		++		
338	SEGSEPALLHSW	++			
339	SEPALLHSW	++			
340	TEFSLNTY	++	+		
341	EEIEGKGSFTYF	++			
342	HEFSSPSHL		++		
343	TEFTTVLY		+		
344	EEATGQFHVY	+			
345	IEFIHPQAF	+	+		
346	VEAPGPVHVYW	+	+		+
347	ALNPYQYQY				+
348	AEIQGNINHV				+

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID	Sequence	Gene Expression			
		NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
349	AEQDMRELTY		+		
350	GECDVFKEL	+			
351	EEVNYINTF				+
352	NEVLTYIKF		+		
353	GEIIMQNNW				+
354	TEDPTILRI		+		
355	SDMVRPHLF		+	+	+
356	EEGRVYLF	+	+		
357	RELENCFQIQ				+
358	KEADIHFLI	+	+	+	
359	DELFSIALY				+
360	AEVPTGVII	+			
361	SENLFFASF	+			
362	SEKGVYQVY				+
363	AELDKLTSV				+
364	AETPIQNVI	+			
365	SEMNVNMKY	+			
366	AENLFRAP		+		+
367	GEVHPSEMI		+		+
368	GEFPVRVQV		+		
369	EEIERFFKL				+
370	YEDLSQKY				+
371	GELALKKKI				+
372	TEGIIMKDF	+			
373	MEMQKSPVF				+
374	DEVNFLVY		+	+	
375	VYSDLHAFYY				++
376	KYVKDFHKF				+
377	VYVGAVNRI		+		

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID		Gene Expression			
No	Sequence	NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
378	KFLGPAEHLTF	+			
388	FSIPEGALVAV		+		
389	TLMEQPLTTL				+
401	DSDESYMEKSLY				+
402	DTDSQRLAY				+
405	ETEEGIYWRY		++		
409	FVDPLVTNY				+
419	LSELKPMSY		+		
427	NSDEQKITEMVY				+
429	NTEDSSMSGYLY	+			
432	NVDPVQHTY	+			
438	STDNFNCKY	+	+		
442	TSDFSRFTNY				+
450	YSDDGQKWTY	++			
454	KVYTPSISK				+
455	RIADIFVKK	+	+		
456	SMFTAILKK				+
457	SINKPTSER				+
458	GIADFVLKY				+
459	RPMQQARAQL		+++		
460	MPMAGDMNGL		++		
461	RPILIIIVTL		+		
462	RPFHTRATV	++	++	+	+
463	TPKAGPTL	++	++	+	+
464	YPRPGTPAA				+
465	VPRPIFSQL				+
466	APYKSVTSL	+	+		
467	KPFSSFTSM				+
468	SPMYGQAGL				+

TABLE 9-continued

Expression scores. The table lists peptides from genes that are very highly over-expressed in lung cancer tissues (NSCLCadeno = non-small cell lung carcinoma adenocarcinoma; NSCLCsquam = non-small cell lung carcinoma squamous cell; NSCLCother = non-small cell lung carcinoma, other subtypes; SCLC = small cell lung carcinoma) compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, bile duct, blood cells, blood vessels, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, head&neck, kidney, large intestine, liver, lung, lymph node, nerve, parathyroid, pancreas, pituitary, pleura, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, ureter. In case expression data for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID		Gene Expression			
No	Sequence	NSCLCadeno	NSCLCsquam	NSCLCother	SCLC
469	YPENGVVQM				+
470	SPNSYFRVL				+
471	KPRPDVTNEL				+
472	NPRATDAQL				+
476	AEEEIMKKI	+++	+++	+	+++
477	QENSYQSRL	++	+++		
478	SEIEQEIGSL	++	++		
479	AEIQPQTQV	+	+		+
480	GEVSGLTKDF				+
481	RELQHEHSL	+	+		
482	TEREWADEW				+
483	EENDQSTHKW		+		
484	AEVGFVRPF				+
485	SEIEDSTKQVF				+
486	SEDDPILQI				+
487	AEDQLHHSF				+
488	TEFPPIIKMY				+
489	SEIGKAVGF				+

Example 3

[0363] In Vitro Immunogenicity for MHC Class I Presented Peptides

[0364] In order to obtain information regarding the immunogenicity of the TUMAPs of the present invention, the inventors performed investigations using an in vitro T-cell priming assay based on repeated stimulations of CD8+ T cells with artificial antigen presenting cells (aAPCs) loaded with peptide/MHC complexes and anti-CD28 antibody. This way the inventors could show immunogenicity for HLA-A*02:01, HLA-A*24:02, HLA-A*01:01, HLA-A*03:01, HLA-B*07:02, HLA-B*08:01 and HLA-B*44:02 restricted TUMAPs of the invention, demonstrating that these peptides are T-cell epitopes against which CD8+ precursor T cells exist in humans (Table 10a and Table 10b).

[0365] In Vitro Priming of CD8+ T Cells

[0366] In order to perform in vitro stimulations by artificial antigen presenting cells loaded with peptide-MHC complex (pMHC) and anti-CD28 antibody, the inventors first isolated CD8+ T cells from fresh HLA-A*02, HLA-A*24, HLA-A*01, HLA-A*03, HLA-B*07, HLA-B*08 or HLA-B*44 leukapheresis products via positive selection using CD8 microbeads (Miltenyi Biotec, Bergisch-Gladbach, Germany) of healthy donors obtained from the University clinics Mannheim, Germany, after informed consent.

[0367] PBMCs and isolated CD8+ lymphocytes were incubated in T-cell medium (TCM) until use consisting of RPMI-Glutamax (Invitrogen, Karlsruhe, Germany) supplemented with 10% heat inactivated human AB serum (PAN-Biotech, Aidenbach, Germany), 100 U/ml Penicillin/100 µg/ml Streptomycin (Cambrex, Cologne, Germany), 1 mM

sodium pyruvate (CC Pro, Oberdorla, Germany), 20 µg/ml Gentamycin (Cambrex), 2.5 ng/ml IL-7 (PromoCell, Heidelberg, Germany) and 10 U/ml IL-2 (Novartis Pharma, Nornberg, Germany) were also added to the TCM at this step.

[0368] Generation of pMHC/anti-CD28 coated beads, T-cell stimulations and readout was performed in a highly defined in vitro system using four different pMHC molecules per stimulation condition and 8 different pMHC molecules per readout condition.

[0369] The purified co-stimulatory mouse IgG2a anti human CD28 Ab 9.3 (Jung et al., 1987) was chemically biotinylated using Sulfo-N-hydroxysuccinimidobiotin as recommended by the manufacturer (Perbio, Bonn, Germany). Beads used were 5.6 µm diameter streptavidin coated polystyrene particles (Bangs Laboratories, Illinois, USA).

[0370] pMHC used for positive and negative control stimulations were A*02:01/MLA-001 (peptide ELA-GIGILTV (SEQ ID NO. 532) from modified Melan-A/MART-1) and A*02:01/DDX5-001 (YLLPAIVHI from DDX5, SEQ ID NO. 533), respectively.

[0371] 800.000 beads/200 µl were coated in 96-well plates in the presence of 4x12.5 ng different biotin-pMHC, washed and 600 ng biotin anti-CD28 were added subsequently in a volume of 200 µl. Stimulations were initiated in 96-well plates by co-incubating 1x10⁶ CD8⁺ T cells with 2x10⁵ washed coated beads in 200 µl TCM supplemented with 5 ng/ml IL-12 (PromoCell) for 3 days at 37° C. Half of the medium was then exchanged by fresh TCM supplemented with 80 U/ml IL-2 and incubating was continued for 4 days at 37° C. This stimulation cycle was performed for a total of three times. For the pMHC multimer readout using 8 different pMHC molecules per condition, a two-dimensional combinatorial coding approach was used as previously described (Andersen et al., 2012) with minor modifications encompassing coupling to 5 different fluorochromes. Finally, multimeric analyses were performed by staining the cells with Live/dead near IR dye (Invitrogen, Karlsruhe, Germany), CD8-FITC antibody clone SK1 (BD, Heidelberg, Germany) and fluorescent pMHC multimers. For analysis, a BD LSRII SORP cytometer equipped with appropriate lasers and filters was used. Peptide specific cells were calculated as percentage of total CD8⁺ cells. Evaluation of multimeric analysis was done using the FlowJo software (Tree Star, Oreg., USA). In vitro priming of specific multimer+CD8⁺ lymphocytes was detected by comparing to negative control stimulations. Immunogenicity for a given antigen was detected if at least one evaluable in vitro stimulated well of one healthy donor was found to contain a specific CD8⁺ T-cell line after in vitro stimulation (i.e. this well contained at least 1% of specific multimer+ among CD8⁺ T-cells and the percentage of specific multimer+ cells was at least 10x the median of the negative control stimulations).

[0372] In Vitro Immunogenicity for Lung Cancer (Including NSCLC and SCLC) Peptides

[0373] For tested HLA class I peptides, in vitro immunogenicity could be demonstrated by generation of peptide specific T-cell lines. Exemplary flow cytometry results after TUMAP-specific multimer staining for 16 peptides of the invention are shown in FIGS. 3A through 11B together with corresponding negative controls. Results for 152 peptides from the invention are summarized in Table 10a and Table 10b.

in vitro immunogenicity of HLA class I peptides of the invention		
Exemplary results of in vitro immunogenicity experiments conducted by the applicant for the peptides of the invention. <20% = +; 20%-49% = ++; 50%-69% = +++; > = 70% = ++++		
Seq ID No	Sequence	Wells positive [%]
491	KYLEKYNL	++
492	NYEDHFPLL	++
493	TYKYVDINTF	+
494	RYLEKFYGL	+
495	SYNDALLTF	+++
496	VFMKDGPFYF	+
498	EYIRALQQL	+
500	VWSDVTPLTF	+
504	VYEKNGYIYF	++++
510	KVLEHVVRV	+
513	KLVELEHTL	+
515	KIFEMLEGV	+
516	YTFSGDVQL	+
519	KIQEILTQV	+
520	KIQEMQHFL	+
525	RLDDLKMTV	+
528	RLLDSVSRL	+

TABLE 10b

in vitro immunogenicity of HLA class I peptides of the invention			
Exemplary results of in vitro immunogenicity experiments conducted by the applicant for the peptides of the invention. <20% = +; 20%-49% = ++; 50%-69% = +++; > = 70% = ++++			
Seq ID No	Sequence	Wells positive [%]	HLA
136	ATDLVVLDRY	"+"	A*01
143	FIDYPKKEDY	"+"	A*01
153	KLDRSVFTAY	"++++"	A*01
160	LTEAVLNRY	"++"	A*01
164	NTDNNLAVY	"+"	A*01
173	RTEFNLNQY	"++++"	A*01
174	SADDIRGIQSLY	"+"	A*01
185	TSDSNLNKY	"+"	A*01
187	VADLHLYLY	"++"	A*01
189	VSDSECLSRV	"++"	A*01

TABLE 10b-continued

in vitro immunogenicity of HLA class I peptides of the invention Exemplary results of in vitro immunogenicity experiments conducted by the applicant for the peptides of the invention. <20% = +; 20%-49% = ++; 50%-69% = +++; > = 70% = ++++			
Seq ID No	Sequence	Wells positive [%]	HLA
193	VTEFSLNTY	"+"	A*01
201	YVGKEHMFY	"+"	A*01
395	ASEASRLAHY	"++"	A*01
398	ASEQQALHTVQY	"+"	A*01
405	ETEEGIYWRY	"+"	A*01
430	NTEGLHHLY	"+"	A*01
436	QTETGTPYMLY	"+"	A*01
451	YSDSLVQKGY	"+"	A*01
452	YVDAVLGKGHQY	"+"	A*01
84	YVDINTFRL	"+"	A*02
85	YIDEFQSLV	"++"	A*02
87	TLYPYQISQL	"++"	A*02
88	VQMVITEAQKV	"++"	A*02
89	ILSTTMVTV	"++"	A*02
93	TLQEKILQV	"+"	A*02
94	VLPDIETLIGV	"++"	A*02
95	ITIGVLARV	"++"	A*02
96	HLVGGLHTV	"++"	A*02
97	VLALVNSTV	"++"	A*02
101	FIISDWRFVL	"+"	A*02
125	VLQPFLPSI	"++"	A*02
127	GLDGSLVFL	"++"	A*02
128	FLGTTPTL	"+"	A*02
129	VLVDKDAVYV	"++"	A*02
130	NLWGGQGLLG	"++"	A*02
131	LLKEFVQRV	"++"	A*02
132	ALWLVDPLTV	"++"	A*02
133	MTLPVDAVISV	"+"	A*02
392	SLFKDQMEL	"+"	A*02
393	ILLPYLQTL	"+"	A*02
205	SLDGAARPK	"++"	A*03
208	GLASRILDAK	"+"	A*03
209	RTQIPMSEK	"+"	A*03

TABLE 10b-continued

in vitro immunogenicity of HLA class I peptides of the invention Exemplary results of in vitro immunogenicity experiments conducted by the applicant for the peptides of the invention. <20% = +; 20%-49% = ++; 50%-69% = +++; > = 70% = ++++			
Seq ID No	Sequence	Wells positive [%]	HLA
210	ATSGVPVYK	"++"	A*03
214	RTMSEALVRK	"++"	A*03
218	KTLVAELLILK	"++"	A*03
1	QYDPTPLTW	"++"	A*24
2	VWSNVTPLKF	"++"	A*24
4	SYEKVINYL	"++"	A*24
6	KYKDYFPVI	"++"	A*24
8	PFLPPAACFF	"++"	A*24
10	VWSDVTPLNF	"++"	A*24
11	YYSKSVGFMQW	"++"	A*24
13	HYTYILEVF	"++"	A*24
15	KYALLQLDL	"++"	A*24
16	TYNPDFSSL	"++"	A*24
59	KYSTTFMV	"++"	A*24
60	TYLSIFDQL	"++"	A*24
61	NYAENITL	"++"	A*24
62	LYQEILAQL	"++"	A*24
65	VYPASKMPPFI	"++"	A*24
66	IYFRDSSFL	"++"	A*24
72	RYEGILYTI	"++"	A*24
76	WYGWHFPEL	"++"	A*24
79	RYLADLPTL	"++"	A*24
83	TYCQNIKEF	"++"	A*24
375	VYSDLHAFYY	"++"	A*24
379	NYIVPDKQIF	"++"	A*24
380	VFQEKHHVI	"++"	A*24
383	RYKQDVERF	"++"	A*24
384	KYVKVFDKF	"++"	A*24
386	VYNDHSIYVW	"++"	A*24
220	SPSVSQLSVL	"++"	B*07
221	VPDVAQFVL	"++"	B*07
222	NPFYPEVEL	"++"	B*07
223	YPKDIYSSF	"++"	B*07
224	GPQPWHAAL	"++"	B*07

TABLE 10b-continued

in vitro immunogenicity of HLA class I peptides of the invention Exemplary results of in vitro immunogenicity experiments conducted by the applicant for the peptides of the invention. <20% = +; 20%-49% = ++; 50%-69% = +++; > = 70% = ++++			
Seq ID No	Sequence	Wells positive [%]	HLA
225	LPGDGGGIL	"++++"	B*07
226	SPRMSGLLSQT	"+++"	B*07
228	YPRGNHWAVGHL	"++"	B*07
231	RPRALRDLQL	"++"	B*07
232	RPRALRDLQLL	"+++"	B*07
233	KPYQGNPTF	"+"	B*07
237	RPAATAVISL	"+"	B*07
241	SARLATDAL	"+++"	B*07
242	SPRWLPVSL	"++++"	B*07
244	FPYVRDFVM	"+"	B*07
245	RIREHVPQL	"++"	B*07
248	IPNWARQDL	"++++"	B*07
249	VPSSRILQL	"+++"	B*07
250	SPRDFLSGL	"+"	B*07
252	SPDIRNTTV	"+"	B*07
274	TPYQEHVAL	"+"	B*07
285	FPSFLTNSL	"++++"	B*07
292	SPQRLRGLLL	"+++"	B*07
293	RPRSALPRLLLP	"++"	B*07
294	GPTPNTGAAL	"+++"	B*07
460	MPMAGDMNGL	"++"	B*07
462	RPFHTRATV	"++"	B*07
463	TPKAGPTL	"+"	B*07
473	LPRALLSSL	"++"	B*07
474	LPRLLPAL	"++++"	B*07
320	MEVDPIGHVYIF	"+"	B*44
322	KEVDPAGHSY	"++"	B*44
323	SEFMQVIF	"+"	B*44
325	QEQDVDLVQKY	"+"	B*44
326	QEMQHFLGL	"+"	B*44
328	FEYDFLLQRI	"+"	B*44
329	NEHPSNNW	"+"	B*44
330	KEGDLGGKQW	"+"	B*44

TABLE 10b-continued

in vitro immunogenicity of HLA class I peptides of the invention Exemplary results of in vitro immunogenicity experiments conducted by the applicant for the peptides of the invention. <20% = +; 20%-49% = ++; 50%-69% = +++; > = 70% = ++++			
Seq ID No	Sequence	Wells positive [%]	HLA
331	EDAQGHIW	"++"	B*44
333	AETLSTIQI	"+"	B*44
334	AEDEPAA AHL	"+"	B*44
337	TENRYCVQL	"++"	B*44
338	SEGSEPALLHSW	"+"	B*44
339	SEPALLHSW	"++"	B*44
342	HEFSSPSHL	"+"	B*44
476	AEEEIMKKI	"+"	B*44
477	QENSYQSRL	"+"	B*44
297	RAQLKLVAL	"+"	B*08
298	FNKRKPLSL	"+"	B*08
299	MAQFKEISL	"++++"	B*08
300	VASPKHCVL	"+"	B*08
303	LPFPKFTV	"++"	B*08
305	ALKLRVAVL	"+"	B*08
306	ILKVKVGL	"+"	B*08
307	ILLPRTVSL	"+"	B*08
308	MLKQKVEEL	"+"	B*08
311	EIRIRVVQM	"+"	B*08
312	EAMLRNKEL	"+"	B*08
313	ELKKKEYEEL	"+"	B*08
314	AIISRLVAL	"++"	B*08
315	DIYQRALNL	"+"	B*08
316	VIKEKALTL	"+"	B*08
318	EAAIRSVEL	"++"	B*08

Example 4

Synthesis of Peptides

[0374] All peptides were synthesized using standard and well-established solid phase peptide synthesis using the Fmoc-strategy. Identity and purity of each individual peptide have been determined by mass spectrometry and analytical RP-HPLC. The peptides were obtained as white to off-white lyophilizes (trifluoro acetate salt) in purities of >50%. All TUMAPs are preferably administered as trifluoro-acetate salts or acetate salts, other salt-forms are also possible.

Example 5

[0375] MHC Binding Assays

[0376] Candidate peptides for T cell based therapies according to the present invention were further tested for their MHC binding capacity (affinity). The individual peptide-MHC complexes were produced by UV-ligand exchange, where a UV-sensitive peptide is cleaved upon UV-irradiation, and exchanged with the peptide of interest as analyzed. Only peptide candidates that can effectively bind and stabilize the peptide-receptive MHC molecules prevent dissociation of the MHC complexes. To determine the yield of the exchange reaction, an ELISA was performed based on the detection of the light chain ($\beta 2m$) of stabilized MHC complexes. The assay was performed as generally described in Rodenko et al. (Rodenko et al., 2006).

[0377] 96 well MAXISorp plates (NUNC) were coated over night with 2 ug/ml streptavidin in PBS at room temperature, washed 4x and blocked for 1 h at 37° C. in 2% BSA containing blocking buffer. Refolded HLA-A*02:01/MLA-001 monomers served as standards, covering the range of 15-500 ng/ml. Peptide-MHC monomers of the UV-exchange reaction were diluted 100-fold in blocking buffer. Samples were incubated for 1 h at 37° C., washed four times, incubated with 2 ug/ml HRP conjugated anti- $\beta 2m$ for 1 h at 37° C., washed again and detected with TMB solution that is stopped with NH_4SO_4 . Absorption was measured at 450 nm. Candidate peptides that show a high exchange yield (preferably higher than 50%, most preferred higher than 75%) are generally preferred for a generation and production of antibodies or fragments thereof, and/or T cell receptors or fragments thereof, as they show sufficient avidity to the MHC molecules and prevent dissociation of the MHC complexes.

TABLE 11

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*01 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
134	AAEIGDKSWLY	"++++"
135	ASEDSVLLY	"++++"
136	ATDLVVLDY	"++++"
137	ATSKFMEFY	"++++"
138	DSDSCHFNLY	"++++"
139	ECDMAFHIY	"++++"
140	ESDREELNY	"+++"
141	ESDVGVVVY	"+++"
142	EVAEPSVLFDLY	"++++"
143	FIDYPKKEDY	"++++"
144	FLDSQNL SAY	"++++"
145	FVDKPVAY	"++++"
146	GLNTGSALSY	"++"
147	GSSDSSTLPKL	"++"

TABLE 11-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*01 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
148	GTEFTTILY	"++++"
149	GTEFTTVLY	"++++"
150	GTELLSLVY	"++++"
151	HSDLKVGEY	"+++"
152	HTDSLHLLI	"+++"
153	KLDRSVFTAY	"+++"
154	LLDISQKNLY	"+++"
155	LLDPNPHMY	"++++"
156	LLDSLREQY	"+++"
157	LMDRPIFY	"++++"
158	LSDLLKQGY	"++++"
159	LSDTSVIQFY	"++++"
160	LTEAVLNRY	"+++"
161	LVDDGTHGQY	"+++"
162	LVDNSIRELQY	"+++"
163	NSDSSLTLREFY	"+++"
164	NTDNNLAVY	"++++"
165	NTDPTAPPY	"+++"
166	NTQITDIGRY	"+++"
167	QSDPGTSVLGY	"+++"
168	QTDHPQPILDRY	"++++"
169	RLDTPLYFSY	"++++"
170	RSDDTAVVY	"++++"
171	RSDPVTNLVLY	"++++"
172	RTDSCSSAQAY	"+++"
173	RTEFNLNQY	"++++"
174	SADDIRGIQSLY	"++++"
176	SRTINVSNLVY	"+++"
177	SSDEVNFLVY	"++++"
178	SSDSSTLPKL	"++"
179	STAKSATWTY	"++++"
180	STDPWIQ MAY	"++++"
181	TADGKTYYY	"+++"
182	TDYHVRVY	"+++"
183	TLEDIATSHLY	"++++"

TABLE 11-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*01 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
184	TSAPEDSSFY	"+++"
185	TSDSNLNKY	"++++"
186	TTDIIIEKY	"+++"
187	VADLHLVLY	"+++"
188	VSDAKLDKY	"+++"
189	VSDSECLSRV	"++++"
190	VTGGINPLIDRY	"+++"
191	VTDGSLYEGVAY	"++++"
192	VTEESFDSKIFY	"++++"
193	VTEFSLNTY	"++++"
194	VVADTKMIEY	"+"
195	VVDSVGGVLY	"++++"
196	WMFFVINY	"+"
197	YADTVRPEFY	"+++"
198	YLDPVQRDLV	"++++"
199	YLPQHTIETY	"++"
200	YSDDEVTKY	"++++"
201	YVGKEHMFY	"++++"
394	ASEAEMRLFY	"++++"
395	ASEASRLAHY	"++++"
396	ASEFGNHVLY	"++++"
397	ASEITSKGASLY	"++++"
398	ASEQQALHTVQV	"++++"
399	ATDIPCLLY	"++++"
400	ATDISRQNEY	"+++"
401	DSDESYMEKSLY	"++++"
402	DTDSQRLAY	"+++"
403	ELDSKVEVLTY	"+++"
404	ETARKFLYY	"++++"
405	ETEEGIYWRY	"++++"
406	ETEQTKEWDY	"++++"
407	FSDNDKLYLY	"++++"
408	FTEQWTDGY	"+++"
409	FVDPLVTNY	"++++"
410	GSDHQSPSSSY	"++++"

TABLE 11-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*01 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
411	GTVYEDLRY	"++++"
412	ILDEVIMGY	"++++"
413	ISDRYYTALY	"++++"
414	KTDESLTKY	"+++"
415	LLDPRSHTY	"+++"
416	LLDTAQKNLY	"++++"
417	LLEDKHFQSY	"++++"
418	LSDPSPGPKSY	"+++"
419	LSELPMSY	"++++"
420	LTEDKETLQY	"++++"
421	LTELLERAAFY	"++++"
422	MIDVTKSY	"++++"
423	NLDAVHDITVAY	"++++"
424	NLDEEKQLLY	"+++"
425	NLDIIQVEY	"++++"
426	NLDQATRVAY	"+++"
427	NSDEQKITEMVY	"++++"
428	NSELSCQLY	"++++"
429	NTEDSSMSGVLY	"++++"
430	NTEGLHHLY	"++++"
431	NTSDMMGRMSY	"++++"
432	NVDPVQHTY	"+++"
433	QIDTGENLY	"++++"
434	QTDCAPIINGY	"++++"
435	QTDDTWRTEY	"++++"
436	QTETGTPYMLY	"++++"
437	STDGKHWEY	"++++"
438	STDNFNCKY	"+++"
439	TLDAGKFQIY	"+++"
440	TLDENPGVRY	"+++"
441	TLDSALNAASY	"++++"
442	TSDFSRTNY	"++++"
443	TTDFPSESSFEY	"++++"
444	TTDTVIRSY	"+++"
445	VLDQGKITEY	"+++"

TABLE 11-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*01 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
446	VTAQVVGTERY	"++++"
447	VVDEDHELIY	"+++"
448	YLDIPNPRY	"+++"
449	YLDRG TGNVSFY	"++++"
450	YSDDGQKWTY	"++++"
451	YSDSLVQKGY	"++++"
452	YVDAVLGKGHQY	"++++"

TABLE 12

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*02 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
84	YVDINTFRL	"++++"
85	YIDFQSLV	"++++"
86	FVIDGFDEL	"++++"
87	TLYPYQISQL	"++++"
88	VQMVITEAQKV	"++++"
89	ILSTTMVTV	"++++"
91	FALPGLLHA	"+++"
92	NLRDLLSEV	"+++"
93	TLQEKILQV	"++++"
94	VLPDIETLIGV	"++++"
95	ITIGVLARV	"++++"
96	HLVGGLHTV	"++++"
97	VLALVNSTV	"++++"
98	LQSSGLTLLL	"++++"
99	FLKEKVPGI	"++++"
100	RQYPTPFQL	"++++"
101	FIISDWRFVL	"+++"
102	SLLEQAIAL	"++++"
103	FLYYPDPVL	"++++"
104	GMLDIFWGV	"++++"
105	SLLTHTIPTA	"++++"
106	FIIDTTYPAYV	"++++"

TABLE 12-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*02 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
107	LLQGAIESV	"++++"
109	LLGSIGLLGV	"++++"
110	LLADFQALL	"++++"
111	ALCLLLHLL	"+"
112	SVSDGIHSV	"++++"
113	AVLTGLVEV	"++++"
114	ILDERQVLL	"++++"
115	MLLETQDALYV	"++++"
116	VLMEENSKL	"++++"
117	FLDPNARPLV	"++++"
118	ALSSVLHSI	"++++"
119	RTADITVTV	"++++"
120	ALLANLPAV	"++++"
121	ALVDTLTGI	"++++"
122	ALLEMFPEITV	"++++"
123	LMAFFLAVV	"++"
124	SVASVLLYL	"++++"
125	VLQPFLPSI	"++++"
126	FLSTVTSV	"++++"
127	GLDGS LVFL	"++++"
128	FLGTTPTL	"++++"
129	VLYDKDAVYV	"++++"
130	NLWGGQGLLG	"++++"
131	LLKEFVQRV	"++++"
132	ALWLVDP LTV	"++++"
133	MTLPVDAVISV	"++++"
388	FSIPEGALVAV	"++++"
389	TLMEQPLTTL	"++++"
390	HIMPTVHTV	"++++"
391	SLIDMRGIETV	"++++"
392	SLFKDQMEL	"++++"
393	ILLPYLQTL	"++++"

TABLE 13

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*03 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
202	KLAELEGALQK	"++++"
203	KVKDTPGLGK	"++++"
204	AVFDKFIRY	"++++"
205	SLDGAARPK	"++++"
206	KLIDLQVMY	"++++"
207	RSPFNGLTMY	"++++"
208	GLASRILDAK	"++++"
209	RTQIPMSEK	"++++"
210	ATSGVPVYK	"++++"
211	TVNPVAIHK	"++++"
212	KAYEQVMHY	"++++"
214	RTMSEALVRK	"++++"
215	MMFSGPQILKL	"++++"
216	KLYAWELAF	"+++"
217	RILNQILYY	"++++"
218	KTLVAELLILK	"+++"
219	RLRSSLVFK	"++++"
453	AINTSIKNK	"++++"
454	KVYTPSISK	"++++"
455	RIADIFVKK	"++++"
456	SMFTAILKK	"++++"
457	SINKPTSER	"++++"
458	GIADFVLKY	"++++"

TABLE 14

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*24 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
1	QYDPTPLTW	"++++"
2	VWSNVTPLKF	"++++"
3	YLEKFYGL	"++"
4	SYEKVINYL	"++++"
5	RYMKDYLI	"++++"
6	KYKDYFPVI	"++++"

TABLE 14-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*24 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
7	VQQWSVAVF	"+++"
8	PFLPPAACFF	"++++"
10	VWSDVTPLNF	"++++"
11	YYSKSVGFMQW	"++++"
12	STIRGELFFF	"+"
13	HYTYILEVF	"++++"
14	SYSSCYSF	"+++"
15	KYALLQDL	"++++"
16	TYNPDFSSL	"+++"
17	YYADKKTIVL	"+++"
18	DYIGSVEKW	"++++"
19	ILKEDPFLF	"+"
20	EFTTVLYNF	"++++"
21	SYEVRSTF	"+++"
22	TQPGDWTLF	"++++"
23	KFIISDWRF	"++++"
24	MYPDLSELLM	"++++"
25	SYNGYVFYL	"++++"
26	KTPTNYLFL	"++++"
27	NYTLYPITF	"++++"
28	YYSIISHTL	"++++"
29	VYPLLSRLYW	"++++"
30	QYLPGWTVLF	"++++"
31	QYQNVLTW	"++++"
32	SLPDLTPTF	"++++"
33	KSSVIASLLF	"+++"
34	MQPRMFFLF	"++++"
35	KYLEESVWL	"++++"
36	KQMEDGHTLF	"++"
37	QWPWQASLQF	"++++"
38	KYTNWKAPL	"++++"
39	LIFMLANVF	"+"
40	QYEPPSAPSTTF	"+++"
42	TLFNTIYRF	"++++"
43	IQMDEPMAF	"+"

TABLE 14-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*24 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
44	AYLSAVGTF	"++++"
45	KYFVPPQLF	"++++"
46	AFPVTSIFHTF	"++++"
47	KYADYFLEV	"++++"
48	VFIDHPVHLKF	"++++"
49	LYISEVRNI	"++++"
50	SYPELVKMW	"++++"
51	KYALLLQEL	"++++"
52	KYMKIFHKF	"++++"
53	KYITNLEDL	"++++"
54	LLIKLLQTF	"+++"
55	RWMDQRLVF	"++++"
56	VYMIPELEL	"++++"
57	YPSIIQEF	"++++"
58	QFAAPLRGIYF	"++++"
59	KYSTTFMV	"++"
60	TYLSIFDQL	"+++"
61	NYAENILTL	"+++"
62	LYQEILACL	"++++"
63	VMPSDSFFF	"++++"
64	NYAIFDEGHML	"++++"
65	VYPASKMPFI	"++++"
66	IYFRDSSFL	"++++"
67	RYPGKFYRV	"++++"
68	IYQQIIQTY	"++++"
69	IMPEKFEFW	"++++"
70	PYTNVTFDF	"++++"
71	SYMVLAPVF	"++++"
72	RYEGILYTI	"++++"
73	SYIGLPLTL	"+++"
74	VYDQYFITL	"++++"
75	NYIYSISVF	"++++"
76	WYGNHFPPEL	"+++"
77	AYTLGHEFV	"+"
78	TWFPKTPMLF	"++++"

TABLE 14-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-A*24 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
79	RYLADLPTL	"++++"
80	YYSPLRDLL	"++++"
81	LYPEGLRLL	"++++"
82	RFLPSPVVI	"++++"
83	TYCQNIKEF	"++++"
375	VYSDLHAFYY	"++++"
376	KVKDFHKEF	"++++"
377	VYVGAVNRI	"++++"
378	KFLGPAEHLTF	"++++"
379	NYIVPDQKIF	"+++"
380	VFQEKHHVI	"+++"
381	TYSKKHFRI	"++++"
382	IYSHHPTL	"+++"
383	RYKQDVERF	"+++"
384	KYVKVFDKF	"++++"
385	MYINEVERL	"++++"
386	VYNDHSIYVW	"++++"
387	RWLPQKNAAQF	"+++"

TABLE 15

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*07 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
220	SPSVSQLSVL	"++++"
221	VPDVAQFVL	"++++"
222	NPFYPEVEL	"+++"
223	YPKDIYSSF	"++++"
224	GPQPWHAAL	"++++"
225	LPFDGPGGIL	"++++"
226	SPRMSGLLSQT	"++++"
227	YPRGNHWAUGH	"++++"
228	YPRGNHWAUGH	"++++"
229	VPLPAGGGTV	"+++"
230	VPLPAGGGTVL	"+++"

TABLE 15-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*07 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
231	RPRALRDLQL	"++++"
232	RPRALRDLQLL	"++++"
233	KPYQGNPTF	"++++"
234	RAKNAGVTI	"++++"
235	MPLKHYLLL	"++++"
236	RVRGGEDGDRAL	"++++"
237	RPAATAVISL	"+++"
238	KPGPPWAAF	"++++"
239	YVPSASLFML	"++++"
240	SPREVTTVL	"++++"
241	SARLATDAL	"++++"
242	SPRWLPVSL	"++++"
243	RPIENRILIL	"++++"
244	FPYVRDFVM	"++++"
245	RIREHVPQL	"+++"
246	TPLPAVIVL	"++++"
247	RALLARLLL	"+++"
248	IPNWARQDL	"++++"
249	VPSSRILQL	"++++"
250	SPRDFLSGL	"++++"
251	VPRSSGQTV	"++++"
252	SPDIRNTTV	"++++"
253	RVIDAVRFTL	"+++"
254	NPFPHLITL	"++++"
255	MPLLENLYL	"++++"
256	SPRVPSIEL	"++++"
257	LPRIPFADV	"++++"
258	LPRGPLASL	"++++"
259	RPPAAGLRGISL	"++++"
260	YPQHPLNA	"+++"
261	APSARVGV	"+++"
262	SAYPQRLEI	"+"
263	HPAPYGDLL	"++++"
265	SPRQPPRLV	"++++"
267	HPELVNHIVF	"+++"

TABLE 15-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*07 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
268	YPLFRGINL	"++++"
269	APRAPRLML	"++++"
270	APGPRFLVT	"++++"
271	MPLPWSLALP	"+++"
272	MPLPWSLALPL	"++++"
273	MPLLWLGRF	"++"
274	TPYQEHVAL	"+++"
275	APHPPLSVV	"+++"
276	LPRAGGAPL	"+++"
278	HPMIDINGIIVF	"++"
279	SPARASPAL	"+++"
280	VPISSEETPVL	"+++"
281	RPRAPVTPA	"++++"
282	MPQIETRVIL	"+++"
283	RPHSLSSEL	"++++"
284	FPVTSIFHTF	"++"
285	FPSFLTNSL	"++++"
286	VPTLRSEL	"++++"
287	APREEQQRSL	"+++"
288	FPQKFIDLL	"++"
289	VPENHSVAL	"++++"
290	APYRPPDISL	"++++"
291	SPQRLRGLL	"++++"
292	SPQRLRGLLL	"+++"
293	RPRSALPRLLLP	"++++"
294	GPTPNTGAAL	"++++"
295	KPEGTRIAV	"++++"
459	RPMQQARAQL	"+++"
460	MPMAGDMNGL	"++++"
462	RPFHTRATV	"++++"
463	TPKAGPTL	"++++"
464	YPRPGTPAA	"++++"
465	VPRPIFSQL	"++++"
466	APYKSVTSL	"++++"
467	KPFSSFTSM	"++++"

TABLE 15-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*07 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
468	SPMYGQAGL	"++++"
469	YPENGVVQM	"++"
470	SPNSYFRVL	"++++"
471	KPRPDVTNEL	"++++"
472	NPRATDAQL	"++++"
473	LPRALLSSL	"++++"
474	LPRLLPAL	"++++"
475	RPHKPGLYL	"++++"

TABLE 16

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*08 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
296	MPMQDIKM	"++++"
297	RAQLKLVAL	"++++"
298	FNKRKPLSL	"++"
299	MAQFKEISL	"++++"
300	VASPKHCVL	"++"
301	YMHKLLVL	"++++"
302	HLLQKQTSI	"++"
303	LPFPKFTV	"++++"
304	ELKKLYCQI	"++++"
305	ALKLRVAVL	"++++"
306	ILKVKVGL	"++++"
307	ILLPRTVSL	"++++"
308	MLKQKVEEL	"++++"
309	DAIQRKYSC	"++"
310	LPPKKFVL	"++++"
311	EIRIRVVQM	"++++"
312	EAMLRNKEL	"++++"
313	ELKKKEYEEL	"++++"
314	AIISRLVAL	"++++"
315	DIYQRALNL	"++++"
316	VIKEKALTL	"++"

TABLE 16-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*08 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; >75% = ++++		
Seq ID No	Sequence	Peptide exchange
317	LVKVKVLL	"++++"
318	EAAIRSVEL	"++++"

TABLE 17

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*44 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; > 75% = ++++		
Seq ID No	Sequence	Peptide exchange
319	AEMLERVIKNI	"++++"
320	MEVDPIGHVYIF	"++++"
321	AEMLESVIKNI	"++"
322	KEVDPAGHSY	"++"
323	SEFMQVIF	"++"
324	TDSIHAWTF	"++"
325	QEQDVDLVQKY	"++"
326	QEMQHFLGL	"++++"
327	YEIEARNQVF	"++++"
328	FEYDFLLORI	"++++"
329	NEHPSNNW	"++"
330	KEGDLGKQW	"++"
331	EDAQGHIW	"++"
332	MEVPVIKI	"++"
333	AETLSTIQI	"++"
334	AEDEPAAHL	"++"
335	KELEATKQY	"++"
336	ASSSGPMRWW	"++"
337	TENRYCVQL	"++++"
338	SEGSEPALLHSW	"++"
339	SEPALLHSW	"++"
340	TEFSLNTY	—
341	EEIEGKGSFTYF	"++"
342	HEFSSPSHL	"++"
343	TEFTTVLY	"++"
344	EEATGQFHVY	"++"
345	IEFIHPQAF	"++++"

TABLE 17-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*44 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; > 75% = ++++		
Seq ID No	Sequence	Peptide exchange
346	VEAPGPVHVYW	"++++"
347	ALNPYQYQY	"+++"
348	AEIQGNINHV	"+++"
349	AEQDMRELT	"+++"
350	GECDVFKEIL	"+++"
351	EEVNYINTF	"+++"
352	NEVLTYIKF	"++++"
353	GEIIMQNNW	"++++"
354	TEDPTILRI	"+++"
355	SDMVRPHLF	"++"
356	EEGRVYLF	"+++"
357	RELENCFQIQ	"+++"
358	KEADIHFLI	"++++"
359	DELFSSIALY	"++++"
360	AEVPTGVII	"+++"
361	SENLFASF	"++++"
362	SEKGVIQVY	"+++"
363	AELDKLTSV	"+++"
364	AETPIQNVI	"+++"
365	SEMNVNMKY	"++++"
366	AENLFRAF	"++"
367	GEVHPSEMI	"+++"
368	GEFPPRVQV	"++"
369	EEIERFFKL	"+++"
370	YEDLSQKY	"+"
371	GELALKKKI	"++"
372	TEGIIMKDF	"++"
373	MEMQKSPVF	"+++"
374	DEVNFLVY	"+"
476	AEEEEIMKKI	"++"
477	QENSYSQRL	"+++"
478	SEIEQEIGSL	"+++"
479	AEIQPQTQV	"+++"
480	GEVSGLTADF	"++"
481	RELQHEHSL	"+++"

TABLE 17-continued

MHC class I binding scores. Binding of HLA-class I restricted peptides to HLA-B*44 was ranged by peptide exchange yield: >10% = +; >20% = ++; >50 = +++; > 75% = ++++		
Seq ID No	Sequence	Peptide exchange
482	TEREWADEW	"++++"
483	EENDQSTHKW	"++++"
484	AEVGFVRFF	"++++"
485	SEIEDSTKQVF	"++++"
486	SEDDPILQI	"++++"
487	AEDQLHHSF	"++++"
488	TEFPIIKMY	"++"
489	SEIGKAVGF	"++++"

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SEQUENCE: 2
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10

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LLLSIGLLG V		11
SEQ ID NO: 110	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 110		
LLADFQALL		9
SEQ ID NO: 111	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 111		
ALCLLLHLL		9
SEQ ID NO: 112	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 112		
SVSDGIHSV		9
SEQ ID NO: 113	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 113		
AVLTGLVEV		9
SEQ ID NO: 114	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 114		
ILDERQVLL		9
SEQ ID NO: 115	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 115		
MLLETQDALY V		11
SEQ ID NO: 116	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 116		
VLMEENSKL		9
SEQ ID NO: 117	moltype = AA length = 10	
FEATURE	Location/Qualifiers	

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source	1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 117 FLDPNARPLV		10
SEQ ID NO: 118 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 118 ALSSVLHSI		9
SEQ ID NO: 119 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 119 RTADITVTV		9
SEQ ID NO: 120 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 120 ALLANLPAV		9
SEQ ID NO: 121 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 121 ALVDTLTGI		9
SEQ ID NO: 122 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 122 ALLEMPFEIT V		11
SEQ ID NO: 123 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 123 LMAFFLAVV		9
SEQ ID NO: 124 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 124 SVASVLLYL		9
SEQ ID NO: 125 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 125 VLQFFLPSI		9
SEQ ID NO: 126 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 126		

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FLSTVTSV		8
SEQ ID NO: 127	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 127		
GLDGSLVFL		9
SEQ ID NO: 128	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 128		
FLGTTPTL		8
SEQ ID NO: 129	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 129		
VLYDKDAVYV		10
SEQ ID NO: 130	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 130		
NLWGGQGLLG V		11
SEQ ID NO: 131	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 131		
LLKEFVQRV		9
SEQ ID NO: 132	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 132		
ALWLVDPLTV		10
SEQ ID NO: 133	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 133		
MTLPVDAVIS V		11
SEQ ID NO: 134	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 134		
AAEIGDKSWL Y		11
SEQ ID NO: 135	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 135		
ASEDSVLLY		9
SEQ ID NO: 136	moltype = AA length = 10	
FEATURE	Location/Qualifiers	

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source	1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 136 ATDLVVLDY		10
SEQ ID NO: 137 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 137 ATSKFMIFY		9
SEQ ID NO: 138 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 138 DSDSCHFNY		9
SEQ ID NO: 139 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 139 ECDMAFHIY		9
SEQ ID NO: 140 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 140 ESDREELNY		9
SEQ ID NO: 141 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 141 ESDVGVVY		9
SEQ ID NO: 142 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 142 EVAEPSVLFD LY		12
SEQ ID NO: 143 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 143 FIDYPKKEDY		10
SEQ ID NO: 144 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 144 FLDSQNLSAY		10
SEQ ID NO: 145 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 145		

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FVDKPVAY		8
SEQ ID NO: 146	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 146		
GLNTGSALSY		10
SEQ ID NO: 147	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 147		
GSSDSSTLPK L		11
SEQ ID NO: 148	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 148		
GTEFTTILY		9
SEQ ID NO: 149	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 149		
GTEFTTVLY		9
SEQ ID NO: 150	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 150		
GTELLSLVY		9
SEQ ID NO: 151	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 151		
HSDLKVGEY		9
SEQ ID NO: 152	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 152		
HTDSLHLII		9
SEQ ID NO: 153	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 153		
KLDRSVFTAY		10
SEQ ID NO: 154	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 154		
LLDISQKNLY		10
SEQ ID NO: 155	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 155 LLDPNPHMY		9
SEQ ID NO: 156 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 156 LLDSLREQY		9
SEQ ID NO: 157 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 157 LMDRPIFY		8
SEQ ID NO: 158 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 158 LSDLLKQGY		9
SEQ ID NO: 159 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 159 LSDTSVIQFY		10
SEQ ID NO: 160 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 160 LTEAVLNRY		9
SEQ ID NO: 161 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 161 LVDDGTHGQY		10
SEQ ID NO: 162 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 162 LVDNSIRELQ Y		11
SEQ ID NO: 163 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 163 NSDSSLTLRE FY		12
SEQ ID NO: 164 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 164		

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NTDNNLAVY		9
SEQ ID NO: 165	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 165		
NTDPTAPPY		9
SEQ ID NO: 166	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 166		
NTQITDIGRY		10
SEQ ID NO: 167	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 167		
QSDPGTSVLG Y		11
SEQ ID NO: 168	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 168		
QTDHPQPILD RY		12
SEQ ID NO: 169	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 169		
RLDTPLYFSY		10
SEQ ID NO: 170	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 170		
RSDDTAVYY		9
SEQ ID NO: 171	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 171		
RSDPVTNLVL Y		11
SEQ ID NO: 172	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 172		
RTDSCSSAQA QY		12
SEQ ID NO: 173	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 173		
RTEFNLNQY		9
SEQ ID NO: 174	moltype = AA length = 12	
FEATURE	Location/Qualifiers	

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source	1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 174 SADDIRGIQS LY		12
SEQ ID NO: 175 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 175 SDVTPLTF		8
SEQ ID NO: 176 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 176 SRTINVSPLY		10
SEQ ID NO: 177 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 177 SSDEVNPLVY		10
SEQ ID NO: 178 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 178 SSDSSTLPKL		10
SEQ ID NO: 179 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 179 STAKSATWTY		10
SEQ ID NO: 180 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 180 STDPWIQMay		10
SEQ ID NO: 181 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 181 TADGKTYYY		9
SEQ ID NO: 182 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 182 TDYHVRVY		8
SEQ ID NO: 183 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 183		

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TLEDIATSHL Y		11
SEQ ID NO: 184	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 184		
TSAHPEDSSF Y		11
SEQ ID NO: 185	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 185		
TSDSNLNKY		9
SEQ ID NO: 186	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 186		
TTDIEKY		8
SEQ ID NO: 187	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 187		
VADLHLYLY		9
SEQ ID NO: 188	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 188		
VSDAKLDKY		9
SEQ ID NO: 189	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 189		
VSDSECLSR Y		10
SEQ ID NO: 190	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 190		
VTDGINPLID RY		12
SEQ ID NO: 191	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 191		
VTDGSLYEGV AY		12
SEQ ID NO: 192	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 192		
VTEESFDSKF Y		11
SEQ ID NO: 193	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 193 VTEFSLNTY		9
SEQ ID NO: 194 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 194 VVADTKMIEY		10
SEQ ID NO: 195 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 195 VVDSVGGYLY		10
SEQ ID NO: 196 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 196 WMFFVINY		8
SEQ ID NO: 197 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 197 YADTVRPEFY		10
SEQ ID NO: 198 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 198 YLDPVQRDLV		10
SEQ ID NO: 199 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 199 YLPQHTIETY		10
SEQ ID NO: 200 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 200 YSDADVTKY		9
SEQ ID NO: 201 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 201 YVGKEHMFY		9
SEQ ID NO: 202 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 202		

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KLAELEGALQ K		11
SEQ ID NO: 203	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 203		
KVKDTPGLGK		10
SEQ ID NO: 204	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 204		
AVFDKFIRY		9
SEQ ID NO: 205	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 205		
SLDGAARPK		9
SEQ ID NO: 206	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 206		
KLIDLSQVMY		10
SEQ ID NO: 207	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 207		
RSFNGLTMY		10
SEQ ID NO: 208	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 208		
GLASRIILDAK		10
SEQ ID NO: 209	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 209		
RTQIPMSEK		9
SEQ ID NO: 210	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 210		
ATSGVPVYK		9
SEQ ID NO: 211	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 211		
TVNPVAIHK		9
SEQ ID NO: 212	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 212 KAYEQVMHY		9
SEQ ID NO: 213 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 213 LNINMTSPMG TK		12
SEQ ID NO: 214 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 214 RTMSEALVR K		11
SEQ ID NO: 215 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 215 MMFSGPQILK L		11
SEQ ID NO: 216 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 216 KLYAWELAF		9
SEQ ID NO: 217 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 217 RILNQILYY		9
SEQ ID NO: 218 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 218 KTLVAELLIL K		11
SEQ ID NO: 219 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 219 RLRSSLVFK		9
SEQ ID NO: 220 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 220 SPSVSQLSVL		10
SEQ ID NO: 221 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 221		

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VPDVAQFVL		9
SEQ ID NO: 222	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 222		
NPFYPEVEL		9
SEQ ID NO: 223	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 223		
YPKDIYSSF		9
SEQ ID NO: 224	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 224		
GPQFWHAAL		9
SEQ ID NO: 225	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 225		
LPPDGPGGIL		10
SEQ ID NO: 226	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 226		
SPRMSGLLSQ T		11
SEQ ID NO: 227	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 227		
YPRGNHWAVG H		11
SEQ ID NO: 228	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 228		
YPRGNHWAVG HL		12
SEQ ID NO: 229	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 229		
VPLPAGGGTV		10
SEQ ID NO: 230	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 230		
VPLPAGGGTV L		11
SEQ ID NO: 231	moltype = AA length = 10	
FEATURE	Location/Qualifiers	

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source	1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 231 RPRALRDLQL		10
SEQ ID NO: 232 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 232 RPRALRDLQL L		11
SEQ ID NO: 233 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 233 KPYQGNPTF		9
SEQ ID NO: 234 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 234 RAKNAGVTI		9
SEQ ID NO: 235 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 235 MPLKHYLLL		9
SEQ ID NO: 236 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 236 RVRGGEDGDR AL		12
SEQ ID NO: 237 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 237 RPAATAVISL		10
SEQ ID NO: 238 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 238 KPGPPWAAF		9
SEQ ID NO: 239 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 239 YVPSASLFML		10
SEQ ID NO: 240 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 240		

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SPREVTTVL		9
SEQ ID NO: 241	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 241		
SARLATDAL		9
SEQ ID NO: 242	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 242		
SPRWLPVSL		9
SEQ ID NO: 243	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 243		
RPIENRILIL		10
SEQ ID NO: 244	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 244		
FPYVRDFVM		9
SEQ ID NO: 245	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 245		
RIREHVPQL		9
SEQ ID NO: 246	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 246		
TPLPAVIVL		9
SEQ ID NO: 247	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 247		
RALLARLLL		9
SEQ ID NO: 248	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 248		
IPNWARQDL		9
SEQ ID NO: 249	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 249		
VPSSRILQL		9
SEQ ID NO: 250	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

-continued

source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 250 SPRDFLSGL		9
SEQ ID NO: 251 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 251 VPRSSGQTV		9
SEQ ID NO: 252 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 252 SPDIRNTTV		9
SEQ ID NO: 253 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 253 RVIDAVRFTL		10
SEQ ID NO: 254 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 254 NPPFHLITL		9
SEQ ID NO: 255 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 255 MPLLENLYL		9
SEQ ID NO: 256 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 256 SPRVPSIEL		9
SEQ ID NO: 257 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 257 LPRIPFADV		9
SEQ ID NO: 258 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 258 LPRGPLASL		9
SEQ ID NO: 259 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 259		

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RPPAAGLRGI	SL	12
SEQ ID NO: 260	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 260		
YPQHPGLNA		9
SEQ ID NO: 261	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 261		
APSARVGVC		9
SEQ ID NO: 262	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 262		
SAYPQRLEI		9
SEQ ID NO: 263	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 263		
HPAPYGDLI		9
SEQ ID NO: 264	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 264		
RPILIIITL		9
SEQ ID NO: 265	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 265		
SPRQPPRLV		9
SEQ ID NO: 266	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 266		
HAYPPGPGL		9
SEQ ID NO: 267	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 267		
HPELVNHIVF		10
SEQ ID NO: 268	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 268		
YPLFRGINL		9
SEQ ID NO: 269	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

-continued

source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 269 APRAPRLML		9
SEQ ID NO: 270 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 270 APGPRFLVT		9
SEQ ID NO: 271 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 271 MPLPWSLALP		10
SEQ ID NO: 272 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 272 MPLPWSLALP L		11
SEQ ID NO: 273 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 273 MPLLWLRGF		9
SEQ ID NO: 274 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 274 TPYQEHVAL		9
SEQ ID NO: 275 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 275 APHPPLSVV		9
SEQ ID NO: 276 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 276 LPRAGGAFI		9
SEQ ID NO: 277 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 277 MPLFEPRVF		9
SEQ ID NO: 278 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 278		

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HPMIDINGII VF		12
SEQ ID NO: 279	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 279		
SPARASPAL		9
SEQ ID NO: 280	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 280		
VPISEEGTPV L		11
SEQ ID NO: 281	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 281		
RPRAPVTPA		9
SEQ ID NO: 282	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 282		
MPQIETRVIL		10
SEQ ID NO: 283	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 283		
RPHSLSSEL		9
SEQ ID NO: 284	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 284		
FPVTSIFHTF		10
SEQ ID NO: 285	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 285		
FPSFLTNSL		9
SEQ ID NO: 286	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 286		
VPTLRSEL		8
SEQ ID NO: 287	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 287		
APREEQQRSL		10
SEQ ID NO: 288	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

-continued

source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 288 FPQKFIDLL		9
SEQ ID NO: 289 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 289 VPENHSVAL		9
SEQ ID NO: 290 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 290 APYRPPDISL		10
SEQ ID NO: 291 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 291 SPQRLRGLL		9
SEQ ID NO: 292 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 292 SPQRLRGLLL		10
SEQ ID NO: 293 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 293 RPRSALPRL LP		12
SEQ ID NO: 294 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 294 GPTPNTGAAL		10
SEQ ID NO: 295 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 295 KPEGTRIAV		9
SEQ ID NO: 296 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 296 MPMQDIKM		8
SEQ ID NO: 297 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 297		

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RAQLKLVAL		9
SEQ ID NO: 298	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 298		
FNKRKPLSL		9
SEQ ID NO: 299	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 299		
MAQFKEISL		9
SEQ ID NO: 300	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 300		
VASPKHCVL		9
SEQ ID NO: 301	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 301		
YMHKLLVL		8
SEQ ID NO: 302	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 302		
HLLQKQTSI		9
SEQ ID NO: 303	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 303		
LPFPKFTV		8
SEQ ID NO: 304	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 304		
ELKKLYCQI		9
SEQ ID NO: 305	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 305		
ALKLRVAVL		9
SEQ ID NO: 306	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 306		
ILKVKVGL		8
SEQ ID NO: 307	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 307 ILLPRTVSL		9
SEQ ID NO: 308 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 308 MLKQKVEEL		9
SEQ ID NO: 309 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 309 DAIQRKYSC		9
SEQ ID NO: 310 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 310 LPPKKFVL		8
SEQ ID NO: 311 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 311 EIRIRVVQM		9
SEQ ID NO: 312 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 312 EAMLRNKEL		9
SEQ ID NO: 313 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 313 ELKKKEYEEL		10
SEQ ID NO: 314 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 314 AIISRLVAL		9
SEQ ID NO: 315 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 315 DIYQALNL		9
SEQ ID NO: 316 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 316		

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VIKEKALTL		9
SEQ ID NO: 317	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 317		
LVKVKVLL		8
SEQ ID NO: 318	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 318		
EAAIRSVEL		9
SEQ ID NO: 319	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 319		
AEMLERVIKN Y		11
SEQ ID NO: 320	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 320		
MEVDPIGHVY IF		12
SEQ ID NO: 321	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 321		
AEMLESVIKN Y		11
SEQ ID NO: 322	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 322		
KEVDPAGHSY		10
SEQ ID NO: 323	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 323		
SEFMQVIF		8
SEQ ID NO: 324	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 324		
TDSIHAWTF		9
SEQ ID NO: 325	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 325		
QEQQDVLVQK Y		11
SEQ ID NO: 326	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 326 QEMQHFLGL		9
SEQ ID NO: 327 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 327 YEIERNQVF		10
SEQ ID NO: 328 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 328 FEYDFLLQRI		10
SEQ ID NO: 329 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 329 NEHPSNNW		8
SEQ ID NO: 330 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 330 KEGDLGGKQW		10
SEQ ID NO: 331 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 331 EDAQGHIV		8
SEQ ID NO: 332 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 332 MEVPVIKI		8
SEQ ID NO: 333 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 333 AETLSTIQI		9
SEQ ID NO: 334 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 334 AEDEPAAHL		10
SEQ ID NO: 335 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 335		

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KELEATKQY		9
SEQ ID NO: 336	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 336		
ASSSGPMRWW		10
SEQ ID NO: 337	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 337		
TENRYCVQL		9
SEQ ID NO: 338	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 338		
SEGSEPALLH SW		12
SEQ ID NO: 339	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 339		
SEPALLHSW		9
SEQ ID NO: 340	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 340		
TEFSLNTY		8
SEQ ID NO: 341	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 341		
EEIEGKGSFT YF		12
SEQ ID NO: 342	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 342		
HEFSSPSHL		9
SEQ ID NO: 343	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 343		
TEFTTVLY		8
SEQ ID NO: 344	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 344		
EEATGQFHVY		10
SEQ ID NO: 345	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 345 IEFIHPQAF		9
SEQ ID NO: 346 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 346 VEAPGPVHVY W		11
SEQ ID NO: 347 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 347 ALNPYQYQY		9
SEQ ID NO: 348 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 348 AEIQGNINHV		10
SEQ ID NO: 349 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 349 AEQDMRELTY		10
SEQ ID NO: 350 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 350 GECDVFKEIL		10
SEQ ID NO: 351 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 351 EEVNYINTF		9
SEQ ID NO: 352 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 352 NEVLTYIKF		9
SEQ ID NO: 353 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 353 GEIIMQNNW		9
SEQ ID NO: 354 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 354		

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TEDPTILRI		9
SEQ ID NO: 355	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 355		
SDMVRFHLP		9
SEQ ID NO: 356	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 356		
EEGRVYLF		8
SEQ ID NO: 357	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 357		
RELENCFQIQ		10
SEQ ID NO: 358	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 358		
KEADIHFLI		9
SEQ ID NO: 359	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 359		
DELFSIALLY		9
SEQ ID NO: 360	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 360		
AEVPTGVII		9
SEQ ID NO: 361	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 361		
SENLPFASF		9
SEQ ID NO: 362	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 362		
SEKGVIVQY		9
SEQ ID NO: 363	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 363		
AELDKLTSV		9
SEQ ID NO: 364	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 364 AETPIQNVI		9
SEQ ID NO: 365 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 365 SEMNVMKY		9
SEQ ID NO: 366 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 366 AENLFRAF		8
SEQ ID NO: 367 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 367 GEVHPSEMI		9
SEQ ID NO: 368 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 368 GEFPVRVQV		9
SEQ ID NO: 369 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 369 EEIERFFKL		9
SEQ ID NO: 370 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 370 YEDLSQKY		8
SEQ ID NO: 371 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 371 GELALKKKI		9
SEQ ID NO: 372 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 372 TEGIIMKDF		9
SEQ ID NO: 373 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 373		

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MEMQKSPVF		9
SEQ ID NO: 374	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 374		
DEVNFLVY		8
SEQ ID NO: 375	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 375		
VYSDLHAFYY		10
SEQ ID NO: 376	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 376		
KYVKDFHKF		9
SEQ ID NO: 377	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 377		
VYVGAVNRI		9
SEQ ID NO: 378	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 378		
KFLGPAEHLT F		11
SEQ ID NO: 379	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 379		
NYIVPDKQIF		10
SEQ ID NO: 380	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 380		
VFQEKHHVI		9
SEQ ID NO: 381	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 381		
TYSKKHFRI		9
SEQ ID NO: 382	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 382		
IYHSHHPTL		9
SEQ ID NO: 383	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 383 RYKQDVERF		9
SEQ ID NO: 384 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 384 KYVKVFDKF		9
SEQ ID NO: 385 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 385 MYINEVERL		9
SEQ ID NO: 386 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 386 VYNDHSIYVW		10
SEQ ID NO: 387 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 387 RWLPQKNAAQ F		11
SEQ ID NO: 388 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 388 FSIPEGALVA V		11
SEQ ID NO: 389 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 389 TLMEQPLTTL		10
SEQ ID NO: 390 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 390 HIMPTVHTV		9
SEQ ID NO: 391 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 391 SLIDMRGIET V		11
SEQ ID NO: 392 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 392		

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SLFKDQMEI		9
SEQ ID NO: 393	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 393		
ILLPYLQTL		9
SEQ ID NO: 394	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 394		
ASEAEMRLFY		10
SEQ ID NO: 395	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 395		
ASEASRLAHY		10
SEQ ID NO: 396	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 396		
ASEFGNHLY		10
SEQ ID NO: 397	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 397		
ASEITSGAS LY		12
SEQ ID NO: 398	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 398		
ASEQQALHTV QY		12
SEQ ID NO: 399	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 399		
ATDIPCLLY		9
SEQ ID NO: 400	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 400		
ATDISRQNEY		10
SEQ ID NO: 401	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 401		
DSDESYMEKS LY		12
SEQ ID NO: 402	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 402 DTDSQRLAY		9
SEQ ID NO: 403 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 403 ELDSKVEVLT Y		11
SEQ ID NO: 404 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 404 ETARKFLYY		9
SEQ ID NO: 405 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 405 ETEEGIYWRY		10
SEQ ID NO: 406 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 406 ETEQTKEFDY		10
SEQ ID NO: 407 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 407 FSDNDKLYLY		10
SEQ ID NO: 408 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 408 FTEQWTDGY		9
SEQ ID NO: 409 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 409 FVDPLVTNY		9
SEQ ID NO: 410 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 410 GSDHQSPSSS SY		12
SEQ ID NO: 411 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 411		

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GTVYEDLRY		9
SEQ ID NO: 412	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 412		
ILDEVIMGY		9
SEQ ID NO: 413	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 413		
ISDRYYTALY		10
SEQ ID NO: 414	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 414		
KTDESLTKY		9
SEQ ID NO: 415	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 415		
LLDPRSYHTY		10
SEQ ID NO: 416	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 416		
LLDTAQKNLY		10
SEQ ID NO: 417	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 417		
LLEDKHFQSY		10
SEQ ID NO: 418	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 418		
LSDPSGPKSY		10
SEQ ID NO: 419	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 419		
LSELKPMSY		9
SEQ ID NO: 420	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 420		
LTEDKETLQY		10
SEQ ID NO: 421	moltype = AA length = 11	
FEATURE	Location/Qualifiers	

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source	1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 421 LTELLERAAF Y		11
SEQ ID NO: 422 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 422 MIDVTKSYY		9
SEQ ID NO: 423 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 423 NLDAVHDITV AY		12
SEQ ID NO: 424 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 424 NLDEEKQLLY		10
SEQ ID NO: 425 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 425 NLDIIQQEY		9
SEQ ID NO: 426 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 426 NLDQATRVAY		10
SEQ ID NO: 427 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 427 NSDEQKITEM VY		12
SEQ ID NO: 428 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 428 NSELSCQLY		9
SEQ ID NO: 429 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 429 NTEDSSMSGY LY		12
SEQ ID NO: 430 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 430		

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NTEGLHHLY		9
SEQ ID NO: 431	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 431		
NTSDMMGRMS Y		11
SEQ ID NO: 432	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 432		
NVDPVQHTY		9
SEQ ID NO: 433	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 433		
QIDTGENLY		9
SEQ ID NO: 434	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 434		
QTDCAPMNGY		10
SEQ ID NO: 435	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 435		
QTDDTWRTEY		10
SEQ ID NO: 436	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 436		
QTETGTPYML Y		11
SEQ ID NO: 437	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 437		
STDGKHWWEY		10
SEQ ID NO: 438	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 438		
STDNFNCKY		9
SEQ ID NO: 439	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 439		
TLDAGKFQIY		10
SEQ ID NO: 440	moltype = AA length = 10	
FEATURE	Location/Qualifiers	

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source	1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 440 TLDENPGVRY		10
SEQ ID NO: 441 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 441 TLDNALNAAS YY		12
SEQ ID NO: 442 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 442 TSDFSRTNY		10
SEQ ID NO: 443 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 443 TTDFPSESSF EY		12
SEQ ID NO: 444 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 444 TTDTVIRSY		9
SEQ ID NO: 445 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 445 VLDQKGITEY		10
SEQ ID NO: 446 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 446 VTAQVVGTER Y		11
SEQ ID NO: 447 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 447 VVDEDHელიY		10
SEQ ID NO: 448 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 448 YLDIPNPRY		9
SEQ ID NO: 449 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 449		

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YLDRGTGNVS FY		12
SEQ ID NO: 450	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 450		
YSDDGQKWTY Y		11
SEQ ID NO: 451	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 451		
YSDSLVQKGY		10
SEQ ID NO: 452	moltype = AA length = 12	
FEATURE	Location/Qualifiers	
source	1..12	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 452		
YVDAVLGKGH QY		12
SEQ ID NO: 453	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 453		
AINTSIKNK		9
SEQ ID NO: 454	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 454		
KVYTPSISK		9
SEQ ID NO: 455	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 455		
RIADIFVKK		9
SEQ ID NO: 456	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 456		
SMFTAILKK		9
SEQ ID NO: 457	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 457		
SINKPTSER		9
SEQ ID NO: 458	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 458		
GIADFVLKY		9
SEQ ID NO: 459	moltype = AA length = 10	
FEATURE	Location/Qualifiers	

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source	1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 459 RPMQQARAQL		10
SEQ ID NO: 460 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 460 MPMAGDMNGL		10
SEQ ID NO: 461 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 461 RPILIIIVTL		9
SEQ ID NO: 462 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 462 RPFHTRATV		9
SEQ ID NO: 463 FEATURE source	moltype = AA length = 8 Location/Qualifiers 1..8 mol_type = protein organism = Homo sapiens	
SEQUENCE: 463 TPKAGPTL		8
SEQ ID NO: 464 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 464 YPRPGTPAA		9
SEQ ID NO: 465 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 465 VPRPIFSQL		9
SEQ ID NO: 466 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 466 APYKSVTSL		9
SEQ ID NO: 467 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 467 KPFSSFTSM		9
SEQ ID NO: 468 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 468		

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SPMYGQAGL		9
SEQ ID NO: 469	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 469		
YPENGVVQM		9
SEQ ID NO: 470	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 470		
SPNSYFRVL		9
SEQ ID NO: 471	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 471		
KPRPDVINEL		10
SEQ ID NO: 472	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 472		
NPRATDAQL		9
SEQ ID NO: 473	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 473		
LPRALLSSL		9
SEQ ID NO: 474	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 474		
LPRLLPAL		8
SEQ ID NO: 475	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 475		
RPHKPGLYL		9
SEQ ID NO: 476	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 476		
AEEEEIMKKI		9
SEQ ID NO: 477	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 477		
QENSYQSRL		9
SEQ ID NO: 478	moltype = AA length = 10	
FEATURE	Location/Qualifiers	

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source	1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 478 SEIEQEIGSL		10
SEQ ID NO: 479 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 479 AEIQPQTQV		9
SEQ ID NO: 480 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 480 GEVSGLTKDF		10
SEQ ID NO: 481 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 481 RELQHEHSL		9
SEQ ID NO: 482 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 482 TEREWADW		9
SEQ ID NO: 483 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 483 EENDQSTHKW		10
SEQ ID NO: 484 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 484 AEVGFVRFF		9
SEQ ID NO: 485 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 485 SEIEDSTKQV F		11
SEQ ID NO: 486 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 486 SEDDPILQI		9
SEQ ID NO: 487 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 487		

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AEDQLHHSF		9
SEQ ID NO: 488	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 488		
TEFPITKMY		9
SEQ ID NO: 489	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 489		
SEIGKAVGF		9
SEQ ID NO: 490	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 490		
SYVKVLHHL		9
SEQ ID NO: 491	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 491		
KYLEKYNL		9
SEQ ID NO: 492	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 492		
NYEDHFPLL		9
SEQ ID NO: 493	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 493		
TYKYVDINTF		10
SEQ ID NO: 494	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 494		
RYLEKFYGL		9
SEQ ID NO: 495	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 495		
SYNDALLTF		9
SEQ ID NO: 496	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 496		
VFMKDGFFYF		10
SEQ ID NO: 497	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 497 NYPKSIHSF		9
SEQ ID NO: 498 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 498 EYIRALQQL		9
SEQ ID NO: 499 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 499 VYFVAPAKF		9
SEQ ID NO: 500 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 500 VWSDVTPLTF		10
SEQ ID NO: 501 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 501 GYIDNVTLI		9
SEQ ID NO: 502 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 502 SVHKITSTF		9
SEQ ID NO: 503 FEATURE source	moltype = AA length = 12 Location/Qualifiers 1..12 mol_type = protein organism = Homo sapiens	
SEQUENCE: 503 VHFEDTGKTL LF		12
SEQ ID NO: 504 FEATURE source	moltype = AA length = 10 Location/Qualifiers 1..10 mol_type = protein organism = Homo sapiens	
SEQUENCE: 504 VYEKNGYIYF		10
SEQ ID NO: 505 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 505 AYISGLDVF		9
SEQ ID NO: 506 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 506		

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RYVFPLPYL		9
SEQ ID NO: 507	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 507		
VYIAELEKI		9
SEQ ID NO: 508	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 508		
IYVTGGHLP		9
SEQ ID NO: 509	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 509		
ALLEEEEGV		9
SEQ ID NO: 510	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 510		
KVLEHVVRV		9
SEQ ID NO: 511	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 511		
KIWEELSVLE V		11
SEQ ID NO: 512	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 512		
VLGEEQEGV		9
SEQ ID NO: 513	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 513		
KLVELEHTL		9
SEQ ID NO: 514	moltype = AA length = 11	
FEATURE	Location/Qualifiers	
source	1..11	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 514		
VQLDSIEDLE V		11
SEQ ID NO: 515	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 515		
KIFEMLEGV		9
SEQ ID NO: 516	moltype = AA length = 9	
FEATURE	Location/Qualifiers	

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source	1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 516 YTFSGDVQL		9
SEQ ID NO: 517 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 517 TLYNPERTIT V		11
SEQ ID NO: 518 FEATURE source	moltype = AA length = 11 Location/Qualifiers 1..11 mol_type = protein organism = Homo sapiens	
SEQUENCE: 518 GLLEDERALQ L		11
SEQ ID NO: 519 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 519 KIQEILTQV		9
SEQ ID NO: 520 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 520 KIQEMQHFL		9
SEQ ID NO: 521 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 521 FVYGEPREL		9
SEQ ID NO: 522 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 522 TLDEKVAEL		9
SEQ ID NO: 523 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 523 HLIAEIHTA		9
SEQ ID NO: 524 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 524 KVWSDVTPL		9
SEQ ID NO: 525 FEATURE source	moltype = AA length = 9 Location/Qualifiers 1..9 mol_type = protein organism = Homo sapiens	
SEQUENCE: 525		

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RLDDLKMTV		9
SEQ ID NO: 526	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 526		
VLSPFILTL		9
SEQ ID NO: 527	moltype = AA length = 8	
FEATURE	Location/Qualifiers	
source	1..8	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 527		
LLDSVSRL		8
SEQ ID NO: 528	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 528		
RLDSVSRL		9
SEQ ID NO: 529	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 529		
HPSAHDVIL		9
SEQ ID NO: 530	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 530		
APAAWLRSA		10
SEQ ID NO: 531	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 531		
AEIEADRSY		9
SEQ ID NO: 532	moltype = AA length = 10	
FEATURE	Location/Qualifiers	
source	1..10	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 532		
ELAGIGILTV		10
SEQ ID NO: 533	moltype = AA length = 9	
FEATURE	Location/Qualifiers	
source	1..9	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 533		
YLLPAIVHI		9

1. A peptide consisting of the amino acid sequence VTEFSLNTY (SEQ ID NO: 193) in the form of a pharmaceutically acceptable salt.

2. The peptide of claim 1, wherein said peptide has the ability to bind to an MHC class-I molecule, and wherein said peptide, when bound to said MHC, is capable of being recognized by CD8 T cells.

3. The peptide of claim 1, wherein the pharmaceutically acceptable salt is chloride salt.

4. The peptide of claim 1, wherein the pharmaceutically acceptable salt is acetate salt.

5. A composition comprising the peptide of claim 1, wherein the composition comprises an adjuvant and a pharmaceutically acceptable carrier.

6. The composition of claim 5, wherein the peptide is in the form of a chloride salt.

7. The composition of claim 5, wherein the peptide is in the form of an acetate salt.

8. The composition of claim 5 wherein the adjuvant is selected from the group consisting of anti-CD40 antibody, imiquimod, resiquimod, GM-CSF, cyclophosphamide, sunitinib, bevacizumab, interferon-alpha, interferon-beta, CpG oligonucleotides and derivatives, poly-(I:C) and derivatives, RNA, sildenafil, particulate formulations with poly(lactide co-glycolide) (PLG), virosomes, interleukin (IL)-1, IL-2, IL-4, IL-7, IL-12, IL-13, IL-15, IL-21, and IL-23.

9. The composition of claim 8, wherein the adjuvant is IL-2.

10. The composition of claim 8, wherein the adjuvant is IL-7.

11. The composition of claim 8, wherein the adjuvant is IL-12.

12. The composition of claim 8, wherein the adjuvant is IL-15.

13. The composition of claim 8, wherein the adjuvant is IL-21.

14. A pegylated peptide consisting of the amino acid sequence of VTEFSLNTY (SEQ ID NO: 193) or a pharmaceutically acceptable salt thereof.

15. The peptide of claim 14, wherein the pharmaceutically acceptable salt is chloride salt.

16. The peptide of claim 14, wherein the pharmaceutically acceptable salt is acetate salt.

17. A composition comprising the pegylated peptide of claim 14 or pharmaceutically acceptable salt thereof, and a pharmaceutically acceptable carrier.

18. The composition of claim 5, wherein the pharmaceutically acceptable carrier is selected from the group consisting of saline, Ringer's solution, dextrose solution, and sustained release preparation.

19. The peptide in the form of a pharmaceutically acceptable salt of claim 1, wherein said peptide is produced by solid phase peptide synthesis or produced by a yeast cell or bacterial cell expression system.

20. A composition comprising the peptide of claim 1, wherein the composition is a pharmaceutical composition and comprises water and a buffer.

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