

PROCESS FOR PREPARING VACCINE COMPOSITIONS

Sequence Listing

The instant application contains a Sequence Listing which has been submitted
electronically in ASCII format and is hereby incorporated by reference in its entirety. Said
ASCII copy, created on August 29, 2019, is named N414322WO_SL.txt and is 1,450,065 bytes
in size.

Field

The disclosure relates to peptides and compositions that find use in vaccines and
immunotherapy, to nucleic acids and vectors that encode such peptides, to methods of designing
and producing such peptides, to methods of predicting whether an individual subject will
respond to treatment with such peptides, to subject-specific compositions comprising such
peptides, and to methods of treatment using such peptides.

Background

For decades, scientists have assumed that chronic diseases were beyond the reach of a
person's natural defences. Recently, however, significant tumor regressions observed in
individuals treated with antibodies that block immune inhibitory molecules have accelerated the
field of cancer immunotherapy. These clinical findings demonstrate that re-activation of existing
T cell responses results in meaningful clinical benefit for individuals. These advances have
renewed enthusiasm for developing cancer vaccines that induce tumor specific T cell responses.

Despite the promise, current immunotherapy is effective only in a fraction of individuals.
In addition, most cancer vaccine trials have failed to demonstrate statistically significant efficacy
because of a low rate of tumor regression and antitumor T cell responses in individuals. Similar
failures were reported with therapeutic and preventive vaccines that sought to include T cell
responses in the fields of HIV and allergy. There is a need to overcome the clinical failures of
immunotherapies and vaccines.

Summary

In antigen presenting cells (APC) protein antigens are processed into peptides. These
peptides bind to HLA molecules and are presented on the cell surface as peptide-HLA
complexes to T cells. Different individuals express different HLA molecules, and different HLA

molecules present different peptides. The inventors have demonstrated that an epitope that binds to a single HLA class I allele expressed in a subject is essential, but not sufficient to induce tumor specific T cell responses. Instead tumour specific T cell responses are optimally activated when an epitope is recognised and presented by the HLA molecules encoded by at least three HLA class I genes of an individual (PCT/EP2018/055231, PCT/EP2018/055232, PCT/EP2018/055230, EP 3370065 and EP 3369431).

Based on this discovery the inventors have developed a method for designing and preparing peptides to induce T cell responses in the highest proportion of subjects in a given target human population and have used this method to design a set of peptides for use in treating cancer.

Accordingly, in a first aspect the disclosure provides a peptide of up to 50 amino acids in length and comprising the amino acid sequence of any of SEQ ID NOs: 1 to 2786 and/or 5432-5931.

In a further aspect, the disclosure provides a polynucleic acid or a vector that encodes a peptide of up to 50 amino acids in length and comprising the amino acid sequence of any of SEQ ID NOs: 1 to 2786 and/or 5432-5931.

In a further aspect, the disclosure provides a panel of two or more of the peptides or two or more of the polynucleic acids or vectors, wherein each peptide comprises, or each polynucleic acid or vector encodes a peptide that comprises, a different amino acid sequence selected from SEQ ID NOs: 1 to 2786 and/or 5432-5931.

In a further aspect, the disclosure provides a pharmaceutical composition or kit, comprising one or more of the peptides, polynucleic acids, vectors or panels, wherein the composition or kit optionally comprise at least one pharmaceutically acceptable diluent, carrier, or preservative.

In a further aspect, the disclosure provides a method of predicting that a specific human subject will have a cytotoxic T cell response and/or a helper T cell response to administration of the pharmaceutical composition or the peptides, polynucleic acids or vectors of the kit, the method comprising

- (i) a. determining that the one or more peptides, or encoded peptides, of the pharmaceutical composition or kit, comprise at least one amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and

- b. predicting that the subject will have a cytotoxic T cell response to administration of the pharmaceutical composition; or
- (ii) a. determining that the one or more peptides, or encoded peptides, of the pharmaceutical composition or kit comprise at least one amino acid sequence that is a T cell epitope capable of binding to at least three HLA class II molecules of the subject; and
- b. predicting that the subject will have a helper T cell response to administration of the pharmaceutical composition.

5 In a further aspect, the disclosure provides a method of vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject, the method comprising administering to the subject the pharmaceutical composition or the peptides, polynucleic acids or vectors of the kit.

In further aspects, the disclosure provides

- the pharmaceutical composition or the peptides, polynucleic acids or vectors of the kit described above for use in a method of vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject; and
- use of the peptides or polynucleic acids as described above in the manufacture of a medicament for vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject.

20 In a further aspect, the disclosure provides a method of preparing a pharmaceutical composition or kit for use in a method of treating cancer in a specific human subject, the method comprising

- a. selecting two or more peptides, or one or more polynucleic acids or vectors according that encode at least two peptides, wherein each peptide, or encoded peptide, comprises an amino acid sequence selected from SEQ ID NOs: 1 to 2786 and/or 5432-5931 that comprises a T cell epitope capable of binding to at least three HLA class I alleles and/or a T cell epitope capable of binding to at least three HLA class II alleles of the specific human subject; and
- b. preparing a pharmaceutical composition or kit comprising the two or more peptides, or one or more polynucleic acids or vectors selected in step a.

30 In a further aspect, the disclosure provides a method of designing, or preparing a peptide, or a polynucleic acid or vector that encodes a peptide, or a panel of peptides, or one or more

polynucleic acid or vectors that encode a panel of peptides, for use in a method of inducing a T cell response against a target polypeptide, the method comprising

- (i) selecting or defining a model human population comprising a plurality of subjects each defined by HLA class I genotype and/or by HLA class II genotype;
- 5 (ii) identifying for each subject of the model population:
 - (a) amino acid sequences of the target polypeptide that are a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
 - (b) amino acid sequences of the target polypeptide that are a T cell epitope capable of binding to at least three HLA class II molecules of the subject;
 - 10 (c) amino acid sequences of the target polypeptide that comprise a T cell epitope capable of binding to at least three HLA class I molecules of the subject and a T cell epitope capable of binding to at least three HLA class II molecules of the subject; or
 - (d) amino acid sequences of the target polypeptide that both
 - 15 i. are a T cell epitope capable of binding to at least three HLA class II molecules; and
 - ii. comprise an amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
 - (iii) selecting a polypeptide fragment window length of between 9 and 50 amino acids;
 - 20 (iv) identifying a fragment of the target polypeptide that
 - (a) has the length selected in step (iii); and
 - (b) comprises an amino acid sequence identified in any one of step (ii) (a) to (d) in the highest proportion of subjects in the model population;
 - 25 (v) optionally testing the fragment identified in step (iv) against additional pre-defined criteria, rejecting the fragment if the further pre-defined criteria are not met, and repeating step (iv) to identify an alternative fragment of the target polypeptide that
 - (a) has the length selected in step (iii); and
 - 30 (b) comprises an amino acid sequence identified in step (iv) in the next highest proportion of subjects in the model population;
 - (vi) optionally repeating step (iv) and further optionally step (v) in one or more further rounds, wherein a further fragment of the target polypeptide is identified in each

round, and wherein in each round subjects are excluded from the model population if any of the fragments selected in step (iv) and not rejected in step (v) of any of the preceding rounds comprises an amino acid sequence identified in step (ii) for that subject; and

- 5 (vii) designing or preparing a peptide, a polynucleic acid or vector that encodes a peptide, a panel of peptides, or one or more polynucleic acids or vectors that encode a panel of peptides, wherein each peptide comprises one or more of the target polypeptide fragments identified in step (iv), (v) or (vi), optionally wherein the polypeptide fragment is flanked at the N and/or C terminus by additional
10 amino acids that are not part of the sequence of the target polypeptide antigen.

In a further aspect, the disclosure provides a panel peptides, polynucleic acids or vectors designed and/or prepared according to the method, or comprising or encoding two or more peptides designed and/or prepared according to the method.

- In a further aspect, the disclosure provides a panel of peptides, or one or more
15 polynucleic acids or vectors encoding a panel of peptides, for use in a method of inducing a T cell response against one or more target polypeptides in a subject of a target human population, wherein each of the peptides, or encoded peptides, comprises an amino acid sequence that is

- (a) 9 to 50 amino acids in length; and
(b) comprises a fragment of the one or more target polypeptides, wherein the
20 fragment comprises, in at least 10% of subjects of the intent-to-treat human population:
- a. an amino acid sequence of the target polypeptide that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
 - 25 b. an amino acid sequence of the target polypeptide that is a T cell epitope capable of binding to at least three HLA class II molecules of the subject;
 - c. an amino acid sequence of the target polypeptide that comprise a T cell epitope capable of binding to at least three HLA class I molecules of the subject and a T cell epitope capable of binding to at least three
30 HLA class II molecules of the subject; or
 - d. an amino acid sequence of the target polypeptide that both

- i. is a T cell epitope capable of binding to at least three HLA class II molecules; and
- ii. comprise an amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject.

In a further aspect, the disclosure provides a pharmaceutical composition or kit comprising the panel of peptides, or one or more polynucleic acids or vectors encoding the panel of peptides, wherein the composition or kit optionally comprises at least one pharmaceutically acceptable diluent, carrier, or preservative.

In a further aspect, the disclosure provides a method of vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject, the method comprising administering to the subject a pharmaceutical composition or the panel of peptides, polynucleic acids or vectors of the kit.

The disclosure will now be described in more detail, by way of example and not limitation, and by reference to the accompanying drawings. Many equivalent modifications and variations will be apparent, to those skilled in the art when given this disclosure. Accordingly, the exemplary embodiments of the disclosure set forth are considered to be illustrative and not limiting. Various changes to the described embodiments may be made without departing from the scope of the disclosure. All documents cited herein, whether supra or infra, are expressly incorporated by reference in their entirety.

The present disclosure includes the combination of the aspects and preferred features described except where such a combination is clearly impermissible or is stated to be expressly avoided. As used in this specification and the appended claims, the singular forms “a”, “an”, and “the” include plural referents unless the content clearly dictates otherwise. Thus, for example, reference to “a peptide” includes two or more such peptides.

Section headings are used herein for convenience only and are not to be construed as limiting in any way.

Description of the Figures

Fig. 1
ROC curve of HLA restricted PEPI biomarkers.

Fig. 2

ROC curve of ≥ 1 PEPI3+ Test for the determination of the diagnostic accuracy. AUC = 0.73 classifies a fair diagnostic value for the PEPI biomarker.

Fig. 3

Distribution of HLA class I PEPI3+ compared to CD8+ T cell responses measured by a state of art assay among peptide pools used in the CD8+ T cell response assays. A: HLA class I restricted PEPI3+s. The 90% Overall Percent of Agreement (OPA) among the T cell responses and PEPI3+ peptides demonstrate the utility of the invented peptides for prediction of vaccine induced T cell response set of individuals ($p < 0.001$). B: Class I HLA restricted epitopes (PEPI1+). The OPA between predicted epitopes and CD8+ T cell responses was 25% (not statistically significant). True positive (TP), both peptide and T cell responses were detected (shaded); True negative (TN): neither peptides nor T cell responses were detected (shaded); False negative (FN), only T cell responses were detected; False positive (FP), only peptide were detected.

Fig. 4

Correlation between PEPI Test predicted CD4 peptides and T-cell reactivity measured with peptide pools in patients treated with SLP vaccine. A: ≥ 3 HLA class II allele-binding PEPIs; B: single HLA class II allele-binding epitopes. Gray: true positive (TP) and true negative (TN) responses; White: false negative (FN) and false positive (FP) responses. TP: both peptide and T cell responses were detected; TN: neither peptides nor T cell responses were detected; FN: only T cell responses were detected; FP: only peptides were detected.

Fig. 5

Multiple HLA binding peptides that define the HPV-16 LPV vaccine specific T cell response set of 20 VIN-3 and 5 cervical cancer patients. PEPI counts were compared to clinical responses after treatment with LPV. Predicted CD8+ T cell responders according to HLA class I PEPIs (A) and CD4+ T cell responders according to HLA class II PEPIs (B). Correlation between HLA class I (C) and class II (D) PEPI count and clinical response at 3 months follow-up in VIN-3 patients. Predicted T cell responders: PEPI count ≥ 1 . Gray column, patient with HPV16 E6- and/or E7-specific T cell response; Dashed column, patient without T cell responses. CR, complete clinical responder; PR, partial clinical responder; NR, clinical non-responder.

Fig. 6

The multiple HLA class I binding peptides that define the HPV vaccine specific T cell response set of 2 patients. A: Four HPV antigens in the HPV vaccine. Boxes represent the length of the amino acid sequences from the N terminus to the C terminus. B: Process to identify the multiple

HLA binding peptides of two patients: HLA sequences of the patients labelled as 4-digit HLA genotype right from the patient's ID. The location of the 1st amino acid of the 54 and 91 epitopes that can bind to the patient 12-11 and patient 14-5 HLAs (PEPI1+) respectively are depicted with lines. PEPI2 represents the peptides selected from PEPI1+s that can bind to multiple HLAs of a patient (PEPI2+). PEPI3 represent peptides that can bind to ≥ 3 HLAs of a patient (PEPI3+). PEPI4 represent peptides that can bind to ≥ 4 HLAs of a patient (PEPI4+). PEPI5 represent peptides that can bind to ≥ 5 HLAs of a patient (PEPI5+). PEPI6 represent peptides that can bind to 6 HLAs of a patient (PEPI6). C: The DNA vaccine specific PEPI3+ set of two patients characterizes their vaccine specific T cell responses.

10 Fig. 7

TSA expression probability targeted by IMA901 vaccine.

Fig. 8

HLA Class I allele binding properties of TUMAPs of IMA901 peptide vaccine for 2,915 common alleles. (A) and for the Class I genotype (6 alleles) of 51 HLA-A*02+ RCC patients.

15 Percentages at the bottom indicate the proportion of HLAs the TUMAPs can bind to. Lines in darker grey indicate binding HLA alleles. (B) Probability indicates the proportion of patients who can present the indicated number of TUMAPs with their three or more HLAs. AP indicates number of antigens which can generate at least one PEPI. In this case, since both the antigens and the predicted PEPIs are 9mers (SEQ ID NOS 5958-5966, respectively, in order of appearance), AP=TUMAP=PEPI.

20 Fig. 9

Correlation between immune response measured for any TUMAP and immune response against expressed antigen on the tumor (AGP).

Fig. 10

25 Correlation study between immune response rates (IRR) and PEPI Score, between objective response rates (ORR) and MultiPEPI Scores and between objective response rates (ORR) and MultiAg PEPI Scores. A: Preliminary experiment to explore the relationship between PEPI Score and immune response rate of therapeutic vaccines ($r^2=0.7$, $p=0.001$) B: IRR - PEPI Score plot. ($r^2=0.47$, $p=0.001$). C: MultiPEPI Score and clinical response rate of therapeutic vaccines ($r^2=0.75$, $p=0.001$). D: ORRs plotted against the MultiPEPI Score ($r^2=0.12$, $p=0.124$). E: ORRs plotted against the MultiAg PEPI Score for vaccines with multiple antigens ($r^2=0.64$; $p=0.009$). F: ORRs plotted against the MultiPEPI Score for vaccines with multiple antigens ($r^2=0.87$; $p=0.0002$). G: ORRs plotted against the MultiPEPI Score in patients with target antigen positive

disease ($r^2=0.56$ and $p=0.005$). Dark grey dashed lines indicate the 95% confidence interval; light grey dashed line indicates the trendline.

Fig. 11

OBERTO trial design (NCT03391232)

5 Fig. 12

Antigen expression in CRC cohort of OBERTO trial (n=10). A: Expression frequencies of PolyPEPI1018 source antigens determined based on 2391 biopsies. B: PolyPEPI1018 vaccine design specified as 3 out of 7 TSAs are expressed in CRC tumors with above 95% probability. C: In average, 4 out of the 10 patients had pre-existing immune responses against each target
10 antigens, referring to the real expression of the TSAs in the tumors of the patients. D: 7 out of the 10 patients had pre-existing immune responses against minimum of 1 TSA, in average against 3 different TSAs.

Fig. 13

Immunogenicity of PolyPEPI1018 in CRC patients confirms proper target antigen and
15 target peptide selection. Upper part: target peptide selection and peptide design of PolyPEPI1018 vaccine composition (SEQ ID NO: 5967). Two 15mers from CRC specific CTA (TSA) selected to contain 9mer PEPI3+ predominant in representative Model population. Table: PolyPEPI1018 vaccine has been retrospectively tested during a preclinical study in a CRC cohort and was
20 proven to be immunogenic in all tested individuals for at least one antigen by generating PEPI3+s. Clinical immune responses were measured specific for at least one antigen in 90% of patients, and multi-antigen immune responses were also found in 90% of patients against at least 2, and in 80% of patients against at least 3 antigens as tested with IFN γ fluorospot assay specifically measured for the vaccine-comprising peptides.

Fig. 14

25 Clinical response for PolyPEPI1018 treatment. A: Swimmer plot of clinical responses of OBERTO trial (NCT03391232). B: Association progression free survival (PFS) and AGP count. C: Association tumour volume and AGP count.

Fig. 15

Illustration of hotspot analysis. Analysis identifies hotspots in sample of 7 patients (Pat1-Pat7)
30 in a peptide of amino acid sequence PIVQNIQGQMVHQAI SPRTLNAWVKVVEEK (SEQ ID NO: 5932). Crosses indicate position of a T cell epitope (9 mer) capable of binding to at least three HLA class I alleles (HLA class I-binding PEPI3+). Light shade indicates a T cell epitope (15 mer) capable of binding to at least four HLA class II alleles (HLA class II-binding PEPI4+).

Dark shade indicates HLA class II-binding PEPI4+ with an embedded HLA class I-binding PEPI3+. The 20 mer containing a HLA class I-binding PEPI3+ in the maximum number of the 7 patients is indicated. The 20 mer containing HLA class II-binding PEPI4+ with an embedded HLA class I-binding PEPI3+ in the maximum number of the 7 patients is indicated as 1st Hotspot 20 mer. This 1st Hotspot might be selected in a first cycle of a method of the present disclosure. In a second cycle, Pat1, Pat2 and Pat4 may be disregarded and the indicated second Hotspot selected.

Fig. 16

Distribution of hotspot amino acid sequence selection after 30 cycles. Selection of fewer than 30 peptides indicates that no more sequences meeting the HLA-binding criteria (20 mer containing HLA class II-binding PEPI4+ with an embedded HLA class I-binding PEPI3+) could be identified in the model population.

Fig. 17

Process for Personalized Vaccination. Process consists of saliva sample collection and tumor sample collection for tumor pathology. Based on the determined HLA genotype of the patient and tumor type of the patient, 12 tumor and patient specific peptides are selected and personalized vaccine comprising the selected 12 peptides is prepared. Vaccine will be then administered to the patient by the oncologist.

Fig. 18

Feasibility study for a “simulated” Breast Cancer Clinical trial. This example demonstrates that >80 % of patients could be treated with “patient-specific” vaccine selected from a „Warehouse” of 100 different peptides.

Fig. 19

Probability of vaccine antigen expression in the Patient-A’s tumor cells. There is over 95% probability that 5 out of the 13 target antigens in the vaccine regimen is expressed in the patient’s tumor. Consequently, the 13 peptide vaccines together can induce immune responses against at least 5 ovarian cancer antigens with 95% probability (AGP95). It has 84% probability that each peptide will induce immune responses in the Patient-A. AGP50 is the mean (expected value) =7.9 (it is a measure of the effectiveness of the vaccine in attacking the tumor of Patient-A).

Fig. 20

Treatment schedule of Patient-A.

Fig. 21

T cell responses of patient-A. A. Left: Vaccine peptide-specific T cell responses (20-mers). right:

CD8+ cytotoxic T cell responses (9-mers). Predicted T cell responses are confirmed by bioassay.

Fig. 22

MRI findings of Patient-A treated with personalised (PIT) vaccine. This late stage, heavily pretreated ovarian cancer patient had an unexpected objective response after the PIT vaccine treatment. These MRI findings suggest that PIT vaccine in combination with chemotherapy significantly reduced her tumor burden, not appear on normal cells of the tissue in which the tumor developed.

Fig. 23

Probability of vaccine antigen expression in the Patient-B's tumor cells and treatment schedule of Patient-B. A: There is over 95% probability that 4 out of the 13 target antigens in the vaccine is expressed in the patient's tumor. B: Consequently, the 12 peptide vaccines together can induce immune responses against at least 4 breast cancer antigens with 95% probability (AGP95). It has 84% probability that each peptide will induce immune responses in the Patient-B. AGP50 = 6.45; it is a measure of the effectiveness of the vaccine in attacking the tumor of Patient-B. C: Treatment schedule of Patient-B.

Fig. 24

T cell responses of Patient-A. Left: Vaccine peptide-specific T cell responses (20-mers) of P. Right: Kinetic of vaccine-specific CD8+ cytotoxic T cell responses (9-mers). Predicted T cell responses are confirmed by bioassay.

Fig. 25

Treatment schedule of Patient-C.

Fig. 26

T cell responses of Patient-C. A: Vaccine peptide-specific T cell responses (20-mers). B: Vaccine peptide-specific CD8+ T cell responses (9-mers). C-D: Kinetics of vaccine-specific CD4+ T cells and CD8+ cytotoxic T cell responses (9-mers), respectively. Long lasting immune responses both CD4 and CD 8 T cell specific are present after 14 months.

Fig. 27

Treatment schedule of Patient-D.

Fig. 28

Immune responses of Patient-D for PIT treatment. A: CD4+ specific T cell responses (20mer) and B: CD8+ T cell specific T cell responses (9mer). 0.5-4 months refer to the timespan following the last vaccination until PBMC sample collection.

Description of the Sequences

SEQ ID NOs: 1 to 2786 set forth the “hotspot” sequences from cancer antigens described in Table 25A.

5 SEQ ID NOs: 2787 to 5431 set forth the “hotspot” sequences from cancer antigens described in Table 28.

SEQ ID NOs: 5432 to 5931 set forth the “hotspot” sequences from cancer antigens described in Table 25B.

SEQ ID NO: 5932 sets forth the amino acid sequence shown in Figure 15.

10 SEQ ID NOs: 5933 to 5945 set forth sequences of personalized vaccine of Patient-A and are described in Table 31.

SEQ ID NOs: 5946 to 5957 set forth sequences of personalized vaccine of Patient-B and are described in Table 33.

SEQ ID NOs: 5958-5966 set forth the 9mer sequences shown in Figure 8.

15 SEQ ID NO: 5967 sets forth the PolyPEPI1018 vaccine peptide shown in Figure 13.

Detailed Description*HLA Genotypes*

20 HLAs are encoded by the most polymorphic genes of the human genome. Each person has a maternal and a paternal allele for the three HLA class I molecules (HLA-A*, HLA-B*, HLA-C*) and four HLA class II molecules (HLA-DP*, HLA-DQ*, HLA-DRB1*, HLA-DRB3*/4*/5*). Practically, each person expresses a different combination of 6 HLA class I and 8 HLA class II molecules that present different epitopes from the same protein antigen.

25 The nomenclature used to designate the amino acid sequence of the HLA molecule is as follows: gene name*allele:protein number, which, for instance, can look like: HLA-A*02:25. In this example, “02” refers to the allele. In most instances, alleles are defined by serotypes – meaning that the proteins of a given allele will not react with each other in serological assays. Protein numbers (“25” in the example above) are assigned consecutively as the protein is discovered. A new protein number is assigned for any protein with a different amino acid sequence (e.g. even a one amino acid change in sequence is considered a different protein number). Further information on the nucleic acid sequence of a given locus may be appended to the HLA nomenclature, but such information is not required for the methods described herein.

30 The HLA class I genotype or HLA class II genotype of an individual may refer to the actual amino acid sequence of each class I or class II HLA of an individual, or may refer to the

nomenclature, as described above, that designates, minimally, the allele and protein number of each HLA gene. In some embodiments, the HLA genotype of an individual is obtained or determined by assaying a biological sample from the individual. The biological sample typically contains subject DNA. The biological sample may be, for example, a blood, serum, plasma, saliva, urine, expiration, cell or tissue sample. In some embodiments the biological sample is a saliva sample. In some embodiments the biological sample is a buccal swab sample. An HLA genotype may be obtained or determined using any suitable method. For example, the sequence may be determined via sequencing the HLA gene loci using methods and protocols known in the art. In some embodiments, the HLA genotype is determined using sequence specific primer (SSP) technologies. In some embodiments, the HLA genotype is determined using sequence specific oligonucleotide (SSO) technologies. In some embodiments, the HLA genotype is determined using sequence based typing (SBT) technologies. In some embodiments, the HLA genotype is determined using next generation sequencing. Alternatively, the HLA set of an individual may be stored in a database and accessed using methods known in the art.

HLA-epitope binding

A given HLA of a subject will only present to T cells a limited number of different peptides produced by the processing of protein antigens in an APC. As used herein, “display” or “present”, when used in relation to HLA, references the binding between a peptide (epitope) and an HLA. In this regard, to “display” or “present” a peptide is synonymous with “binding” a peptide.

As used herein, the term “epitope” or “T cell epitope” refers to a sequence of contiguous amino acids contained within a protein antigen that possesses a binding affinity for (is capable of binding to) one or more HLAs. An epitope is HLA- and antigen-specific (HLA-epitope pairs, predicted with known methods), but not subject specific.

The term “personal epitope”, or “PEPI” as used herein distinguishes a subject-specific epitope from an HLA specific epitope. A “PEPI” is a fragment of a polypeptide consisting of a sequence of contiguous amino acids of the polypeptide that is a T cell epitope capable of binding to one or more HLA class I molecules of a specific human subject. In other words a “PEPI” is a T cell epitope that is recognised by the HLA class I set of a specific individual. In contrast to an “epitope”, PEPIs are specific to an individual because different individuals have different HLA molecules which each bind to different T cell epitopes. In appropriate cases a “PEPI” may also refer to a fragment of a polypeptide consisting of a sequence of contiguous amino acids of the

polypeptide that is a T cell epitope capable of binding to one or more HLA class II molecules of a specific human subject.

“PEPI1” as used herein refers to a peptide, or a fragment of a polypeptide, that can bind to one HLA class I molecule (or, in specific contexts, HLA class II molecule) of an individual.

5 “PEPI1+” refers to a peptide, or a fragment of a polypeptide, that can bind to one or more HLA class I molecule of an individual.

“PEPI2” refers to a peptide, or a fragment of a polypeptide, that can bind to two HLA class I (or II) molecules of an individual. “PEPI2+” refers to a peptide, or a fragment of a polypeptide, that can bind to two or more HLA class I (or II) molecules of an individual, i.e. a
10 fragment identified according to a method disclosed herein.

“PEPI3” refers to a peptide, or a fragment of a polypeptide, that can bind to three HLA class I (or II) molecules of an individual. “PEPI3+” refers to a peptide, or a fragment of a polypeptide, that can bind to three or more HLA class I (or II) molecules of an individual.

“PEPI4” refers to a peptide, or a fragment of a polypeptide, that can bind to four HLA
15 class I (or II) molecules of an individual. “PEPI4+” refers to a peptide, or a fragment of a polypeptide, that can bind to four or more HLA class I (or II) molecules of an individual.

“PEPI5” refers to a peptide, or a fragment of a polypeptide, that can bind to five HLA class I (or II) molecules of an individual. “PEPI5+” refers to a peptide, or a fragment of a polypeptide, that can bind to five or more HLA class I (or II) molecules of an individual.

20 “PEPI6” refers to a peptide, or a fragment of a polypeptide, that can bind to all six HLA class I (or six HLA class II) molecules of an individual.

Generally speaking, epitopes presented by HLA class I molecules are about nine amino acids long. For the purposes of this disclosure, however, an epitope may be more or less than nine amino acids long, as long as the epitope is capable of binding HLA. For example, an
25 epitope that is capable of being presented by (binding to) one or more HLA class I molecules may be between 7, or 8 or 9 and 9 or 10 or 11 amino acids long.

Table 1. Example software for determining epitope-HLA binding

Using techniques known in the art, it is possible to determine the epitopes that will bind to a known HLA. Any suitable method may be used, provided that the same method is used to
30 determine multiple HLA-epitope binding pairs that are directly compared. For example, biochemical analysis may be used. It is also possible to use lists of epitopes known to be bound by a given HLA. It is also possible to use predictive or modelling software to determine which epitopes may be bound by a given HLA. Examples are provided in Table 1. In some cases a T

cell epitope is capable of binding to a given HLA if it has an IC₅₀ or predicted IC₅₀ of less than 5000 nM, less than 2000 nM, less than 1000 nM, or less than 500 nM.

Table 1 - Example software for determining epitope-HLA binding

EPITOPE PREDICTION TOOLS	WEB ADDRESS
BIMAS, NIH	www-bimas.cit.nih.gov/molbio/hla_bind/
PPAPROC, Tubingen Univ.	
MHCPred, Edward Jenner Inst. of Vaccine Res.	
EpiJen, Edward Jenner Inst. of Vaccine Res.	http://www.ddg-pharmfac.net/epijen/EpiJen/EpiJen.htm
NetMHC, Center for Biological Sequence Analysis	http://www.cbs.dtu.dk/services/NetMHC/
SVMHC, Tubingen Univ.	http://abi.inf.uni-tuebingen.de/Services/SVMHC/
SYFPEITHI, Biomedical Informatics, Heidelberg	http://www.syfpeithi.de/bin/MHCServer.dll/EpitopePrediction.htm
ETK EPITOOLKIT, Tubingen Univ.	http://etk.informatik.uni-tuebingen.de/epipred/
PREDEP, Hebrew Univ. Jerusalem	http://margalit.huji.ac.il/Teppred/mhc-bind/index.html
RANKPEP, MIF Bioinformatics	http://bio.dfci.harvard.edu/RANKPEP/
IEDB, Immune Epitope Database	http://tools.immuneepitope.org/main/html/tcell_tools.html
EPITOPE DATABASES	WEB ADDRESS
MHCBN, Institute of Microbial Technology, Chandigarh, INDIA	http://www.imtech.res.in/raghava/mhcbn/
SYFPEITHI, Biomedical Informatics, Heidelberg	http://www.syfpeithi.de/
AntiJen, Edward Jenner Inst. of Vaccine Res.	http://www.ddg-pharmfac.net/antijen/AntiJen/antijenhomepage.htm
EPIMHC database of MHC ligands, MIF Bioinformatics	http://immunax.dfci.harvard.edu/epimhc/
IEDB, Immune Epitope Database	http://www.iedb.org/

HLA molecules regulate T cell responses. Until recently, the triggering of an immune response to individual epitopes was thought to be determined by recognition of the epitope by the product of single HLA allele, i.e. HLA-restricted epitopes. However, HLA-restricted epitopes induce T cell responses in only a fraction of individuals. Peptides that activate a T cell response in one individual are inactive in others despite HLA allele matching. Therefore, it was previously unknown how an individual's HLA molecules present the antigen-derived epitopes that positively activate T cell responses.

The inventors discovered that multiple HLA expressed by an individual need to present the same peptide in order to trigger a T cell response. Therefore the fragments of a polypeptide antigen (epitopes) that are immunogenic for a specific individual (PEPIs) are those that can bind to multiple class I (activate cytotoxic T cells) or class II (activate helper T cells) HLAs expressed by that individual. This discovery is described in PCT/EP2018/055231, PCT/EP2018/055232, PCT/EP2018/055230, EP 3370065 and EP 3369431.

Peptides

In some aspects the disclosure provides a peptide that comprises the amino acid sequence of any one of SEQ ID NOs: 1 to 2786 as shown in Table 25A and/or SEQ ID NOs: 5432 to 5931 as shown in Table 25B and/or SEQ ID NOs: 2787 to 5431 shown in Table 28. Each of SEQ ID NOs: 1 to 5931 is a 20-mer fragment of a TAA, wherein the fragment comprises at least one HLA class II-binding PEPI4+ and at least one HLA class I-binding PEPI3+ embedded in the HLA class II-binding PEPI4+ in subjects of a model population of ~16,000 subjects.

The 20-mer fragments were identified as described herein to maximise the number of subjects in the model population that would mount T cell responses to a corresponding TAA in response to administration of at least one peptide comprising one of the 20-mers for each TAA. A panel of peptides each comprising a different one or more of the 20-mer fragments, or a suitable sub-selection thereof, therefore represents an ideal panel of peptides from which to select peptides for use in vaccinating against cancer or providing immunotherapy to treat cancer in individual human subjects.

In some cases the peptides or the panel peptides of the present disclosure may (each) comprise one or more of the sequences of SEQ ID NOs: 1 to 2786 and/or 2787 to 5431 and/or 5432 to 5931 that are fragments of polypeptide antigens associated with one or more specific cancers or types of cancer, such as those of Table 24, or any other described herein. Peptides may be selected from such a panel to treat a corresponding cancer. In some cases the

polypeptide antigens may have a minimum expression rate in the cancer, such as being expressed in at least about 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% of such cancers. In some cases the polypeptide antigens may be those that are most frequently expressed in the cancer, for example the 50, 45, 40, 35, 30, 25, 20, 15, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 most commonly expressed antigens, for example as set out in Table 24.

In some cases the peptides or the panel peptides may (each) comprise peptides that comprise the sequences of SEQ ID NOs: 1 to 2786 and/or 2787 to 5431 and/or 5432 to 5931 that are fragments of a specific polypeptide antigen or family of polypeptide antigens, such as any described herein. Peptides may be selected from such a panel to treat a corresponding cancer that is associated with expression of the antigen.

In some cases the peptides or the panel peptides may (each) comprise peptides that comprise the sequences of SEQ ID NOs: 1 to 2786 and/or 2787 to 5431 and/or 5432 to 5931 that were identified by the inventors as described herein in the first 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 cycles of the method described herein. The peptides identified in earlier cycles are those that are able to induce T cell responses against the corresponding target antigen in the highest proportion of subjects in the model population.

In some cases the panel of peptides comprises peptides that together comprise any 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40 or 50, 100, 200, 300, 400 or 500 of the amino acid sequences of Table 25 or Table 28, or of the amino acid sequences of Table 25 or Table 28 that are a fragment of a TAA that is associated with a cancer selected from those listed in Table 24, and/or that were obtained in the first 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 cycles as described herein.

In some cases the panel comprises or encodes at least two, or at least 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acid sequence selected from SEQ ID NOs: 1 to 2786 and/or 2787 to 5431 and/or 5432 to 5931, each of which comprises a T cell epitope capable of binding to at least three HLA class I alleles and/or a T cell epitope capable of binding to at least three HLA class II alleles of an individual human subject. Such a panel is a personalised, subject-specific selection of peptides that can be used to induce T cell responses in the specific subject.

In some cases the peptides of the disclosure may be up to 50, 45, 40, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21 or 20 amino acids in length. The peptide comprises or consists of an amino acid sequence selected from any of SEQ ID NO: 1 to 2786 and/or 2787 to

5431 and/or 5432 to 5931, which is a fragment of one or more TAAs as shown in Table 24. In some cases the fragment may comprise or consist of a longer fragment of a TAA of which the sequence of SEQ ID NO: 1 to 2786 and/or 2787 to 5431 and/or 5432 to 5931 is a part. The terms “fragment” or “fragment of a polypeptide” as used herein refer to a string of amino acids or an amino acid sequence typically of reduced length relative to the or a reference polypeptide and comprising, over the common portion, an amino acid sequence identical to the reference polypeptide. Such a fragment according to the disclosure may be, where appropriate, included in a larger polypeptide of which it is a constituent.

In some cases the fragment having the amino acid sequence of any one of SEQ ID NOs: 1 to 2786, or the longer fragment of a TAA comprising the amino acid sequence of any one of SEQ ID NOs: 1 to 2786, is flanked at the N and/or C terminus of the peptide by additional amino acids that are not part of the consecutive sequence of the TAA. In some cases the sequence may be flanked by up to 30 or 25 or 20 or 15 or 10, or 9 or 8 or 7 or 6 or 5 or 4 or 3 or 2 or 1 additional amino acid at the N and/or C terminus.

In some aspects the disclosure provides a polynucleic acid or vector that encodes one or more peptides, wherein the encoded peptides comprise the amino acid sequence of any one of SEQ ID NOs: 1 to 2786 and/or 2787 to 5431 and/or 5432 to 5931 and/or 2787 to 3997, as shown in Tables 25 and 28, or panels thereof. All of the disclosure herein relating to peptides comprising the amino acid sequence of any of SEQ ID NOs: 1 to 2786 and shown in Table 25 (and methods and compositions relating to such peptides) also applies equally to polynucleic acids or vectors encoding one or more peptides comprising the amino acid sequence of any of SEQ ID NOs: 1 to 2786 and/or 2787 to 5431 and/or 5432 to 5931 and/or 2787 to 3997.

Methods of designing and producing peptides

In some embodiments the disclosure provides methods of designing and preparing one or more peptides, or polynucleotides or vectors that encode peptides, that can optimally be used to induce T cell responses against one or more given polypeptide antigens in a given target population of subjects.

Target polypeptides

As used herein, the term “polypeptide” refers to a full-length protein, a portion of a protein, or a peptide characterized as a string of amino acids. As used herein, the term “peptide” refers to a short polypeptide. The peptides are typically between 9, or 10, or 11, or 12, or 13, or

14, or 15 or 16 or 17 or 18 or 19 or 20 and 20, or 21, or 22, or 23, or 24, or 25, or 26, or 27, or 28, or 29, or 30, or 35, or 40, or 45, or 50 amino acid in length. In some cases the peptide is not a 9-mer or a 15-mer. Short peptides may not be processed by antigen presenting cells and therefore bind exogenously to the HLA molecules. Thus, injected short peptides may bind in
 5 large numbers to the HLA molecules of all nucleated cells that have surface HLA class I, leading to tolerance. On the other hand polypeptides are not processed as efficiently as long peptides. Accordingly in some cases the peptides may be about 20 or 25 to about 30 or 35 amino acids in length.

The method may comprise the step of selecting one or more target polypeptide antigens.
 10 The target polypeptide antigen may be any polypeptide or fragment of a polypeptide against which it is desirable to mount a T cell response in a subject of the target population, for example a CD4+ T cell response or a CD8+ T cell response. Typically the target polypeptide is a polypeptide that is expressed by a pathogenic organism (for example, a bacteria or a parasite), a virus, a cancer cell or other disease-associated cell. In some cases the polypeptide may be
 15 present in a sample taken from a subject, such as a subject of the specific or target human population.

The polypeptide may be a Tumor Specific Antigen (TSA) and/or cancer- or tumor-associated antigen (TAA). TAAs are proteins expressed in cancer or tumor cells. Examples of TAAs include new antigens (neoantigens, which are expressed during tumorigenesis and altered
 20 from the analogous protein in a normal or healthy cell), products of oncogenes and tumor suppressor genes, overexpressed or aberrantly expressed cellular proteins (e.g. HER2, MUC1), antigens produced by oncogenic viruses (e.g. EBV, HPV, HCV, HBV, HTLV), cancer testis antigens (CTA, e.g. MAGE family, NY-ESO) and cell-type-specific differentiation antigens (e.g. MART-1). TAA sequences may be found experimentally, or in published scientific papers, or
 25 through publicly available databases, such as the database of the Ludwig Institute for Cancer Research (www.cta.lncc.br/), Cancer Immunity database (cancerimmunity.org/peptide/) and the TANTIGEN Tumor T cell antigen database (cvc.dfci.harvard.edu/tadb/). Exemplary TAAs are listed in Tables 2 and 22. A TSA is an antigen produced by a particular type of tumor that does not appear on normal cells of the tissue in which the tumor developed. TSAs include shared
 30 antigens, neoantigens, and unique antigens. In some cases the polypeptide is not expressed or is minimally expressed in normal healthy cells or tissues, but is expressed (in those cells or tissues) in a high proportion of (with a high frequency in) subjects having a particular disease or condition, such as a type of cancer or a cancer derived from a particular cell type or tissue.

Alternatively, the polypeptide may be expressed at low levels in normal healthy cells, but at high levels (overexpressed) in diseased (e.g. cancer) cells or in subjects having the disease or condition. In some cases the polypeptide is expressed in, or expressed at a high level relative to normal healthy cells or subjects, in at least 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 5 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or more of such individuals, or of a subject-matched human subpopulation or model or target population. For example the population may be matched by ethnicity, geographical location, gender, age, disease, disease type or stage, genotype, and/or expression of one or more biomarkers. Expression frequencies (rates) may be determined from published figures and scientific 10 publications.

In some cases the target polypeptide is a cancer testis antigens (CTA). CTA are not typically expressed beyond embryonic development in healthy cells. In healthy adults, CTA expression is limited to male germ cells that do not express HLAs and cannot present antigens to T cells. Therefore, CTAs are considered expressional neoantigens when expressed in cancer 15 cells. CTA expression is (i) specific for tumor cells, (ii) more frequent in metastases than in primary tumors and (iii) conserved among metastases of the same patient (Gajewski ed. Targeted Therapeutics in Melanoma. Springer New York. 2012).

In some cases the target polypeptide is one that is associated with or expressed by cancer cells or cancer cells of a particular type or cancer of a particular cell type of tissue. In some 20 cases the cancer is a solid tumour. In some cases the cancer is a carcinoma, sarcoma, lymphoma, leukemia, germ cell tumor, or blastoma. The cancer may be a hormone related or dependent cancer (e.g., an estrogen or androgen related cancer) or a non-hormone related or dependent cancer. The tumor may be malignant or benign. The cancer may be metastatic or non-metastatic. The cancer may or may not be associated with a viral infection or viral oncogenes. 25 In some cases the cancer is one or more selected from melanoma, lung cancer, renal cell cancer, colorectal cancer, bladder cancer, glioma, head and neck cancer, ovarian cancer, non-melanoma skin cancer, prostate cancer, kidney cancer, stomach cancer, liver cancer, cervix uteri cancer, oesophagus cancer, non-Hodgkin lymphoma, leukemia, pancreatic cancer, corpus uteri cancer, lip cancer, oral cavity cancer, thyroid cancer, brain cancer, nervous system cancer, gallbladder 30 cancer, larynx cancer, pharynx cancer, myeloma, nasopharynx cancer, Hodgkin lymphoma, testis cancer, breast cancer, gastric cancer, colorectal cancer, renal cell cancer, hepatocellular cancer, pediatric cancer and Kaposi sarcoma.

The polypeptide may be a viral protein that is expressed intracellularly. Examples include HPV16 E6, E7; HIV Tat, Rev, Gag, Pol, Env; HTLV-Tax, Rex, Gag, Env, Human herpes virus proteins, Dengue virus proteins. The polypeptide may be a parasite protein that is expressed intracellularly, for example malaria proteins.

- 5 Non-limiting examples of suitable polypeptides include those listed in one or more of Tables 2 to 5.

Table 2 - LIST OF NAMED TUMOUR ANTIGENS WITH CORRESPONDING ACCESSION NUMBERS. CTAs/TSAs = bold and *							
		5T4	Q13641.1	A1BG	P04217.1	A33	Q99795.1
A4GALT	Q9NPC4.1	AACT	P01011.1	AAG	Q9M6E9.1	ABI1	Q81ZP0.1
ABI2	Q9NYB9.1	ABL1	P00519.1	ABL-BCR	Q8WUG5.1	ABLIM3	O94929.1
ABLL	P42684.1	ABTB1	Q969K4.1	ACACA	Q13085.1	ACBD4	Q8NC06.1
ACO1	P21399.1	ACRBP	Q8NEB7.1*	ACTL6A	O96019.1	ACTL8	Q9H568.1*
ACTN4	O43707.1	ACVR1	Q04771.1	ACVR1B	P36896.1	ACVR2B	Q13705.1
ACVRL1	P37023.1	ACS2B	Q68CK6.1	ACSL5	Q9ULC5.1	ADAM-15	Q13444.1
ADAM17	P78536.1	ADAM2	Q99965.1*	ADAM29	Q9UKF5.1*	ADAM7	Q9H2U9.1
ADAP1	O75689.1	ADFP	Q99541.1	ADGRA3	Q8IWK6.1	ADGRF1	Q5T601.1
ADGRF2	Q81ZF7.1	ADGRL2	O95490.1	ADHFE1	Q8IWW8.1	ABN	Q8WTP8.1
AFF1	P51825.1	AFF4	Q9UHB7.1	AFP	P02771.1	AGAP2	Q99490.1
AGO1	Q9UL18.1	AGO3	Q9H9G7.1	AGO4	Q9HCK5.1	AGR2	O95994.1
AIFM2	Q9BRQ8.1	AIM2	O14862.1	AKAP-13	Q12802.1	AKAP-3	O75969.1*
AKAP-4	Q5JQC9.1*	AKIP1	Q9NQ31.1	AKT1	P31749.1	AKT2	P31751.1
AKT3	Q9Y243.1	ALDH1A1	P00352.1	ALK	Q9UM73.1	ALKBH1	Q13686.1
ALPK1	Q96QP1.1	AMIGO2	Q86SJ2.1	ANG2	O15123.1	ANKRD45	Q5TZF3.1*
ANO1	Q5XXA6.1	ANP32A	P39687.1	ANXA2	P07355.1	APC	P25054.1
APEH	P13798.1	APOA2	P20652.1	APOD	P05090.1	APOL1	O14791.1
AR	P10275.1	ARAF	P10398.1	ARF4L	P49703.1	ARHGEF5	Q12774.1
ARID3A	Q99856.1	ARID4A	P29374.1	ARL6IP5	O75915.1	ARMC3	B4DXS3.1*
ARMC8	Q8IUR7.1	ARTC1	P52961.1	ARX	Q96QS3.1*	ATAD2	Q6PL18.1
AT1C	P31939.1	AURKC	Q9UQB9.1	AXIN1	O15169.1	AXL	P30530.1
BAAT	Q14032.1	BAFF	Q9Y275.1	BAGE-1	Q13072.1*	BAGE-2	Q86Y30.1*
BAGE-3	Q86Y29.1*	BAGE-4	Q86Y28.1	BAGE-5	Q86Y27.1*	BAI1	O14514.1
BAL	P19835.1	BALF2	P03227.1	BALF4	P03188.1	BALF5	P03198.1
BARF1	P03228.1	BBRF1	P03213.1	BCAN	Q96GW7.1	BCAP31	P51572.1
BCL-2	P10415.1	BCL2L1	Q07817.1	BCL6	P41182.1	BCL9	O00512.1
BCR	P11274.1	BCRF1	P03180.1	BDLF3	P03224.1	BGLF4	P13288.1
BHLF1	P03181.1	BHRF1	P03182.1	BILF1	P03208.1	BILF2	P03218.1
BIN1	O00499.1	BING-4	O15213.1	BIRC7	Q96CA5.1	BLLF1	P03200.1
BLLF2	P03199.1	BMI1	P35226.1	BMLF1	Q04360.1	BMPR1B	O00238.1
BMRF1	P03191.1	BNLF2a	P0C739.1	BNLF2b	Q8AZJ3.1	BNRF1	P03179.1
BRAF1	P15056.1	BRD4	O60885.1	BRDT	Q58F21.1*	BRI3BP	Q8WY22.1
BRINP1	O60477.1	BRLF1	P03209.1	BTBD2	Q9BX70.1	BUB1B	O60566.1
BVRF2	P03234.1	BXLF1	P03177.1	BZLF1	P03206.1	C15orf60	Q7Z4M0.1*
CA 12-5	Q8WXI7.1	CA 19-9	Q969X2.1	CA195	Q5TG92.1	CA9	Q16790.1
CABYR	O75952.1*	CADM4	Q8NFZ8.1	CAGE1	Q8CT20.1*	CALCA	P01258.1
CALR3	Q96L12.1	CAN	P35658.1	CASC3	O15234.1	CASC5	Q8NG31.1*
CASP5	P51878.1	CASP8	Q14790.1	CBFA2T2	O43439.1	CBFA2T3	O75081.1
CBL	P22681.1	CBLB	Q13191.1	CC3	Q9BUP3.1	CCDC110	Q8TBZ0.1*
CCDC33	Q8N5R6.1*	CCDC36	Q8IYA8.1*	CCDC6	Q16204.1	CCDC62	Q6P9F0.1*
CCDC68	Q9H2F9.1	CCDC83	Q8IWF9.1*	CCL13	Q99616.1	CCL2	P13500.1
CCL7	P80098.1	CCNA1	P78396.1*	CCNA2	P20248.1	CCNB1	P14635.1
CCND1	P24385.1	CCNE2	O96020.1	CCNI	Q14094.1	CCNL1	Q9UK58.1
CCR2	P41597.1	CD105	P17813.1	CD123	P26951.1	CD13	P15144.1
CD133	O43490.1	CD137	Q07011.1	CD138	P18827.1	CD157	Q10588.1
CD16A	P08637.1	CD178	P48023.1	CD19	P15391.1	CD194	P51679.1
CD2	P06729.1	CD20	P11836.1	CD21	P20023.1	CD22	P20273.1
CD229	Q9HBG7.1	CD23	P06734.1	CD27	P26842.1	CD28	P10747.1
CD30	P28908.1	CD317	Q10589.1	CD33	P20138.1	CD350	Q9ULW2.1
CD36	P16671.1	CD37	P11049.1	CD4	P01730.1	CD40	P25942.1
CD40L	P29965.1	CD45	P08575.1	CD47	Q08722.1	CD51	P06756.1
CD52	P31358.1	CD55	P08174.1	CD61	P05106.1	CD70	P32970.1
CD74	P08922.1	CD75	P15907.1	CD79B	P40259.1	CD80	P33681.1
CD86	P42081.1	CD8a	P01732.1	CD8b	P10966.1	CD95	P25445.1

CD98	P08195.1	CDC123	O75794.1	CDC2	P06493.1	CDC27	P30260.1
CDC73	Q6P1J9.1	CDCA1	Q9BZD4.1*	CDCP1	Q9H5V8.1	CDH3	P22223.1
CDK2AP1	O14519.1	CDK4	P11802.1	CDK7	P50613.1	CDKN1A	P38936.1
CDKN2A	P42771.1	CEA	P06731.1	CEACAM1	Q86UE4.1	CENPK	Q9BS16.1
CEP162	Q5TB80.1	CEP290	O15078.1*	CEP55	Q53EZ4.1*	CFL1	P23528.1
CH3L2	Q15782.1	CHEK1	O14757.1	CK2	P19784.1	CLCA2	Q9UQC9.1
CLOCK	O15516.1	CLPP	Q16740.1	CMC4	P56277.1	CML66	Q96RS6.1
CO-029	P19075.1	COTL1	Q14019.1	COX2	P35354.1	COX6B2	Q6YFQ2.1*
CPSF1	Q10570.1	CPXCR1	Q8N123.1*	CREBL2	O60519.1	CREG1	O75629.1
Cripto	P13385.1	CRISP2	P16562.1*	*CRK	P46108.1	CRKL	P46109.1
CRLF2	Q9HC73.1	CSAGE	Q6PB30.1	CT45	Q5HYN5.1*	CT45A2	Q5DJT8.1*
CT45A3	Q8NHU0.1*	CT45A4	Q8N7B7.1*	CT45A5	Q6NSH3.1*	CT45A6	P0DMU7.1*
CT46	Q86X24.1*	CT47	Q5JQC4.1*	CT47B1	P0C2P7.1*	CTAGE2	Q96RT6.1*
cTAGE5	O15320.1*	CTCFL	Q8NI51.1*	CTDSP2	O14595.1	CTGF	P29279.1
CTLA4	P16410.1	CTNNA2	P26232.1*	CTNNB1	P35222.1	CTNND1	O60716.1
CTSH	P09668.1	CTSP1	A0RZH4.1*	CTTN	Q14247.1	CXCR4	P61073.1
CXorf48	Q8WUE5.1*	CXorf61	Q5H943.1*	Cyclin-E	P24864.1	CYP1B1	Q16678.1
CypB	P23284.1	CYR61	O00622.1	CS1	P28290.1	CSAG1	Q6PB30.1*
CSDE1	O75534.1	CSF1	P09603.1	CSF1R	P07333.1	CSF3R	Q99062.1
CSK	P41240.1	CSK23	Q8NEV1.1	DAPK3	O43293.1	DAZ1	Q9NQZ3.1
DBPC	Q9YT7.1	DCAF12	Q5T6F0.1*	DCT	P40126.1	DCUN1D1	Q96GG9.1
DCUN1D3	Q8IWE4.1	DDR1	Q08345.1	DDX3X	O00571.1	DDX6	P26196.1
DEDD	O75618.1	DEK	P35659.1	DENR	O43583.1	DEPDC1	Q5TB30.1
DFNA5	O60443.1	DGAT2	Q96PD7.1	DHFR	P00374.1	DKK1	O94907.1
DKK3	Q9UBP4.1	DKKL1	Q9UK85.1*	DLEU1	O43261.1	DMBT1	Q9UGM3.1
DMRT1	Q9Y5R6.1*	DNAJB8	Q8NHS0.1*	DNAJC8	O75937.1	DNMT3A	Q9Y6K1.1
DPPA2	Q7Z7J5.1*	DR4	O00220.1	DR5	O14763.1	DRG1	Q9Y295.1*
DSCR8	Q96T75.1	E2F3	O00716.1	E2F6	O75461.1	E2F8	A0AVK6.1
EBNA1	P03211.1	EBNA2	P12978.1	EBNA3	P12977.1	EBNA4	P03203.1
EBNA6	P03204.1	EBNA-LP	Q8AZK7.1	E-cadherin	P12830.1	ECT2	Q9H8V3.1
ECTL2	Q008S8.1	EDAG	Q9BXL5.1*	EEF2	P13639.1	EFNA1	P20827.1
EFS	O43281.1	EFTUD2	Q15029.1	EGFL7	Q9UHF1.1	EGFR	p00533.1
ET24	O14681.1	EIF4EBP1	Q13541.1	ELF3	P78545.1	ELF4	Q99607.1
ELOVL4	Q9GZR5.1*	EMP1	P54849.1	ENAH	Q8N8S7.1	Endosialin	Q9HCU0.1
ENO1	P06733.1	ENO2	P09104.1	ENO3	P13929.1	ENTPD5	O75356.1
EpCAM	P16422.1	EPHA2	P29317.1	EPHA3	P29320.1	EPHB2	P29323.1
EPHB4	P54760.1	EPHB6	O15197.1	EPS8	Q12929.1	ERBB3	P21860.1
ERBB4	Q15303.1	EREG	O14944.1	ERG	P11308.1	ERVK-18	O42043.1
ERVK-19	O71037.1	ESR1	P03372.1	ETAA1	Q9NY74.1	ETS1	P14921.1
ETS2	P15036.1	ETV1	P50549.1	ETV5	P41161.1	ETV6	P41212.1
EVI5	O60447.1	EWSR1	Q01844.1	EYA2	O00167.1	EZH2	Q15910.1
FABP7	O15540.1	FAM133A	Q8N9E0.1*	FAM13A	O94988.1	FAM46D	Q8NEK8.1*
FAM58BP	P0C7Q3.1	FANCG	O15287.1	FATE1	Q969F0.1*	FBXO39	Q8N4B4.1*
FBXW11	Q9UKB1.1	FCHSD2	O94868.1	FER	P16591.1	FES	P07332.1
FEV	Q99581.1	FGF10	O15520.1	FGF23	Q9GZV9.1	FGF3	P11487.1
FGF4	P08620.1	FGF5	P12034.1	FGFR1	P11362.1	FGFR2	P21802.1
FGFR3	P22607.1	FGFR4	P22455.1	FGR	P09769.1	FLI1	Q01543.1
FLT3	P36888.1	FMNL1	O95466.1	FMOD	Q06828.1	FMR1NB	Q8N0W7.1*
FN1	P02751.1	Fn14	Q9NP84.1	FNIP2	Q9P278.1	FOLR1	P15328.1
FOS	P01100.1	FosB	P53539.1	FOSL1	P15407.1	FOXM1	Q08050.1
FOXO1	Q12778.1	FOXO3	O43524.1	FRAT1	Q92837.1	FRMD3	A2A2Y4.1
FSIP1	Q8NA03.1	FSIP2	Q5CZC0.1	FSTL3	O95633.1	FTHL17	Q9BXU8.1*
FUND2	Q9BWH2.1	FUS	P35637.1	FUT1	P19526.1	FUT3	P21217.1
FYN	P06241.1	GAB2	Q9UQC2.1	GADD45G	O95257.1	GAGE-1	Q13065.1
GAGE12B/C/D/E	A1L429.1	GAGE12F	P0CL80.1	GAGE12G	P0CL81.1	GAGE12H	A6NDE8.1
GAGE12I	P0CL82.1	GAGE12J	A6NER3.1	GAGE-2	Q6NT46.1	GAGE-3	Q13067.1
GAGE-4	Q13068.1	GAGE-5	Q13069.1	GAGE-6	Q13070.1	GAGE-7	O76087.1
GAGE-8	Q9UEU5.1	GALGT2	Q00973.1	GAS7	O60861.1	GASZ	Q8WWH4.1
GATA-3	P23771.1	GBU4-5	Q587J7.1	GCDFP-15	P12273.1	GFAP	P14136.1
GFI1	Q99684.1	Ghrelin	Q9UBU3.1	GHSR	Q92847.1	GLPC1	O14908.1
GITR	Q9Y5U5.1	GKAP1	Q5VSY0.1	GLI1	P08151.1	Glypican-3	P51654.1
GML	Q99445.1	GNA11	P29992.1	GNAQ	P50148.1	GNB2L1	P63244.1
GOLGA5	Q8TBA6.1	gp100	P40967.1	gp75	P17643.1	Gp96	P14625.1
GPAT2	Q6NUI2.1*	GPATCH2	Q9NW75.1*	GPC-3	P51654.1	GFNMB	Q14956.1
GPR143	P51810.1	GPR89A	B7ZAQ6.1	GRB2	P62993.1	GRP78	P11021.1
GUCY1A3	Q02108.1	H3F3A	P84243.1	HAGE	Q9NXZ2.1*	hANP	P01160.1
HBEGF	Q99075.1	hCG-beta	P01233.1	HDAC1	Q13547.1	HDAC2	Q92769.1
HDAC3	O15379.1	HDAC4	P56524.1	HDAC5	Q9UQL6.1	HDAC6	Q9UBN7.1
HDAC7	Q8WU14.1	HDAC8	Q9BY41.1	HDAC9	Q9UKV0.1	HEATR1	Q9H583.1
Hepsin	P05981.1	Her2/neu	P04626.1	HERC2	O95714.1	HERV-K104	P61576.1

HEXB	P07686.1	HEXIM1	O94992.1	HGRG8	Q9Y5A9.1	HIPK2	Q9H2X6.1
HJURP	Q8NCD3.1	HMGB1	P09429.1	HMOX1	P09601.1	HNRPL	P14866.1
HOM-TES-85 Q9P127.1*		HORMAD1 Q86X24.1*		HORMAD2 Q8N7B1.1*		HPSE	Q9Y251.1
HPV16 E6	P03126.1	HPV16 E7	P03129.1	HPV18 E6	P06463.1	HPV18 E7	P06788.1
HRAS	P01112.1	HSD17B13	Q7Z5P4.1	HSP105	Q92598.1	HSP60	P10809.1
HSPA1A	P08107.1	HSPB9 Q9BQ86.1*		HST-2	P10767.1	HT001	Q2TB18.1
hTERT	O14746.1	HUS1	O60921.1	ICAM-1	P05362.1	IDH1	O75874.1
IDO1	P14902.1	IER3	P46695.1	IGF1R	P08069.1	IGFS11 Q5DX21.1*	
IL13RA2 Q14627.1*		IMP-3 Q9NV31.1*		ING3	Q9NXR8.1	INPPL1	O15357.1
INTS6	Q9UL03.1	IRF4	Q15306.1	IRS4	O14654.1	ITGA5	P08648.1
ITGB8	P26012.1	ITPA	Q9BY32.1	ITPR2	Q14571.1	JAK2	O60674.1
JAK3	P52333.1	JARID1B Q9UGL1.1*		JAZF1	Q86VZ6.1	JNK1	P45983.1
JNK2	P45984.1	JNK3	P53779.1	JTB	O76095.1	JUN	P05412.1
JUP	P14923.1	K19	P08727.1	KAAG1	Q9UBP8.1	Kallikrein 14	
Kallikrein 4	Q9Y5K2.1	KAT6A	Q92794.1	KDM1A	O60341.1	Q9P0G3.1	
KIAA0100 Q14667.1*		KIAA0336	Q8IWJ2.1	KIAA1199	Q8WUJ3.1	KIAA1641	A6QL64.1
KIF11	P52732.1	KIF1B	O60333.1	KIF20A	O95235.1	KIT	P10721.1
KLF4	O43474.1	KLHL41	O60662.1	KLK10	O43240.1	KMT2D	O14686.1
KOC1	O00425.1	K-ras	P01116.1	KRIT1	O00522.1	KW-12	P62913.1
KW-2	Q96RS0.1	KW-5 (SEBD4)	Q9H0Z9.1	KW-7	O75475.1	L1CAM	P32004.1
L53	Q96EL3.1	L6	Q9BTT4.1	LAG3	P18627.1	Lage-1 O75638.1*	
LATS1	O95835.1	LATS2	Q9NRM7.1	LCMT2	O60294.1	LCPI	P13796.1
LDHC P07864.1*		LDLR	P01130.1	LEMD1 Q68G75.1*		Lengsin	Q5TDP6.1
LETMD1	Q6P1Q0.1	LGALS3BP	Q08380.1	LGALS8	O00214.1	LIN7A	O14910.1
LPI Q6XZB0.1*		LIV-1	Q13433.1	LLGL1	Q15334.1	LMO1	P25800.1
LMO2	P25791.1	LMP1	P03230.1	LMP2	P13285.1	LOC647107 Q8TAI5.1*	
LOXL2	Q9Y4K0.1	LRP1	Q07954.1	LRRN2	O75325.1	LTF	P02788.1
LTK	P29376.1	LZTS1	Q9Y250.1	LY6K Q17RY6.1*		LYN	P07948.1
LYPD6B Q8NI32.1*		MAEA	Q7L5Y9.1	MAEL Q96JY0.1*		MAF	O75444.1
MAFF	Q9ULX9.1	MAFG	O15525.1	MAFK	O60675.1	MAGE-A1 P43355.1*	
MAGE-A10 P43363.1*		MAGE-A11 P43364.1*		MAGE-A12 P43365.1*		MAGE-A2 P43356.1*	
MAGE-A2B Q6F448.1*		MAGE-A3 P43357.1*		MAGE-A4 P43358.1*		MAGE-A5 P43359.1*	
MAGE-A6 P43360.1*		MAGE-A8 P43361.1*		MAGE-A9 P43362.1*		MAGE-B1 P43366.1*	
MAGE-B2 O15479.1*		MAGE-B3 O15480.1*		MAGE-B4 O15481.1*		MAGE-B5 Q9BZ81.1*	
MAGE-B6 Q8N7X4.1*		MAGE-C1 O60732.1*		MAGE-C2 Q9UBF1.1*		MAGE-C3 Q8TD91.1*	
mammaglobin-A		MANF	P55145.1	MAP2K2	P36507.1	MAP2K7	O14733.1
Q13296.1							
MAP3K7	O43318.1	MAP4K5	Q9Y4K4.1	MART1	Q16655.1	MART-2	Q5VITY9.1
MAS1	P04201.1	MC1R	Q01726.1	MCAK Q99661.1*		MCF2	P10911.1
MCF2L	O15068.1	MCL1	Q07820.1	MCTS1	Q9ULC4.1	MCSP	Q6UVK1.1
MDK	P21741.1	MDM2	Q00987.1	MDM4	O15151.1	ME1	P48163.1
ME491	P08962.1	MECOM	Q03112.1	MELK	Q14680.1	MEN1	O00255.1
MERTK	Q12866.1	MET	P08581.1	MFGE8	Q08431.1	MFHAS1	Q9Y4C4.1
MFI2	P08582.1	MGAT5	Q09328.1	Midkine	P21741.1	MIF	P14174.1
MKI67	P46013.1	MLH1	P40692.1	MLL	Q03164.1	MLLT1	Q03111.1
MLLT10	P55197.1	MLLT11	Q13015.1	MLLT3	P42568.1	MLLT4	P55196.1
MLLT6	P55198.1	MMP14	P50281.1	MMP2	P08253.1	MMP7	P09237.1
MMP9	P14780.1	MOB3B	Q86TA1.1	MORC1 Q86VD1.1*		MPHOSPH1 Q96Q89.1*	
MPL	P40238.1	MRAS	O14807.1	MRP1	P33527.1	MRP3	O15438.1
MRPL28	Q13084.1	MRPL30	Q8TCC3.1	MRPS11	P82912.1	MSLN	Q13421.1
MTA1	Q13330.1	MTA2	O94776.1	MTA3	Q9BTC8.1	MTCP1	P56278.1
MTSS1	O43312.1	MUC-1	P15941.1	MUC-2	Q02817.1	MUC-3	Q02505.1
MUC-4	Q99102.1	MUC-5AC	P98088.1	MUC-6	Q6W4X9.1	MUM1	Q2TAK8.1
MUM2	Q9Y5R8.1	MYB	P10242.1	MYC	P01106.1	MYCL	P12524.1
MYCLP1	P12525.1	MYCN	P04198.1	MYD88	Q99836.1	MYEOV	Q96EZ4.1
MYO1B	O43795.1	NA88-A P0C5K6.1*		NAE1	Q13564.1	Napsin-A	O96009.1
NAT6	Q93015.1	NBAS	A2RRP1.1	NBPF12	Q5TAG4.1	NCOA4	Q13772.1
NDC80	O14777.1	NDUFC2	O95298.1	Nectin-4	Q96NY8.1	NEK2	P51955.1
NEMF	O60524.1	NENF	Q9UMX5.1	NEURL1	O76050.1	NFIB	O00712.1
NFKB2	Q00653.1	NF-X1	Q12986.1	NFYC	Q13952.1	NGAL	P80188.1
NGEP	Q6IWH7.1	NKG2D-L1	Q9BZM6.1	NKG2D-L2	Q9BZM5.1	NKG2D-L3	Q9BZM4.1
NKG2D-L4	Q8TD07.1	NKX3.1	Q99801.1	NLGN4X	Q8NOW4.1	NLRP4 Q96MN2.1*	
NNMT	P40261.1	NOL4 O94818.1*		NOTCH2	Q04721.1	NOTCH3	Q9UM47.1
NOTCH4	Q99466.1	NOV	P48745.1	NPM1	P06748.1	NR6A1 Q15406.1*	
N-RAS	P01111.1	NRCAM	Q92823.1	NRP1	O14786.1	NSE1	Q96KN4.1
NSE2	Q96KN1.1	NTRK1	P04629.1	NUAK1	O60285.1	NUGGC	Q68CJ6.1
NXF2 Q9GZY0.1*		NXF2B Q5JRM6.1*		NY-BR-1	Q9BXX3.1	NYD-TSPG	Q9BWW7.1
NY-ESO-1 P78358.1*		NY-MEL-1	P57729.1	OCA2	Q04671.1	ODF1 Q14990.1*	
ODF2 Q5BJF6.1*		ODF3 Q96PU9.1*		ODF4 Q2M2E3.1*		OGG1	O15527.1
OGT	O15294.1	OIP5 O43482.1*		OS9	Q13438.1	OTOA Q05BM7.1*	

OX40	P43489.1	OX40L	P23510.1	P53	P04637.1	P56-LCK	P06239.1
PA2G4	Q9UQ80.1	PAGE1	O75459.1*	PAGE2	Q7Z2X2.1*	PAGE2B	Q5JRK9.1*
PAGE3	Q5JUK9.1*	PAGE4	O60829.1*	PAGE5	Q96GU1.1*	PAK2	Q13177.1
PANO1	IOJ062.1	PAP	Q06141.1	PAPOLG	Q9BWT3.1	PARK2	O60260.1
PARK7	Q99497.1	PARP12	Q9H0J9.1	PASD1	Q8IV76.1*	PAX3	P23760.1
PAX5	Q02548.1	PBF	P00751.1	PBK	Q96KB5.1*	PBX1	P40424.1
PCDC1	Q15116.1	PCM1	Q15154.1	PCNXL2	A6NKB5.1	PDGFB	P01127.1
PDGFRA	P16234.1	PEPP2	Q9HAU0.1*	PGF	P49763.1	PGK1	P00558.1
PHLDA3	Q9Y5J5.1	PHLPP1	O60346.1	PIAS1	O75925.1	PIAS2	O75928.1
PIK3CA	P42336.1	PIK3CD	O00329.1	PIK3R2	O00459.1	PIM1	P11309.1
PIM2	Q9P1W9.1	PIM3	Q86V86.1	PIR	O00625.1	PIWIL1	Q96J94.1*
PIWIL2	Q8TC59.1*	PIWIL3	Q7Z3Z3.1	PIWIL4	Q7Z3Z4.1	PKN3	Q6P5Z2.1
PLA2G16	P53816.1	PLAC1	Q9HBJ0.1*	PLAG1	Q6DJT9.1	PLEKHG5	O94827.1
PLK3	Q9H4B4.1	PLS3	P13797.1	PLVAP	Q9BX97.1	PLXNB1	O43157.1
PLXNB2	O15031.1	PML	P29590.1	PML-RARA	Q96QH2.1	POTEA	Q68J7.1*
POTEB	Q6S5H4.1*	POTEC	B2RU33.1*	POTED	Q86YR6.1*	POTEE	Q6S8J3.1*
POTEG	Q6S5H5.1*	POTEH	Q6S545.1*	PP2A	P63151.1	PPAPDC1B	Q8NEB5.1
PPFIA1	Q13136.1	PIIG	Q13427.1	PPP2R1B	P30154.1	PRAME	P78395.1*
PRDX5	P30044.1	PRKAA1	Q13131.1	PRKCI	P41743.1	PRM1	P04553.1*
PRM2	P04554.1*	PRMT3	O60678.1	PRMT6	Q96LA8.1	PDL1	Q9NZQ7.1
PROM1	O43490.1	PRSS54	Q6PEW0.1*	PRSS55	Q6UWB4.1*	PRTN3	P24158.1
PRUNE	Q86TPI.1	PRUNE2	Q8WUY3.1	PSA	P07288.1	PSCA	D3DWT6.1
PSMA	Q04609.1	PSMD10	O75832.1	PSGR	Q9H255.1	PSP-94	Q1L6U9.1
PTEN	P60484.1	PTH-rP	P12272.1	PTK6	Q13882.1	PTPN20A	Q4JDL3.1*
PTPRK	Q15262.1	PTRRZ	P23471.1	PTTG-1	O95997.1	PTTG2	Q9NZH5.1
PTTG3	Q9NZH4.1	PXDNL	A1KZ92.1	RAB11FIP3	O75154.1	RAB8A	P61006.1
RAD1	O60671.1	RAD17	O75943.1	RAD51C	O43502.1	RAF1	P04049.1
RAGE-1	Q9UQ07.1	RAP1A	P62834.1	RARA	P10276.1	RASSF10	A6NKB9.1
RB1	P06400.1	RBL2	Q08999.1	RBM46	Q8TBY0.1*	RBP4	P02753.1
RCAS1	O00559.1	RCVRN	P35243.1	RECQL4	O94761.1	RET	P07949.1
RGS22	Q8NE09.1*	RGS5	O15539.1	RHAMM	O75330.1	RhoC	P08134.1
RHOXF2	Q9BQY4.1	RL31	P62888.1	RNASET2	O00584.1	RNF43	Q68DV7.1
RNF8	O76064.1	RON	Q04912.1	ROFN1A	Q9HAT0.1*	ROR1	Q01973.1
RPA1	O95602.1	RPL10A	P62906.1	RPL7A	P62424.1	RPS2	P15880.1
RPS6KA5	O75582.1	RPSA	P08865.1	RQCD1	Q92600.1*	RRAS2	P62070.1
RSL1D1	O76021.1	RTKN	Q9BST9.1	RUNX1	Q01196.1	RUNX2	Q13950.1
RYK	P34925.1	SAGE1	Q9NXZ1.1*	SART2	Q9UL01.1	SART3	Q15020.1
SASH1	O94885.1	sCLU	P10909.1	SCRN1	Q12765.1	SDCBP	O00560.1
SDF-1	P48061.1	SDHD	O14521.1	SEC31A	O94979.1	SEC63	Q9UGP8.1
Semaphorin 4D	Q92854.1	SEMGI	P04279.1*	SFN	P31947.1	SH2B2	O14492.1
SH2D1B	O14796.1	SH3BP1	Q9Y3L3.1	SHB	Q15464.1	SHC3	Q92529.1
SIRT2	Q8IXJ6.1	SIVA1	O15304.1	SKI	P12755.1	SLBP	A9UHW6.1
SLC22A10	Q63ZE4.1	SLC25A47	Q6Q0C1.1	SLC35A4	Q96G79.1	SLC45A3	Q96JT2.1
SLC4A1AP	Q9BWU0.1	SLC06A1	Q86UG4.1*	SLITRK6	Q9H5Y7.1	Sm23	Q27701.1
SMAD5	Q99717.1	SMAD6	O43541.1	SMO	Q99835.1	Smt3B	P61956.1
SNRPD1	P62314.1	SOS1	Q07889.1	SOX-2	P48431.1	SOX-6	P35712.1
SOX-11	P35716.1	SPA17	Q15506.1*	SPACA3	Q8IXA5.1*	SPAG1	Q07617.1*
SPAG17	Q6Q759.1*	SPAG4	Q9NPE6.1*	SPAG6	O75602.1*	SPAG8	Q99932.1*
SPAG9	O60271.1*	SPANXA1	Q9NS26.1*	SPANXB	Q9NS25.1*	SPANXC	Q9NY87.1*
SPANXD	Q9BXN6.1*	SPANXE	Q8TAD1.1*	SPANXN1	Q5VSR9.1*	SPANXN2	Q5MJ10.1*
SPANXN3	Q5MJ09.1*	SPANXN4	Q5MJ08.1*	SPANXN5	Q5MJ07.1*	SPATA19	Q7Z5L4.1*
SPEF2	Q9C093.1*	SPI1	P17947.1	SPINLW1	O95925.1*	SPO11	Q9Y5K1.1*
SRC	P12931.1	SSPN	Q14714.1	SSX-1	Q16384.1*	SSX-2	Q16385.1*
SSX-3	Q99909.1*	SSX-4	O60224.1*	SSX-5	O60225.1*	SSX-6	Q7RTT6.1*
SSX-7	Q7RTT5.1*	SSX-9	Q7RTT3.1*	ST18	O60284.1	STAT1	P42224.1
STEAP1	Q9UHE8.1	STK11	Q15831.1	STK25	O00506.1	STK3	Q13188.1
STN	Q9H668.1	SUPT7L	O94864.1	Survivin	O15392.1	SUV39H1	O43463.1
SYCE1	Q8N0S2.1	SYCP1	Q15431.1	SYCP3	Q8IZU3.1	SYT	Q15532.1
TA-4	Q96RI8.1	TACC1	O75410.1	TAF1B	Q53T94.1	TAF4	O00268.1
TAF7L	Q5H9L4.1*	TAG-1	Q02246.1*	TAL1	P17542.1	TAL2	Q16559.1
TAPBP	O15533.1	TATI	P00995.1	TAX1BP3	O14907.1	TBC1D3	Q8IZP1.1
TBP-1	P17980.1	TCL1A	P56279.1	TCL1B	O95988.1	TDHP	Q9BT92.1
TDRD1	Q9BXT4.1*	TDRD4	Q9BXT8.1*	TDRD6	O60522.1*	TEKT5	Q96M29.1*
TEX101	Q9BY14.1*	TEX14	Q8IWB6.1*	TEX15	Q9BXT5.1*	TEX38	Q6PEX7.1*
TF	P02787.1	TFDP3	Q5H9I0.1*	TFE3	P19532.1	TGFBFR1	P36897.1
TGFBFR2	P37173.1	THEG	Q9P2T0.1*	TIE2	Q02763.1	TIPRL	O75663.1
TLR2	O60603.1	TMEFF1	Q8IYR6.1*	TMEFF2	Q9UIK5.1*	TMEM108	Q6UXF1.1*
TMEM127	O75204.1	TMPRSS12	Q86WS5.1*	TNC	P24821.1	TNFRSF17	Q02223.1
TNFRSF15	O95150.1	TNK2	Q07912.1	TOMM34	Q15785.1	TOP2A	P11388.1
TOP2B	Q02880.1	TOR3A	Q9H497.1	TP73	O15350.1	TPA1	8N543.1

TPGS2	Q68CL5.1	TPI1	P60174.1	TPL2	P41279.1	TPM4	P67936.1
TPO	P40225.1	TPPP2	P59282.1*	TPR	P12270.1	TPTE	P56180.1*
TRAF5	O00463.1	TRAG-3	Q9Y5P2.1*	TRGC2	P03986.1	TRIM24	O15164.1
TRIM37	O94972.1	TRIM68	Q6AZZ1.1	TRPM8	Q7Z2W7.1	TSGA10	Q9BZW7.1*
TSP50	Q9UI38.1*	TSPAN6	O43657.1	TSPY1	Q01534.1*	TSPY2	A6NKD2.1*
TSPY3	Q6B019.1*	TSPYL1	Q9H0U9.1	TSSK6	Q9BXA6.1*	TTC23	Q5W5X9.1
TTK	P33981.1*	TULP2	O00295.1*	TUSC2	O75896.1	TWEAK	O43508.1
TXNIP	Q9H3M7.1	TYMS	P04818.1	TYR	P14679.1	U2 snRNP B	P08579.1
U2AF1	Q01081.1	UBD	O15205.1	UBE2A	P49459.1	UBE2C	O00762.1
UBE2V1	Q13404.1	UBE4B	O95155.1	UBR5	O95071.1	UBXD5	Q5T124.1
UFL1	O94874.1	URI1	O94763.1	URLC10	Q17RY6.1	UROCI	Q96N76.1
USP2	O75604.1	USP4	Q13107.1	VAV1	P15498.1	VCX3A	Q9NNX9.1
VEGFR1	P17948.1	VEGFR2	P35968.1	VHL	P40337.1	VIM	P08670.1
VWA5A	O00534.1	WHSC2	Q9H3P2.1	WISP1	O95388.1	WNK2	Q9Y3S1.1
WNT10B	O00744.1	WNT3	P56703.1	WNT-5a	P41221.1	WT1	P19544.1
WWP1	Q9H0M0.1	XAGE-1	Q9HD64.1*	XAGE-2	Q96GT9.1*	XAGE-3	Q8WTP9.1*
XAGE-4	Q8WWM0.1	XAGE-5	Q8WWM1.1*	XBP1	P17861.1	XPO1	O14980.1
XRCC3	O43542.1	YB-1	P67809.1	YEATS4	O95619.1	YES1	P07947.1
YKL-40	P36222.1	ZBTB7A	O95365.1	ZBTB7C	A1YPR0.1	ZEB1	P37275.1
ZFYVE19	Q96K21.1	ZNF165	P49910.1*	ZNF185	O15231.1	ZNF217	O75362.1
ZNF320	A2RRD8.1	ZNF395	Q9H8N7.1	ZNF645	Q8N7E2.1*	ZUBR1	Q5T4S7.1
ZW10	O43264.1	ZWINT	O95229.1	Ropporin-1A	Q9HAT0	WBP2NL	Q6ICG8.1

Table 2 optionally excludes Ropporin-1A Q9HAT0 and/or WBP2NL Q6ICG8.1.

Table 3 - LIST OF ACCESSION NUMBERS FOR VIRAL ANTIGENS FROM IEDB							
	Q76R62.1	P03182.1	P09258.1	P09310.1	P03227.1	P89466.1	P04601.1
P13285.1	P09991.1	P03468.1	A2T3Q0.1	P0C6X7.1	P89448.1	P12978.1	P09257.1
P50641.1	P14075.1	20178567.1	Q01023.1	P03188.1	P04585.1	P0C767.1	P12977.1
P89467.1	Q9W850.1	Q00683.1	P04591.1	P03211.1	9628706.1	P03460.1	P08666.1
P03485.1	Q04360.1	Q913Y7.1	P89449.1	Q81871.1	P03452.1	P17763.1	P89430.1
P03410.1	P04012.1	P27958.1	Q6WB99.1	P25212.1	Q9PZT1.1	P68593.1	P03203.1
P29996.1	9629374.1	P59633.1	O42053.1	P0C6L3.1	P59635.1	Q9YZN9.1	Q6WB95.1
P10233.1	P89475.1	Q6WB98.1	Q6SW67.1	Q7TFA0.1	P0CK17.1	P59594.1	1980491.1
P14079.1	P15423.1	1891762.1	P09259.1	P09269.1	Q77Q38.1	Q786F2.1	Q6SW99.1
P24771.1	F5HB98.1	9629370.1	P68336.1	P03300.1	1980486.1	Q69027.1	P28284.1
P13290.1	9626585.1	P06923.1	P14076.1	P03346.1	O42062.1	P07566.1	P03204.1
Q69091.1	P09255.1	P03206.1	O36634.1	P10205.1	F5HCM1.1	P0CK16.1	Q6WB97.1
Q85601.1	P89468.1	Q69467.1	P03218.1	Q786F3.1	P59637.1	1891763.1	Q6WB94.1
P03231.1	Q9IK92.1	Q6WBA1.1	P03466.1	P14335.1	P26670.1	Q9PZT0.1	1985356.1
Q2HR63.1	P59634.1	Q6SW59.1	P03277.1	P59595.1	Q69028.1	P03383.1	P03261.1
P03200.1	P04578.1	P06484.1	F5HC97.1	S5TC82.1	P18095.1	Q96895.1	P18094.1
9629372.1	P50791.1	P03230.1	P13845.1	9629712.1	P03209.1	P03129.1	Q76R61.1
P03228.1	P0C206.1	Q9WMB5.1	P03226.1	Q9QR69.1	O36633.1	O42049.1	P03496.1
P03428.1	P03431.1	P0C0U1.1	P03433.1	P03508.1	1980456.1	P0C739.1	P69726.1
P69723.1	1980490.1	532129755.1	P03120.1	P04020.1	P06922.1	P03114.1	P03314.1
P06790.1	P06788.1	P06927.1	P03101.1	P03107.1	P06794.1	530787712.1	P04013.1
Q80872.1	P04014.1	P03126.1	P36811.1	P06463.1	P26554.1	P04016.1	P14078.1
P03191.1	1980471.1	P06821.1	P0C797.1	F5HF49.1	P0C045.1	P04296.1	P04485.1
P10230.1	P10221.1	P06487.1	P10215.1	P04293.1	P10211.1	P10209.1	P10225.1
P10224.1	P10238.1	P10185.1	P08392.1	P10231.1	P06492.1	P04290.1	P08393.1
P08543.1	P10210.1	P08617.1	F5HB53.1	P04019.1	P04015.1	P89442.1	P89452.1
P89462.1	P59632.1	O36635.1	P07210.1	Q83884.1	Q8JUX5.1	P03089.1	Q66479.1
P03185.1	P0CAP6.1	P04618.1	56160929.1	1980519.1	P08669.1	P14348.1	P03212.1
P03179.1	45617- other.1	1511872.1	302317869.1	P69899.1	P09247.1	Q05127.1	P18272.1
Q9YMG2.1	Q05128.1	302371215.1	302371218.1	Q5XX08.1	302371214.1	P14336.1	138948- other.1
P08292.1	1803956.1	P35253.1	1891726.1	P09308.1	P03189.1	667489389.1	P09272.1
34365530.1	Q05320.1	P59596.1	P32886.1	55097.1	P03316.1	P03276.1	Q81870.1
Q81862.1	64320.1	1933190.1					

Table 4 -LIST OF ACCESSION NUMBERS FOR BACTERIAL ANTIGENS FROM IEDB							
	B8ZUD1.1	P09621.1	P9WPE5.1	Q2GI62.1	POA5B8.1	O50443.1	Q5NEZ3.1
P9WQF5.1	P9WK95.1	O05311.1	P9WQD7.1	P9WKG3.1	P9WHE5.1	P0CD83.1	P9WHB9.1
P9WH91.1	P9WHB3.1	P9WNK7.1	A0A0F3MKF3.1	A1JIP3.1	B2RKSE.1	P0A1D3.1	P0A6F5.1
P0C0Z7.1	P0C923.1	P61439.1	Q9Z708.1	POA521.1	P9WPE7.1	Q79FJ2.1	B8ZR84.1
I6Y3P5.1	Q2FYP2.1	P9WG41.1	P96890.1	O06625.1	I6X654.1	Q8YIE1.1	P9WQ81.1
I6XWA1.1	P11311.1	O53900.1	P9WIR7.1	P9WQB1.1	B8ZUC6.1	O06802.1	P9WMM1.1

P9WG37.1	Q2FWC4.1	Q2GGE3.1	O33347.1	P9WJ09.1	P9WJ11.1	P9WF23.1	O69703.1
I6X4K0.1	B2RM93.1	P71888.1	P9WFW3.1	P9WPV1.1	P9WPU7.1	P9WPFV3.1	P9WPU5.1
O50391.1	P9WID7.1	P9WPC3.1	P96901.1	O84848.1	Q2FUX4.1	A0A0M1YNY3.1	P49944.1
P9WPQ9.1	Q45010.1	Q2FZK7.1	P9WMN3.1	P9WPQ1.1	Q45013.1	O53666.1	Q5NEH1.1
P9WHR5.1	P9WIE5.1	Q5NEQ3.1	P9WNF3.1	F2QBN0.1	B8ZTB7.1	P0C922.1	P9WMJ9.1
Q5NGW2.1	P01556.1	Q8DMZ4.1	P33768.1	Q2FUY2.1	Q5NG56.1	X8CE55.1	Q5NGE4.1
P94973.1	O06827.1	P96872.1	I6X9Y7.1	I6XFX8.1	O50442.1	O53697.1	O53978.1
P95137.1	P95144.1	O53519.1	Q79FZ8.1	P9WJF5.1	P71629.1	P9WJS3.1	P9WBP7.1
Q7D9T1.1	P9WHS1.1	O06393.1	P9WP69.1	P9WPN5.1	P9WNX3.1	O53380.1	I6YAU3.1
P0A4V2.1	P9WQP3.1	P0C2T2.1	P9WQP1.1	P9WQN9.1	O53311.1	P9WIS7.1	O06159.1
H2GU79.1	Q2G2Q0.1	P9WNV1.1	P9WNV5.1	Q8YE98.1	Q59191.1	P9WGY7.1	P9WGY9.1
Q2G2W1.1	P9WGH1.1	P9WNG9.1	P9WNG7.1	O84591.1	Q9Z7A6.1	P9WGR1.1	P96404.1
I6YGS0.1	Q6MX18.1	P9WNK5.1	O53692.1	P9WNK3.1	P9WNK1.1	P9WNJ9.1	P9WNJ7.1
P9WNJ5.1	P9WNJ3.1	P9WNJ1.1	P9WNI9.1	P96903.1	P9WNB1.1	P9WJE1.1	P9WJD9.1
P9WJD7.1	P9WJD3.1	P9WJC5.1	P9WJC3.1	P9WJC1.1	P9WNQ3.1	P9WJE5.1	P9WJC7.1
O84646.1	I6YDV4.1	P11439.1	Q5NFI1.1	P9WNE5.1	P14738.1	P11089.1	H7C7G3.1
L7N6B9.1	I6XFI7.1	O05578.1	P96218.1	P9WN39.1	P9WN59.1	Q8YB13.1	P9WN83.1
P9WJA9.1	P9WMY9.1	Q5NH51.1	O53673.1	P9WIP9.1	P0CE15.1	P72041.1	Q5NEM8.1
Q5NI16.1	P9WJA3.1	P0A4Q1.1	P9WIP1.1	P9WIN9.1	P9WNF5.1	O50846.1	Q59947.1
H7C7N8.1	Q5NEC6.1	O84606.1	P9WQJ9.1	P9WQJ7.1	P9WQ71.1	O53611.1	P9WKL1.1
P9WKJ7.1	D5V9Y8.1	P0CC04.1	P23700.1	P9WJN5.1	Q5NHJ0.1	Q5NEY9.1	P15917.1
Q2G155.1	O34094.1	Q8F8E1.1	O69661.1	H6MMU4.1	P9WK61.1	P9WK55.1	Q8YGS9.1
O50811.1	P9WQ59.1	P9WIN7.1	P9WIR1.1	O50430.1	D5VCH6.1	Q5NHI7.1	P9WUF9.1
I6XFY8.1	B2RH54.1	Q46409.1	P30690.1	A0A0J5IWN3.1	A0PSI5.1	A4TAC4.1	B1MB69.1
B2HSY2.1	B8ZSN3.1	E4WHS0.1	P9WK17.1	V5XE39.1	I6X7G8.1	I6Y461.1	I6YGB1.1
I6YC99.1	Q79FY7.1	I6X5Z8.1	I6Y479.1	I6YA32.1	O05461.1	Q2G1E2.1	P9WK19.1
I6YAW3.1	Q5NGG4.1	O51624.1	P9WJW5.1	Q50584.1	B2RHG1.1	Q5NFI7.1	P9WQN7.1
P9WHH3.1	O84639.1	Q5NF24.1	P9WJH1.1	P9WJH5.1	O53203.1	P55969.1	O50418.1
Q5NGE0.1	H7C7K8.1	O54584.1	G1UB30.1	Q5NH85.1	G1UB25.1	P0A3N8.1	E1X6Y5.1
Q5NEP7.1	Q8YHH0.1	P38006.1	P43838.1	P43839.1	P0CL67.1	P0CL66.1	Q0SLZ0.1
Q07337.1	G5IXI6.1	O07721.1	O53254.1	P75330.1	I6Y936.1	L7N649.1	L7N656.1
L7N693.1	Q79FK4.1	Q79FR3.1	Q79FR5.1	Q79G04.1	Q79FS8.1	Q6MWX1.1	Q79FV6.1
Q79FS5.1	Q79FQ7.1	Q79FP3.1	Q79FP2.1	Q79FK9.1	Q79FE6.1	I6XEF1.1	Q79FD4.1
Q6MX26.1	Q6MX50.1	L7N680.1	O53695.1	I6X8R2.1	O53246.1	I6Y0L1.1	Q2G282.1
P14283.1	P04977.1	P9WMX7.1	P9WFR1.1	P9WN09.1	O86345.1	P9WGU1.1	P9WGT9.1
P9WGT7.1	P9WPF7.1	P9WIB3.1	P9WMM9.1	P9WHM5.1	P9WQE9.1	Q8DQ08.1	Q8DQ07.1
I6Y231.1	P9WHV9.1	O05877.1	O07236.1	O86370.1	O06404.1	O06410.1	B8ZRL2.1
O06807.1	O33269.1	Q79FA9.1	Q79FK6.1	Q8VKN2.1	L7N675.1	Q79FK5.1	L0T7Y7.1
Q79FI9.1	Q79FE1.1	Q6MWX9.1	O84616.1	O84647.1	P9WQ27.1	O84288.1	I6X9S5.1
P9WJW3.1	P9WPS9.1	P95149.1	O53632.1	I6Y293.1	L0T243.1	P9WPA3.1	P9WKC9.1
P96402.1	P71810.1	O06417.1	P96365.1	L0T5B2.1	P96264.1	P9WJK5.1	P9WJQ9.1
O84419.1	O84818.1	Q8YG32.1	O06608.1	O07175.1	P9WGA3.1	O53323.1	P96354.1
P9WIM9.1	B8ZRT2.1	P9WK93.1	P13423.1	O84583.1	P9WGG3.1	P9WIM1.1	P9WKJ3.1
P9WNZ7.1	P9WK31.1	Q50701.1	P9WID3.1	Q8YC41.1	P9WPL3.1	P9WNI3.1	P9WNI7.1
P9WNI5.1	P9WQ49.1	P9WMG1.1	Q2GGR3.1	P9WK71.1	O33192.1	P9WND5.1	P9WFL9.1
P9WMB7.1	P9WJ79.1	P9WND7.1	Q63RA7.1	Q63ID0.1	I6YET7.1	Q9S010.1	P9WGC9.1
Q50700.1	Q5NFR6.1	P9WGG3.1	P9WHI1.1	P9WHV3.1	Q5NIA7.1	P9WG27.1	P9WFF3.1
P9WGA1.1	P9WIB9.1	P9WGL3.1	O51381.1	P9WI83.1	P9WI79.1	P9WFT7.1	Q8YGS6.1
P05788.1	P17835.1	P9WIK9.1	Q5NHP7.1	P9WJU5.1	P9WGE7.1	Q2G2B2.1	P04958.1
P9WG67.1	P9WKE1.1	O07226.1	P9WJ13.1	P9WHF3.1	P9WF43.1	Q7D7L0.1	P9WMF9.1
P9WGN1.1	P9WKJ9.1	P60230.1	P9WKH7.1	O53699.1	P9WHT7.1	P9WJS5.1	Q5NII0.1
Q8YDZ3.1	Q9RPX7.1	P9WN67.1	O05576.1	Q5NHL4.1	P9WN15.1	P9WMD5.1	P9WMP5.1
P9WG85.1	P9WJW7.1	P9WIH1.1	P9WIG1.1	P9WIG3.1	P9WIF5.1	P9WIF1.1	P9WIE7.1
P9WHW9.1	P9WI41.1	P9WI39.1	P9WI37.1	P9WI25.1	Q11031.1	P9WI47.1	P9WI23.1
P9WI19.1	P9WI11.1	P9WI45.1	P9WIO7.1	P9WIO5.1	Q79FH3.1	P9WI43.1	P9WHZ7.1
P9WHZ5.1	P9WHZ3.1	P9WHY9.1	P9WHY7.1	P9WHY5.1	Q6MX07.1	P9WHY3.1	Q6MWY2.1
Q50703.1	P9WHX3.1	P96221.1	Q7D589.1	P9WMA3.1	P9WKW1.1	P9WKS9.1	P9WMT9.1
P9WGC1.1	P9WLZ5.1	P9WLZ3.1	P9WLX1.1	P9WLV9.1	P9WLS7.1	P9WLQ1.1	P9WLJ1.1
P9WLH9.1	P9WLF3.1	P9WL97.1	P9WL87.1	P9WL85.1	P9WL83.1	P9WL67.1	P9WL63.1
P9WL51.1	P9WL47.1	P9WNH3.1	P9WGL7.1	P9WQM5.1	P9WPD9.1	A0A098A1N7.1	A0A098A2B0.1
A2RGM0.1	A5LVF6.1	A5MKZ9.1	B8ZQI8.1	B8ZQM3.1	B8ZQT5.1	B8ZR82.1	B8ZRH1.1
B8ZS71.1	B8ZS85.1	B8ZS86.1	B8ZSJ5.1	B8ZSL3.1	B8ZSL7.1	B8ZSM6.1	B8ZT30.1
B8ZTD0.1	B8ZTS2.1	B8ZTV5.1	B8ZU53.1	B8ZUA4.1	B8ZUE5.1	B8ZUF0.1	B8ZUT6.1
B8ZUX6.1	C0R9U8.1	C6DPT8.1	C6DQ35.1	E1XJN6.1	G8W6L3.1	G8W6L7.1	G8W6U7.1
H6MNY3.1	H6MQD5.1	H8HRN0.1	H8HW90.1	H8L8K3.1	I6TQ53.1	I6TX52.1	P0C5B9.1
Q1BYS7.1	R4MDK6.1	S5F815.1	W6GWM1.1	P9WFC9.1	P9WFFJ9.1	P14916.1	P69996.1
P9WFC5.1	Q8VQK6.1	P9WHS3.1	A5MKI6.1				

Table 5 - LIST OF ACCESSION NUMBERS FOR FUNGAL ANTIGENS FROM IEDB and UNIPROT

Q5ANA3.1	Q5A3P6.1	Q59VM7.1	Q5A1A9.1	Q5APF0.1	Q8J0P4.1	Q4WHG0.1	Q4WQ87.1
Q59X67.1	Q59Z17.1	Q59ZI3.1	Q5AA33.1	B8N4Q9.1	Q4WAW6.1	Q4WAJ6.1	Q4X1V0.1
A0A1D8PQ86.1	Q59ZB1.1	Q873N2.1	Q59L72.1	B8NIF0.1	P46075.1	Q4WCL1.1	Q4WRP2.1
Q59L12.1	Q59LC9.1	P48989.1	Q5AFC2.1	B8N406.1	Q4WGL5.1	Q9HEQ8.1	Q4WVI6.1
P46593.1	P82611.1	Q5ADV5.1	Q59SG9.1	P41750.1	O00092.1	Q4WEN1.1	Q4WCV3.1
P0DJ06.1	O94038.1	Q59WD3.1	Q59RQ0.1	B8NM71.1	Q4WLW8.1	Q4WI37.1	Q4WNI1.1
P29717.1	P46589.1	Q59W04.1	Q59RK9.1	B8MYS6.1	Q8X176.1	Q4WZS1.1	Q4WQH4.1
Q9UW14.1	Q5AF56.1	Q59VN0.1	P31353.1	B8N8Q9.1	Q96UX3.1	Q4WDA4.1	Q4WDE1.1
Q92207.1	P83773.1	Q59WB9.1	Q5ACM4.1	B8N8R3.1	Q4WPF5.1	Q4WLS7.1	Q4WJT7.1
Q5A8T7.1	Q59YU1.1	Q59P53.1	Q5ACI8.1	B8N417.1	Q92450.1	Q4WWM6.1	Q4WLG1.1
Q5A8T4.1	Q59YV2.1	Q5A432.1	Q5AB93.1	B8N8R0.1	Q4WAW9.1	Q4WPF8.1	Q4WQR6.1
P43076.1	Q5ABE5.1	Q5AK64.1	Q5ALL8.1	B8NM74.1	A4GYZ0.1	Q6MYT0.1	Q4WZS2.1
Q5AP53.1	Q59LF2.1	A0A1D8PNZ7.1	Q5A4X8.1	B8N106.1	Q4WAW3.1	Q4WTL0.1	Q4WXP0.1
Q5AL52.1	Q8NJN3.1	Q59Q30.1	Q5AD34.1	B8NH4.1	Q70J59.1	Q4WXV2.1	Q4WU59.1
P43079.1	Q5ALN1.1	A0A1D8PN12.1	Q59V02.1	B8NJG8.1	Q4X1A4.1	Q4X0Z3.1	Q4WUG4.1
Q5AD07.1	Q59S72.1	Q5AK24.1	Q5AHC0.1	B8NM66.1	E9R876.1	Q4WN25.1	Q4WIK9.1
Q5A0E5.1	Q59K86.1	Q5AFT2.1	Q59Y11.1	B8MYL0.1	M4VQY9.1	Q4WN21.1	Q4WYP0.1
Q5AKU6.1	Q5AGD1.1	Q5A0W6.1	Q59QA5.1	B8NM62.1	Q4WF53.1	Q4X1N0.1	Q4X0B5.1
Q59RL7.1	P79023.1	P0CB63.1	Q5AMJ5.1	B8NGT5.1	Q4WZ64.1	Q4WQV2.1	Q4WYK9.1
G1UB61.1	Q59LP6.1	Q59U11.1	Q5AMF7.1	B8NM64.1	Q4WAZ0.1	Q4WZP2.1	Q4WY33.1
Q5ABC6.1	Q5AP87.1	P83775.1	Q5ABW2.1	B8NV37.1	Q4WR16.1	Q4WVK2.1	Q4X1F8.1
A0A1D8PQB9.1	P22274.1	Q5APF2.1	Q5APJ9.1	B8N151.1	Q4WLB9.1	Q4WUA0.1	Q4WA45.1
P87020.1	Q5AC48.1	Q59VP2.1	Q5AM72.1	B8NEJ3.1	Q4WQS0.1	A4DA84.1	Q4WKD7.1
P0CY27.1	Q5AP59.1	Q5AEE1.1	Q5ACU3.1	B8N8M2.1	Q4WEP7.1	Q4WJX0.1	Q4WCH5.1
Q59XX2.1	Q59MV1.1	Q5AMR5.1	Q5A1V3.1	B8MYV0.1	E9R9Y3.1	Q4W3P8.1	Q4WXY3.1
Q59U10.1	Q5AL27.1	Q59SU5.1	Q59RF7.1	B8N7I7.1	P41748.1	Q4X1D7.1	Q4WPL7.1
Q59RW5.1	Q5AJD2.1	Q59VP1.1	Q5ACN3.1	B8NJG3.1	Q4WY93.1	Q4W9Z9.1	Q4X136.1
Q59MQ0.1	P0CU38.1	Q5ADQ0.1	Q5AHE8.1	B8N8R1.1	P87184.1	Q4WE62.1	Q4WZ44.1
Q5ABU7.1	Q59QC5.1	Q5AK59.1	Q5AHA4.1	B8NJH2.1	Q4WBS1.1	Q4WZL3.1	Q4WTC7.1
Q9Y7F0.1	Q5A5N6.1	Q59RH5.1	Q5AEG7.1	B8NQ51.1	Q70DX9.1	Q4WB37.1	Q4WMK2.1
Q5AC08.1	Q59Q79.1	Q5ACW8.1	Q59V01.1	B8NM63.1	Q4WG16.1	Q4W9Z4.1	Q4WNC9.1
P30575.1	Q5AH38.1	Q5AGM0.1	Q5AK97.1	B8NM73.1	Q96X30.1	Q4WDD0.1	Q4WY67.1
Q5AAG6.1	Q5AMN3.1	Q59VN2.1	Q5A1B2.1	B8NYX0.1	Q4WV19.1	Q4WKB9.1	Q4WU12.1
O74189.1	Q5A1Z5.1	O94069.1	Q5AJK6.1	B8N3P7.1	Q4WAZ6.1	Q4WU07.1	Q4WA61.1
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P0CY34.1	Q59L25.1	Q59XQ1.1	Q59MD0.1	B8MXJ7.1	Q4WTV7.1	Q4WX13.1	Q4WA60.1
Q5A1D3.1	Q5A922.1	O94048.1	Q5AG46.1	B8NJB0.1	Q4WV71.1	Q4WV71.1	Q4WX36.1
Q5AJU7.1	Q5AFG1.1	Q5ADX2.1	Q59VW6.1	B8NPS7.1	Q4WZ65.1	Q4X0C2.1	Q4WA62.1
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P83774.1	Q59X11.1	Q59XW9.1	Q5A6M2.1	B8N9H4.1	Q4WNE1.1	Q4X054.1	Q4WHW1.1
Q59Q46.1	Q5ABQ7.1	Q59WU8.1	Q5A5M7.1	B8NNK9.1	Q4WQZ6.1	Q4X1I3.1	Q4WYG7.1
Q59X23.1	Q59PZ3.1	Q5AAR0.1	Q5A6N8.1	B8NI03.1	Q4WWC6.1	Q4W9V1.1	Q4WJH4.1
P46614.1	O13332.1	Q5AQ62.1	Q9UVJ4.1	B8NM76.1	Q6Q487.1	Q4WDF1.1	Q4WJM6.1
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P82610.1	A0A1D8PPG4.1	Q5A847.1	Q59RA0.1	B8NJG9.1	Q4WM08.1	Q4WTH0.1	Q4WMU9.1
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Q59WG7.1	P53698.1	Q59Y41.1	Q5ALX5.1	B8MY73.1	Q4WVK7.1	Q4WVW6.1	Q4WQI6.1
Q5AFN8.1	Q5AJX2.1	Q59S52.1	Q5A748.1	B8N6W5.1	P78746.1	Q4WP83.1	Q4WCJ7.1
Q59TP1.1	Q5AP55.1	Q59U73.1	Q5ALU2.1	B8N3L3.1	Q4WPF8.1	Q4WAY7.1	Q4WTT8.1
Q5AF39.1	Q59PG6.1	Q9Y872.1	Q5A2B9.1	B8NPS8.1	Q4WX43.1	Q4WX89.1	Q4WWR2.1
Q5AP97.1	Q59NP1.1	Q5AGA9.1	Q5ALX3.1	B8NTI4.1	Q4WQL4.1	Q4WYT0.1	Q4WWL0.1
Q5A5U9.1	Q59PD3.1	Q59VL7.1	Q5A1M3.1	B8MYS7.1	Q4WBE1.1	Q4WNT9.1	Q4WZT9.1
Q5AF41.1	Q5ACW2.1	Q59KJ7.1	Q5A4H4.1	B8NM70.1	Q4WQT2.1	Q4WVS4.1	Q4X0I7.1
O13318.1	Q5ANB2.1	Q5AP90.1	Q5AA26.1	B8MYS8.1	Q4WBT5.1	A4D9J5.1	Q4WU00.1
Q5AA09.1	Q5AJD0.1	Q5AD72.1	Q5ANL6.1	B8N6M6.1	Q4WQZ2.1	Q4W9B7.1	Q4WRW0.1
Q5A762.1	Q5A4P9.1	Q59S59.1	P87218.1	B8NCU7.1	Q4WD47.1	Q4WNC6.1	Q4W9V0.1
P46587.1	P78599.1	Q5APM7.1	Q59KF3.1	B8N5T6.1	Q4WCZ8.1	Q4WJW8.1	Q4WYJ7.1
Q5A287.1	Q5APC8.1	Q5A2Z1.1	Q59N29.1	B8MVS3.1	Q4WB01.1	Q4WH96.1	Q4WHY5.1
Q5949.1	Q59LU0.1	Q59TD3.1	Q5AOL7.1	B8NCM8.1	Q4WBK6.1	Q4X0I5.1	Q4WEP0.1
Q5ADM9.1	Q5APT8.1	P84149.1	Q59UG4.1	B8NW36.1	Q4WRQ7.1	Q4WMS9.1	Q4WXD3.1
Q5AH02.1	Q59PR3.1	Q5AI97.1	Q5AHK2.1	B8NJG7.1	Q4WTQ6.1	Q4WAH4.1	Q4WJ02.1
Q5A4X5.1	Q5A2W2.1	Q5A2A2.1	Q5ADP6.1	B8N7Z6.1	Q4WJ21.1	Q4WII3.1	Q4WTP6.1
Q5A4E3.1	Q5A4E2.1	Q5A044.1	Q5AK62.1	B8NGU1.1	Q4WPO8.1	Q4WJA1.1	Q4WN54.1
Q5A761.1	Q5A309.1	Q59P03.1	Q59YF0.1	B8NC10.1	Q4WR62.1	Q4W9R7.1	Q4WCW2.1
Q9UW23.1	A0A1D8PL26.1	Q59TU0.1	Q5AAJ7.1	B8N4P0.1	Q4WD56.1	Q4WPP2.1	Q4WPM6.1
P53704.1	P0CU37.1	Q5APK7.1	Q5A8H7.1	B8NPN0.1	Q4WIN6.1	Q4WNC6.1	Q4WNN3.1
Q59VR1.1	Q5AF95.1	Q59ST1.1	Q59U81.1	B8NQ08.1	Q4U3E8.1	Q4WNI0.1	Q4WSI0.1
G1UB67.1	Q59MW2.1	Q5A7N3.1	Q5APB6.1	B8N3N5.1	Q4X195.1	Q4WDG1.1	Q4WNY4.1
P52496.1	Q59S50.1	Q5ANP2.1	Q59WD5.1	Q00049.1	P0C955.1	Q4X0Z7.1	Q4WVF4.1
Q9HEW1.1	Q5AD78.1	Q59933.1	Q5ABA2.1	B8NDP1.1	Q4WRH9.1	Q4WMS3.1	Q4WP02.1
Q5AGB6.1	Q5AMM4.1	Q3MPQ4.1	Q5A861.1	B8NEM4.1	Q4WVD1.1	Q4WNA2.1	Q4WWH6.1
Q5A1W9.1	Q5AAW3.1	Q59MP1.1	Q5AH87.1	Q9P8Z9.1	Q4WID6.1	Q4WJH6.1	Q4WVE5.1
P30418.1	Q59MG1.1	Q59MB6.1	P33181.1	B8MZJ8.1	Q4WFX9.1	Q4WYS1.1	Q4WHP3.1
Q59SN6.1	Q5ACK7.1	Q5A216.1	Q59Q43.1	B8NX10.1	Q4WRE4.1	Q4WJ01.1	Q4WRE2.1
Q5A343.1	Q5A218.1	Q9UVL1.1	Q5A860.1	B8NV05.1	Q4WC60.1	Q4WGL2.1	Q4WYX0.1
Q5ABZ2.1	Q59SJ9.1	Q59YS7.1	Q59ZW9.1	B8NEI6.1	Q4WR18.1	Q4WPA9.1	Q4WRB8.1
Q59MJ1.1	Q5AD49.1	Q5AGA0.1	A0A1D8PI78.1	B8MZI5.1	Q4WQY6.1	Q4WPE6.1	Q4WI88.1
Q5AJ71.1	Q59NX9.1	Q5A687.1	Q59R24.1	B8NSJ0.1	Q4WYK4.1	Q4WWW9.1	Q4WQL0.1
Q74201.1	Q5A119.1	Q59R28.1	Q5AHJ5.1	B8NDR8.1	Q4WI96.1	Q4WKB5.1	Q4WDZ0.1
Q5AK54.1	Q59K07.1	Q5AJ56.1	P0C0X3.1	B8NDQ2.1	Q4WVH4.1	Q4WA38.1	Q4WA70.1
O93852.1	Q5AKA5.1	Q5AD59.1	Q59KL6.1	B8N9M0.1	A4D9R2.1	Q4WHL1.1	Q4WQ82.1
Q5AIR7.1	Q59QC2.1	Q5AG73.1	P43072.1	B8NLL6.1	P0C956.1	Q4X1X0.1	Q4WMX7.1
Q5A8K2.1	Q5AL45.1	Q5AND1.1	Q5AF54.1	B8N9X2.1	Q4WR22.1	Q4WRX2.1	Q4X0V2.1
Q8TGB2.1	P0CY19.1	Q59NG5.1	Q59W44.1	B8NM08.1	Q4WQY8.1	Q4WDH9.1	Q4WI16.1
Q5A477.1	Q5AGC4.1	Q59N20.1	P48990.1	B8NSD4.1	Q4WJJ3.1	Q4WVG1.1	Q4WXA1.1
Q5AP95.1	Q5ALP1.1	Q59WJ5.1	Q59U67.1	B8N122.1	Q4X265.1	Q4WDE0.1	Q4WCV5.1
Q5AF03.1	Q5AK42.1	Q5AA50.1	Q5ANB7.1	B8NCF0.1	Q9UVX3.1	Q4WCX4.1	Q4W9M7.1
Q5AMQ4.1	Q5APG7.1	Q5A319.1	Q5A3Y5.1	B8NKS1.1	Q4WR19.1	Q4X122.1	Q4WQY9.1
Q5ANI6.1	Q59Y20.1	Q5AD27.1	Q59SI2.1	B8N3R8.1	Q4WTF3.1	Q4WZF1.1	Q4WX30.1
P78595.1	Q5ALL3.1	Q5AHI7.1	Q5APA2.1	B8NG55.1	Q4WLY1.1	Q4WMU1.1	Q4WUT7.1
Q874I4.1	Q5AAT0.1	Q5ANE3.1	P12461.1	B8N0Q7.1	Q4WMU3.1	Q4WGB7.1	Q4WQI2.1
Q9UWF6.1	Q59QD6.1	Q59S06.1	Q59TN1.1	B8N513.1	Q4WQG5.1	A4DA73.1	Q4X022.1
Q9UW12.1	Q5AML1.1	P87185.1	Q5A416.1	B8N4F5.1	Q4WPE9.1	Q4WD81.1	Q4WQZ0.1

Q5AAL9.1	Q5ACM9.1	Q5AM50.1	Q43133.1	B8NT06.1	Q4WAZ4.1	Q4WHG0.1	Q4WE58.1
Q5AD56.1	Q59Z14.1	Q9B8C8.1	Q59MI8.1	B8NH2.1	Q4WLN7.1	Q4WAJ6.1	Q4WJR4.1
Q5A7S7.1	Q5AAG1.1	Q9B8C9.1	Q5A302.1	B8MWR8.1	Q4WRB0.1	Q4WCL1.1	Q4WQZ1.1
P28870.1	Q59YL9.1	Q9B8D2.1	Q5AH60.1	B8N4G0.1	Q4WC55.1	Q9HEQ8.1	Q4WQY7.1
Q59NX5.1	Q59PL9.1	Q9B8D1.1	Q5A692.1	B8N9M5.1	Q4WMV5.1	Q4WEN1.1	Q4WQY5.1
Q5ABG1.1	Q59QL0.1	Q59M69.1	Q59Q39.1	Q00278.1	Q4WAZ2.1	Q4WI37.1	Q4WXT2.1
Q5AP52.1	Q5A1U8.1	Q59VX9.1	Q59NW5.1	B8NPX1.1	Q92197.1	Q4WZS1.1	Q8J130.1
P0CY31.1	Q74198.1	Q59YD8.1	Q5A6Q4.1	B8NYW8.1	Q4WSE8.1	Q4WDA4.1	Q4WJX5.1
P13649.1	Q5A013.1	Q59QH0.1	P43075.1	B8N219.1	Q4WX94.1	Q4WLS7.1	Q4X1I8.1
Q5AG77.1	P87163.1	Q5A8A2.1	Q59Q36.1	B8NQK0.1	Q4WLD0.1	Q4WWM6.1	Q4WVW4.1
Q9UW13.1	Q5AI86.1	Q9B8D7.1	Q92410.1	Q12732.1	Q4WUK5.1	Q4WP81.1	Q4WTH1.1
P0CU34.1	Q5AM80.1	Q9UW25.1	Q5A1M4.1	Q9HEY7.1	Q8TGG5.1	Q6MYT0.1	Q4WLI9.1
P40954.1	Q5A6Q7.1	Q59XY9.1	Q5ANC8.1	Q6UEG8.1	Q4WTK9.1	Q4WTL0.1	Q4WQJ5.1
Q04802.1	Q5AGV4.1	Q5A2T0.1	Q5A4K7.1	Q42716.1	Q4WVU5.1	Q4WXV2.1	Q4WQJ2.1
P0CY35.1	Q5AJ82.1	Q5AGW8.1	Q5ADL8.1	Q9UW95.1	Q4WLM7.1	Q4X0Z3.1	Q4WK56.1
Q5AAU5.1	Q5AIA1.1	Q5ADS3.1	Q59RQ2.1	Q9Y8D9.1	Q4W9P4.1	Q4WN25.1	Q4WJS2.1
Q59VQ8.1	Q5A9Z6.1	Q5ACR4.1	Q5APC0.1	A2SZW8.1	Q4WIT0.1	Q4WN21.1	Q4WJT9.1
Q59VF4.1	Q5AGC1.1	P0CU36.1	Q5A931.1	Q2U2U3.1	Q4WQB9.1	Q4X1N0.1	Q4WUV8.1
Q5A0X8.1	Q59ZV5.1	Q5A2Y7.1	Q59VW7.1	Q00258.1	Q4WKG6.1	Q4WQV2.1	Q4WX68.1
O13426.1	Q59VP7.1	Q5A368.1	Q5AKU5.1	Q12437.1	Q4WMR0.1	Q4WZP2.1	Q4WHN8.1
Q5A0M4.1	Q5A7P3.1	Q9B8D6.1	Q59MN0.1	E9QYP0.1	Q4WYE5.1	Q4WVK2.1	Q4WJU8.1
Q59PF9.1	Q5A6K8.1	Q9B8D0.1	Q59WH7.1	Q4WS76.1	Q4WZ01.1	Q4WUA0.1	Q4WBT4.1
Q5AFP3.1	Q5AD13.1	Q5A2K0.1	Q96WL3.1	Q4WMJ7.1	Q4W930.1	A4DA84.1	Q4WZV6.1
Q5AEK8.1	Q04782.1	Q5A1Q5.1	Q59ZX6.1	P28296.1	Q4WBR0.1	Q4WJX0.1	Q4WUV9.1
Q5AFK0.1	Q5A0J9.1	Q5AEM5.1	Q59MU1.1	E9RAH5.1	Q4WHD1.1	Q4W38.1	Q4WL2.1
Q5APD4.1	Q59ZZ6.1	Q5AK25.1	Q5A0J0.1	Q4WW81.1	Q4WTB3.1	Q4X1D7.1	Q4WFS2.1
Q5ADQ9.1	Q5AH25.1	Q5AK10.1	Q59WK2.1	Q50EL0.1	Q4WRV9.1	Q4W9Z9.1	Q4WBM1.1
P83779.1	Q59XM1.1	Q5AI15.1	P43073.1	Q4WY82.1	Q4X267.1	Q4WE62.1	Q4WAU7.1
Q5AAH2.1	Q59NN8.1	Q5AEM8.1	P87220.1	Q4WSF6.1	Q4WVZ3.1	Q4WZL3.1	Q4WZS3.1
O74254.1	Q5AP65.1	Q5A4J4.1	Q5ABD9.1	E9RCK4.1	Q4WR24.1	Q4WB37.1	Q4WPU9.1
Q5AL49.1	Q5AFF7.1	Q59YK4.1	P83781.1	Q4WZA8.1	Q4WPM8.1	Q4W9Z4.1	Q4WVZ0.1
P53697.1	Q59VR3.1	Q59WV0.1	Q5ANB1.1	Q4WAW7.1	Q4WE86.1	Q4WDD0.1	Q4WCX9.1
Q5ACL7.1	Q5AFH3.1	Q5AHB1.1	Q5A0E2.1	Q92405.1	A4DA70.1	Q4WKB9.1	Q4WJ38.1
Q5AEM6.1	P83780.1	Q5APK0.1	Q5AMG5.1	Q4WRY5.1	Q4WW45.1	Q4WU07.1	Q4WRC2.1
Q8TG40.1	Q5A4G9.1	Q59PW0.1	Q5A6T8.1	Q7Z7W6.1	Q4WVG2.1	Q4WBL6.1	Q4WWW5.1
Q59X38.1	Q59NQ9.1	O74711.1	Q59WG5.1	Q4WZ67.1	Q4WQG9.1	Q4WX13.1	Q4WC84.1
Q59VQ3.1	A0A1D8PNP3.1	Q5ADN9.1	Q5AI80.1	Q4WZB3.1	Q4WQN1.1	Q4WV71.1	Q4WTW3.1
Q5A7Q2.1	Q5A9Z1.1	Q5ACP5.1	Q5AB49.1	Q4WLN1.1	Q4WCF1.1	Q4X0C2.1	Q4WV6.1
Q5AJV5.1	A0A1D8PK89.1	Q5A1E1.1	Q59R32.1	Q4WR82.1	Q4WZC3.1	Q4WU4.1	Q4WKD9.1
Q5A3Z6.1	Q59WB3.1	Q59L86.1	Q5A061.1	O14434.1	Q4WYX7.1	Q4WGS4.1	Q4WP10.1
Q5A201.1	Q59ZC8.1	Q5AD23.1	Q59P50.1	Q4WMK0.1	Q4X0A5.1	Q4WP13.1	C5JZM2.1
O93827.1	Q5A1L6.1	Q5A5U6.1	Q59WC6.1	Q4WPX2.1	Q4WUD3.1	Q4WHG5.1	P0DJ06.1
Q5AAI8.1	A0A1D8PN14.1	Q5ADQ7.1	Q5AI48.1	O43099.1	Q4WS49.1	Q4WPF7.1	P46598.1
Q5A2J7.1	Q5A8X7.1	Q59WJ4.1	Q59ZU1.1	Q4WJ81.1	Q4WCX7.1	Q4WH83.1	P87020.1
P22011.1	Q59X39.1	Q5AGV7.1	Q5AG56.1	P67875.1	Q4WXX5.1	Q4WXX1.1	P38110.1
Q9HGT6.1	Q5ACW6.1	Q59NR8.1	Q59T36.1	Q4WZB4.1	Q4WNB5.1	Q8NJM2.1	C1GK29.1
Q9UW26.1	P0CB54.1	Q5A5K7.1	Q9P840.1	E9QUT3.1	O42799.1	Q4WWD3.1	
Q59LX5.1	A0A1D8PN88.1	Q5A210.1	Q5AHB8.1	Q4WAZ9.1	Q4WHA3.1	Q4WPU8.1	
Q59PT0.1	A0A1D8PMB1.1	Q59N10.1	Q5AKU3.1	Q4WZ70.1	Q4W9M3.1	Q4WN99.1	
Q3MNT0.1	Q5ABR2.1	Q5A1B3.1	Q59ZW4.1	E9RBR0.1	Q4WVH5.1	P0C959.1	

Model Population

The method may comprise the step of selecting or defining a model human population. A suitable model population is one that is relevant to the human population or a subpopulation in which it is intended to use the peptides designed or prepared by the method to induce a T cell response. This may be referred to as the target population or the intent-to-treat population. The peptides or the encoded peptides designed or produced by the method are for use in a method of

inducing a T cell response against the target polypeptide in a subject of the intent-to-treat population. A relevant population is one that is representative or similar to the intent-to-treat population. In some cases the model population is representative for the whole human race. In other cases the model population may be a disease- and/or subject-matched population (subpopulation), for example a subpopulation matched to the intent-to-treat population by ethnicity, geographical location, gender, age, disease or cancer, disease or cancer type or stage, genotype, and/or expression of one or more biomarkers (for example, women having the BRCA mutation for a breast cancer vaccine), and/or partially by HLA genotype (for example subjects have one or more particular HLA alleles). In some cases the intent-to-treat population may be subjects having cancer or a type of cancer, such as any described herein. For example, the model population may have HLA class I and/or class II genomes that are representative of those found in the world population, or a subject and/or disease matched subpopulation. In some cases the model population is representative for at least 70%, or 75% or 80% or 84% or 85% or 86% or 90% or 95% of the intent-to-treat population by HLA diversity and/or HLA frequency. In some cases the model population may comprise at least 100, or 200 or 300 or 400 or 500 or 1000 or 5000 or 10000 or 15000 subjects.

Each subject in the model population is minimally defined by their HLA class I or class II genotype, e.g. complete 4-digit HLA class I genotype. Data concerning the HLA genotype of the model population may be stored or recorded in or retrieved from a database or be an *in silico* model human population.

HLA-binding criteria

The method comprises the step of identifying, for each subject of the model population, amino acid sequences within the target polypeptide that meet certain HLA-binding criteria, such as comprising a T cell epitope that can bind to multiple HLA class I and/or class II HLA molecules as described herein. For example, amino acid sequences that comprise a T cell epitope that is capable of binding to at least three HLA class I alleles of a subject and/or a T cell epitope that is capable of binding to at least three or four HLA class II alleles of the subject are optimal for inducing CD4+ T cell and/or CD8+ T cell responses. In some cases the HLA class I-binding T cell epitope and the HLA class II binding T cell epitope may overlap. In some cases the HLA class I binding T cell epitope may be fully embedded in the sequence of the HLA class II binding T cell epitope. In some cases the multiple HLA class I and class II binding epitopes

are within a minimum distance on one another, such as both within a 50, or 45, or 40, or 35, or 30, or 25 amino acid fragment of the target polypeptide.

The method comprises selecting a polypeptide fragment window length. The polypeptide fragment window length defines the fragment length across the target polypeptide used to
5 identify hotspots where the maximum number of subjects in the model population have an amino acid sequence that meets the HLA-binding criteria. The polypeptide fragment window length may be from 9 to 50 amino acids long.

Peptides that comprise a hotspot sequence as identified by the method described herein may be particularly useful for inducing T cell responses in a high proportion of the subjects of
10 the intent-to-treat population population. Peptides comprising such sequences may accordingly be designed or prepared according to the present disclosure and used in methods of treatment. The peptide may consist of the amino acid sequence of the hotspot fragment of the target polypeptide or may comprise the sequence of a longer fragment of the target polypeptide of which the hotspot sequence is a part. In some cases the target polypeptide fragment may be
15 flanked at the N and/or C terminus of the peptide by additional amino acids that are not part of the consecutive sequence of the target polypeptide antigen. In some cases the fragment may be flanked by up to 30 or 25 or 20 or 15 or 10, or 9 or 8 or 7 or 6 or 5 or 4 or 3 or 2 or 1 additional amino acid at the N and/or C terminus.

In some cases the method of the disclosure may be repeated in an iterative process to
20 identify further fragments of the target polypeptide antigen that meet the HLA-binding criteria in subjects of the model population. In some case the method may be repeated in up to 50, 45, 40, 35, 30, 25, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 cycles of the method described herein.

In some cases, the object of the iterative process may be to identify the minimum number
25 of peptides or hotspots that will induce the desired T cell responses (cytotoxic T cell response and/or helper T cell response) in the maximum number of subjects in the model or intent-to-treat population. In this case it is desirable to remove from the model population those subjects for whom the hotspots or peptides selected in any previous rounds already meet the desired criteria before repeating the method in a further cycle. The iterative method may in some cases be
30 continued until either no more sequences meeting the HLA-binding criteria can be identified or a pre-defined number of cycles, number of hotspots, or pre-defined minimal coverage of the model or intent-to-treat population is reached.

In some cases further predefined criteria may be applied to the hotspot selection process. If a particular hotspot sequence does not meet such additional criteria then the hotspot may be disregarded and another amino acid sequence of the selected window length and meeting the HLA-binding criteria for the next highest number of subjects in the model population may be selected, until a sequence is reached that meets the additional predefined criteria. In an iterative process, the subjects of the model population for which the selected sequence meets all of the HLA-binding criteria and other criteria should be removed from the model population before proceeding to the next cycle.

In one example, the additional predefined criteria may relate to features of the peptide sequence that influence manufacturing feasibility. For example, in some cases a peptide/hotspot sequence may be rejected in it comprises a particular amino acid residue, such as a cysteine, or a particular amino acid motif, or if the peptide/hotspot sequence has less than a minimum level of hydrophilicity.

The method of the disclosure may be used to provide peptides that are useful for inducing T cell responses against a given polypeptide, or to provide an ideal set of peptides from which to select a peptide for inducing T cell responses against one or more given polypeptides in a specific subject of a given human population.

In other cases the method may be repeated for a set of polypeptides, for example a set of polypeptides that are associated with the same disease or condition, such as polypeptides that are expressed by the same pathogen or type of pathogen, or associated with the same cancer or type of cancer, such as those disclosed herein. The method may then provide an ideal set of peptides from which to select peptides to treat the disease or condition in a specific subject of a given human population.

Panels of peptides

In some cases the disclosure provides a panel of peptides or a panel of polynucleic acids or vectors encoding a panel of peptides. The panel may be suitable for use in a method of inducing a T cell response against one or more target polypeptides in a subject of an intent-to-treat human population. The intent-to-treat human population may be a population as described herein and may be defined by the HLA genotype distribution in the subjects of the intent-to-treat population as described herein.

In some cases the panel is a panel designed and/or prepared according to the methods described herein. In other cases the panel comprises or encodes two or more peptides designed and/or prepared according to the method described herein.

In other cases the panel comprises or encodes two or more peptides, wherein each peptide
 5 comprises a fragment of the one or more target polypeptide, wherein the fragment comprises, in a high proportion of the intent-to-treat population, a sequence that meets any of the HLA-binding criteria described herein. In some cases a “high” percentage may be at least or more than 1%, 2%, 5%, 10%, 12%, 15%, 16%, 17%, 18%, 19%, 20%, 21%, 22%, 23%, 24%, 25%, 26%, 27%, 28%, 29%, 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%,
 10 44%, 45%, 46%, 47%, 48%, 49% or 50% of an intent-to-treat population as described herein.

The peptides of the panel may have any of the characteristics of a peptide described herein. For example, each peptide may be 9-50 amino acids in length; may comprise a fragment of the one or more target polypeptides that is 9-50 amino acids in length and meets the HLA-binding requirements; the target polypeptide fragment may be flanked at the N and/or C terminus
 15 of the peptide by additional amino acids that are not part of the consecutive sequence of the target polypeptide antigen; and/or the target polypeptide(s) may be any described herein, for example any of those listed in Tables 2 to 5.

In some cases the target polypeptide of each peptide of the panel may be the same; i.e. each peptide comprises a different fragment of the target polypeptide, each of which meets the
 20 HLA-binding requirements in a high proportion of the intent-to-treat population. The panel then represents a selection of peptides that may be used to induce T cell responses against the same target polypeptide in different HLA-matched subjects. In some cases the fragments of the target polypeptide in the peptides of the panel do not overlap or do not comprise any common T cell epitopes or PEPs.

In other cases the panel may comprise peptides that are designed to induce T cell
 25 responses against different target polypeptides, that is the selected fragments of the target polypeptides comprised in the peptides are from different target polypeptides. In some cases the panel comprises such fragments from at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39 or 40 different
 30 target polypeptides.

The different target polypeptides may be any different polypeptides that it is useful to target or that can be selectively targeted with different PEPs as described herein. In some cases different target polypeptide antigens are non-homologues or non-paralogues or have less than

95%, or 90%, or 85% or 80% or 75% or 70% or 60% or 50% sequence identity across the full length of each polypeptide.

In some cases the different target polypeptides targeted by the peptides of a panel are each expressed by or associated with the same disease, condition, pathogen or cancer, such as
5 any described herein. Such a panel of peptides may be ideal for use in treatment of the disease or condition in a subject in need thereof, particularly if the peptides are HLA/PEPI matched to the specific subject as described herein.

In some cases one or more or each of the target polypeptides is present in a sample taken from a human subject. This indicates that the polypeptide(s) are expressed in the subject, for
10 example a cancer- or tumor-associated antigen, TSA or CTA expressed by cancer cells of the subject.

In some cases 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more or each of the target polypeptide antigens is a TSA and/or a CTA.

15 *Selection of polypeptides and patients*

The peptides described herein may be used to induce T cell responses or provide vaccination or immunotherapy in a subject in need therefore. More than one peptide will typically be selected for treatment of a subject. Each peptide may be selected for treatment of a subject based on (i) the disease or condition to be treated in the subject; and/or (ii) the HLA
20 genotype of the subject.

Each peptide selected for treatment of a subject may comprise a fragment as described herein of a target polypeptide antigen that is associated with the disease or condition to be treated in the subject, or expressed by target cells of the treatment, such as cancer cells. The disease or condition and the target polypeptide antigens may be any described herein. Typically each
25 peptide selected for treatment of the subject will comprise a fragment as described herein of a different target polypeptide antigen. The target polypeptide antigens may be selected because they are known to be expressed by target cells in the subject. For example the target polypeptide antigens may have been detected in a sample obtained from the subject, such as a tumor biopsy. In other cases, the target polypeptide antigens may be selected based on their expression rate in
30 the cells that are targeted by the treatment, for example the expression rate of a particular TAA in cancer or a particular type of cancer, such as any described herein. Typically the peptides selected for the treatment of the subject are those that comprise a fragment as described herein of the polypeptide antigens associated with the condition at the highest expression rates for the

condition to be treated. Further the fragments typically have been predicted to induce a T cell response in the specific subject, as further described herein.

Polypeptide antigens, and particularly short peptides derived from polypeptide antigens, that are commonly used in vaccination and immunotherapy, induce immune responses in only a fraction of human subjects. The peptides of the present disclosure are specifically selected to induce immune responses in a high proportion of the general population, or a high proportion of a given intent-to-treat population. However, but they may not be effective in all individuals or all subjects of the intent-to-treat population due to HLA genotype heterogeneity.

In some cases the present disclosure provides a method of predicting that a specific human subject will have a T cell response (cytotoxic and/or helper) to administration of any of the peptides, panels of peptides or pharmaceutical compositions or kits described herein. As provided herein T cell epitope presentation by multiple HLAs of an individual is generally needed to trigger a T cell response. The best predictor of a cytotoxic (CD8+) T cell response to a given polypeptide is the presence of at least one T cell epitope that is presented by at least three HLA class I alleles of a subject (≥ 1 PEPI3+). Similarly the presence of at least one T cell epitope that is presented by at least three or four HLA class II alleles of a subject may be predictive of a helper (CD4+) T cell response. If such T cell epitopes correspond to a fragment of a target polypeptide antigen, such as any target polypeptide antigen described herein, then the subject is predicted to mount a T cell response that targets cells in the subject that express the target polypeptide, if present. Accordingly in some cases the method may be for predicting a T cell response in a subject to a target polypeptide antigen, such as any described herein.

The inventors have further discovered that the presence in a vaccine or immunotherapy composition of at least two T cell epitopes that (i) correspond to fragments of one or more target polypeptide antigens, and (ii) can bind to at least three HLA class I alleles of an individual is predictive for a clinical response. For example, if an individual has a total of ≥ 2 PEPI3+ within the active ingredient peptide(s) of a vaccine or immunotherapy composition, and these PEPI3+s are derived from polypeptide antigens that are in fact expressed by target cells in the individual (for example, target tumor cells of the individual express the target tumor-associated antigens), then the individual is a likely clinical responder (i.e. a clinically relevant immune responder).

A “clinical response” or “clinical benefit” as used herein may be the prevention or a delay in the onset of a disease or condition, the amelioration of one or more symptoms, the induction or prolonging of remission, or the delay of a relapse or recurrence or deterioration, or any other improvement or stabilisation in the disease status of a subject. Where appropriate, a

“clinical response” may correlate to “disease control” or an “objective response” as defined by the Response Evaluation Criteria In Solid Tumors (RECIST) guidelines.

Accordingly some aspects of the disclosure relate to a method of predicting that a specific human subject will have a clinical response to a method of treatment as described herein or to
5 administration of a pharmaceutical composition or the peptides, nucleic acids or vectors of a pharmaceutical kit described herein.

In some cases the method comprises determining that the active ingredient peptide(s) for treatment of the subject comprise two or more different amino acid sequences each of which is a) a fragment of a target polypeptide antigen expressed by target cells of the subject (for example,
10 polypeptide antigens that have been detected in a biopsy); and b) a T cell epitope capable of binding to at least three HLA class I of the subject.

In some cases the likelihood that a subject will have a clinical response to a peptide vaccine or immunotherapy composition, such as those described herein, can be determined without knowing whether the target antigens are expressed in target cells, such as cancer cells of
15 the subject and/or without determining the HLA class I genotype of the subject. Known antigen expression frequencies in the disease (e.g. MAGE-A3 in a tumor type like gastric cancer) and/or known frequencies for HLA class I and class II genotype of subjects in the target population (e.g. ethnic population, general population, diseased population) may be used instead.

The likelihood that a subject will respond to treatment is increased by (i) the presence of
20 more multiple HLA-binding PEPs in the active ingredient polypeptides; (ii) the presence of PEPs in more target polypeptide antigens; and (iii) expression of the target polypeptide antigens in the subject or in diseased cells of the subject. The probability that target cells in the subject (over-)express a specific or any combination of target polypeptide antigens may be determined using population expression frequency data (expression rates), e.g. probability of expression of
25 an antigen in gastric cancer. The population expression frequency data may relate to a subject- and/or disease-matched population or the intent-to-treat population. For example, the frequency or probability of expression of a particular cancer-associated antigen in a particular cancer or subject having a particular cancer, for example breast cancer, can be determined by detecting the antigen in tumor, e.g. breast cancer tumor samples. Such expression frequencies may be
30 determined from published figures and scientific publications. In some cases a method of the disclosure may comprise a step of determining the expression frequency of a relevant target polypeptide antigen in a relevant population.

Disclosed is a range of pharmacodynamic biomarkers to predict the activity/effect of vaccines in individual human subjects as well as in populations of human subjects. These biomarkers expedite more effective vaccine development and also decrease the development cost and may be used to assess and compare different compositions. Exemplary biomarkers are as follows.

- **AG95 – potency of a vaccine:** The number of antigens in a cancer vaccine that a specific tumor type expresses with 95% probability. AG95 is an indicator of the vaccine's potency, and is independent of the immunogenicity of the vaccine antigens. AG95 is calculated from the tumor antigen expression rate data. Such data may be obtained from experiments published in peer reviewed scientific journals. Technically, AG95 is determined from the binomial distribution of antigens in the vaccine, and takes into account all possible variations and expression rates.
- **PEPI3+ count – immunogenicity of a vaccine in a subject:** Vaccine-derived PEPI3+ are personal epitopes that bind to at least 3 HLAs of a subject and induce T cell responses. PEPI3+ can be determined using the PEPI3+ Test in subjects who's complete 4-digit HLA genotype is known.
- **AP count – antigenicity of a vaccine in a subject:** Number of vaccine antigens with PEPI3+. Vaccines contain sequences from target polypeptide antigens expressed by diseased cells. AP count is the number of antigens in the vaccine that contain PEPI3+, and the AP count represents the number of antigens in the vaccine that can induce T cell responses in a subject. AP count characterizes the vaccine-antigen specific T cell responses of the subject since it depends only on the HLA genotype of the subject and is independent of the subject's disease, age, and medication. The correct value is between 0 (no PEPI presented by the antigen) and maximum number of antigens (all antigens present PEPIs).
- **AP50 – antigenicity of a vaccine in a population:** The mean number of vaccine antigens with a PEPI in a population. The AP50 is suitable for the characterization of vaccine-antigen specific T cell responses in a given population since it depends on the HLA genotype of subjects in a population.
- **AGP count – effectiveness of a vaccine in a subject:** Number of vaccine antigens expressed in the tumor with PEPI. The AGP count indicates the number of tumor antigens that vaccine recognizes and induces a T cell response against (hit the target). The AGP count depends on the vaccine-antigen expression rate in the subject's tumor and the HLA genotype

of the subject. The correct value is between 0 (no PEPI presented by expressed antigen) and maximum number of antigens (all antigens are expressed and present a PEPI).

- 5 • **AGP50 – effectiveness of a cancer vaccine in a population:** The mean number of vaccine antigens expressed in the indicated tumor with PEPI (i.e., AGP) in a population. The AGP50 indicates the mean number of tumor antigens that the T cell responses induced by the vaccine can recognize. AGP50 is dependent on the expression rate of the antigens in the indicated tumor type and the immunogenicity of the antigens in the target population. AGP50 can estimate a vaccine's effectiveness in different populations and can be used to compare different vaccines in the same population. The computation of AGP50 is similar to that used

10 for AG50, except the expression is weighted by the occurrence of the PEPI3+ in the subject on the expressed vaccine antigens. In a theoretical population, where each subject has a PEPI from each vaccine antigen, the AGP50 will be equal to AG50. In another theoretical population, where no subject has a PEPI from any vaccine antigen, the AGP50 will be 0. In general, the following statement is valid: $0 \leq \text{AGP50} \leq \text{AG50}$.
- 15 • **mAGP – a candidate biomarker for the selection of likely responders:** Likelihood that a cancer vaccine induces T cell responses against multiple antigens expressed in the indicated tumor. mAGP is calculated from the expression rates of vaccine-antigens in the tumor and the presence of vaccine derived PEPIs in the subject. Technically, based on the AGP distribution, the mAGP is the sum of probabilities of the multiple AGP (≥ 2 AGPs).

20 The results of a prediction as set out above may be used to inform a physician's decisions concerning treatment of the subject. Accordingly, in some cases the method of the disclosure predicts that a subject will have or is likely to have a T cell response and/or a clinical response to a treatment as described herein, and the method further comprises selecting the treatment for the human subject. In some cases a subject is selected for treatment if their likelihood of a response

25 targeted at a predefined number of target polypeptide antigens, optionally wherein the target polypeptide antigens are (predicted to be) expressed, is above a predetermined threshold. In some cases the number of target polypeptide antigens or epitopes is two. In some cases the number of target polypeptide antigens or epitopes is three, or four, or five, or six, or seven, or eight, or nine, or ten. The method may further comprise administering the treatment to the

30 human subject. Alternatively, the method may predict that the subject will not have an immune response and/or a clinical response and further comprise selecting a different treatment for the subject.

Pharmaceutical Compositions, Methods of Treatment and Modes of Administration

In some aspects the disclosure relates to a pharmaceutical composition or kit comprising one or more of the peptides, polynucleic acids or vectors described herein. Such pharmaceutical compositions or kits may be for use in a method of inducing an immune response, treating, 5 vaccinating or providing immunotherapy to a subject. The pharmaceutical composition or kit may be a vaccine or immunotherapy composition or kit. Such treatment may comprise administering the pharmaceutical composition or the peptides, polynucleic acids or vectors of the kit to the subject.

The pharmaceutical compositions or kits described herein may comprise, in addition to 10 one or more peptides, nucleic acids or vectors, a pharmaceutically acceptable excipient, carrier, diluent, buffer, stabiliser, preservative, adjuvant or other materials well known to those skilled in the art. Such materials are preferably non-toxic and preferably do not interfere with the pharmaceutical activity of the active ingredient(s). The pharmaceutical carrier or diluent may be, for example, water containing solutions. The precise nature of the carrier or other material may 15 depend on the route of administration, e.g. oral, intravenous, cutaneous or subcutaneous, nasal, intramuscular, intradermal, and intraperitoneal routes.

The pharmaceutical compositions of the disclosure may comprise one or more “pharmaceutically acceptable carriers”. These are typically large, slowly metabolized macromolecules such as proteins, saccharides, polylactic acids, polyglycolic acids, polymeric 20 amino acids, amino acid copolymers, sucrose (Paoletti et al., 2001, Vaccine, 19:2118), trehalose (WO 00/56365), lactose and lipid aggregates (such as oil droplets or liposomes). Such carriers are well known to those of ordinary skill in the art. The pharmaceutical compositions may also contain diluents, such as water, saline, glycerol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present. Sterile 25 pyrogen-free, phosphate buffered physiologic saline is a typical carrier (Gennaro, 2000, Remington: The Science and Practice of Pharmacy, 20th edition, ISBN:0683306472).

The pharmaceutical compositions of the disclosure may be lyophilized or in aqueous form, i.e. solutions or suspensions. Liquid formulations of this type allow the compositions to be administered direct from their packaged form, without the need for reconstitution in an aqueous 30 medium, and are thus ideal for injection. The pharmaceutical compositions may be presented in vials, or they may be presented in ready filled syringes. The syringes may be supplied with or without needles. A syringe will include a single dose, whereas a vial may include a single dose or multiple doses.

Liquid formulations of the disclosure are also suitable for reconstituting other medicaments from a lyophilized form. Where a pharmaceutical composition is to be used for such extemporaneous reconstitution, the disclosure provides a kit, which may comprise two vials, or may comprise one ready-filled syringe and one vial, with the contents of the syringe
5 being used to reconstitute the contents of the vial prior to injection.

The pharmaceutical compositions of the disclosure may include an antimicrobial, particularly when packaged in a multiple dose format. Antimicrobials may be used, such as 2-phenoxyethanol or parabens (methyl, ethyl, propyl parabens). Any preservative is preferably present at low levels. Preservative may be added exogenously and/or may be a component of the
10 bulk antigens which are mixed to form the composition (e.g. present as a preservative in pertussis antigens).

The pharmaceutical compositions of the disclosure may comprise detergent e.g. Tween (polysorbate), DMSO (dimethyl sulfoxide), DMF (dimethylformamide). Detergents are generally present at low levels, e.g. <0.01%, but may also be used at higher levels, e.g. 0.01 – 50%.

15 The pharmaceutical compositions of the disclosure may include sodium salts (e.g. sodium chloride) and free phosphate ions in solution (e.g. by the use of a phosphate buffer).

In certain embodiments, the pharmaceutical composition may be encapsulated in a suitable vehicle either to deliver the peptides into antigen presenting cells or to increase the stability. As will be appreciated by a skilled artisan, a variety of vehicles are suitable for
20 delivering a pharmaceutical composition of the disclosure. Non-limiting examples of suitable structured fluid delivery systems may include nanoparticles, liposomes, microemulsions, micelles, dendrimers and other phospholipid-containing systems. Methods of incorporating pharmaceutical compositions into delivery vehicles are known in the art.

In order to increase the immunogenicity of the composition, the pharmacological
25 compositions may comprise one or more adjuvants and/or cytokines.

Suitable adjuvants include an aluminum salt such as aluminum hydroxide or aluminum phosphate, but may also be a salt of calcium, iron or zinc, or may be an insoluble suspension of acylated tyrosine, or acylated sugars, or may be cationically or anionically derivatised saccharides, polyphosphazenes, biodegradable microspheres, monophosphoryl lipid A (MPL),
30 lipid A derivatives (e.g. of reduced toxicity), 3-O-deacylated MPL [3D-MPL], quil A, Saponin, QS21, Freund's Incomplete Adjuvant (Difco Laboratories, Detroit, Mich.), Merck Adjuvant 65 (Merck and Company, Inc., Rahway, N.J.), AS-2 (Smith-Kline Beecham, Philadelphia, Pa.), CpG oligonucleotides, bioadhesives and mucoadhesives, microparticles, liposomes,

polyoxyethylene ether formulations, polyoxyethylene ester formulations, muramyl peptides or imidazoquinolone compounds (e.g. imiquamod and its homologues). Human immunomodulators suitable for use as adjuvants in the disclosure include cytokines such as interleukins (e.g. IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc), macrophage colony stimulating factor (M-CSF), tumour necrosis factor (TNF), granulocyte, macrophage colony stimulating factor (GM-CSF) may also
 5 be used as adjuvants.

In some embodiments, the compositions comprise an adjuvant selected from the group consisting of Montanide ISA-51 (Seppic, Inc., Fairfield, N.J., United States of America), QS-21 (Aquila Biopharmaceuticals, Inc., Lexington, Mass., United States of America), GM-CSF,
 10 cyclophosphamide, bacillus Calmette-Guerin (BCG), corynebacterium parvum, levamisole, azimezone, isoprinosine, dinitrochlorobenzene (DNCB), keyhole limpet hemocyanins (KLH), Freund's adjuvant (complete and incomplete), mineral gels, aluminum hydroxide (Alum), lysolecithin, pluronic polyols, polyanions, oil emulsions, dinitrophenol, diphtheria toxin (DT).

By way of example, the cytokine may be selected from the group consisting of a
 15 transforming growth factor (TGF) such as but not limited to TGF- α and TGF- β ; insulin-like growth factor-I and/or insulin-like growth factor-II; erythropoietin (EPO); an osteoinductive factor; an interferon such as but not limited to interferon- α , - β , and - γ ; a colony stimulating factor (CSF) such as but not limited to macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF). In some embodiments, the cytokine is selected
 20 from the group consisting of nerve growth factors such as NGF- β ; platelet-growth factor; a transforming growth factor (TGF) such as but not limited to TGF- α and TGF- β ; insulin-like growth factor-I and insulin-like growth factor-II; erythropoietin (EPO); an osteoinductive factor; an interferon (IFN) such as but not limited to IFN- α , IFN- β , and IFN- γ ; a colony stimulating factor (CSF) such as macrophage-CSF (M-CSF); granulocyte-macrophage-CSF (GM-CSF); and
 25 granulocyte-CSF (G-CSF); an interleukin (IL) such as but not limited to IL-1, IL-1.alpha., IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12; IL-13, IL-14, IL-15, IL-16, IL-17, IL-18; LIF; kit-ligand or FLT-3; angiostatin; thrombospondin; endostatin; a tumor necrosis factor (TNF); and LT.

It is expected that an adjuvant or cytokine can be added in an amount of about 0.01 mg to
 30 about 10 mg per dose, preferably in an amount of about 0.2 mg to about 5 mg per dose. Alternatively, the adjuvant or cytokine may be at a concentration of about 0.01 to 50%, preferably at a concentration of about 2% to 30%.

In certain aspects, the pharmaceutical compositions of the disclosure are prepared by physically mixing the adjuvant and/or cytokine with the PEPIs under appropriate sterile conditions in accordance with known techniques to produce the final product.

Examples of suitable compositions of polypeptide fragments and methods of administration are provided in Esseku and Adeyeye (2011) and Van den Mooter G. (2006). Vaccine and immunotherapy composition preparation is generally described in Vaccine Design ("The subunit and adjuvant approach" (eds Powell M. F. & Newman M. J. (1995) Plenum Press New York). Encapsulation within liposomes, which is also envisaged, is described by Fullerton, US Patent 4,235,877.

In some embodiments, the compositions disclosed herein are prepared as a nucleic acid vaccine. In some embodiments, the nucleic acid vaccine is a DNA vaccine. In some embodiments, DNA vaccines, or gene vaccines, comprise a plasmid with a promoter and appropriate transcription and translation control elements and a nucleic acid sequence encoding one or more polypeptides of the disclosure. In some embodiments, the plasmids also include sequences to enhance, for example, expression levels, intracellular targeting, or proteasomal processing. In some embodiments, DNA vaccines comprise a viral vector containing a nucleic acid sequence encoding one or more polypeptides of the disclosure. In additional aspects, the compositions disclosed herein comprise one or more nucleic acids encoding peptides determined to have immunoreactivity with a biological sample. For example, in some embodiments, the compositions comprise one or more nucleotide sequences encoding 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more peptides comprising a fragment that is a T cell epitope capable of binding to at least three HLA class I molecules and/or at least three or four HLA class II molecules of a patient. In some embodiments, the peptides are derived from an antigen that is expressed in cancer. In some embodiments the DNA or gene vaccine also encodes immunomodulatory molecules to manipulate the resulting immune responses, such as enhancing the potency of the vaccine, stimulating the immune system or reducing immunosuppression. Strategies for enhancing the immunogenicity of DNA or gene vaccines include encoding of xenogeneic versions of antigens, fusion of antigens to molecules that activate T cells or trigger associative recognition, priming with DNA vectors followed by boosting with viral vector, and utilization of immunomodulatory molecules. In some embodiments, the DNA vaccine is introduced by a needle, a gene gun, an aerosol injector, with patches, via microneedles, by abrasion, among other forms. In some forms the DNA vaccine is incorporated into liposomes or other forms of nanobodies. In some embodiments, the DNA vaccine includes a delivery system

selected from the group consisting of a transfection agent; protamine; a protamine liposome; a polysaccharide particle; a cationic nanoemulsion; a cationic polymer; a cationic polymer liposome; a cationic nanoparticle; a cationic lipid and cholesterol nanoparticle; a cationic lipid, cholesterol, and PEG nanoparticle; a dendrimer nanoparticle. In some embodiments, the DNA vaccines is administered by inhalation or ingestion. In some embodiments, the DNA vaccine is introduced into the blood, the thymus, the pancreas, the skin, the muscle, a tumor, or other sites.

In some embodiments, the compositions disclosed herein are prepared as an RNA vaccine. In some embodiments, the RNA is non-replicating mRNA or virally derived, self-amplifying RNA. In some embodiments, the non-replicating mRNA encodes the peptides disclosed herein and contains 5' and 3' untranslated regions (UTRs). In some embodiments, the virally derived, self-amplifying RNA encodes not only the peptides disclosed herein but also the viral replication machinery that enables intracellular RNA amplification and abundant protein expression. In some embodiments, the RNA is directly introduced into the individual. In some embodiments, the RNA is chemically synthesized or transcribed *in vitro*. In some embodiments, the mRNA is produced from a linear DNA template using a T7, a T3, or an Sp6 phage RNA polymerase, and the resulting product contains an open reading frame that encodes the peptides disclosed herein, flanking UTRs, a 5' cap, and a poly(A) tail. In some embodiments, various versions of 5' caps are added during or after the transcription reaction using a vaccinia virus capping enzyme or by incorporating synthetic cap or anti-reverse cap analogues. In some embodiments, an optimal length of the poly(A) tail is added to mRNA either directly from the encoding DNA template or by using poly(A) polymerase. The RNA may encode one or more peptides comprising a fragment that is a T cell epitope capable of binding to at least three HLA class I and/or at least three or four HLA class II molecules of a patient. In some embodiments, the fragments are derived from an antigen that is expressed in cancer. In some embodiments, the RNA includes signals to enhance stability and translation. In some embodiments, the RNA also includes unnatural nucleotides to increase the half-life or modified nucleosides to change the immunostimulatory profile. In some embodiments, the RNAs is introduced by a needle, a gene gun, an aerosol injector, with patches, via microneedles, by abrasion, among other forms. In some forms the RNA vaccine is incorporated into liposomes or other forms of nanobodies that facilitate cellular uptake of RNA and protect it from degradation. In some embodiments, the RNA vaccine includes a delivery system selected from the group consisting of a transfection agent; protamine; a protamine liposome; a polysaccharide particle; a cationic nanoemulsion; a cationic polymer; a cationic polymer liposome; a cationic nanoparticle; a cationic lipid and

cholesterol nanoparticle; a cationic lipid, cholesterol, and PEG nanoparticle; a dendrimer nanoparticle; and/or naked mRNA; naked mRNA with in vivo electroporation; protamine-complexed mRNA; mRNA associated with a positively charged oil-in-water cationic nanoemulsion; mRNA associated with a chemically modified dendrimer and complexed with polyethylene glycol (PEG)-lipid; protamine-complexed mRNA in a PEG-lipid nanoparticle; mRNA associated with a cationic polymer such as polyethylenimine (PEI); mRNA associated with a cationic polymer such as PEI and a lipid component; mRNA associated with a polysaccharide (for example, chitosan) particle or gel; mRNA in a cationic lipid nanoparticle (for example, 1,2-dioleoyloxy-3-trimethylammoniumpropane (DOTAP) or dioleoylphosphatidylethanolamine (DOPE) lipids); mRNA complexed with cationic lipids and cholesterol; or mRNA complexed with cationic lipids, cholesterol and PEG-lipid. In some embodiments, the RNA vaccine is administered by inhalation or ingestion. In some embodiments, the RNA is introduced into the blood, the thymus, the pancreas, the skin, the muscle, a tumor, or other sites, and/or by an intradermal, intramuscular, subcutaneous, intranasal, intranodal, intravenous, intrasplenic, intratumoral or other delivery route.

Polynucleotide or oligonucleotide components may be naked nucleotide sequences or be in combination with cationic lipids, polymers or targeting systems. They may be delivered by any available technique. For example, the polynucleotide or oligonucleotide may be introduced by needle injection, preferably intradermally, subcutaneously or intramuscularly. Alternatively, the polynucleotide or oligonucleotide may be delivered directly across the skin using a delivery device such as particle-mediated gene delivery. The polynucleotide or oligonucleotide may be administered topically to the skin, or to mucosal surfaces for example by intranasal, oral, or intrarectal administration.

Uptake of polynucleotide or oligonucleotide constructs may be enhanced by several known transfection techniques, for example those including the use of transfection agents. Examples of these agents include cationic agents, for example, calcium phosphate and DEAE-Dextran and lipofectants, for example, lipofectam and transfectam. The dosage of the polynucleotide or oligonucleotide to be administered can be altered.

Administration is typically in a "prophylactically effective amount" or a "therapeutically effective amount" (as the case may be, although prophylaxis may be considered therapy), this being sufficient to result in a clinical response or to show clinical benefit to the individual, e.g. an effective amount to prevent or delay onset of the disease or condition, to ameliorate one or more symptoms, to induce or prolong remission, or to delay relapse or recurrence.

The dose may be determined according to various parameters, especially according to the substance used; the age, weight and condition of the individual to be treated; the route of administration; and the required regimen. The amount of antigen in each dose is selected as an amount which induces an immune response. A physician will be able to determine the required route of administration and dosage for any particular individual. The dose may be provided as a single dose or may be provided as multiple doses, for example taken at regular intervals, for example 2, 3 or 4 doses administered hourly. Typically peptides, polynucleotides or oligonucleotides are typically administered in the range of 1 pg to 1 mg, more typically 1 pg to 10 µg for particle mediated delivery and 1 µg to 1 mg, more typically 1-100 µg, more typically 5-50 µg for other routes. Generally, it is expected that each dose will comprise 0.01-3 mg of antigen. An optimal amount for a particular vaccine can be ascertained by studies involving observation of immune responses in subjects.

Examples of the techniques and protocols mentioned above can be found in Remington's Pharmaceutical Sciences, 20th Edition, 2000, pub. Lippincott, Williams & Wilkins.

In some cases the method of treatment may comprise administration to a subject of more than one peptide, polynucleic acid or vector. These may be administered together/simultaneously and/or at different times or sequentially. The use of combinations of different peptides, optionally targeting different antigens, may be important to overcome the challenges of genetic heterogeneity of tumors and HLA heterogeneity of individuals. The use of peptides of the disclosure in combination expands the group of individuals who can experience clinical benefit from vaccination. Multiple pharmaceutical compositions of PEPs, manufactured for use in one regimen, may define a drug product. In some cases different peptides, polynucleic acids or vectors of a single treatment may be administered to the subject within a period of, for example, 1 year, or 6 months, or 3 months, or 60 or 50 or 40 or 30 days.

Routes of administration include but are not limited to intranasal, oral, subcutaneous, intradermal, and intramuscular. The subcutaneous administration is particularly preferred. Subcutaneous administration may for example be by injection into the abdomen, lateral and anterior aspects of upper arm or thigh, scapular area of back, or upper ventrodorsal gluteal area.

The compositions of the disclosure may also be administered in one, or more doses, as well as, by other routes of administration. For example, such other routes include, intracutaneously, intravenously, intravascularly, intraarterially, intraperitoneally, intrathecally, intratracheally, intracardially, intralobally, intramedullary, intrapulmonarily, and intravaginally. Depending on the desired duration of the treatment, the compositions according to the disclosure

may be administered once or several times, also intermittently, for instance on a monthly basis for several months or years and in different dosages.

Solid dosage forms for oral administration include capsules, tablets, caplets, pills, powders, pellets, and granules. In such solid dosage forms, the active ingredient is ordinarily combined with one or more pharmaceutically acceptable excipients, examples of which are detailed above. Oral preparations may also be administered as aqueous suspensions, elixirs, or syrups. For these, the active ingredient may be combined with various sweetening or flavoring agents, coloring agents, and, if so desired, emulsifying and/or suspending agents, as well as diluents such as water, ethanol, glycerin, and combinations thereof.

One or more compositions of the disclosure may be administered, or the methods and uses for treatment according to the disclosure may be performed, alone or in combination with other pharmacological compositions or treatments, for example chemotherapy and/or immunotherapy and/or vaccine. The other therapeutic compositions or treatments may for example be one or more of those discussed herein, and may be administered either simultaneously or sequentially with (before or after) the composition or treatment of the disclosure.

In some cases the treatment may be administered in combination with checkpoint blockade therapy/checkpoint inhibitors, co-stimulatory antibodies, cytotoxic or non-cytotoxic chemotherapy and/or radiotherapy, targeted therapy or monoclonal antibody therapy. It has been demonstrated that chemotherapy sensitizes tumors to be killed by tumor specific cytotoxic T cells induced by vaccination (Ramakrishnan *et al. J Clin Invest.* 2010; 120(4):1111-1124). Examples of chemotherapy agents include alkylating agents including nitrogen mustards such as mechlorethamine (HN2), cyclophosphamide, ifosfamide, melphalan (L-sarcosine) and chlorambucil; anthracyclines; epothilones; nitrosoureas such as carmustine (BCNU), lomustine (CCNU), semustine (methyl-CCNU) and streptozocin (streptozotocin); triazines such as decarbazine (DTIC; dimethyltriazenoimidazole-carboxamide; ethylenimines/methylmelamines such as hexamethylmelamine, thiotepa; alkyl sulfonates such as busulfan; Antimetabolites including folic acid analogues such as methotrexate (amethopterin); alkylating agents, antimetabolites, pyrimidine analogs such as fluorouracil (5-fluorouracil; 5-FU), floxuridine (fluorodeoxyuridine; FUdR) and cytarabine (cytosine arabinoside); purine analogues and related inhibitors such as mercaptopurine (6-mercaptopurine; 6-MP), thioguanine (6-thioguanine; TG) and pentostatin (2'-deoxycoformycin); epipodophylotoxins; enzymes such as L-asparaginase; biological response modifiers such as IFN α , IL-2, G-CSF and GM-CSF; platinum coordination

complexes such as cisplatin (cis-DDP), oxaliplatin and carboplatin; anthracenediones such as mitoxantrone and anthracycline; substituted urea such as hydroxyurea; methylhydrazine derivatives including procarbazine (N-methylhydrazine, MIH) and procarbazine; adrenocortical suppressants such as mitotane (o,p'-DDD) and aminoglutethimide; taxol and
 5 analogues/derivatives; hormones/hormonal therapy and agonists/antagonists including adrenocorticosteroid antagonists such as prednisone and equivalents, dexamethasone and aminoglutethimide, progestin such as hydroxyprogesterone caproate, medroxyprogesterone acetate and megestrol acetate, estrogen such as diethylstilbestrol and ethinyl estradiol equivalents, antiestrogen such as tamoxifen, androgens including testosterone propionate and
 10 fluoxymesterone/equivalents, antiandrogens such as flutamide, gonadotropin-releasing hormone analogs and leuprolide and non-steroidal antiandrogens such as flutamide; natural products including vinca alkaloids such as vinblastine (VLB) and vincristine, epipodophyllotoxins such as etoposide and teniposide, antibiotics such as dactinomycin (actinomycin D), daunorubicin (daunomycin; rubidomycin), doxorubicin, bleomycin, plicamycin (mithramycin) and mitomycin
 15 (mitomycin C), enzymes such as L-asparaginase, and biological response modifiers such as interferon alphenomes.

In some cases the method of treatment is a method of vaccination or a method of providing immunotherapy. As used herein, "immunotherapy" is the treatment of a disease or condition by inducing or enhancing an immune response in an individual. In certain
 20 embodiments, immunotherapy refers to a therapy that comprises the administration of one or more drugs to an individual to elicit T cell responses. In a specific embodiment, immunotherapy refers to a therapy that comprises the administration or expression of polypeptides that contain one or more PEPs to an individual to elicit a T cell response to recognize and kill cells that display the one or more PEPs on their cell surface in conjunction with a class I HLA. In another
 25 specific embodiment, immunotherapy comprises the administration of one or more PEPs to an individual to elicit a cytotoxic T cell response against cells that display tumor associated antigens (TAAs), tumor specific antigens (TSAs) or cancer testis antigens (CTAs) comprising the one or more PEPs on their cell surface. In another embodiment, immunotherapy refers to a therapy that comprises the administration or expression of polypeptides that contain one or more PEPs
 30 presented by class II HLAs to an individual to elicit a T helper response to provide co-stimulation to cytotoxic T cells that recognize and kill diseased cells that display the one or more PEPs on their cell surface in conjunction with a class I HLAs. In still another specific embodiment, immunotherapy refers to a therapy that comprises administration of one or more

drugs to an individual that re-activate existing T cells to kill target cells. The theory is that the cytotoxic T cell response will eliminate the cells displaying the one or more PEPs, thereby improving the clinical condition of the individual. In some instances, immunotherapy may be used to treat tumors. In other instances, immunotherapy may be used to treat intracellular pathogen-based diseases or disorders.

In some cases the disclosure relates to the treatment of cancer or any specific type of cancer described herein. In some other cases the disclosure relates to the treatment of a viral, bacterial, fungal or parasitic infection, or any other disease or condition that may be treated by immunotherapy.

Further Embodiments of the Disclosure

1. A pharmaceutical composition, comprising two or more different peptides, wherein each peptide is up to 50 amino acids in length and comprises the amino acid sequence of any of SEQ ID NOs: 1 to 2786 and/or 5432 to 5931.

2. The pharmaceutical composition of item 1, comprising at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, or at least 12 different peptides, wherein each peptide is up to 50 amino acids in length and comprises the amino acid sequence of any of SEQ ID Nos: 1 to 2786 and/or 5432 to 5931.

3. A pharmaceutical composition comprising one or more polynucleic acids or vectors that encode two or more peptides wherein each peptide is up to 50 amino acids in length and comprises the amino acid sequence of any of SEQ ID NOs: 1 to 2786 and/or 5432 to 5931.

4. The pharmaceutical composition of item 2 comprising at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, or at least 12 polynucleic acids or vectors.

5. The pharmaceutical composition of item 1 or item 3, wherein each peptide or encoded peptide comprises at least one amino acid sequence selected from one of the following groups:

(a) the sequences listed in Table 25A and/or 25B and indicated in Table 25A or 25B to be a fragment of a breast cancer-associated antigen listed in Table 24;

(b) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a lung cancer-associated antigen listed in Table 24;

(c) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a prostate cancer-associated antigen listed in Table 24;

- (d) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a colorectal cancer-associated antigen listed in Table 24;
- (e) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a bladder cancer-associated antigen listed in Table 24;
- 5 (f) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a ovarian cancer-associated antigen listed in Table 24;
- (g) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a pancreatic cancer-associated antigen listed in Table 24;
- (h) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a brain cancer-associated antigen listed in Table 24;
- 10 (i) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a leukemia-associated antigen listed in Table 24;
- (j) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a lymphoma-associated antigen listed in Table 24;
- 15 (k) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a hepatocellular cancer-associated antigen listed in Table 24;
- (l) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a melanoma-associated antigen listed in Table 24;
- (m) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a thyroid cancer-associated antigen listed in Table 24;
- 20 (n) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a pediatric cancer-associated antigen listed in Table 24;
- (o) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a gastric cancer-associated antigen listed in Table 24;
- 25 (p) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a kidney cancer-associated antigen listed in Table 24;
- (q) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a head and neck cancer-associated antigen listed in Table 24; and
- (r) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a cervical cancer-associated antigen listed in Table 24.
- 30
- 6. The pharmaceutical composition according to any of items 1-5 further comprising a pharmaceutically acceptable adjuvant, diluent, carrier, preservative, or a combination thereof.
- 7. A kit comprising:

- a. a first pharmaceutical composition comprising one or more peptides, wherein each peptide comprises a different one of the amino acid sequence of any one of SEQ ID NOs: 1 to 2786 and/or 5432 to 5931; and
 - b. a second different pharmaceutical composition comprising one or more peptides,
5 wherein each peptide comprises a different one of the amino acid sequence of any one of SEQ ID NOs: 1 to 2786 and/or 5432 to 5931.
8. The kit of item 7, further comprising a package insert.
9. A method of inducing a cytotoxic T cell response and/or a helper T cell response in a subject of a target population, the method comprising administering a pharmaceutical
10 composition according to any one of item 1 to item 7.
10. The method of item 9, further comprising prior to the administering step, determining if the subject is likely to have an have a clinical response to administration of the pharmaceutical composition by
 - a. determining that each peptide, or encoded peptide of the pharmaceutical
15 composition comprises at least one amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and
 - b. predicting that the subject will have a cytotoxic T cell response to each peptide, each encoded peptide, polynucleic acid or vector of the pharmaceutical composition.
11. A method of vaccination, providing immunotherapy or inducing a cytotoxic T cell
20 response in a subject, the method comprising administering to the subject a pharmaceutical composition according to any one of item 1 to item 6.
12. The method of item 11 wherein the peptides, polynucleic acids or vectors of the pharmaceutical composition have been predicted to induce a cytotoxic T cell response and/or a helper T cell response in the subject using a method comprising:
25
 - a. determining that each peptide, or encoded peptide of the pharmaceutical composition comprises at least one amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and
 - b. predicting that the subject will have a cytotoxic T cell response to each peptide, encoded peptide, polynucleic acid or vector of the pharmaceutical composition.
- 30 13. The method of item 12, wherein the peptides or encoded peptides of the pharmaceutical composition are fragments of two or more different cancer associated antigens selected from those listed in Table 22.
14. The method according to any one of item 9 to item 14 that is a method of treating cancer,

optionally bladder cancer, brain cancer, breast cancer, colorectal cancer, gastric cancer, hepatocellular cancer, leukemia, lung cancer, lymphoma, melanoma, ovarian cancer, pancreatic cancer, pediatric cancer, thyroid cancer or prostate cancer.

- 15 5 encodes
- a peptide, or a panel of peptides, or one or more polynucleic acid or vectors that encode a panel of peptides, for use in a method of inducing a T cell response against a target polypeptide, the method comprising
- 10 (i) selecting or defining a model human population comprising a plurality of subjects each defined by HLA class I genotype and/or by HLA class II genotype;
- (ii) identifying for each subject of the model population:
- (a) amino acid sequences of the target polypeptide that are a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
- (b) amino acid sequences of the target polypeptide that are a T cell epitope capable of binding to at least four HLA class II molecules of the subject;
- 15 (c) amino acid sequences of the target polypeptide that comprise a T cell epitope capable of binding to at least three HLA class I molecules of the subject and a T cell epitope capable of binding to at least four HLA class II molecules of the subject; or
- 20 (d) amino acid sequences of the target polypeptide that both
- a. are a T cell epitope capable of binding to at least four HLA class II molecules; and
- b. comprise an amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
- 25 (iii) selecting a polypeptide fragment window length of between 9 and 50 amino acids;
- (iv) identifying a fragment of the target polypeptide that
- (c) has the length selected in step (iii); and
- (d) comprises an amino acid sequence identified in any one of step (ii) (a) to (d)
- 30 in the highest proportion of subjects in the model population;
- (v) optionally testing the fragment identified in step (iv) against additional pre-defined criteria, rejecting the fragment if the further pre-defined criteria are not

met, and repeating step (iv) to identify an alternative fragment of the target polypeptide that

(a) has the length selected in step (iii); and

(b) comprises an amino acid sequence identified in step (iv) in the next highest proportion of subjects in the model population;

(vi) optionally repeating step (iv) and further optionally step (v) in one or more further rounds, wherein a further fragment of the target polypeptide is identified in each round, and wherein in each round subjects are excluded from the model population if any of the fragments selected in step (iv) and not rejected in step (v) of any of the preceding rounds comprises an amino acid sequence identified in step (ii) for that subject; and

(vii) designing or preparing a peptide, a polynucleic acid or vector that encodes a peptide, a panel of peptides, or one or more polynucleic acids or vectors that encode a panel of peptides, wherein each peptide comprises one or more of the target polypeptide fragments identified in step (iv), (v) or (vi), optionally wherein the polypeptide fragment is flanked at the N and/or C terminus by additional amino acids that are not part of the sequence of the target polypeptide antigen.

16. The method according to item 15, wherein the target polypeptide is expressed by pathogenic organism, a virus or a cancer cell, or is a cancer testes antigen, optionally wherein the target polypeptide is selected from the antigens listed in any of Tables 2 to 5.

17. The method according to item 15 or item 16, further comprising selecting two or more peptides, polynucleic acids or vectors designed or prepared according to the method of item 15 or 16 for use in a method of vaccinating, providing immunotherapy to, or inducing a cytotoxic and/or helper T cell response in a subject, optionally wherein each of the two or more peptides or encoded peptides comprises an amino acid sequence that is

(a) a fragment of a polypeptide that is expressed by a pathogenic organism, a virus or a cancer cell; and

(b) a T cell epitope capable of binding to at least three HLA class I molecules of the subject or a T cell epitope capable of binding to at least four HLA class II molecules of the subject;

and wherein the method further comprises administering the one or more peptides, polynucleic acids or vectors to the subject.

18. A pharmaceutical composition comprising a panel of peptides, polynucleic acids or

vectors designed and/or prepared according to the method of item 15 or item 16, or comprising or encoding two or more peptides designed and/or prepared according to the method of item 15 or item 16.

19. A pharmaceutical composition comprising a panel of peptides, or one or more
5 polynucleic acids or vectors encoding a panel of peptides, for use in a method of inducing a T cell response against one or more target polypeptides in a subject of a target human population, wherein each of the peptides, or encoded peptides, comprises an amino acid sequence that is
- (a) 9 to 50 amino acids in length; and
 - 10 (b) comprises a fragment of the one or more target polypeptides, wherein the fragment comprises, in at least 10% of subjects of the intent-to-treat human population:
 - a. an amino acid sequence of the target polypeptide that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
 - b. an amino acid sequence of the target polypeptide that is a T cell epitope
15 capable of binding to at least four HLA class II molecules of the subject;
 - c. an amino acid sequence of the target polypeptide that comprise a T cell epitope capable of binding to at least three HLA class I molecules of the subject and a T cell epitope capable of binding to at least four HLA class II molecules of the subject; or
 - 20 d. an amino acid sequence of the target polypeptide that both
 - i. is a T cell epitope capable of binding to at least four HLA class II molecules; and
 - ii. comprise an amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject
- 25 20. The pharmaceutical composition according to item 18 or item 19, further comprising a pharmaceutically acceptable adjuvant, diluent, carrier, preservative, or a combination thereof.
21. A method of vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject, the method comprising administering to the subject a pharmaceutical composition according to any of item 18 to item 20.
- 30 22. The method of item 21, wherein one or more or each of the peptides or the encoded peptides of the pharmaceutical composition comprises an amino acid sequence that is
- (a) a fragment of a polypeptide that is expressed by a pathogenic organism, a virus or a cancer cell; and

- (b) a T cell epitope capable of binding to at least three HLA class I molecules of the subject or a T cell epitope capable of binding to at least four HLA class II molecules of the subject.

Examples

5 Example 1 – HLA-epitope binding prediction process and validation

Predicted binding between particular HLA and epitopes (9 mer peptides) was based on the Immune Epitope Database tool for epitope prediction (www.iedb.org).

The HLA I-epitope binding prediction process was validated by comparison with HLA class I-epitope pairs determined by laboratory experiments. A dataset was compiled of HLA I-epitope pairs reported in peer reviewed publications or public immunological databases.

The rate of agreement with the experimentally determined dataset was determined (Table 6). The binding HLA I-epitope pairs of the dataset were correctly predicted with a 93% probability. Coincidentally the non-binding HLA I-epitope pairs were also correctly predicted with a 93% probability.

15 Table 6. Analytical specificity and sensitivity of the HLA-epitope binding prediction process.

<i>HLA-epitope pairs</i>	<i>True epitopes (n=327)</i> <i>(Binder match)</i>	<i>False epitopes (n=100)</i> <i>(Non-binder match)</i>
<i>HIV</i>	91% (32)	82% (14)
<i>Viral</i>	100% (35)	100% (11)
<i>Tumor</i>	90% (172)	94% (32)
<i>Other (fungi, bacteria, etc.)</i>	100% (65)	95% (36)
<i>All</i>	93% (304)	93% (93)

The accuracy of the prediction of multiple HLA binding epitopes was also determined (Table 7). Based on the analytical specificity and sensitivity using the 93% probability for both true positive and true negative prediction and 7% (=100% - 93%) probability for false positive and false negative prediction, the probability of the existence of a multiple HLA binding epitope in a person can be calculated. The probability of multiple HLA binding to an epitope shows the relationship between the number of HLAs binding an epitope and the expected minimum number of real binding. Per PEPI definition three is the expected minimum number of HLA to bind an epitope (bold).

25 Table 7. Accuracy of multiple HLA binding epitopes predictions.

Expected minimum number of real HLA binding	Predicted number of HLAs binding to an epitope						
	0	1	2	3	4	5	6
1	35%	95%	100%	100%	100%	100%	100%
2	6%	29%	90%	99%	100%	100%	100%
3	1%	4%	22%	84%	98%	100%	100%
4	0%	0%	2%	16%	78%	96%	99%
5	0%	0%	0%	1%	10%	71%	94%
6	0%	0%	0%	0%	0%	5%	65%

The validated HLA-epitope binding prediction process was used to determine all HLA-epitope binding pairs described in the Examples below.

5 **Example 2 – Epitope presentation by multiple HLA predicts cytotoxic T lymphocyte (CTL) response**

This study investigates whether the presentation of one or more epitopes of a polypeptide antigen by one or more HLA class I molecule of an individual is predictive for a CTL response.

The study was carried out by retrospective analysis of six clinical trials, conducted on 71
10 cancer patients and 9 HIV-infected patients (Table 8). Patients from these studies were treated with an HPV vaccine, three different NY-ESO-1 specific cancer vaccines, one HIV-1 vaccine and a CTLA-4 specific monoclonal antibody (Ipilimumab) that was shown to reactivate CTLs against NY-ESO-1 antigen in melanoma patients. All of these clinical trials measured antigen specific CD8+ CTL responses (immunogenicity) in the study subjects after vaccination. In some
15 cases, correlation between CTL responses and clinical responses were reported.

No patient was excluded from the retrospective study for any reason other than data availability. The 157 patient datasets (Table 8) were randomized with a standard random number generator to create two independent cohorts for training and evaluation studies. In some cases, the cohorts contained multiple datasets from the same patient, resulting in a *training*
20 *cohort* of 76 datasets from 48 patients and a *test/validation cohort* of 81 datasets from 51 patients.

Table 8. Summary of patient datasets

Clinical trial	Immunotherapy	Target Antigen	Disease	# Patients*	# Data sets (#antigen x #patient)	Immunoassay performed in the clinical trials**	HLA genotyping method
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1	VGX-3100	HPV16-E6 HPV16-E7 HPV18-E6 HPV18-E7 HPV16/18	Cervical cancer	17/18	5 x 17	IFN- γ ELISPOT	High Resolution SBT
2	HIVIS vaccine	HIV-1 Gag HIV-1 RT	AIDS	9/12	2 x 9	IFN- γ ELISPOT	Low-Medium Resolution SSO
3	rNY-ESO-1	NY-ESO-1	Breast-and ovarian cancers, melanoma and sarcoma	18/18	1 x 18	In vitro and Ex vivo IFN- γ ELISPOT	High Resolution SBT
4	Ipilimumab	NY-ESO-1	Metastatic melanoma	19/20	1 x 19	ICS after T-cell stimulation	Low to medium resolution typing, SSP of genomic DNA, high resolution sequencing
5	NY-ESO-1f	NY-ESO-1 (91-110)	Esophageal-, non-small-cell lung- and gastric cancer	10/10	1 x 10	ICS after T-cell stimulation	SSO probing and SSP of genomic DNA
6	NY-ESO-1 overlapping peptides	NY-ESO-1 (79-173)	Esophageal- and lung cancer, malignant melanoma	7/9	1 x 7	ICS after T-cell stimulation	SSO probing and SSP of genomic DNA
Total	6	7		80	157		

The reported CD8+ T cell responses of the training dataset were compared with the HLA class I restriction profile of epitopes (9 mers) of the vaccine antigens. The antigen sequences and the HLA class I genotype of each patient were obtained from publicly available protein sequence

databases or peer reviewed publications and the HLA I-epitope binding prediction process was blinded to patients' clinical CD8+ T cell response data where CD8+ T cells are IFN- γ producing CTL specific for vaccine peptides (9 mers). The number of epitopes from each antigen predicted to bind to at least 1 (PEPI1+), or at least 2 (PEPI2+), or at least 3 (PEPI3+), or at least 4 (PEPI4+), or at least 5 (PEPI5+), or all 6 (PEPI6) HLA class I molecules of each patient was determined and the number of HLA bound were used as classifiers for the reported CTL responses. The true positive rate (sensitivity) and true negative rate (specificity) were determined from the training dataset for each classifier (number of HLA bound) separately.

ROC analysis was performed for each classifier. In a ROC curve, the true positive rate (Sensitivity) was plotted in function of the false positive rate (1-Specificity) for different cut-off points (FIG. 1). Each point on the ROC curve represents a sensitivity/specificity pair corresponding to a particular decision threshold (epitope (PEPI) count). The area under the ROC curve (AUC) is a measure of how well the classifier can distinguish between two diagnostic groups (CTL responder or non-responder).

The analysis unexpectedly revealed that predicted epitope presentation by multiple class I HLAs of a subject (PEPI2+, PEPI3+, PEPI4+, PEPI5+, or PEPI6), was in every case a better predictor of the CD8+ T cell response or CTL response than epitope presentation by merely one or more HLA class I (PEPI1+, AUC = 0.48, Table 9).

Table 9. Determination of diagnostic value of the PEPI biomarker by ROC analysis

Classifiers	AUC
PEPI1+	0.48
PEPI2+	0.51
PEPI3+	0.65
PEPI4+	0.52
PEPI5+	0.5
PEPI6+	0.5

The CTL response of an individual was best predicted by considering the epitopes of an antigen that could be presented by at least 3 HLA class I alleles of an individual (PEPI3+, AUC = 0.65, Table 9). The threshold count of PEPI3+ (number of antigen-specific epitopes presented by 3 or more HLA of an individual) that best predicted a positive CTL response was 1 (Table 10). In other words, at least one antigen-derived epitope is presented by at least 3 HLA class I of a subject (≥ 1 PEPI3+), then the antigen can trigger at least one CTL clone, and the subject is a

likely CTL responder. Using the ≥ 1 PEPI3+ threshold to predict likely CTL responders (" ≥ 1 PEPI3+ test") provided 76% true positive rate (diagnostic sensitivity) (Table 10).

Table 10. Determination of the ≥ 1 PEPI3+ threshold to predict likely CTL responders in the training dataset.

	PEPI3+ Count											
	1	2	3	4	5	6	7	8	9	10	11	12
Sensitivity:	0.76	0.60	0.31	0.26	0.14	0.02	0	0	0	0	0	0
1-Specificity:	0.59	0.24	0.21	0.15	0.09	0.06	0.06	0.03	0.03	0.03	0.03	0.03

5

Example 3 –Retrospective Validation of the ≥ 1 PEPI3+ threshold as novel biomarker for PEPI test

In a retrospective analysis, the test cohort of 81 datasets from 51 patients was used to validate the ≥ 1 PEPI3+ threshold to predict an antigen-specific CD8+ T cell response or CTL response. For each dataset in the test cohort it was determined whether the ≥ 1 PEPI3+ threshold was met (at least one antigen-derived epitope presented by at least three class I HLA of the individual). This was compared with the experimentally determined CD8+ T cell responses (CTL responses) reported from the clinical trials (Table 11).

The retrospective validation demonstrated that a PEPI3+ peptide induces CD8+ T cell response (CTL response) in an individual with 84% probability. 84% is the same value that was determined in the analytical validation of the PEPI3+ prediction, epitopes that binds to at least 3 HLAs of an individual (Table 7). These data provide strong evidences that immune responses are induced by PEPIs in individuals.

Table 11. Diagnostic performance characteristics of the ≥ 1 PEPI3+ test (n=81).

Performance characteristic	Description	Result
Positive predictive value (PPV)	The likelihood that an individual that meets the ≥ 1 PEPI3+ threshold has antigen-specific CTL responses after treatment with immunotherapy.	84%
Sensitivity	The proportion of subjects with antigen-specific CTL responses after treatment with immunotherapy who meet the ≥ 1 PEPI3+ threshold.	75%

Specificity	100% $[D / (B + D)]$	The proportion of subjects without antigen-specific CTL responses after treatment with immunotherapy who do not meet the ≥ 1 PEPI3+ threshold.	55%
Negative predictive value (NPV)	100% $[D/(C +D)]$	The likelihood that an individual who does not meet the ≥ 1 PEPI3+ threshold does not have antigen-specific CTL responses after treatment with immunotherapy.	42%
Overall percent agreement (OPA)	100% $[(A + D)/ N]$	The percentage of predictions based on the ≥ 1 PEPI3+ threshold that match the experimentally determined result, whether positive or negative.	70%
Fisher's exact (p)			0.01

ROC analysis determined the diagnostic accuracy, using the PEPI3+ count as cut-off values (Fig. 2). The AUC value = 0.73. For ROC analysis an AUC of 0.7 to 0.8 is generally considered as fair diagnostic value.

- 5 A PEPI3+ count of at least 1 (≥ 1 PEPI3+) best predicted a CTL response in the test dataset (Table 12). This result confirmed the threshold determined during the training (Table 9).

Table 12. Confirmation of the ≥ 1 PEPI3+ threshold to predict likely CTL responders in the test/validation dataset.

	PEPI3+ Count											
	1	2	3	4	5	6	7	8	9	10	11	12
Sensitivity:	0.75	0.52	0.26	0.23	0.15	0.13	0.08	0.05	0	0	0	0
1-Specificity:	0.45	0.15	0.05	0	0	0	0	0	0	0	0	0

10

Example 4 – Clinical Validation of the ≥ 1 PEPI3+ threshold as novel biomarker for PEPI test

- 15 The PEPI3+ biomarker-based vaccine design has been tested first time in a phase I clinical trial in metastatic colorectal cancer (mCRC) patients in the OBERTO phase I/II clinical trial (NCT03391232). In this study, we evaluated the safety, tolerability and immunogenicity of a single

or multiple dose(s) of PolyPEPI1018 as an add-on to maintenance therapy in subjects with mCRC. PolyPEPI1018 is a peptide vaccine containing 12 unique epitopes derived from 7 conserved TSAs frequently expressed in mCRC (WO2018158455 A1). These epitopes were designed to bind to at least three autologous HLA alleles that are more likely to induce T-cell responses than epitopes presented by a single HLA (See Examples 2 & 3). mCRC patients in the first line setting received the vaccine (dose: 0.2 mg/peptide) just after the transition to maintenance therapy with a fluoropyrimidine and bevacizumab. Vaccine-specific T-cell responses were first predicted by identification of PEPI3+-s *in silico* (using the patient's complete HLA genotype and antigen expression rate specifically for CRC) and then measured by ELISpot after one cycle of vaccination (phase I part of the trial).

Seventy datasets from 10 patients (Phase 1 cohort and dataset of OBERTO trial) was used to prospectively validate that PEPI3+ biomarker predicts antigen-specific CTL responses. For each dataset, predicted PEPI3+-s were determined *in silico* and compared to the vaccine-specific immune responses measured by ELISPOT assay from the patients' blood. Diagnostic characteristics (positive predictive value, negative predictive value, overall percent agreement) determined this way were then compared with the retrospective validation results described in Example 3.

The overall percent agreement was 64%, with high positive predictive value of 79%, representing 79% probability that the patient with predicted PEPI3+ will produce CD8 T cell specific immune response against the analyzed antigen. Clinical trial data were significantly correlated with the retrospective trial results ($p=0.01$) and provides evidence for the PEPI3+ calculation with PEPI test to predict antigen-specific T cell responses based on the complete HLA-genotype of patients (Table 13).

Table 13. Prospective validation of the ≥ 1 PEPI3+ and PEPI test

Parameter	Definition	Retrospective validation n = 81*	Prospective validation (OBERTO) n = 70**
PPV	The likelihood that an individual with		
Positive Predictive Value	a positive PEPI test result has antigen-specific T cell responses	84%	79%

NPV	The likelihood that an individual with		
Negative Predictive Value	a negative PEPI test result does not have antigen-specific T cell responses	42%	51%
OPA			
Overall Percent Agreement	The percentage of results that are true results, whether positive or negative	70%	64%
Fisher's exact probability test (p)		0.01	0.01
*51 patients; 6 clinical trials; 81 dataset **10 patients; Treos phase I clinical trial (OBERTO); 70 datasets			

Example 5 – The ≥ 1 PEPI3+ test predicts CD8+ T cell reactivities

Supporting data were obtained to show that the ≥ 1 PEPI3+ correlates with clinical immunogenicity data but the state-of-art mono-HLA specific epitope determination does not show correlation with vaccine-specific immunogenicity.

The ≥ 1 PEPI3+ calculation was compared with a state-of-art method for predicting a specific human subject's CTL response to peptide antigens.

The HLA genotypes of 28 cervical cancer and VIN-3 patients that received HPV-16 specific synthetic long peptide vaccine (LPV) in two different clinical trials were determined from DNA samples. The LPV consists of long peptides covering the HPV-16 viral oncoproteins E6 and E7. The amino acid sequence of the LPV was obtained from M. J. Welters, et al. Induction of tumor-specific CD4+ and CD8+ T-cell immunity in cervical cancer patients by a human papillomavirus type 16 E6 and E7 long peptides vaccine. *Clin Cancer Res* **14**, 178-187 (2008)., G. G. Kenter, et al. Vaccination against HPV-16 oncoproteins for vulvar intraepithelial neoplasia. *N Engl J Med* **361**, 1838-1847 (2009). M. J. Welters, et al. Success or failure of vaccination for HPV16-positive vulvar lesions correlates with kinetics and phenotype of induced T-cell responses. *Proc Natl Acad Sci U S A* **107**, 11895-11899 (2010). The publications also report the T cell responses of each vaccinated patient to pools of overlapping peptides of the vaccine. 25 (20 having VIN-3 and 5 having cervical cancer) patients had immune response data available, and 25 had clinical response data available.

For each patient, epitopes (9 mers) of the LPV that are presented by at least three patient class I HLA (PEPI3+s) were identified and their distribution among the peptide pools was determined. Peptides that comprised at least one PEPI3+ (≥ 1 PEPI3+) were predicted to induce a

CD8+ T cell response. Peptides that comprised no PEPI3+ were predicted not to induce a CD8+ T cell response.

The ≥ 1 PEPI3+ threshold correctly predicted 529 out of 555 negative CD8+ T cell responses (95% true negative (TN) rate) and 9 out of 45 positive CD8+ T cell responses (20% true positive (TP) rate) measured after vaccination (FIG. 3A). Overall, the agreement between the ≥ 1 PEPI3+ threshold and experimentally determined CD8+ T cell reactivity was 90% ($p < 0.001$). For each patient the distribution among the peptide pools of epitopes that are presented by at least one patient class I HLA (≥ 1 PEPI1+, HLA restricted epitope prediction, prior art method) was also determined. Forty-two HLA class I binding epitopes predicted 45 CD8+ T cell responses (93% TP rate). In contrast, of the 555 negative T cell responses, only 105 were ruled out by HLA binding epitopes (19% TN rate) (FIG. 3B). Overall, the agreement between a single HLA class I allele binding epitope and CD8+ T cell response was 25%, which was not statistically significant.

Example 6 - Prediction of HLA class II restricted CD4+ helper T cell epitopes

The 28 cervical cancer and VIN-3 patients that received the HPV-16 synthetic long peptide vaccine (LPV) in two different clinical trials (as detailed in Example 5) were investigated for CD4+ T helper responses following LPV vaccination (FIG. 4). The TP rate of the prediction of HLA class II restricted epitopes was 95%, since the State of Art tool predicted 112 positive responses (positive CD4+ T cell reactivity to a peptide pool for a person's HLA class II alleles) out of 117. The TN rate was 0% since it could rule out 0 of 33 negative T cell responses. Overall, the agreement between HLA-restricted class II PEPI prediction and CD4+ T cell reactivity was 75% (not significant).

The HLA class II-binding PEPI3+-s predicted 86 of 117 positive CD4+ T-cell responses (73% TP rate) and ruled out 17 of 33 negative T-cell responses (52% TN rate). Overall, the agreement between HLA class II PEPI3+-s and CD4+ T-cell response was 69% ($p = 0.005$) (FIG. 4A).

Example 7 - The ≥ 1 PEPI3+ test predicts T cell responses to full length LPV polypeptides

Using the same studies as reported in Examples 5 and 6, the ≥ 1 PEPI3+ test was used to predict patient CD8+ and CD4+ T cell responses to the full length E6 and E7 polypeptide antigens of the LPV vaccine. Results were compared to the experimentally determined responses reported. The test correctly predicted the CD8+ T cell reactivity (PEPI3+) of 11 out of 15 VIN-3 patients with positive CD8+ T cell reactivity test results (sensitivity 70%, PPV 85%) and of 2 out of 5 cervical

cancer patients (sensitivity 40%, PPV 100%) (FIG. 5A). The CD4+ T cell reactivities (PEPI3+) were correctly predicted 100% both of VIN-3 and cervical cancer patients (FIG. 5B).

Class I and class II HLA restricted PEPI3+ count was also observed to correlate with the reported clinical benefit to LPV vaccinated patients. Patients with higher PEPI3+ counts had either complete or partial response already after 3 months. There was also a correlation between the number of PEPIs and clinical response in VIN-3 patients for HLA class II PEPIs but not HLA class I PEPIs, confirming the post-hoc analysis results from the clinical trial (FIG. 5C and 5D).

10 **Example 8 – Case Study, PEPI3+ correlation with vaccine-specific immunogenicity**

“Vaccine-1” is an HPV16 based DNA vaccine containing full length E6 and E7 antigens with a linker in between. “Vaccine-2” is an HPV18 based DNA vaccine containing full length E6 and E7 antigens with a linker in between (FIG 6A). A Phase II clinical trial investigated the T cell responses of 17 HPV-infected patients with cervical cancer who were vaccinated with both “Vaccine-1” and “Vaccine-2” (“Vaccine-3” vaccination, Bagarazzi et al. Science Translational Medicine, 2012; 4(155):155ra138.).

FIG. 6B shows for two illustrative patients (patient 12-11 and patient 14-5) the position of each epitope (9 mer) presented by at least 1 (PEPI1+), at least 2 (PEPI2+), at least 3 (PEPI3+), at least 4 (PEPI4+), at least 5 (PEPI5+), or all 6 (PEPI6) class I HLA of these patients within the full length sequence of the two HPV-16 and two HPV-18 antigens.

Patient 12-11 had an overall PEPI1+ count of 54 for the combined vaccines (54 epitopes presented by one or more class I HLA). Patient 14-5 had a PEPI1+ count of 91. Therefore, patient 14-5 has a higher PEPI1+ count than patient 12-11 with respect to the four HPV antigens. The PEPI1+s represent the distinct vaccine antigen specific HLA restricted epitope sets of patients 12-11 and 14-5. Only 27 PEPI1+s were common between these two patients. For the PEPI3+ counts (number of epitopes presented by three or more patient class I HLA), the results for patients 12-11 and 14-5 were reversed. Patient 12-11 had a PEPI3+ count of 8, including at least one PEPI3+ in each of the four HPV16/18 antigens. Patient 14-5 had a PEPI3+ count of 0 (FIG. 6C).

The reported immune responses of these two patients matched the PEPI3+ counts, not the PEPI1+ counts. Patient 12-11 developed immune responses to each of the four antigens post-vaccination as measured by ELISpot, whilst patient 14-5 did not develop immune responses to any of the four antigens of the vaccines. A similar pattern was observed when the PEPI1+ and

PEPI3+ sets of all 17 patients in the trial were compared. There was no correlation between the PEPI1+ count and the experimentally determined T cell responses reported from the clinical trial. However, correlation between the T cell immunity predicted by the ≥ 1 PEPI3+ test and the reported T cell immunity was observed. The ≥ 1 PEPI3+ test predicted the immune responders to HPV DNA vaccine.

Moreover, the diversity of the patient's PEPI3+ set resembled the diversity of T cell responses generally found in cancer vaccine trials. Patients 12-3 and 12-6, similar to patient 14-5, did not have PEPI3+s predicting that the HPV vaccine could not trigger T cell immunity. All other patients had at least one PEPI3 predicting the likelihood that the HPV vaccine can trigger T cell immunity. 11 patients had multiple PEPI3+ predicting that the HPV vaccine likely triggers polyclonal T cell responses. Patients 15-2 and 15-3 could mount high magnitude T cell immunity to E6 of both HPV, but poor immunity to E7. Other patients 15-1 and 12-11 had the same magnitude response to E7 of HPV18 and HPV16, respectively.

Example 9 – Design of a Model Population for conducting *in silico* trials and identifying candidate precision vaccine targets for large population

An *in silico* human trial cohort of 433 subjects with complete 4-digit HLA class I genotype (2 x HLA-A*xx:xx; 2 x HLA-B*xx:xx; 2 x HLA-C*xx:xx) and demographic information was compiled. This Model Population has subjects with mixed ethnicity having a total of 152 different HLA alleles that are representative for >85% of presently known allele G-groups.

A database of a “Big Population” containing 7,189 subjects characterized with 4-digit HLA genotype and demographic information was also established. The Big Population has 328 different HLA class I alleles. The HLA allele distribution of the Model Population significantly correlated with the Big Population (Table 14) (Pearson $p < .001$). Therefore, the 433 patient Model Population is representative for a 16 times larger population. The Model Population is representative for 85% of the human race as given by HLA diversity as well as HLA frequency. Table 14. Statistical analysis of HLA distributions in “Model Population” vs. “Big Population”.

Group name 1	Group name 2	Pearson R value	Correlation	P Value
433 Model Population	7,189 Big Population	0.89	Strong	$P < 0.001$

Example 10 – *In silico* trial based on the identification of multiple HLA binding epitopes in a multi-peptide vaccine IMA901 predict the reported clinical trial immune response rate

Probability of targeting multiple antigens in the tumor of RCC patients

5 IMA901 is a therapeutic vaccine for renal cell cancer (RCC) comprising 9 peptides derived from tumor-associated antigens (TUMAPs). It was demonstrated that TUMAPs are naturally presented in human cancer tissue, they are overexpressed antigens shared by a subset of patients with the given cancer entity (Table 15). We estimated the probability that a TSA is expressed in a subject treated with IMA901 vaccine using available data from the scientific
10 literature (FIG. 7). We used the Bayesian convention assuming that the expression probabilities follow a Beta-distribution.

We defined AG50 as the number of TSAs (AG) in the cancer vaccine that a specific tumor type expresses with 50% probability. The AG50 modelling of cancer vaccines assumes that each AG produces an effect proportional to the expression rate of the AG in the tumor type
15 (if each AG in the vaccine is immunogenic).

For IMA901 vaccine targeting 9 antigens (9 TUMAPs), the AG50 value is 4.7, meaning that about half of the antigens are overexpressed in 50% of patients' tumor. Moreover, the probability of targeting 2 expressed antigens is 100% and 3 antigens is 96%. These results suggest high potency of IMA901 vaccine based on target antigen selection.

20 **Table 15. Overexpression of TAAs in RCC tumors selected for IMA901 vaccine**

TAA (AG)	Published expression rate in RCC tumors*	Estimated expression rate (95% CI)
ADF-001	5/11 ¹	46% (21%, 72%)
ADF-002	5/11	46% (21%, 72%)
APO-001	9/11 ²	77% (52%, 95%)
CCN-001	4/11	38% (15%, 65%)
GUC-001	0/2 ²	25% (1%, 71%)
K67-001	2/2	75% (29%, 99%)
MET-001	11/11	92% (74%, 100%)
MUC-001	0/11	8% (0%, 26%)
RGS-001	7/11	62% (35%, 85%)

*expression is defined as overexpression in tumors compared to healthy tissues provided in the source publications

¹Walter S et al, Multi-peptide immune response to cancer vaccine IMA901 after single-dose cyclophosphamide associates with longer patient survival, Nature Medicine, (2012), 18, 1254–1261

²Krüger T et al, Lessons to be learned from primary renal cell carcinomas, Cancer Immunol, Immunother, 2005, 54, 826-836

Probability of inducing immune responses against multiple antigens in the tumor of RCC patients

A total of 96 HLA-A*02+ subjects with advanced RCC were treated with IMA901 in two independent clinical studies (Phase I and Phase II) (Walter S et al, Multi-peptide immune response to cancer vaccine IMA901 after single-dose cyclophosphamide associates with longer patient survival, *Nature Medicine*, (2012), 18, 1254–1261). Each of the 9 peptides in IMA901 have been identified as HLA-A*02-restricted epitopes. Based on currently accepted standards, all 9 peptides are strong candidates to boost T cell responses against renal cancer since their presence has been detected in renal cancer patients, and because the trial patients were specifically selected to have at least one HLA molecule (HLA-A*02) capable of presenting each of the peptides. Despite this restriction the immune response rate of the phase I and phase II clinical trials measured for at least one peptide of the vaccine was 74% and 64%, respectively. We analyzed by *in silico* prediction the HLA binding properties of each TUMAP in IMA901 and found that 8 out of the 9 TUMAPs can bind to many HLA-A*02 alleles confirming the identification process (FIG. 8). However, we found that each TUMAP can bind to many other HLA-B* and HLA-C* alleles (FIG. 8A).

Since the complete 4-digit HLA genotype of subjects who participated in IMA901 clinical trials were not available, we used the genotype data of 51 HLA-A*02 selected RCC subjects from another clinical trial, to characterize the immunogenicity of IMA901 vaccine (REF: Chowell D, Morris LGT, Grigg CM, Weber JK, Samstein RM, et al. Patient HLA class I genotype influences cancer response to checkpoint blockade immunotherapy. *Science*. 2018; 359 (6375): 582-587.). As presented on FIG. 8B, only few TUMAPs are able to bind to multiple HLAs of the same subject. The most immunogenic peptide in this context turned to be MET-001 capable of generating PEPI in 35% of RCC patients. However, CCN-001 could not generate PEPI in any of the patients, in agreement with FIG. 8A; CCN-001 can bind only to HLA-A*02 alleles. Based on FIG. 8A, MUC-001 is theoretically able to bind other alleles, too (both HLA-B and HLA-C), however those alleles were not present in the patients of our model population, therefore this peptide could not generate PEPI, either.

The immunogenicity of IMA901 vaccine determined in the 2 clinical trials was compared with the PEPI response rate determined using the PEPI test in our RCC model population. We found 67% (CI95 53-78%) immune response to at least one peptide of the IMA901 vaccine. According to PEPI test, 33% (CI95 22-47%) of these HLA-A*02+ subjects did not have 3 HLAs binding to any TUMAPs. Interestingly, IMA901 did not induce T cell responses in 25% and 36%

of HLA-A*02 selected subjects in the Phase I and Phase II clinical trials, respectively. Furthermore, PEPI test predicted 30% (CI95 19-43%) of subjects with 1 PEPI to one TUMAP, and 37% (CI95 25-51%) have ≥ 2 PEPIs to at least two IMA901 peptides, which is in agreement with the average 40% and 27% immune response to 1 or ≥ 2 TUMAPs in both clinical trials (Table 16). The differences between the immunogenicity found in the 3 cohorts can be explained by the differences in the HLA genotype of the study subjects as well as the potential errors in measuring T cell responses and in determining PEPIs with the PEPI test (see Example 1). The phase I and phase II study results show the variability of the immune response rates of the same vaccine in different trial cohorts. However, the agreements between PEPI response rates and immunogenicity of peptide vaccines are determined by the host HLA sequences.

Table 16. Immunogenicity of IMA901 vaccine is determined by the host HLA genotype (multiple HLAs)

Immune responses to TUMAPs	Phase I (n=27)*	Phase II (n=61)*	Phase I + II (n=88)	RCC model population (n=51)** (CI95%)
No peptide	25%	36%	33%	33% (22-47%)
≥ 1 peptide	74%	64%	67%	67% (53-78%)
1 peptide	44%	38%	40%	30% (19-43%)
≥ 2 peptides	29%	26%	27%	37% (25-51%)

*reported immunological data for the trials conducted with IMA901 vaccine (REF: Walter Nat Med 2012);

**Predicted by PEPI test

Similarly to the AG50, we defined AP50 as the average number of antigens with PEPI of a vaccine which shows how the vaccine can induce immune response against the antigens targeted by the composition (cancer vaccine specific immune response). AP, therefore is depending of the HLA heterogeneity of the analyzed population and is independent on the expression of the antigen on the tumor. The IMA901 composition can induce immune response against an average of 1.06 vaccine antigens (AP50=1.06) meaning that in the HLA-A*02 selected RCC model population it can induce immune response against at least one vaccine antigen. This result is far less compared to the designed intention of immunogenicity (HLA-matched patients treated with 9 peptides).

Comparison of Immunogenicity and Clinical Response of TUMAPs in the IMA901 Peptide Vaccine

An immune response induced by a vaccine against a single antigen might not be sufficient for clinical activity, as the given antigen might not be expressed in the patient. Therefore, we defined AGP as the immune response which targets an expressed antigen, taking into account

both the immunogenicity and expression probability of the vaccine antigen on the tumor, presented above. AGP depends on the antigen (AG) expression rate in the indicated tumor and the HLA genotype of subjects capable to make PEPI (P) in the study population.

Therefore, we investigated the correlation between immune responses against different number of antigens (TUMAPs) and the immune responses against likely expressed antigens (AGP). We found that an immune response elicited by one peptide (1 TUMAP) corresponds to 0.98 AGP, meaning that there is 98% probability that the immune response induced by any peptide of the IMA901 vaccine will target an expressed antigen on the tumor (FIG. 9). However, immune responses elicited by 2 or 3 TUMAPs correspond to only 1.44 and 2.21 AGP, respectively. 0.35 AGP corresponding to 0 TUMAP indicates the cumulated error of PEPI test prediction (see Example 1).

characterize the potency of a cancer vaccine we defined AGP50, a parameter showing the number of antigens that the vaccine induced CTLs can recognize in a tumor with 50% probability. The computation is similar to the AG50 but in addition to the expression, the occurrence of the PEPI presentation on certain vaccine antigen is also considered. AGP50 for IMA901 vaccine for the RCC model population is 1.10.

In a retrospective analysis, IMA901 clinical trial investigators found that significantly more subjects who responded to multiple TUMAPs of IMA901 experienced disease control (DC, stable disease or partial response) compared with subjects who had no response or responded to only 1 TUMAP (Table 17). Since the presence of PEPIs accurately predicted the responders to TUMAPs, we investigated the relationship between disease control rate in the TUMAP responder subpopulation and AGP. Similarly, to the investigators we analyzed the percentage of patients who are likely to have immune response against an expressed antigen (i.e.: ≥ 1 AGP) for the subpopulations predicted to have immune response to 0, 1 or 2 TUMAPs using our RCC model population. Interestingly, percentage of patients with 1 AGP is similar to the percentage of patients with disease control in the subpopulations: i.e.: 33% of patients had disease control vs 47% (CI95 23-67%) had 1 AGP and considerably more patients had disease control and AGP in the subgroup with immune response to 2 TUMAPs 75% vs 90 % (CI95 70, 97%), respectively. These results suggest that only those patients are likely to experience clinical benefit, who have immune response against at least one expressed tumor antigen. Moreover, the percentage of patients with 1 AGP in our RCC model population is similar to the disease control rate of the phase I and phase II trials conducted with IMA901 vaccine (Table 17).

Table 17. Correlation between clinical benefit and AGP

Subpopulation	% of pts with DC in the clinical subpopulation	% pts with 1 AGP in the model subpopulation (CI95)
No IR	14%	5% (0%,18%)
IR to 1TUMAP	33%	47% (23%,67%)
IR to ≥ 2 TUMAPs	75%	90% (70%,97%)
Phase I	40%	49% (35%,61%)
Phase II	31%	

Analysis of IMA901 vaccine potency in multiple populations

As shown in Table 18, AG50 value of 4.7 was observed for IMA901 vaccine, suggesting high potency based on target antigen selection. However, AP50 for IMA901 in both the
5 unselected general population and HLA-A*02 selected subjects were only 0.75 and 1.12, respectively. Similar results were obtained for unselected RCC model population and HLA-A*02 selected populations. This results demonstrate that HLA-A*02 enrichment improved the antigenicity of IMA901, however did not ensure the immunogenicity of the vaccine. Consequently, the AGP50 values describing the potency of the vaccine are low in each
10 population.

Table 18. Potency of IMA901 vaccine in in unselected population and HLA-A*02 selected subjects

Model Population	AG50	AP50	AGP50
All Subjects (n=433)	4.7	0.75	0.49
HLA-A*02 Subjects (n=180)	4.7	1.12	0.81
RCC population (n=129)	4.7	0.61	0.70
RCC subpopulation A*02 (n=51)	4.7	1.06	1.10

Example 11 – In silico trials based on the identification of multiple HLA binding epitopes predict the reported T cell response rates of clinical trials

The objective of this study was to determine whether a model population, such as the one described in Example 9, may be used to predict CTL reactivity rates of vaccines, i.e. used in an *in silico* efficacy trial and to determine the correlation between the clinical outcome of vaccine trials and PEPI.

20 Published clinical trial results were collected from studies with therapeutic vaccines, which included 1,790 subjects in 64 clinical studies, treated with 42 therapeutic vaccines

covering 61 different antigens (Table 19). The same vaccines used in those clinical trials were used to perform *in silico* trials with the model population of 433 human leukocyte antigen (HLA)-genotyped subjects (described in Example 9). No subjects were excluded for reasons other than data availability. IRR was defined as the proportion of subjects in the study population with T cell responses induced by the study vaccine. ORR was defined as the proportion of subjects in the study population with objective response (complete and partial response) after vaccination. The proportion of subjects with PEPIs (personal epitopes that bind to 3 HLA alleles of a subject), multiple PEPIs, and PEPIs in multiple antigens were computed in the *in silico* trials to obtain the PEPI Score, MultiPEPI Score, and MultiAgPEPI Score, respectively. The immune and objective response rates (IRR and ORR) from the published clinical trials were compared with the PEPI Score, MultiPEPI Score, and MultiAgPEPI Score. All reported and calculated scores are summarized in Table 20.

Table 19. Summary of patient demographics in the published clinical trials

Characteristic	Count	Percentage
Total subjects	1,790	
Total studies	64	
Subjects with HIV infection	12	1%
Subjects with neoplasia or dysplasia	172	9%
Subjects with cancer	1606	90%
Subjects with solid tumors	1503	84%
Subjects with liquid tumors	103	6%
Subjects with metastatic tumors	788	44%
Subjects with non-metastatic tumors	818	46%
HLA selected subjects	918	51%
Non- HLA selected subjects	872	49%
Trials with HLA selected subjects	32	50%
Trials without HLA selected subjects	32	50%

Table 20. Response rates and PEPI Scores

Immunotherapy	IRR	ORR	PEPI Score	Multi PEPI Score	MultiAg PEPI Score
PSMA-Survivin pulsed DC vaccine	---	18%	3%	0%	0%
Peptide vaccine	---	3%	10%	0%	0%
HPV-SLP	83%	60%	73%	70%	34%
	100%	60%	73%	70%	34%
VGX-3100	78%	50%	87%	56%	64%
Melanoma peptide vaccine	52%	12%	42%	6%	6%

GAA peptides vaccine	55%	15%	18%	0%	0%
KRM-20 peptide vaccine	40%	13%	36%	15%	15%
Peptide vaccine	100%	25%	81%	3%	1%
S-288310 peptide vaccine	67%	17%	44%	8%	8%
KIF20A-66 peptide	70%	26%	38%	7%	---
PepCan	65%	52%	62%	26%	---
Iplilimumab (NYESO-1 specific response)	72%	25%	84%	65%	---
p53 SLP70-248	88%	0%	77%	52%	---
	100%	0%	77%	52%	---
	0%	---	77%	52%	---
p53 SLP70-235	21%	---	75%	52%	---
GVX301	64%	0%	65%	7%	---
TroVax vaccine (OXB-301)	65%	0%	94%	83%	---
	57%	0%	94%	83%	---
StimuVax	21%	---	2%	---	---
IMA901	74%	---	48%	27%	27%
	64%	---	48%	27%	27%
ICT107	33%	---	52%	---	---
ProstVac	67%	---	50%	23%	---
	45%	---	50%	23%	---
	76%	---	50%	23%	---
	67%	---	50%	23%	---
	50%	---	50%	23%	---
	72%	---	50%	23%	---
Synchrotope TA2M	46%	---	24%	7%	---
MELITAC 12.1	49%	---	47%	19%	---
HIVIS	50%	---	88%	---	---
	80%	---	93%	---	---
ImMucin	90%	---	95%	70%	---
	100%	47%	95%	70%	---
NY-ESO-1 OLP	71%	---	84%	65%	---
	82%	0%	84%	65%	---
WT1 vaccine	83%	---	80%	77%	---
WT1 peptide vaccine	72%	6%	86%	---	---
RHAMM-R3 peptide vaccine	44%	0%	0%	---	---
GMMG-MM5 peptides	35%	---	86%	21%	21%
INGN-225 p53 vaccine	58%	4%	82%	61%	---
HR2822	8%	---	3%	---	---
GV1001	17%	---	3%	---	---
	45%	---	3%	---	---
Vx-001	51%	---	33%	---	---
	66%	7%	33%	---	---
	58%	4%	33%	---	---
	71%	0%	33%	---	---
NY-ESO-1f	90%	0%	55%	18%	---
GL-0817 (MAGE-A3 Trojan)	33%	---	29%	3%	---
	57%	0%	29%	3%	---
	0%	0%	29%	3%	---
DPX0907 (per peptide)	0%	---	22%	---	---
	11%	---	18%	---	---
	11%	---	7%	---	---

	11%	---	39%	---	---
	17%	---	12%	---	---
	17%	---	5%	---	---
	22%	---	31%	---	---
CV9103 mRNA vaccine	80%	---	100%	---	---
TG4010 vaccine	38%	13%	43%	6%	---
	26%	0%	43%	6%	---
	21%	---	43%	6%	---
	---	0%	---	---	---
SVN-2B peptide vaccine	60%	---	35%	---	---
TSPP peptide vaccine	---	5%	72%	31%	---
Her2/neu peptide vaccine (p369)	62%	---	4%	---	---
Her2/neu peptide vaccine (p688)	31%	---	1%	---	---
Her2/neu peptide vaccine (p971)	54%	---	0%	---	---
MART-1 Peptide Vaccine	15%	---	0%	---	---

We investigated the correlation between ≥ 1 PEPI3+ Score and immune response rate in a previous study of 12 peptide vaccines derived from cancer antigens that induced T cell responses in a subpopulation of 172 subjects from 19 clinical trials, that were identified from peer reviewed publications. The experimentally determined response rates reported from the trials were compared with the ≥ 1 PEPI3+ Scores and linear correlation between ≥ 1 PEPI3+ Score and response rate ($R^2 = 0.70$) was found ($p=0.001$) (FIG. 10A). The correlation between ≥ 1 PEPI3+ Score and immune response rate was then confirmed by the analysis of 59 clinical trials involving 1,343 subjects who were treated with 40 different vaccines. Each vaccine was analyzed by comparing the published IRR from the clinical trial to the PEPI Score from the model population (FIG. 10B). The correlation between the IRR and PEPI Score was significant ($r^2=0.465$ and $p=0.001$). This result demonstrated that the PEPI Score determined by *in silico* trials in the MP accurately predicts the IRRs observed in clinical trials.

To test whether polyclonal T cell response increases the likelihood of tumor shrinkage, ORR and MultiPEPI Score were compared. Preliminary experiments analyzed the relationship between clinical response (either ORR or DCR) and MultiPEPI Score in 17 clinical trials conducted with peptide- and DNA-based immunotherapy vaccines. The results from these experiments demonstrated a significant correlation between clinical response rate and MultiPEPI Score ($r^2 = 0.75$, $p<0.001$). To confirm these findings, ORR data from 27 clinical trials with 21 different vaccines, involving 600 subjects, were collected and analyzed (**Error! Reference source not found.**). The MultiPEPI Score was calculated as the percentage of subjects in the model population with multiple PEPIs from the study vaccine. The results from this experiment

demonstrated that ORR does not correlate with MultiPEPI Score (**Error! Reference source not found.**).

Results from previous studies suggested that T cell responses against multiple antigens were associated with longer progression free- and overall survival. Consequently, we hypothesized that the induction of T cell responses against multiple tumor antigens increases the likelihood of tumor shrinkage. To test this hypothesis, ORR data from 10 clinical trials conducted with 9 different vaccines, involving 263 subjects, that were treated with multiantigen-targeting vaccine were collected and analyzed. The MultiAg PEPI Score was calculated as the percentage of subjects with vaccine-specific PEPIs on at least two antigens. The results from this experiment demonstrated a significant correlation between ORR and MultiAg PEPI Score ($r^2=0.64$; $p=0.01$), and ORR and MultiPEPI Score ($r^2=0.88$ and $p=0.001$) (**Error! Reference source not found.** and F, respectively). These results suggest that T cell responses against multiple tumor antigens may recognize a larger tumor cell population, thereby increasing the likelihood of tumor shrinkage.

The next analysis explored whether PEPI-specific T cell responses against antigens expressed in the tumor of interest, increase the likelihood of tumor shrinkage. A total of 15 clinical trials enrolled subjects with target antigen positive disease and 11 clinical trials had no subject preselection based on antigen expression. The proportion of subjects with objective response was significantly higher in CTs with target antigen-positive subjects compared with CTs without pre-selection (21.0% vs. 3.6%, respectively, $p=0.03$)

The correlation between ORR and MultiPEPI Score was statistically significant in subjects with confirmed expression of target antigens ($r^2=0.56$, $p=0.005$) (FIG. 10G). These results emphasize the importance of the presence of cognate PEPI in the tumor, and also that the presence of the cognate PEPI in the tumor increases the likelihood of tumor shrinkage.

This study demonstrated that the link between a subject's HLA genotype and PEPI is the most important factor in predicting clinical response to a vaccine. This study also showed that the PEPI Score can predict the clinical outcome of therapeutic vaccines.

Example 12 - Study design of OBERTO Phase I/II Clinical Trial and preliminary safety data

OBERTO trial is a Phase I/II trial of PolyPEPI1018 Vaccine and CDx for the Treatment of Metastatic Colorectal Cancer (NCT03391232). Study design is shown on FIG. 11.

Enrollment criteria

- Histologically confirmed metastatic adenocarcinoma originating from the colon or the rectum
- Presence of at least 1 measurable reference lesion according to RECIST 1.1
- PR or stable disease during first-line treatment with a systemic chemotherapy regimen and 1 biological therapy regimen
- Maintenance therapy with a fluoropyrimidine (5-fluorouracil or capecitabine) plus the same biologic agent (bevacizumab, cetuximab or panitumumab) used during induction, scheduled to initiate prior to the first day of treatment with the study drug
- Last CT scan at 3 weeks or less before the first day of treatment

10 Subject Withdrawal and Discontinuation.

- During the initial study period (12W), if a patient experiences disease progression and needs to start a second-line therapy, the patient will be withdrawn from the study.
- During the second part of the study (after 2nd dose) if a patient experiences disease progression and needs to start a second-line therapy, the patient will remain in the study, receive the third vaccination as scheduled and complete follow-up.
- Transient local erythema and edema at the site of vaccination were observed as expected, as well as a flu-like syndrome with minor fever and fatigue. These reactions are already well-known for peptide vaccination and usually are associated with the mechanism of action, because fever and flu-like syndrome might be the consequence and sign for the induction of immune responses (this is known as typical vaccine reactions for childhood vaccinations).
- Only one serious adverse event (SAE) “possibly related” to the vaccine was recorded (Table 21).
- One dose limiting toxicity (DLT) not related to the vaccine occurred (syncope).

25

Safety results are summarized in Table 21.

Table 21. Serious adverse events reported in the OBERTO clinical trial. No related SAE occurred (only 1 “possibly related”).

Patient ID	SAE	Relatedness
010001	Death due to disease progression	Unrelated
010004	Embolism	Unlikely Related
010004	Abdominal pain	Unrelated

010007	Bowel Obstruction	Unrelated
020004	Non-Infectious Acute Encephalitis	Possibly Related

Example 13 – Expression frequency based target antigen selection during vaccine design and it's clinical validation for mCRC

Shared tumor antigens enable precise targeting of all tumor types – including the ones
 5 with low mutational burden. Population expression data collected previously from 2,391 CRC
 biopsies represents the variability of antigen expression in CRC patients worldwide (FIG. 12A).

PolyPEPI1018 is a peptide vaccine we designed to contain 12 unique epitopes derived from
 7 conserved testis specific antigens (TSAs) frequently expressed in mCRC. In our model we
 supposed, that by selecting the TSA frequently expressed in CRC, the target identification will be
 10 correct and will eliminate the need for tumor biopsy. We have calculated that the probability of 3
 out of 7 TSAs being expressed in each tumor is greater than 95%. (FIG. 12B)

In a phase I study we evaluated the safety, tolerability and immunogenicity of
 PolyPEPI1018 as an add-on to maintenance therapy in subjects with metastatic colorectal cancer
 (mCRC) (NCT03391232) (See also in Example 4).

15 Immunogenicity measurements proved pre-existing immune responses and indirectly
 confirmed target antigen expression in the patients. Immunogenicity was measured with enriched
 Fluorospot assay (ELISPOT) from PBMC samples isolated prior to vaccination and in different
 time points following a following single immunization with PolyPEPI1018 to confirm vaccine-
 induced T cell responses; PBMC samples were *in vitro* stimulated with vaccine-specific peptides
 20 (9mers and 30mers) to determine vaccine-induced T cell responses above baseline. In average 4,
 at least 2 patients had pre-existing CD8 T cell responses against each target antigen (FIG. 12C). 7
 out of 10 patients had pre-existing immune responses against at least 1 antigen (average 3) (FIG
 12D). These results provide proof for the proper target selection, because CD8+ T cell response
 for a CRC specific target TSA prior to vaccination with PolyPEPI1018 vaccine confirms the
 25 expression of that target antigen in the analyzed patient. Targeting the real (expressed) TSAs is the
 prerequisite for an effective tumor vaccine.

Example 14 - Pre-clinical and Clinical Immunogenicity of PolyPEPI1018 Vaccine proves proper peptide selection

30 PolyPEPI1018 vaccine contains six 30mer peptides, each designed by joining two
 immunogenic 15mer fragments (each involving a 9mer PEPI, consequently there are 2 PEPIs in

each 30mer by design) derived from 7 TSAs (FIG 13). These antigens are frequently expressed in CRC tumors based on analysis of 2,391 biopsies (FIG 12).

Preclinical immunogenicity results calculated for the Model Population (n=433) and for a CRC cohort (n=37) resulted in 98% and 100% predicted immunogenicity based on PEPI test predictions and this was clinically proved in the OBERTO trial (n=10), with immune responses measured for at least one antigen in 90% of patients. More interestingly, 90% of patients had vaccine peptide specific immune responses against at least 2 antigens and 80% had CD8+ T cell response against 3 or more different vaccine antigens, showing evidence for appropriate target antigen selection during the design of PolyPEPI1018. CD4+ T cell specific and CD8+ T cell specific clinical immunogenicity is detailed in Table 22. High immune response rates were found for both effector and memory effector T cells, both for CD4+ and CD8+ T cells, and 9 of 10 patients' immune responses were boosted or *de novo* induced by the vaccine. Also, the fractions of CRC-reactive, polyfunctional CD8+ and CD4+ T cells have been increased in patient's PBMC after vaccination by 2.5- and 13-fold, respectively.

Table 22. Clinical immunogenicity results for PolyPEPI1018 in mCRC.

Immunological responses	% Patients (n)
CD4+ T cell responses	100% (10/10)
CD8+ T cell responses against ≥3 antigens	80% (8/10)
Both CD8+ and CD4+ T cell responses	90% (9/10)
<i>Ex vivo</i> detected CD8+ T cell response	71% (5/7)
<i>Ex vivo</i> detected CD4+ T cell response	86% (6/7)
Average increase of the fraction of polyfunctional (IFN- γ and TNF- α positive) CD8+ T cells compared to pre-vaccination	0.39%
Average increase of the fraction of polyfunctional (IL-2 and TNF- α positive) CD4+ T cells compared to pre-vaccination	0.066%

Example 15 - Clinical response for PolyPEPI1018 treatment

The OBERTO clinical trial (NCT03391232), that has been further described in Examples 4, 12, 13 and 14 was analyzed for preliminary objective tumor response rates (RECIST 1.1) (FIG. 14). Of the eleven vaccinated patients on maintenance therapy, 5 had stable disease (SD) at the time point of the preliminary analysis (12 weeks), 3 experienced unexpected tumor responses (partial response, PR) observed on treatment (maintenance therapy + vaccination) and 3 had

progressed disease (PD) according to RECIST 1.1 criteria. Stable disease as best response was achieved in 69% of patients on maintenance therapy (capecitabine and bevacizumab). Patient 020004 had durable treatment effect after 12 weeks, and patient 010004 had long lasting treatment effect, qualified for curative surgery. Following the 3rd vaccination this patient had no evidence of disease thus being complete responder, as shown on the swimmer plot on FIG. 14.

After one vaccination, ORR was 27%, DCR was 63%, and in patients receiving at least 2 doses (out of the 3 doses), 2 of 5 had ORR (40%) and DCR was as high as 80% (SD+PR+CR in 4 out of 5 patients) (Table 23).

Table 23. Clinical response for PolyPEPI1018 treatment after ≥ 1 and ≥ 2 vaccination dose

Number of vaccination dose	Objective Response Rate (CR+PR)	Disease Control Rate (SD + PR+CR)
≥ 1	27% (3/11)	63% (7/11)
≥ 2	40% (2/5)	80% (4/5)

Based on the data of the 5 patients receiving multiple doses of PolyPEPI1018 vaccine in the OBERTO-101 clinical trial, preliminary data suggests that higher AGP count (>2) is associated with longer PFS and elevated tumor size reduction (FIG.14B and C).

Example 16 – Selection of peptides for treatment of cancer

Based on the discovery of the role of PEPs in T cell activation as described herein, a method was developed for designing peptides for the treatment of cancer. Specifically the peptides were designed to stimulate T cell responses against known tumor associated antigens in the maximum number of human subjects.

192 TSAs were selected that are known to be expressed in one or more of 19 cancer indications (Table 24). Data concerning expression rates of the TSA in the different cancer indications, where available in peer reviewed publications, was used to rank the TSA in each indication by expression frequency. The ranking order for the TSA is different in each indication.

Table 24 – TSA by indication and Expression Rate (ER)

BREAST				LUNG				PROSTATE			
#	AG ID NO	Antigen	%	#	AG ID NO	Antigen	%	#	AG ID NO	Antigen	%
1	111	PIWIL1	100%	1	179	KIF20A	95%	1	115	PLAC1	100%
2	112	PIWIL2	94%	2	173	CEP55	94%	2	112	PIWIL2	100%
3	131	SPAG9	88%	3	32	DCAF12	89%	3	106	PAGE4	100%
4	8	AKAP-4	85%	4	19	CDCA1	85%	4	62	JARID1B	100%

5	36	EpCAM	76%	5	36	EpCAM	78%	5	36	EpCAM	98%
6	62	JARID1B	76%	6	130	SPAG1	71%	6	27	CTCFL	98%
7	27	CTCFL	74%	7	192	ZNF645	68%	7	133	SPATA19	88%
8	154	TSGA10	70%	8	115	PLAC1	68%	8	19	CDCA1	85%
9	140	Survivin	68%	9	112	PIWIL2	66%	9	140	Survivin	83%
10	19	CDCA1	64%	10	116	PRAME	63%	10	92	NKX3.1	70%
11	102	ODF4	63%	11	63	KOC1	62%	11	8	AKAP-4	65%
12	110	PEPP2	60%	12	140	Survivin	59%	12	32	DCAF12	59%
13	71	MAGE-A11	59%	13	131	SPAG9	56%	13	145	TDRD1	47%
14	160	XAGE-1	58%	14	62	JARID1B	55%	14	31	DBPC	40%
15	42	FMR1NB	55%	15	153	TRAG-3	54%	15	66	LDHC	38%
16	168	ATAD2	52%	16	77	MAGE-A6	51%	16	20	CRISP2	38%
17	191	WBP2NL	50%	17	39	FAM46D	50%	17	90	MUC-1	34%
18	31	DBPC	50%	18	171	CCDC110	50%	18	39	FAM46D	33%
19	116	PRAME	49%	19	22	CT46	47%	19	108	PASD1	29%
20	59	HOM-TES-85	47%	20	7	AKAP-3	46%	20	136	SSX-2	28%
21	96	NY-BR-1	47%	21	81	MAGE-B2	43%	21	130	SPAG1	27%
22	129	SP17	47%	22	161	XAGE-1b	43%	22	94	NR6A1	25%
23	79	MAGE-A9	44%	23	185	SPAG8	43%	23	4	ADAM2	25%
24	43	FSIP1	42%	24	69	MAGE-A1	42%	24	34	DMRT1	24%
25	2	ACRBP	40%	25	170	CASC5	41%	25	67	LEMD1	23%
26	7	AKAP-3	40%	26	73	MAGE-A2	40%	26	77	MAGE-A6	23%
27	145	TDRD1	38%	27	177	HSPB9	40%	27	55	HAGE	22%
28	41	FBXO39	38%	28	93	NLRP4	38%	28	18	CCDC62	22%
29	123	SCP-1	37%	29	64	KU-CT-1	38%	29	98	NY-ESO-1	21%
30	66	LDHC	35%	30	14	BRDT	37%	30	73	MAGE-A2	18%
31	67	LEMD1	35%	31	74	MAGE-A3	37%	31	154	TSGA10	15%
32	70	MAGE-A10	34%	32	152	TPTE	36%	32	74	MAGE-A3	15%
33	69	MAGE-A1	31%	33	27	CTCFL	36%	33	95	NXF2	14%
34	49	GAGE-7	31%	34	30	CXorf61	34%	34	69	MAGE-A1	13%
35	130	SPAG1	31%	35	55	HAGE	32%	35	149	TEX15	13%
36	22	CT46	29%	36	21	CT45	32%	36	33	DKKL1	13%
37	185	SPAG8	29%	37	150	THEG	31%	37	146	TEKT5	11%
38	74	MAGE-A3	28%	38	158	VCX	31%	38	129	SP17	10%
39	138	SSX-4	27%	39	72	MAGE-A12	31%	39	116	PRAME	10%
40	132	SPAN-Xc	26%	40	31	DBPC	30%	40	100	ODF2	10%
41	184	SPAG6	21%	41	35	DPPA2	30%	41	99	ODF1	10%
42	33	DKKL1	20%	42	20	CRISP2	29%	42	70	MAGE-A10	10%
43	86	MAGE-C2	19%	43	184	SPAG6	29%	43	64	KU-CT-1	10%
44	85	MAGE-C1	16%	44	108	PASD1	29%	44	65	Lage-1	8%
45	20	CRISP2	15%	45	66	LDHC	29%	45	135	SSX-1	7%
46	98	NY-ESO-1	15%	46	51	GASZ	29%	46	86	MAGE-C2	6%
47	77	MAGE-A6	15%	47	65	Lage-1	28%	47	72	MAGE-A12	5%
48	21	CT45	15%	48	42	FMR1NB	28%	48	111	PIWIL1	4%
49	55	HAGE	14%	49	75	MAGE-A4	27%	49	2	ACRBP	4%

50	44	FTHL17	14%	50	86	MAGE-C2	27%	50	117	PRSS55	1%
51	30	CXorf61	13%	51	160	XAGE-1	25%	51	142	TAF7L	0%
52	65	Lage-1	12%	52	44	FTHL17	25%	52	134	SPO11	0%
53	72	MAGE-A12	12%	53	8	AKAP-4	25%	53	102	ODF4	0%
54	153	TRAG-3	10%	54	70	MAGE-A10	24%	54	101	ODF3	0%
55	10	BAGE-1	9%	55	167	COX6B2	24%	55	88	MORC1	0%
56	135	SSX-1	9%	56	168	ATAD2	23%	56	81	MAGE-B2	0%
57	75	MAGE-A4	9%	57	166	ZNF165	21%	57	80	MAGE-B1	0%
58	76	MAGE-A5	9%	58	149	TEX15	21%	58	75	MAGE-A4	0%
59	63	KOC1	8%	59	182	PTTG-1	20%	59	63	KOC1	0%
60	136	SSX-2	7%	60	2	ACRBP	20%	60	44	FTHL17	0%
61	159	WT1	7%	61	85	MAGE-C1	19%	61	42	FMR1NB	0%
62	127	SLCO6A1	7%	62	88	MORC1	18%	62	10	BAGE-1	0%
63	115	PLAC1	4%	63	98	NY-ESO-1	17%	63	168	ATAD2	0%
64	23	CT47	4%	64	132	SPAN-Xc	17%	CRC			
65	121	SAGE1	2%	65	169	CABYR	16%	#	AG ID NO	Antigen	%
66	95	NXF2	2%	66	111	PIWIL1	15%	1	180	MCAK	100%
67	149	TEX15	0%	67	95	NXF2	15%	2	113	PIWIL3	96%
68	147	TEX101	0%	68	29	CXorf48	15%	3	67	LEMD1	94%
69	142	TAF7L	0%	69	121	SAGE1	15%	4	159	WT1	91%
70	139	SSX-5	0%	70	23	CT47	14%	5	31	DBPC	90%
71	137	SSX-3	0%	71	16	CAGE1	14%	6	155	TSP50	89%
72	134	SPO11	0%	72	80	MAGE-B1	13%	7	36	EpCAM	88%
73	101	ODF3	0%	73	138	SSX-4	13%	8	140	Survivin	87%
74	88	MORC1	0%	74	163	XAGE-1d	13%	9	1	5T4	85%
75	17	CALR3	0%	75	61	IL13RA2	12%	10	7	AKAP-3	83%
76	4	ADAM2	0%	76	33	DKKL1	12%	11	27	CTCFL	80%
OVARIAN				77	129	SP17	12%	12	112	PIWIL2	80%
#	AG ID NO	Antigen	%	78	141	SYCE1	11%	13	16	CAGE1	74%
1	36	EpCAM	92%	79	59	HOM-TES-85	11%	14	8	AKAP-4	74%
2	131	SPAG9	90%	80	10	BAGE-1	10%	15	131	SPAG9	71%
3	8	AKAP-4	89%	81	136	SSX-2	10%	16	63	KOC1	65%
4	113	PIWIL3	88%	82	146	TEKT5	10%	17	2	ACRBP	63%
5	140	Survivin	85%	83	142	TAF7L	9%	18	168	ATAD2	58%
6	153	TRAG-3	83%	84	17	CALR3	9%	19	130	SPAG1	55%
7	27	CTCFL	82%	85	135	SSX-1	8%	20	60	IGFS11	55%
8	62	JARID1B	71%	86	113	PIWIL3	7%	21	146	TEKT5	50%
9	111	PIWIL1	68%	87	5	ADAM29	7%	22	171	CCDC110	50%
10	2	ACRBP	65%	88	127	SLCO6A1	7%	23	111	PIWIL1	48%
11	179	KIF20A	65%	89	145	TDRD1	5%	24	108	PASD1	44%
12	159	WT1	63%	90	176	HORMAD2	5%	25	78	MAGE-A8	44%
13	129	SP17	62%	91	139	SSX-5	4%	26	35	DPPA2	44%
14	112	PIWIL2	61%	92	123	SCP-1	1%	27	166	ZNF165	43%
15	116	PRAME	59%	93	4	ADAM2	1%	28	177	HSPB9	40%
16	33	DKKL1	57%	94	162	XAGE-1c	0%	29	19	CDCA1	40%

17	7	AKAP-3	48%	95	156	TSPY1	0%	30	41	FBXO39	39%
18	66	LDHC	43%	96	134	SPO11	0%	31	106	PAGE4	33%
19	63	KOC1	43%	97	83	MAGE-B4	0%	32	26	cTAGE5	31%
20	70	MAGE-A10	38%	98	82	MAGE-B3	0%	33	97	NYD-TSPG	30%
21	79	MAGE-A9	37%	99	68	LIPI	0%	34	115	PLAC1	27%
22	75	MAGE-A4	37%	100	41	FBXO39	0%	35	132	SPAN-Xc	24%
23	154	TSGA10	35%	101	40	FATE1	0%	36	51	GASZ	22%
24	143	TAG-1	35%	BLADDER				37	39	FAM46D	22%
25	21	CT45	33%	#	AG ID NO	Antigen	%	38	77	MAGE-A6	22%
26	59	HOM-TES-85	32%	1	19	CDCA1	100%	39	74	MAGE-A3	22%
27	130	SPAG1	31%	2	89	MPHOSPH1	90%	40	40	FATE1	21%
28	35	DPPA2	31%	3	112	PIWIL2	82%	41	24	CTAGE1	19%
29	74	MAGE-A3	30%	4	131	SPAG9	81%	42	75	MAGE-A4	18%
30	124	SCP3a	25%	5	140	Survivin	62%	43	73	MAGE-A2	18%
31	69	MAGE-A1	24%	6	79	MAGE-A9	61%	44	29	CXorf48	17%
32	98	NY-ESO-1	23%	7	78	MAGE-A8	57%	45	17	CALR3	16%
33	65	Lage-1	22%	8	36	EpCAM	54%	46	66	LDHC	15%
34	115	PLAC1	21%	9	24	CTAGE1	53%	47	55	HAGE	15%
35	31	DBPC	20%	10	25	CTAGE2	49%	48	69	MAGE-A1	14%
36	85	MAGE-C1	20%	11	109	PBK	43%	49	65	Lage-1	13%
37	161	XAGE-1b	18%	12	74	MAGE-A3	42%	50	18	CCDC62	13%
38	123	SCP-1	15%	13	154	TSGA10	38%	51	107	PAGE5	11%
39	88	MORC1	14%	14	69	MAGE-A1	34%	52	21	CT45	10%
40	20	CRISP2	14%	15	98	NY-ESO-1	31%	53	95	NXF2	9%
41	144	TAG-2a	13%	16	65	Lage-1	30%	54	119	RAGE-1	8%
42	138	SSX-4	13%	17	72	MAGE-A12	29%	55	76	MAGE-A5	7%
43	162	XAGE-1c	11%	18	145	TDRD1	29%	56	22	CT46	7%
44	136	SSX-2	7%	19	2	ACRBP	28%	57	153	TRAG-3	7%
45	73	MAGE-A2	7%	20	70	MAGE-A10	28%	58	72	MAGE-A12	6%
46	163	XAGE-1d	6%	21	85	MAGE-C1	27%	59	123	SCP-1	6%
47	160	XAGE-1	5%	22	75	MAGE-A4	27%	60	136	SSX-2	5%
48	135	SSX-1	2%	23	77	MAGE-A6	25%	61	154	TSGA10	5%
49	139	SSX-5	0%	24	73	MAGE-A2	25%	62	86	MAGE-C2	4%
50	137	SSX-3	0%	25	55	HAGE	24%	63	152	TPTE	4%
51	134	SPO11	0%	26	44	FTHL17	22%	64	116	PRAME	4%
52	132	SPAN-Xc	0%	27	149	TEX15	21%	65	98	NY-ESO-1	3%
53	18	CCDC62	0%	28	63	KOC1	20%	66	70	MAGE-A10	3%
54	4	ADAM2	0%	29	22	CT46	20%	67	135	SSX-1	2%
PANCREATIC				30	116	PRAME	19%	68	139	SSX-5	2%
#	AG ID NO	Antigen	%	31	86	MAGE-C2	19%	69	85	MAGE-C1	1%
1	171	CCDC110	100%	32	95	NXF2	19%	70	121	SAGE1	1%
2	181	MSLN	96%	33	136	SSX-2	13%	71	149	TEX15	0%
3	130	SPAG1	93%	34	121	SAGE1	12%	72	145	TDRD1	0%
4	36	EpCAM	85%	35	138	SSX-4	11%	73	142	TAF7L	0%
5	174	DKK1	84%	36	142	TAF7L	10%	74	137	SSX-3	0%

6	140	Survivin	83%	37	132	SPAN-Xc	9%	75	134	SPO11	0%
7	159	WT1	72%	38	135	SSX-1	7%	76	104	PAGE1	0%
8	111	PIWIL1	71%	39	123	SCP-1	2%	77	88	MORC1	0%
9	179	KIF20A	63%	40	156	TSPY1	0%	78	81	MAGE-B2	0%
10	1	5T4	62%	41	81	MAGE-B2	0%	79	80	MAGE-B1	0%
11	31	DBPC	60%	42	80	MAGE-B1	0%	80	68	LIPI	0%
12	172	CEA	60%	43	59	HOM-TES-85	0%	81	44	FTHL17	0%
13	63	KOC1	54%	LEUKEMIAS				82	33	DKKL1	0%
14	115	PLAC1	44%	#	AG ID NO	Antigen	%	83	20	CRISP2	0%
15	64	KU-CT-1	33%	1	131	SPAG9	100%	84	10	BAGE-1	0%
16	123	SCP-1	31%	2	38	FAM133A	83%	85	4	ADAM2	0%
17	27	CTCF	29%	3	26	cTAGE5	74%	86	10	BAGE-1	0%
18	69	MAGE-A1	27%	4	24	CTAGE1	72%	87	4	ADAM2	0%
19	170	CASC5	27%	5	85	MAGE-C1	70%	LYMPHOMAS			
20	178	hTERT	21%	6	74	MAGE-A3	65%	#	AG ID NO	Antigen	%
21	138	SSX-4	21%	7	98	NY-ESO-1	65%	1	123	SCP-1	39%
22	46	GAGE-2	17%	8	62	JARID1B	60%	2	74	MAGE-A3	17%
23	74	MAGE-A3	11%	9	166	ZNF165	52%	3	138	SSX-4	16%
24	65	Lage-1	7%	10	65	Lage-1	49%	4	136	SSX-2	16%
25	136	SSX-2	4%	11	124	SCP3a	47%	5	59	HOM-TES-85	14%
26	98	NY-ESO-1	4%	12	28	CTNNA2	45%	6	85	MAGE-C1	13%
27	75	MAGE-A4	2%	13	86	MAGE-C2	37%	7	98	NY-ESO-1	11%
28	70	MAGE-A10	1%	14	75	MAGE-A4	36%	8	69	MAGE-A1	9%
29	137	SSX-3	0%	15	135	SSX-1	31%	9	135	SSX-1	6%
30	135	SSX-1	0%	16	138	SSX-4	30%	10	156	TSPY1	0%
31	132	SPAN-Xc	0%	17	139	SSX-5	24%	11	86	MAGE-C2	0%
32	85	MAGE-C1	0%	18	116	PRAME	23%	PEDIATRIC			
BRAIN				19	72	MAGE-A12	21%	#	AG ID NO	Antigen	%
#	AG ID NO	Antigen	%	20	69	MAGE-A1	20%	1	37	EPHA2	100%
1	166	ZNF165	100%	21	136	SSX-2	12%	2	77	MAGE-A6	80%
2	109	PBK	100%	22	156	TSPY1	12%	3	135	SSX-1	76%
3	178	hTERT	100%	23	123	SCP-1	11%	4	74	MAGE-A3	76%
4	175	EZH2	100%	24	73	MAGE-A2	11%	5	116	PRAME	75%
5	37	EPHA2	95%	25	79	MAGE-A9	9%	6	122	SART3	73%
6	61	IL13RA2	95%	26	68	LIPI	6%	7	138	SSX-4	67%
7	157	TYR	91%	27	4	ADAM2	6%	8	73	MAGE-A2	60%
8	140	Survivin	87%	28	148	TEX14	5%	9	61	IL13RA2	58%
9	54	gp100	85%	29	80	MAGE-B1	5%	10	160	XAGE-1	53%
10	71	MAGE-A11	85%	30	105	PAGE2	4%	11	136	SSX-2	44%
11	154	TSGA10	83%	31	132	SPAN-Xc	4%	12	69	MAGE-A1	44%
12	44	FTHL17	82%	32	137	SSX-3	4%	13	98	NY-ESO-1	42%
13	159	WT1	81%	33	83	MAGE-B4	3%	14	75	MAGE-A4	41%
14	111	PIWIL1	76%	34	70	MAGE-A10	0%	15	72	MAGE-A12	41%
15	112	PIWIL2	64%	MELANOMA				16	86	MAGE-C2	40%
16	165	XAGE-3	60%	#	AG ID NO	Antigen	%	17	85	MAGE-C1	39%

17	131	SPAG9	60%	1	62	JARID1B	100%	18	70	MAGE-A10	33%
18	128	SOX-6	60%	2	140	Survivin	96%	19	164	XAGE-2	14%
19	179	KIF20A	58%	3	116	PRAME	90%	20	65	Lage-1	7%
20	116	PRAME	56%	4	87	MART1	89%	Kidney			
21	3	ACTL8	54%	5	157	TYR	87%	#	AG ID NO	Antigen	%
22	1	5T4	50%	6	54	gp100	82%	1	19	CDCA1	100%
23	103	OIP5	48%	7	132	SPAN-Xc	70%	2	131	SPAG9	88%
24	186	SPINLW1	47%	8	77	MAGE-A6	65%	3	17	CALR3	80%
25	74	MAGE-A3	42%	9	179	KIF20A	64%	4	66	LDHC	57%
26	45	GAGE-1	42%	10	151	TMEM31	63%	5	36	EpCAM	55%
27	69	MAGE-A1	41%	11	73	MAGE-A2	62%	6	79	MAGE-A9	55%
28	63	KOC1	38%	12	74	MAGE-A3	60%	7	111	PIWIL1	52%
29	55	HAGE	38%	13	119	RAGE-1	60%	8	112	PIWIL2	49%
30	29	CXorf48	35%	14	171	CCDC110	60%	9	107	PAGE5	44%
31	86	MAGE-C2	34%	15	71	MAGE-A11	54%	10	116	PRAME	40%
32	108	PASD1	31%	16	161	XAGE-1b	50%	11	140	Survivin	40%
33	73	MAGE-A2	28%	17	72	MAGE-A12	49%	12	119	RAGE-1	37%
34	127	SLCO6A1	19%	18	63	KOC1	46%	13	149	TEX15	33%
35	160	XAGE-1	18%	19	85	MAGE-C1	45%	14	74	MAGE-A3	27%
36	95	NXF2	18%	20	70	MAGE-A10	45%	15	68	LPII	25%
37	36	EpCAM	16%	21	86	MAGE-C2	45%	16	18	CCDC62	25%
38	123	SCP-1	14%	22	108	PASD1	44%	17	63	KOC1	22%
39	129	SP17	13%	23	17	CALR3	44%	18	75	MAGE-A4	17%
40	85	MAGE-C1	13%	24	66	LDHC	44%	19	20	CRISP2	14%
41	134	SPO11	12%	25	163	XAGE-1d	43%	20	64	KU-CT-1	13%
42	75	MAGE-A4	11%	26	98	NY-ESO-1	37%	21	130	SPAG1	11%
43	59	HOM-TES-85	10%	27	69	MAGE-A1	37%	22	69	MAGE-A1	11%
44	27	CTCF1	9%	28	136	SSX-2	35%	23	31	DBPC	10%
45	39	FAM46D	8%	29	65	Lage-1	35%	24	4	ADAM2	9%
46	84	MAGE-B6	6%	30	75	MAGE-A4	30%	25	123	SCP-1	8%
47	136	SSX-2	4%	31	162	XAGE-1c	29%	26	73	MAGE-A2	7%
48	138	SSX-4	4%	32	39	FAM46D	28%	27	55	HAGE	6%
49	98	NY-ESO-1	4%	33	149	TEX15	27%	28	156	TSPY1	5%
50	65	Lage-1	2%	34	27	CTCF1	27%	29	121	SAGE1	5%
51	153	TRAG-3	0%	35	10	BAGE-1	26%	30	72	MAGE-A12	4%
52	152	TPTE	0%	36	154	TSGA10	25%	31	98	NY-ESO-1	2%
53	187	SSX-7	0%	37	135	SSX-1	25%	32	136	SSX-2	2%
54	139	SSX-5	0%	38	76	MAGE-A5	25%	33	65	Lage-1	2%
55	137	SSX-3	0%	39	33	DKKL1	25%	34	70	MAGE-A10	1%
56	135	SSX-1	0%	40	11	BAGE-2	23%	35	145	TDRD1	0%
57	121	SAGE1	0%	41	107	PAGE5	22%	36	142	TAF7L	0%
58	87	MART1	0%	42	81	MAGE-B2	22%	37	139	SSX-5	0%
59	83	MAGE-B4	0%	43	142	TAF7L	21%	38	138	SSX-4	0%
60	81	MAGE-B2	0%	44	138	SSX-4	21%	39	137	SSX-3	0%
61	80	MAGE-B1	0%	45	80	MAGE-B1	19%	40	135	SSX-1	0%

62	30	CXorf61	0%	46	88	MORC1	19%	41	134	SPO11	0%
63	21	CT45	0%	47	55	HAGE	17%	42	95	NXF2	0%
64	14	BRDT	0%	48	51	GASZ	17%	43	88	MORC1	0%
65	80	MAGE-B1	0%	49	123	SCP-1	16%	44	85	MAGE-C1	0%
66	30	CXorf61	0%	50	164	XAGE-2	14%	45	81	MAGE-B2	0%
67	21	CT45	0%	51	12	BAGE-3	14%	46	80	MAGE-B1	0%
68	14	BRDT	0%	52	164	XAGE-2	14%	47	77	MAGE-A6	0%
HCC				53	12	BAGE-3	14%	48	44	FTHL17	0%
#	AG ID NO	Antigen	%	54	79	MAGE-A9	12%	49	42	FMR1NB	0%
1	19	CDCA1	100%	55	78	MAGE-A8	10%	50	33	DKKL1	0%
2	129	SP17	87%	56	13	BAGE-5	9%	51	14	BRDT	0%
3	159	WT1	86%	57	95	NXF2	8%	52	10	BAGE-1	0%
4	2	ACRBP	70%	58	160	XAGE-1	7%	53	2	ACRBP	0%
5	135	SSX-1	69%	59	134	SPO11	6%	HEAD and NECK			
6	63	KOC1	66%	60	20	CRISP2	6%	#	AG ID NO	Antigen	%
7	109	PBK	64%	61	139	SSX-5	5%	1	140	Survivin	91%
8	81	MAGE-B2	61%	62	121	SAGE1	5%	2	171	CCDC110	67%
9	132	SPAN-Xc	60%	63	4	ADAM2	3%	3	116	PRAME	61%
10	146	TEKT5	60%	64	165	XAGE-3	0%	4	77	MAGE-A6	58%
11	60	IGFS11	60%	65	145	TDRD1	0%	5	81	MAGE-B2	45%
12	69	MAGE-A1	56%	66	68	LIPI	0%	6	79	MAGE-A9	44%
13	27	CTCFL	55%	67	64	KU-CT-1	0%	7	75	MAGE-A4	42%
14	140	Survivin	54%	68	44	FTHL17	0%	8	160	XAGE-1	40%
15	166	ZNF165	52%	69	168	ATAD2	0%	9	135	SSX-1	40%
16	131	SPAG9	52%	GASTRIC				10	74	MAGE-A3	40%
17	171	CCDC110	50%	#	AG ID NO	Antigen	%	11	45	GAGE-1	39%
18	7	AKAP-3	50%	1	140	Survivin	100%	12	73	MAGE-A2	38%
19	40	FATE1	49%	2	35	DPPA2	100%	13	71	MAGE-A11	37%
20	138	SSX-4	48%	3	171	CCDC110	100%	14	72	MAGE-A12	34%
21	80	MAGE-B1	47%	4	36	EpCAM	90%	15	63	KOC1	29%
22	136	SSX-2	46%	5	7	AKAP-3	89%	16	138	SSX-4	29%
23	78	MAGE-A8	45%	6	60	IGFS11	88%	17	86	MAGE-C2	29%
24	36	EpCAM	41%	7	30	CXorf61	80%	18	29	CXorf48	27%
25	115	PLAC1	41%	8	16	CAGE1	77%	19	69	MAGE-A1	23%
26	111	PIWIL1	40%	9	111	PIWIL1	76%	20	145	TDRD1	22%
27	31	DBPC	40%	10	155	TSP50	57%	21	55	HAGE	20%
28	16	CAGE1	39%	11	1	5T4	52%	22	98	NY-ESO-1	20%
29	152	TPTE	39%	12	63	KOC1	52%	23	121	SAGE1	17%
30	86	MAGE-C2	37%	13	31	DBPC	50%	24	136	SSX-2	17%
31	139	SSX-5	37%	14	103	OIP5	48%	25	85	MAGE-C1	15%
32	65	Lage-1	36%	15	108	PASD1	44%	26	70	MAGE-A10	12%
33	77	MAGE-A6	36%	16	168	ATAD2	43%	27	165	XAGE-3	12%
34	72	MAGE-A12	36%	17	146	TEKT5	40%	28	123	SCP-1	12%
35	71	MAGE-A11	36%	18	17	CALR3	40%	29	103	OIP5	12%
36	156	TSPY1	35%	19	74	MAGE-A3	37%	30	18	CCDC62	12%

37	74	MAGE-A3	34%	20	73	MAGE-A2	31%	31	65	Lage-1	11%
38	160	XAGE-1	33%	21	69	MAGE-A1	31%	32	20	CRISP2	11%
39	62	JARID1B	29%	22	70	MAGE-A10	30%	33	149	TEX15	11%
40	153	TRAG-3	26%	23	75	MAGE-A4	24%	34	142	TAF7L	10%
41	123	SCP-1	25%	24	138	SSX-4	23%	35	44	FTHL17	10%
42	73	MAGE-A2	25%	25	29	CXorf48	21%	36	49	GAGE-7	9%
43	29	CXorf48	25%	26	116	PRAME	21%	37	139	SSX-5	7%
44	154	TSGA10	20%	27	123	SCP-1	14%	38	130	SPAG1	7%
45	85	MAGE-C1	20%	28	65	Lage-1	14%	39	10	BAGE-1	6%
46	59	HOM-TES-85	19%	29	135	SSX-1	13%	40	164	XAGE-2	6%
47	98	NY-ESO-1	17%	30	98	NY-ESO-1	12%	41	107	PAGE5	6%
48	70	MAGE-A10	15%	31	39	FAM46D	11%	42	95	NXF2	5%
49	188	TDRD4	14%	32	153	TRAG-3	10%	43	59	HOM-TES-85	4%
50	130	SPAG1	11%	33	86	MAGE-C2	10%	44	96	NY-BR-1	2%
51	75	MAGE-A4	7%	34	166	ZNF165	9%	45	152	TPTE	0%
52	79	MAGE-A9	5%	35	161	XAGE-1b	9%	46	146	TEKT5	0%
53	18	CCDC62	0%	36	121	SAGE1	8%	47	134	SPO11	0%
THYROID				37	21	CT45	8%	48	68	LIPI	0%
#	AG ID NO	Antigen	%	38	18	CCDC62	7%	49	66	LDHC	0%
1	159	WT1	97%	39	95	NXF2	6%	Esophageal			
2	112	PIWIL2	88%	40	85	MAGE-C1	6%	#	AG ID NO	Antigen	%
3	36	EpCAM	83%	41	41	FBXO39	4%	1	1	5T4	100%
4	131	SPAG9	78%	42	136	SSX-2	3%	2	189	TTK	97%
5	63	KOC1	65%	43	40	FATE1	2%	3	159	WT1	88%
6	116	PRAME	60%	44	156	TSPY1	0%	4	36	EpCAM	81%
7	140	Survivin	53%	45	152	TPTE	0%	5	129	SP17	81%
8	108	PASD1	25%	46	139	SSX-5	0%	6	75	MAGE-A4	76%
9	66	LDHC	25%	47	132	SPAN-Xc	0%	7	63	KOC1	74%
10	85	MAGE-C1	22%	48	81	MAGE-B2	0%	8	111	PIWIL1	70%
11	74	MAGE-A3	22%	49	80	MAGE-B1	0%	9	77	MAGE-A6	68%
12	95	NXF2	20%	50	51	GASZ	0%	10	140	Survivin	67%
13	55	HAGE	20%	51	19	CDCA1	0%	11	74	MAGE-A3	66%
14	69	MAGE-A1	17%	52	2	ACRBP	0%	12	27	CTCFL	56%
15	51	GASZ	13%	Cervical				13	79	MAGE-A9	55%
16	129	SP17	10%	#	AG ID NO	Antigen	%	14	153	TRAG-3	55%
17	73	MAGE-A2	9%	1	112	PIWIL2	100%	15	73	MAGE-A2	53%
18	39	FAM46D	8%	2	1	5T4	100%	16	69	MAGE-A1	46%
19	136	SSX-2	8%	3	16	CAGE1	98%	17	22	CT46	35%
20	98	NY-ESO-1	7%	4	140	Survivin	92%	18	127	SLCO6A1	33%
21	65	Lage-1	4%	5	8	AKAP-4	86%	19	65	Lage-1	31%
22	70	MAGE-A10	2%	6	66	LDHC	83%	20	98	NY-ESO-1	31%
23	157	TYR	0%	7	111	PIWIL1	83%	21	21	CT45	28%
24	149	TEX15	0%	8	131	SPAG9	82%	22	70	MAGE-A10	27%
25	145	TDRD1	0%	9	63	KOC1	68%	23	55	HAGE	27%
26	142	TAF7L	0%	10	129	SP17	61%	24	72	MAGE-A12	26%

27	139	SSX-5	0%	11	108	PASD1	58%	25	121	SAGE1	22%
28	138	SSX-4	0%	12	51	GASZ	50%	26	19	CDCA1	22%
29	137	SSX-3	0%	13	98	NY-ESO-1	42%	27	18	CCDC62	21%
30	135	SSX-1	0%	14	39	FAM46D	37%	28	149	TEX15	20%
31	134	SPO11	0%	15	36	EpCAM	36%	29	177	HSPB9	20%
32	123	SCP-1	0%	16	179	KIF20A	35%	30	95	NXF2	17%
33	121	SAGE1	0%	17	134	SPO11	33%	31	169	CABYR	17%
34	119	RAGE-1	0%	18	33	DKKL1	33%	32	179	KIF20A	15%
35	92	NKX3.1	0%	19	27	CTCFL	32%	33	23	CT47	15%
36	88	MORC1	0%	20	65	Lage-1	26%	34	85	MAGE-C1	12%
37	87	MART1	0%	21	75	MAGE-A4	23%	35	86	MAGE-C2	11%
38	86	MAGE-C2	0%	22	138	SSX-4	20%	36	145	TDRD1	10%
39	75	MAGE-A4	0%	23	19	CDCA1	18%	37	42	FMR1NB	8%
40	44	FTHL17	0%	24	69	MAGE-A1	17%	38	138	SSX-4	7%
41	33	DKKL1	0%	25	20	CRISP2	17%	39	10	BAGE-1	6%
42	20	CRISP2	0%	26	74	MAGE-A3	16%	40	123	SCP-1	2%
43	1	5T4	0%	27	159	WT1	5%	41	142	TAF7L	0%
44	1	5T4	0%	28	136	SSX-2	4%	42	136	SSX-2	0%
				29	135	SSX-1	4%	43	135	SSX-1	0%
				30	88	MORC1	0%	44	132	SPAN-Xc	0%
				31	70	MAGE-A10	0%	45	44	FTHL17	0%
				32	4	ADAM2	0%				

A model population was used that comprises 15,693 subjects with up to 500 male and 500 female subjects from each of a broad range of ethnicities. The full 6 HLA class I and DQ & DRB1 class II alleles is available for each subject. The number of HLA class II bindings was duplicated to simulate the full genome.

For each of the 15,693 subjects all 15mer amino acid sequences in each TSA were identified that met the following HLA-binding criteria: (i) predicted to bind to at least four HLA class II alleles of the subject (HLA class II-binding PEPI4+); and (ii) comprise a 9mer amino acid sequence that is predicted to bind to at least three HLA class I of the subject (HLA class I-binding PEPI3+);.

A hotspot was identified in the amino acid sequence of each TSA, wherein the hotspot is a 20mer that comprises a 15mer that meets the HLA binding criteria for the maximum number of subjects in the 15,693 subject population. The hotspot analysis is illustrated in Figure 15.

The hotspot analysis was repeated in a further 29 cycles, or until no more sequences meeting the HLA-binding criteria could be identified. Hotspot sequences were screened against manufacturing feasibility criteria. Any hotspot sequence that contained a cysteine residue, or that had a calculated hydrophilicity of less than 33%, was rejected and a different hotspot

sequence comprising a 15mer that met the HLA binding criteria for the next highest number of subjects was selected instead.

In each cycle subjects for whom the HLA-binding criteria were met for any hotspot sequence selected in any previous cycle were excluded. In this way the hotspots that were selected maximized, for each cycle, the number of subjects in the population for whom a hotspot sequence had been selected that is predicted to induce both CD4+ and CD8+ T cell responses. The hotspot sequences selected in each cycle and the TSA of which they are a fragment are shown in Table 25. A total of 3286 hotspot sequences were selected. Figure 16 shows the distribution of hotspot sequence selection across the 192 CTA.

10 **Table 25A – Hotspot Sequences and corresponding TAA**

Cycle	SEQ ID NO	Sequence	Source Antigen(s) [AA position in Antigen]	Cycle	SEQ ID NO	Sequence	Source Antigen(s) [AA position in Antigen]
1	1	PTSSASSFSSAPFLASAVS	5T4 [34,53]	11	1394	AESMYGDFQEAMTHLQHKLI	FAM46D [204,223]
1	2	VESTPMIMENIQELIRSAQE	ACRBP [275,294]	11	1395	VAQTSLEEFNVLEMEVMRRQ	FATE1 [121,140]
1	3	LNWEGVQYLWSFVLENHRRE	ACTL8 [73,92]	11	1396	KYRKLI ESEL SYFVIVYSVM	FBXO39 [423,442]
1	4	PHNFRVYSYSGTGIMKPLDQ	ADAM2 [67,86]	11	1397	STEPGSFKVD TASNLNSGKE	FSIP1 [35,54]
1	5	RIVEIVVVIDNYLYIRYERN	ADAM29 [198,217]	11	1398	LENFFRYFLRLSDDKMEHAQ	FTHL17 [49,68]
1	6	RETFMNKFIYEIARRHPFLY	AFP [155,174]	11	1399	PVNSQKITLEWASPQNFTSV	GASZ [382,401]
1	7	DEVSFYANRLTNLVIAMARK	AKAP-3 [122,141]	11	1400	NRPLIKPKRRLSAARRAGTS	GATA-3 [298,317]
1	8	IDDL SFYVNR LSSSLVIQMAH	AKAP-4 [214,233]	11	1401	EAF EIVVRHAKNYTNAMFKN	Glypican-3 [113,132]
1	9	RTKKELASALKSALSGHLET	ANXA2 [78,97]	11	1402	QLHDPGSLAEADLSYTWDF	gp100 [243,262]
1	10	ARAVFLALSAQLLQARLMKE	BAGE-1 [3,22]	11	1403	IPEELVSMAERFKAHQKRE	HAGE [613,632]
1	11	GVVFLALSAQLLQARLMKEE	BAGE-2 [4,23]; BAGE-3 [4,23]	11	1404	KQQT DIAVNWAGLHHAKKS	HDAC1 [126,145]
1	12	GAVFLALSAQLLQARLMKEE	BAGE-5 [4,23]	11	1405	HNLLLN YGLYRKMEIYRPHK	HDAC2 [40,59]
1	13	NQEYKDAYKFAADVRLMFMN	BRDT [328,347]	11	1406	RFHSEDIYDFLQRVSPTNMQ	HDAC3 [60,79]
1	14	PSNINQFAAAYFQELTMYRG	CABYR [30,49]	11	1407	TLVVTANRGSSPQVMSRSNG	IGFS11 [371,390]
1	15	KRASQLASKMHSLALMVGL	CAGE1 [608,627]	11	1408	IRSSYFTFQLQNI VKPLPPV	IL13RA2 [223,242]
1	16	QTTQNGRFYAI SARFKPFSN	CALR3 [67,86]	11	1409	RDYTLRTFGEMADAFKSDYF	JARID1B [375,394]
1	17	SPASELIAIQDSHSLGSSKS	CCDC62 [566,585]	11	1410	EEIPLKILAHNNFVGR LIGK	KOC1 [275,294]
1	18	AKRTSRFLSGI INFIHFREA	CDCA1 [114,133]	11	1411	GGLKKLSFAENSTIPDIQK	KU-CT-1 [274,293]
1	19	EGKDP AFTALLTTLQVQRE	CRISP2 [20,39]	11	1412	DLQHGS LFFSTSKITSGKDY	LDHC [64,83]
1	20	QGPTAVRKRFFESI I KEAAR	CT45 [152,171]	11	1413	VKNTRK VAVSLSVHIKNLLK	LIPI [147,166]
1	21	ATAQLQRT PMSALVFPNKIS	CT46 [2,21]	11	1414	KVLEYVIKVSARVRFFP PSL	MAGE-A1 [278,297]
1	22	LDMVHSL LHLRLSHNDHILIE	CT47 [124,143]	11	1415	TSLGLTYDGM LSDVQSM PKT	MAGE-A10 [205,224]
1	23	GNNFIQNFYLPQNYIDQFL	CTAGE1 [22,41]	11	1416	SFSQDILHDKIIDL VHL LRL	MAGE-A11 [216,235]

1	24	FAVLFLWRSFRSVTSRLYVR	CTAGE2 [24,43]	11	1417	APEEKIWEELSVLEASDGRE	MAGE-A12 [216,235]
1	25	FAVLFFLWRSFRSVRSRLYV	cTAGE5 [53,72]	11	1418	ELVHFLLLKYRAREPVTKAE	MAGE-A2 [115,134]; MAGE-A3 [115,134]
1	26	HTRFTQSGTMKIHLQKHGE	CTCFL [404,423]	11	1419	ESAGPPQSPQGASALPTTIS	MAGE-A4 [58,77]
1	27	KKNATMLYTASQAFLRHPDV	CTNNA2 [214,233]	11	1420	GSVVGWQYFFPVIFSKASD	MAGE-A6 [137,156]
1	28	NEDNIYISNSIYFSIAIVSE	CXorf48 [122,141]	11	1421	TKAEMLESVIKNYKNHFPDI	MAGE-A8 [134,153]
1	29	NTGEMSSNSTALALVRPSSS	CXorf61 [27,46]	11	1422	EPRKLLTQDWQVQENYLEYRQ	MAGE-A9 [240,259]
1	30	PPPFYRRRFRVGRPPNQ	DBPC [225,244]	11	1423	MLMHFILRKYKMREPIMKAD	MAGE-B1 [114,133]
1	31	SRVLHGYYAAQQLPSLLKERE	DCAF12 [64,83]	11	1424	FGLELNKVPNGHTYTFIDK	MAGE-B2 [164,183]
1	32	NLLRGIDSLFSAPMDFRGLP	DKKL1 [63,82]	11	1425	SKMKVLEFWAKVNKTVPSPAF	MAGE-B3 [284,303]
1	33	IAERQVRMAAQVALRRQQAQ	DMRT1 [108,127]	11	1426	FRKVSQRTELVLFGALKEVN	MAGE-B4 [151,170]
1	34	GKKIEVYLRLHRHAYPEQRQ	DPPA2 [113,132]	11	1427	SASQKAIIFKRLSKDAVKKK	MAGE-B6 [179,198]
1	35	SERVRTYWIIEELKHKAREK	EpCAM [136,155]	11	1428	LQIPVSPSSSSTLLSLFQSF	MAGE-C1 [233,252]
1	36	KGWDLMQNIMNDMPIYMSV	EPHA2 [50,69]	11	1429	KDYFPVILKRAREFMELLFG	MAGE-C2 [175,194]
1	37	KRDNRVAYMNPIMARWRGP	FAM133A [3,22]	11	1430	NDVLAMKRSSSLPSWKSLLN	MORC1 [759,778]
1	38	RRQFEFSVDSFQIVLDPMLD	FAM46D [166,185]	11	1431	AFTKLNNASSRSHSIFTVKI	MPHOSPH1 [340,359]
1	39	GENQEHLVIAEMMELGSRSR	FATE1 [26,45]	11	1432	RRKNYQQLDIFPARDTYHPM	MUC-1 [1187,1206]
1	40	EHLEVKFMNPNYNAVLTKKFQ	FBXO39 [90,109]	11	1433	RAHLAKNLKLTETQVKIWFQ	NKX3.1 [154,173]
1	41	SGSSYFVLANGHILPNSENA	FMR1NB [92,111]	11	1434	EKLDAFFGFQLSQEIKQQIH	NLRP4 [513,532]
1	42	ISDTKDYFMSKTLGIGRLKR	FSIP1 [515,534]	11	1435	QSYSLIHQLLSAEDLEPLGT	NR6A1 [249,268]
1	43	GWESGLVAMESAFHLEKNVN	FTHL17 [93,112]	11	1436	YKLGELLRRTRKRDIVDSLSA	NXF2 [454,473]
1	44	EEMRSHYVAQTGILWLLMNN	GAGE-1 [109,128]	11	1437	SLVEKTPDEAASLVEGTSDK	NY-BR-1 [263,282]
1	45	SRGKSTYYWPRPRRYVQPPE	GAGE-3 [4,23]	11	1438	KPAELSRGRGILIFSDFKDF	NYD-TSPG [212,231]
1	46	WRGRSTYYWPRPRRYVQPPE	GAGE-6 [3,22]; GAGE-7 [3,22]	11	1439	EAARRQFQSQLADLQQLPDI	ODF2 [583,602]
1	47	EKFKKAMTIGDVSLVQELLD	GASZ [48,67]	11	1440	LTPGPGDYFPEKSTKYVFDS	ODF3 [99,118]
1	48	ALSRHMSLSHISPFSSHSH	GATA-3 [396,415]	11	1441	PFQWRITHSFRWMAQVLASE	ODF4 [67,86]
1	49	BFVGEFFTDVSLYILGSDIN	Glypican-3 [143,162]	11	1442	SVHLAWDLRSRLGAVVFSRV	OIP5 [90,109]
1	50	DGGNKHFLRNQPLTFALQLH	gp100 [226,245]	11	1443	EHGDSSAYENVKFI VNRDI	PASD1 [118,137]
1	51	RLNDLQMSNFVNLKNITYLV	HAGE [375,394]	11	1444	GTGVNVYLMKRSRGLSHSP	PBK [41,60]
1	52	KPHRIRMTNHLNLYGLYRK	HDAC1 [31,50]; HDAC2 [32,51]	11	1445	TEADRVIQRTNSMQQLEQWI	PEPP2 [399,418]
1	53	TIFENLKMNLHAPSQIHDV	HDAC3 [361,380]	11	1446	KRVNTRFFAQSGGRLQNPLP	PIWIL1 [742,761]
1	54	KKVNFDMSLDDIIYKELE	HOM-TES-85 [21,40]	11	1447	AGPIGMRMSPPAWVELKDDR	PIWIL2 [629,648]
1	55	LINLNVIMVTPLSNANQPE	IGF511 [52,71]	11	1448	HDIVNRQKSIAGFVASTNAE	PIWIL3 [657,676]
1	56	PIRSSYFTFQLQNI V KPLPP	IL13RA2 [222,241]	11	1449	LNKWKYKNHDLPARII VYRA	PIWIL4 [674,693]

1	57	KLRYRYTLDDLYPMMNALKL	JARID1B [731,750]	11	1450	KKLKIFAMPMDIKMILKMV	PRAME [211,230]
1	58	PDESWALKAIIEALSCKIELH	KOC1 [45,64]	11	1451	YSEELFFEEELSVVLGTNDLT	PRSS55 [111,130]
1	59	IQNHDIMHAITISPLRSANTV	KU-CT-1 [435,454]	11	1452	EENSRLQERGVAYINADSS	PSMA [436,455]
1	60	PDSRLQLHITMPFSSPMEA	Lage-1 [83,102]	11	1453	YELIRGRRYPLSEKKIMHYM	RAGE-1 [90,109]
1	61	QRNVAIMKSIIPAIVHYSFD	LDHC [111,130]	11	1454	RPRRINMTDTGISPMSTRDP	SAGE1 [226,245]
1	62	SEELNIIQLGNIILSTEKSK	LEMD1 [67,86]	11	1455	AIVEAARLEKVHSLFRRQLA	SART3 [237,256]
1	63	QKYSAHAFQFSFRNVLWLLV	LIPI [12,31]	11	1456	DSDPALQKVNFLPVLEQVGN	SCP-1 [63,82]
1	64	VKVLEYVIKVSARVRFFFPS	MAGE-A1 [277,296]	11	1457	DVIEGKTAVIEKRRKKRSSA	SCP3a [41,60]
1	65	DDTTAMASASSATGSFSYP	MAGE-A10 [349,368]	11	1458	VAFPPRAKDLVVFVKNSAR	SCRN1 [11,30]
1	66	DPTSHSYVLVTSLNLSYDGI	MAGE-A11 [283,302]	11	1459	EAQNKELKTQVALSSETPRT	se57-1 [289,308]
1	67	ALSRKMAELVHFLLLKYRAR	MAGE-A12 [108,127]	11	1460	SSGISFQSKYLSFFILGQTV	SLCO6A1 [219,238]
1	68	GREDSVFAHPRKLLMQDLVQ	MAGE-A2 [233,252]	11	1461	MITQLISLREQLLAHDEQK	SOX-6 [194,213]
1	69	FPVIFSKASSSLQLVFGIEL	MAGE-A3 [147,166]	11	1462	DLNKVILLDPSIIEAKMELE	SPAG1 [713,732]
1	70	VNARVRIAYPSLREAALEE	MAGE-A4 [294,313]	11	1463	GGSGAVMSERVSLAGSIYR	SPAG9 [14,33]
1	71	KSPQGASAIPTAIDFTLWRQ	MAGE-A5 [63,82]	11	1464	FLPITSSDIDVVESEAVSVL	SPATA19 [20,39]
1	72	KKLLTQYFVQENYLEYRQVP	MAGE-A6 [243,262]	11	1465	ILSTSKGLIAGNLRYIEEDG	SPO11 [170,189]
1	73	RAPEEAIWEALSVMGLYDGR	MAGE-A8 [218,237]	11	1466	YMKRKYEAMTKLGFKAILPS	SSX-3 [50,69]
1	74	PAQLEFMFQEALKLKVAELV	MAGE-A9 [97,116]	11	1467	QKVGSLERPRVEVLINRINEV	SYCE1 [44,63]
1	75	DNPSGHTYTLVSKNLNTNDG	MAGE-B1 [168,187]	11	1468	TVRNLRARSQSVKMKDKLKID	TAF7L [113,132]
1	76	SSDPPRFQFLWGPRAAETS	MAGE-B2 [265,284]	11	1469	EVHIVRNGGTSMVMENMAVR	TAG-1 [997,1016]
1	77	LIMKTNMLVQFLMEMYKMKK	MAGE-B3 [111,130]	11	1470	KLVENSLSISNPGLFTSLGP	TDRD1 [144,163]
1	78	SSSVLRDTASSSLAFGIPQE	MAGE-B4 [42,61]	11	1471	TLKLRLRETQDTLQLLVMTK	TEKT5 [428,447]
1	79	PQILNRTSQHLVVAFGVELK	MAGE-B6 [234,253]	11	1472	SREFTNAYKLPLAVGPPSLN	TEX14 [781,800]
1	80	RPVSFFFSYTLASLLQSSHE	MAGE-C1 [777,796]	11	1473	FRQPIFSQYASHQPLPQATY	TEX15 [2742,2761]
1	81	ATVMASELSVMSSNVSFSE	MAGE-C2 [354,373]	11	1474	PSSRILQLSKPKAPATLLEE	THEG [264,283]
1	82	EPVVPNAPPAYEKLSAEQSP	MART1 [94,113]	11	1475	DLKIQIEMEKKVVFSTISLG	TPTE [430,449]
1	83	RSQAGMFIYSNNRLIKMHEK	MORC1 [363,382]	11	1476	KVLKSERDKIFLLYEQAQEE	TSGA10 [55,74]
1	84	EIYNEYIYDLFVPVSSKFQK	MPHOSPH1 [277,296]	11	1477	GAGEAPGALSTADPADQSVQ	TSP50 [39,58]
1	85	GVSFFFLSFHISNLQFNSSL	MUC-1 [1039,1058]	11	1478	YEVEAYRRRHSSNLNFFNW	TSPY1 [241,260]
1	86	VQPTQKQKXHLRFHWQANSE	NA17-A [45,64]	11	1479	YRNGDFFISSKDLGYDYSYL	TYR [433,452]
1	87	EEAFSRASLVSVYNSYPYP	NKX3.1 [202,221]	11	1480	ERRFSRSDQLKRHRRTGV	WT1 [361,380]
1	88	SLLRKKMLPEASLLIAIKPV	NLRP4 [263,282]	11	1481	FINHQI IYAGEKNHQYGKSF	ZNF165 [307,326]
1	89	IERLIYLYHKFHLKVSNEE	NR6A1 [369,388]	12	1482	LADLSPFAFSGSNASVSAPS	5T4 [154,173]
1	90	QSQGSVLAFTRTFIATPGSS	NXF2 [510,529]	12	1483	PKFHSESLSSNPSSFAPVR	ACRBP [254,273]
1	91	KRASQYSGQLKVLIAENTML	NY-BR-1 [1103,1122]	12	1484	WLGASVVAHLSTYQSEWMSR	ACT18 [338,357]
1	92	WTLRFFFSYLSWDVDDLLL	NYD-TSPG [322,341]	12	1485	WRVLFLLSGLGGLRMDSNFD	ADAM2 [2,21]
1	93	KEFTVSGNILTIRLTAAHR	NY-ESO-1 [124,143]	12	1486	VIDNYLYIRYERNDSKLLED	ADAM29 [205,224]
1	94	DEKRELAKLRRTTNRIASS	ODF1 [100,119]	12	1487	KGEEELQKYIQESQALAKRS	AFP [396,415]

1	95	ADKDLVVAEALSTLESWRSR	ODF2 [428,447]	12	1488	QKATDIMDAMLRKLYNMFA	AKAP-3 [368,387]
1	96	EKSTKYVFD SAPSHSISART	ODF3 [109,128]	12	1489	LAKDLIVSALKLIQYHLTQQ	AKAP-4 [540,559]
1	97	NSPLPFQWRITHSFRWMAQV	ODF4 [63,82]	12	1490	VPHLQKVFD RYKSYSPYDML	ANXA2 [222,241]
1	98	ADSVHLAWDLSRSLGAVVFS	OIP5 [88,107]	12	1491	YNPPDHEVV TMARMLQDVFE	BRDT [351,370]
1	99	MGFLRRLIYRRRPMIYVESS	PAGE1 [1,20]	12	1492	DQAPEVTLQADIEVMSTVHI	CABYR [274,293]
1	100	GPDMEAFQQELALLKIEDP	PAGE2 [65,84]	12	1493	KEAQEQEFSLQEEFQKLEK	CAGE1 [477,496]
1	101	RGDQGEAPDVAVFVAPGESQ	PAGE4 [12,31]	12	1494	SGKINRHEHYFNQFHRNEL	CALR3 [365,384]
1	102	GTDVEAFQQELALLKIEDAP	PAGE5 [84,103]	12	1495	EKQDYKQKLKALKIEVNKLK	CCDC62 [204,223]
1	103	NHPVRLQAQPIVPVQRAAE	PASD1 [599,618]	12	1496	EEQEEFQQLSDGIELQQL	CDC41 [175,194]
1	104	RYKASQDFPAAIILKVALN	PBK [130,149]	12	1497	ALQKKYLRMVVLAVYTNPED	CT46 [88,107]
1	105	KEMELWMKAMLDALVQTET	PEPP2 [254,273]	12	1498	LSGPABELRSFNMPSLDKMDG	CTAGE2 [603,622]; CTAGE5 [634,653]
1	106	QYAHKLAFLVGQSIHREPNI	PIWIL1 [833,852]	12	1499	AEAKMTFKIFQMNEERLkia	CTAGE5 [188,207]
1	107	RSVGVFVASINLTITKWYSR	PIWIL2 [755,774]	12	1500	FRQKQLLNAHFRKYHDANFI	CTCF1 [523,542]
1	108	QKSIAGFVASTNAELTKWYS	PIWIL3 [663,682]	12	1501	QPFEEFIDASRLVYDGV	CTNNA2 [602,621]
1	109	RTLKQGMMSIATKIAMQM	PIWIL4 [580,599]	12	1502	GDYGMIDESIYFSSDVVTGN	CXorf48 [48,67]
1	110	KAVSQDMVIYSTEIHYSSKG	PLAC1 [85,104]	12	1503	SRDILNNFPHSIARQKRILV	CXorf61 [63,82]
1	111	RLDQLLRHVMNPLETSLITN	PRAME [312,331]	12	1504	AIKRNNPRKFLRSVGDGETV	DBPC [125,144]
1	112	KNTPGIYTSLVNYNLWIEKV	PRSS55 [279,298]	12	1505	GAVSLDGYFHLWKAENTLSK	DCAF12 [268,287]
1	113	SNPIVLRMMNDQLMFLERAF	PSMA [656,675]	12	1506	DAQESSLGLTGLQSLQGF	DKKL1 [37,56]
1	114	TKFKQSRAMNDFPFKKGSG	RAGE-1 [227,246]	12	1507	GISHPIPLPSAAELLVKREN	DMRT1 [132,151]
1	115	GSTGFSSRLAATQDLFFIHQ	RCA51 [123,142]	12	1508	LVISRKRMAYEKAEIKEM	EpCAM [286,305]
1	116	PPAFINMAATGVSSMSTRDQ	SAGE1 [602,621]	12	1509	GVPFRTVSEWLESIKMQQYT	EPHA2 [903,922]
1	117	KDSITVFSVNLPSMQEPDT	SART3 [701,720]	12	1510	MSEIRFTNLTDQVITLDQV	FAM46D [1,20]
1	118	NNNIEKMITAFEELRVQAEN	SCP-1 [215,234]	12	1511	AVNRLRALLEEQQATWRHRE	FATE1 [143,162]
1	119	KLNQEYSQQFLTLFQQWDL	SCP3a [120,139]	12	1512	VESAVVYVKKFGRYLEHLEV	FBXO39 [75,94]
1	120	RRHELYKAHEWARAIIESDQ	SCRN1 [343,362]	12	1513	KHNQDFIKRNI ELAKESRNP	FSIP1 [249,268]
1	121	TSELKTEGVSPYLMILIRLK	se57-1 [316,335]	12	1514	TSYLYLSMAFYFNRDDVALE	FTHL17 [31,50]
1	122	QSSGISFQSKYLSFFILGQT	SLCO6A1 [218,237]	12	1515	SKDQQKILAAKELQVEEIQ	GASZ [320,339]
1	123	KERQLSTMITQLISLREQLL	SOX-6 [187,206]	12	1516	GPLSVYPPASSSSLSGGHAS	GATA-3 [128,147]
1	124	PDNIPAFAAAYFESLLEKRE	SP17 [32,51]	12	1517	EELVNGMYRIYDMENVLLGL	Glypican-3 [304,323]
1	125	EKDPSLVYQHLLYLSKAERF	SPAG1 [863,882]	12	1518	QVSLKVSNDGPTLIGANASF	gp100 [65,84]
1	126	RDAVKFFVAVPGQVISQSS	SPAG9 [1223,1242]	12	1519	TRNDWRVASELINILERANQ	HAGE [592,611]
1	127	KKMKTSESSTILVVYRRNV	SPAN-Xc [40,59]	12	1520	QLSTGGSVASAVKLNKQQT	HDAC1 [111,130]
1	128	TRIQFIRWSHTRIFQVPSEM	SPATA19 [112,131]	12	1521	SDEYIKFLRSIRPDNMSEYS	HDAC2 [70,89]
1	129	AEIQALTFLLSSDYLSRVYLP	SPO11 [368,387]	12	1522	EDYIDFLQRVSPNTMQGFTK	HDAC3 [64,83]
1	130	RIQVEHPQMTFGRHLRIIPK	SSX-1 [91,110]	12	1523	TESVSHFSDLGQSFSFHSGN	IGFS11 [332,351]

1	131	VERPQMTFGRLOGISPKIMP	SSX-2 [94,113]	12	1524	LVTATVENETYTLKTTNETR	IL13RA2 [283,302]
1	132	QRPQMTFGRLOGIFPKIMPK	SSX-3 [95,114]	12	1525	PARRAKRMRAEAMNIEPE	JARID1B [227,246]
1	133	SEKIVYVYMKLNYEVMKLG	SSX-4 [43,62]	12	1526	KKIRESYENDIASMNLQHL	KOC1 [345,364]
1	134	NQVEHPQMTFGRLOGIFPKI	SSX-5 [92,111]	12	1527	KSDNEEVREAAALANLTT	KU-CT-1 [366,385]
1	135	EFEETAKKVRRAIEQLAAMD	Survivin [123,142]	12	1528	AIGLSVMDLVGSILKNLRRV	LDHC [251,270]
1	136	LFLRSQEAAATVQLFQEEHR	SYCE1 [229,248]	12	1529	KPPYSRLDYTDKAFVDVIHS	LIP1 [213,232]
1	137	ESGQYRANEGTSSIVMEIQK	TAF7L [377,396]	12	1530	IFGKASESLQLVFGIDVKEA	MAGE-A1 [143,162]
1	138	GADAYFYVYSNESVRPYTPF	TAG-1 [765,784]	12	1531	SSPSVVASLPLDQSDEGSSS	MAGE-A10 [92,111]
1	139	RGLPASTLSRLSNRLLRLLE	TAG-2a [35,54]	12	1532	QNWVQEKYLVYRQVPGTDPA	MAGE-A11 [361,380]
1	140	SSEVLEYMNQLSASLKETYA	TDRD1 [285,304]	12	1533	QEGPSTFPDLETSFQVALSR	MAGE-A12 [92,111]
1	141	LPGYRYLMSWRPSLFYKIAN	TEKT5 [41,60]	12	1534	DLESEFQAAISRKMVELVHF	MAGE-A2 [100,119]
1	142	LSQWFEFSETTASTVSTTLH	TEX101 [120,139]	12	1535	VGNWQYFFPVI FSKASSSLQ	MAGE-A3 [140,159]
1	143	RLKAGVISAQNIYSFGFGK	TEX14 [193,212]	12	1536	LEHVVRVNARVRIAYPSLRE	MAGE-A4 [288,307]
1	144	GKINQNYASII TEAFPKPKD	TEX15 [368,387]	12	1537	VGNWQYFFPVI FSKASDSLQ	MAGE-A6 [140,159]
1	145	VSRAQMAVPSSRILQLSKP	THEG [255,274]	12	1538	AASSSTLIMGTLEEVTDSG	MAGE-A8 [38,57]
1	146	SSDRTINLLEVLWPTEWIF	TMEM31 [63,82]	12	1539	EEPSSSVDPQLEFMFQEAL	MAGE-A9 [89,108]
1	147	DLDLTYVTERI IAMSFPSSG	TPTE [236,255]	12	1540	ETTKMKVLEFLAKMNGATPR	MAGE-B1 [279,298]
1	148	RKDQGFLEKEFYHKTNIKMR	TRAG-3 [14,33]	12	1541	AETSKMKVLEFLAKVNGTTP	MAGE-B2 [281,300]
1	149	EELQKVQFEKVSALADLSST	TSGA10 [492,511]	12	1542	LKKPQRALSTTTSDVSYKK	MAGE-B3 [62,81]
1	150	VIMHSRYRAQRFWSWVGQAN	TSP50 [186,205]	12	1543	TTAMTSAYS RATSSSSSQPM	MAGE-B4 [327,346]
1	151	KIMLFFRSNPYFQNKVITKE	TSPY1 [200,219]	12	1544	RTSQHLVVAFGVELKEMDSS	MAGE-B6 [239,258]
1	152	HNRESYMPFPIPLYRNGDFF	TYR [420,439]	12	1545	PLQSPVISFSSSTLSPFSE	MAGE-C1 [850,869]
1	153	RGKKGAATKMAAVTAPEAES	VCX [50,69]	12	1546	EEEEASSASSTLYLVFSPS	MAGE-C2 [34,53]
1	154	NKRYFKLSHLQMSRKHTGE	WT1 [331,350]	12	1547	ERSQRSQIANITTVWRAQPT	MORC1 [668,687]
1	155	VGILHLGSRQKKIRIQLRSQ	XAGE-1 [13,32]; XAGE-1b [13,32]; XAGE-1c [92,111]	12	1548	VQQIQSNYDIAIAELHVQKS	MPHOSPH1 [933,952]
1	156	SRQKKIRIQLRSQVLGREMR	XAGE-1d [20,39]	12	1549	DVSVSDVPFPFSAQSGAGVP	MUC-1 [1138,1157]
1	157	MSWRGRSTYRPRPRSLQPP	XAGE-2 [1,20]	12	1550	LSSELGDLEKHSSLPALKEE	NKX3.1 [184,203]
1	158	MIWRGRSTYRPRPRSVPPP	XAGE-3 [1,20]	12	1551	YISEMLLRNKS VRYLDLSAN	NLRP4 [798,817]
1	159	KSFKSPKLAKHAAVFGDKT	ZNF165 [324,343]	12	1552	EELHRFSDEGMEVIERLIYL	NR6A1 [356,375]
2	160	ELASNHFLYLPRDVLALPLS	ST4 [216,235]	12	1553	VTIPYGIKYDKAWLMNSIQS	NXF2 [127,146]
2	161	SHKTPFVSPLLASQSLSIGN	ACRBP [399,418]	12	1554	ESLDQKLFQLQSKNMWLQQQ	NY-BR-1 [1261,1280]
2	162	NFSVWLGA SVVAHLSTYQSE	ACT18 [334,353]	12	1555	YWRTSSFRMTEHNSVKPWQQ	NYD-TSPG [124,143]
2	163	EANELLHTFLRWKTSYLVLR	ADAM2 [242,261]	12	1556	ELSKSMESMRGHLQAQLRSK	ODF2 [337,356]
2	164	IKVKLLFSKHLVPFTYTDQ	ADAM29 [67,86]	12	1557	PINIWIFELEARNVSIPIGWS	ODF4 [163,182]
2	165	SGEKNI FLASFVHEYSRRHP	AFP [344,363]	12	1558	GGTERAIDQASFTTSMEDWT	OIP5 [22,41]

2	166	SEGIMTYANSVVSDMMVSIM	AKAP-3 [282,301]	12	1559	GPPDPQAFQGPAAYPDPQMR	PASD1 [735,754]
2	167	DQVNIIDYLMNRPQNLRLEMT	AKAP-4 [161,180]	12	1560	PINMEELDESYQKVIELFSV	PBK [280,299]
2	168	STPPSAYGSKAYTNFDAER	ANXA2 [18,37]	12	1561	YSPQRTYRSEVSSPIQRGDV	PEPP2 [556,575]
2	169	QLLQARLMKEESPVVSWRLE	BAGE-1 [13,32]; BAGE-2 [13,32]; BAGE-3 [13,32]; BAGE-5 [13,32]	12	1562	APLISVKPLDNWLLIYTRRN	PIWIL1 [485,504]
2	170	TALDVHFVSTLEPLSNAVKR	BAGE-2 [37,56]; BAGE-3 [37,56]	12	1563	DIPLKQLMVIGMDVYHPSR	PIWIL2 [733,752]
2	171	KEMLAKKHFSYAWPFYNPVD	BRDT [281,300]	12	1564	KRINTRFFLKHGSNFQNPFP	PIWIL3 [763,782]
2	172	AKYSSVYMEAEATALLSDTS	CABYR [372,391]	12	1565	DYPKIIKVQENPAAFVRAIQ	PIWIL4 [518,537]
2	173	ENHPKSMITMPALFKENRND	CAGE1 [756,775]	12	1566	DVMHLSQSPSVSLSVLSSLS	PRAME [338,357]
2	174	FSNKGKTLVIQYTVKHEQKM	CALR3 [84,103]	12	1567	FKRANMDNDIALLLASPIK	PRSS55 [148,167]
2	175	TVFGEKSVITLSSIFTKDLV	CCDC62 [385,404]	12	1568	PRRTILFASWDABEEFGLLS	PSMA [412,431]
2	176	TLSPFRYNVAEIVHIRNKI	CDCA1 [3,22]	12	1569	IGEGTFSEVMKMQSLRDGNY	RAGE-1 [10,29]
2	177	PTSWSSAIQSWYDEILDVY	CRISP2 [104,123]	12	1570	RKQDNVLSNVLSGLINMAGA	SAGE1 [451,470]
2	178	SPSYQKRQRMALLARKQGAG	CT45 [24,43]	12	1571	PIPESVIQNYNKALQQLEKY	SART3 [276,295]
2	179	DALQKKYLRMVVLAVYTNP	CT46 [87,106]	12	1572	FVPPRSSSSQVSQVAVKQTLG	SCP-1 [10,29]
2	180	BEGNEANFDLAVVARRYPA	CT47 [97,116]	12	1573	RKRLEMYTKASLKTSNQKIE	SCP3a [89,108]
2	181	FLFGGNNFIQNFYLPQNYID	CTAGE1 [18,37]	12	1574	RPRDEVQEVVYFSAADHEPE	SCRN1 [30,49]
2	182	ALKKLIHAAKLNASKTLEG	CTAGE2 [282,301]; cTAGE5 [312,331]	12	1575	NLVQRMEKEKRTLLERKLSL	se57-1 [193,212]
2	183	MFTSSRMSSFNRMKTHTSE	CTCFL [263,282]	12	1576	IRFGGFRKRKKAKSSVSKKP	SLCO6A1 [59,78]
2	184	SSDSMLDSATSLIAAKNL	CTNNA2 [853,872]	12	1577	QAFPDMHNSNISKILGSRWK	SOX-6 [641,660]
2	185	RNGVIDYTIFFTLDSVKLPD	CXorf48 [188,207]	12	1578	EKHLQALAPESRALRKDKPA	SPAG1 [62,81]
2	186	DLSRDILNFPHSIARQKRI	CXorf61 [61,80]	12	1579	GLAGSIYREFERLIGRYDEE	SPAG9 [26,45]
2	187	DKPVLAIQVLGTVKWFNVRN	DBPC [86,105]	12	1580	IQDIITSLARNEAPAFITDN	SPO11 [55,74]
2	188	GQGSLLFYDIRAQRFLEERL	DCAF12 [358,377]	12	1581	KGERPGAHQAGPDVLIGQE	SYCE1 [313,332]
2	189	TELHPRVAFWIKLPRRRSH	DKK1 [161,180]	12	1582	VIESLRTLDKKTFYKTADIS	TAF7L [159,178]
2	190	SDSTYYSSFYQPSLFPPYNN	DMRT1 [205,224]	12	1583	PGNISWTFSSSSLSIKWDPV	TAG-1 [916,935]
2	191	MLASWARIAARAVQPKALNS	DPPA2 [185,204]	12	1584	SLSISNPGFTSLGPPLRST	TDRD1 [149,168]
2	192	PGQTLIIYVDEKAPFESMQG	EpCAM [244,263]	12	1585	QFTDTNLAFNARISEVTDVK	TEKT5 [334,353]
2	193	DLAPDTTYLVQVQALTQEGQ	EPHA2 [496,515]	12	1586	KILKKGIYVDVAVNSLQGTAL	TEX14 [41,60]
2	194	EKEKDVRSLSKRKKSYRDD	FAM133A [168,187]	12	1587	SNAAIQIASATMPALSLNND	TEX15 [598,617]
2	195	KNLELKVFSSSLRRQFEFSVD	FAM46D [155,174]	12	1588	SRRVEELSRPKRFYLEYYNN	THEG [191,210]
2	196	EVMRRQLYAVNRRLEEEQ	FATE1 [135,154]	12	1589	SSGRQSFYRNPIKEVVRFLLD	TPTE [253,272]
2	197	NLKVNFFFERIMKYERLARI	FBXO39 [282,301]	12	1590	TERDVAFTDLRRMTTERDSL	TSGA10 [103,122]
2	198	QSLEEDSALEALLNFFFPPT	FMR1NB [114,133]	12	1591	FWSWVGQANDIGLLKLQEL	TSP50 [197,216]
2	199	KLQELSAASPTISSFSRLE	FSIP1 [326,345]	12	1592	KVITKEYLVNITEYRASHST	TSPY1 [214,233]
2	200	LELYTSYLYLSMAFYFNRRD	FTHL17 [27,46]	12	1593	ASPLTGIADASQSSMHNALH	TYR [348,367]
2	201	MSWRGRSTYRPRPRRYVEPP	GAGE-1 [1,20]; GAGE-2 [1,20]; GAGE-8 [1,20]	12	1594	AQFPNHSFKHEDPMGQGSLS	WT1 [169,188]
2	202	MNLSRGKSTYYWPRPRRYVQ	GAGE-3 [1,20]	12	1595	DQSFKNWNSDFINHQIYYAGE	ZNF165 [298,317]

2	203	MSWRGRSTYYWPRPRRYVQP	GAGE-6 [1,20]; GAGE-7 [1,20]	13	1596	GYHYRYEINADPRLTNLSSN	5T4 [398,417]
2	204	DREKDHIFSSYTAFGDLEVF	GASZ [263,282]	13	1597	SGWLQTEFLSFQDGFPTKI	ACRBP [457,476]
2	205	GLYYKLHNINRPLTMKKEGI	GATA-3 [343,362]	13	1598	GSRVELTPMQRVAFEMFFSP	ACTL8 [243,262]
2	206	ELIQKLKSFISFYALPGYI	Glypican-3 [390,409]	13	1599	VNLMQKNFLPHNFRVYSYSG	ADAM2 [58,77]
2	207	VLMAVVLASLIYRRRLMKQD	gp100 [605,624]	13	1600	FQGILQINDFAYEIKPLAFS	ADAM29 [123,142]
2	208	SATWPHSVHRLAQSYLKEPM	HAGE [427,446]	13	1601	LIFLNFTESTRTLHRNEYGI	AFP [9,28]
2	209	GAGKGKYYAVNPLRDGIDD	HDAC1 [215,234]	13	1602	PPSKKSFFYKEVFESRNGDY	AKAP-3 [234,253]
2	210	GAGKGKYYAVNFPMDGIDD	HDAC2 [216,235]	13	1603	SSGKPIPASVVLKRVLLRHT	AKAP-4 [356,375]
2	211	QEAFLYTLDRVMTVSFHKYG	HDAC3 [178,197]	13	1604	VNLTNRNSNAQRQDIAFAYQ	ANXA2 [57,76]
2	212	MASFRKLTLSKVPVPHPSR	HOM-TES-85 [1,20]	13	1605	PDSQQQYVNVKTVKVTEQLR	BRDT [255,274]
2	213	QVQGTVTIRNISALSSGLYQ	IGFS11 [195,214]	13	1606	KTSGMSKKSVESVKLAQLE	CABYR [350,369]
2	214	QLQNIIVKPLPPVYLTFTRES	IL13RA2 [231,250]	13	1607	SNLYLEKRVKELQMKITKQQ	CAGE1 [329,348]
2	215	RGHYERILNPYNFLSGDSL	JARID1B [172,191]	13	1608	KMKNTDYLTYDLSEFENIG	CALR3 [279,298]
2	216	YENDIASMNLQAHILPGLNL	KOC1 [351,370]	13	1609	APGHMSDVEWMSIFKPSKMQ	CCDC62 [525,544]
2	217	ATVLTNMAMQEPLRLNIQNH	KU-CT-1 [419,438]	13	1610	RYNVAEIVIHIRNKILTAD	CDCA1 [8,27]
2	218	GAVLKDFTVSGNLLFMSVRD	Lage-1 [120,139]	13	1611	KTRSGKVFQNMANGNPVK	CT46 [333,352]
2	219	WAIGLSVMDLVGSILKNLRR	LDHC [250,269]	13	1612	SETRASLYPPTLLEGPLRLS	CTAGE2 [498,517]
2	220	LPSTRKLYEKKLVQLLVSP	LEMD1 [27,46]	13	1613	SETRAFLSPPTLLEGPLRLS	cTAGE5 [529,548]
2	221	AQFYNDFVNISIGLTYFQS	LPI [409,428]	13	1614	QLLAERTKEQLFFVETMSGD	CTCF [190,209]
2	222	VSARVRRFFPSLREAAALREE	MAGE-A1 [286,305]	13	1615	GAIRGRAARVIHINAEMEN	CTNNA2 [541,560]
2	223	LESVIRNYEDHFPLLFSEAS	MAGE-A10 [161,180]	13	1616	GLINSNTDNNLAVYDLSDI	Cxorf61 [47,66]
2	224	YAGREHFLFGPEKRLLTQNW	MAGE-A11 [344,363]	13	1617	LHKRKRLLPPVKRSLVYVLKN	DCAF12 [33,52]
2	225	SVIRNFQDFFPVIFSKASEY	MAGE-A12 [138,157]	13	1618	LFSAPMDFRGLPGNYHKEEN	DKKL1 [71,90]
2	226	PDLESEFQAASRKMLVHVH	MAGE-A2 [99,118]	13	1619	VENTPDLVSDSTYSSFYQP	DMRT1 [197,216]
2	227	VVGWQYFFPVI FSKASSL	MAGE-A3 [139,158]	13	1620	YQLDPKFITSILYENNVITI	EpCAM [174,193]
2	228	ETSYVVKLEHVVRVNRVRI	MAGE-A4 [281,300]; MAGE-A8 [283,302]	13	1621	AGMKYLANMNYVHRDLAARN	EPHA2 [725,744]
2	229	ESVFRAALSKKVADLIHFL	MAGE-A5 [102,121]	13	1622	WSLISLSNNTGKNLELKFVS	FAM46D [144,163]
2	230	VVGWQYFFPVI FSKASDSL	MAGE-A6 [139,158]	13	1623	KAAGSASAKRVNMNTATRPK	FATE1 [57,76]
2	231	DGREHSVYWKRLKLLTQEWV	MAGE-A8 [235,254]	13	1624	FYFKIWAFLDVSVFVERILKS	FBXO39 [369,388]
2	232	AHAETSYEKVINYLVMNLAR	MAGE-A9 [276,295]	13	1625	SKTLGIGRLKRPSFLDDPLY	FSIP1 [524,543]
2	233	TEEEIWKFMMNLGAYDGEH	MAGE-B1 [216,235]	13	1626	EHMTDLLKERDITLRHLLTM	GASZ [289,308]
2	234	QFLWGPRAAETSKMKVLEF	MAGE-B2 [272,291]	13	1627	YGNVSRATVQRYPPTHHSQ	GATA-3 [64,83]
2	235	TNKKKVSFSSPLILGATIQK	MAGE-B3 [33,52]	13	1628	SLQVTRIFLQALNLGIEVIN	Glypican-3 [222,241]
2	236	SLTRKTKMLVQFLLYKYMK	MAGE-B4 [108,127]	13	1629	VLPDGGQVIWVNNTI INGSQV	gp100 [96,115]
2	237	GPRAYAETTKMRVLRVLADS	MAGE-B6 [360,379]	13	1630	ALKSHFVGAVIGRGGSKIKN	HAGE [73,92]
2	238	NPASSFFSSALLSIFQSSPE	MAGE-C1 [130,149]	13	1631	SDDYIKFLRSIRPDNMSEYS	HDAC1 [69,88]
2	239	SSASSTLYLVFSPSSFSTSS	MAGE-C2 [40,59]	13	1632	QLSTGGSVAGAVKLNRRQTD	HDAC2 [112,131]

2	240	NAPPAYEKLAEQSPPPYSP	MART1 [99,118]	13	1633	NHAPSVQIHDVPADLLTYDR	HDAC3 [370,389]
2	241	DDPQKFAMELSIIYKYSPPK	MORC1 [159,178]	13	1634	QPEQVILYQGGQMGDAPRF	IGFS11 [69,88]
2	242	YEQANLNMANSIKFSVWVSF	MPHOSPH1 [256,275]	13	1635	QHRAQQLSSGNLKFVQDRV	JARID1B [1263,1282]
2	243	NIKFRPGSVVVQLTLAFREG	MUC-1 [1091,1110]	13	1636	LENFTLKVAYIPDEMAAQQN	KOC1 [144,163]
2	244	HRLFHWQANSERADIPASLR	NA17-A [54,73]	13	1637	AAEADGIDPLINLLSSKRDG	KU-CT-1 [394,413]
2	245	PQKRSRAAFSHTQVIELERK	NKX3.1 [123,142]	13	1638	LKDLADELALVDVALDKLKG	LDHC [41,60]
2	246	GINNVFSFGQSVLLFEVLFY	NLRP4 [673,692]	13	1639	DMNVI VVDWSRGATTFIYNR	LIP1 [126,145]
2	247	IPHLFSYSGHSPLLPQQARS	NR6A1 [226,245]	13	1640	GEPRKLLTQDLVQEKYLEYR	MAGE-A1 [233,252]
2	248	QEMVQAFSAQSGMKLEWSQK	NXF2 [573,592]	13	1641	QSETQGLEGAQAPLAVEEDA	MAGE-A10 [19,38]
2	249	SVVAKLLSHGAVIEVHNKAS	NY-BR-1 [97,116]	13	1642	LLLRKYRVKGLITKAEMLGS	MAGE-A11 [232,251]
2	250	NAEDWNLYWRTSSFRMTEHN	NYD-TSPG [117,136]	13	1643	TKAEMLSVIRNFQDFFPVI	MAGE-A12 [131,150]
2	251	AMPFATPMEAEARRSLAQD	NY-ESO-1 [93,112]	13	1644	KPEEGLEARGEALGLVGAQA	MAGE-A2 [11,30]
2	252	LRPSLRSLERKAIRAIEDEK	ODF1 [83,102]	13	1645	EEGPSTFPDLESEFQAALSR	MAGE-A3 [92,111]; MAGE-A6 [92,111]
2	253	GDGPYSTFLTSSPIRSRSP	ODF2 [809,828]	13	1646	EEGVEAQEEALGLVGAQAPT	MAGE-A4 [13,32]
2	254	DVRVTKFKAQYTMARVEP	ODF3 [189,208]	13	1647	PAHLESFREALDEKVAELV	MAGE-A8 [101,120]
2	255	LGQDGRLLSSTLSLSSNRSL	ODF4 [39,58]	13	1648	KEPVTKAEMLESVIKNYKRY	MAGE-A9 [126,145]
2	256	RLGAVVFSRVNTNNVLEAP	OIP5 [99,118]	13	1649	GEPRKFITQDLVQEKYLKYE	MAGE-B1 [239,258]
2	257	NDQESSQPVGSVIVQEPTTE	PAGE2 [16,35]	13	1650	GEPWKLITKDLVQEKYLEYK	MAGE-B2 [242,261]
2	258	MSARVRSRSGRGDQGEAPD	PAGE4 [1,20]	13	1651	QSRTDPLIMKTNMLVQFLME	MAGE-B3 [105,124]
2	259	RGNDQESSQPVGPVIVQQPT	PAGE5 [33,52]	13	1652	AREEBIWEFLNMLGIYDGKR	MAGE-B4 [215,234]
2	260	SSQRKLNWIPSFPTYDYFNQ	PASD1 [16,35]	13	1653	TKMRVLRVLADSSNTSPGLY	MAGE-B6 [368,387]
2	261	LTLWEMMTLSIPHINLSNDD	PBK [235,254]	13	1654	STFEGFAQSSLQIPVSPSFS	MAGE-C1 [258,277]
2	262	GWEEAYTFEGARYYINHNER	PEPP2 [61,80]	13	1655	SEEVIWEVLNAVGVYAGREH	MAGE-C2 [245,264]
2	263	NSLIQNLFKVTPAMGMQMRK	PIWIL1 [509,528]	13	1656	KLREILLYFFPEHQLPSELE	MORC1 [824,843]
2	264	LVGRNFYDPTSAMVLQQHRL	PIWIL2 [338,357]	13	1657	QQHVFPFRESKLTHYFQSFFN	MPHOSPH1 [426,445]
2	265	LRYYNILFRRTFKLLDFEQV	PIWIL3 [222,241]	13	1658	ETQFNQYKTEAASRYNLTIS	MUC-1 [1118,1137]
2	266	YIPDLASRRRLRIALLYSHSE	PIWIL4 [130,149]	13	1659	TTLLMKLMMAWSDNKIFRDR	NLRP4 [162,181]
2	267	GIRAKAVSQDMVIYSTEIHY	PLAC1 [81,100]	13	1660	LTVYSKQIFGELADVTAKYS	NR6A1 [333,352]
2	268	SPEKEEQYIAQFTSQFLSLQ	PRAME [277,296]	13	1661	MAATLKIIERNFPPELLSLNL	NXF2 [258,277]
2	269	DFKRANMDNDIALLLASPI	PRSS55 [147,166]	13	1662	GFHHIHEQIMEYIRKLSKNH	NY-BR-1 [193,212]
2	270	QSGAAVVHEIVRSFGTLKKE	PSMA [389,408]	13	1663	DDNLKPWLLEVNYSPALTL	NYD-TSPG [377,396]
2	271	VVRLSSYSSTLQSVLGSST	RAGE-1 [357,376]	13	1664	ELERKLEATSQAQNI EFLQVI	ODF2 [668,687]
2	272	QLEPDYFKDMTPTIRKTQKI	RCAS1 [89,108]	13	1665	NRSLGQRQNSPLPFQWRITH	ODF4 [55,74]
2	273	RQFVEFTIKEAARFKKVLI	SAGE1 [860,879]	13	1666	PSSPVAYDIISQELELMKKL	PASD1 [361,380]

2	274	KELEELRAAFTRALEYLKQE	SART3 [440,459]	13	1667	NDLIEERYKASQDFFPAAII	PBK [124,143]
2	275	QHKAEMVALMEKHKHQYDK	SCP-1 [704,723]	13	1668	IPTSPPSHGSI AAYQGYSPPQR	PEPP2 [541,560]
2	276	METQQQEIASVRKSLQSMLE	SCP3a [217,236]	13	1669	KVLRSETVLD FMFNFYHQTE	PIWIL1 [272,291]
2	277	DSEFFLT TASGVSVLPQNRS	SCRN1 [268,287]	13	1670	SQVVNVRTIGQPTRLRSVAQ	PIWIL2 [696,715]
2	278	EISILQE QISHLQFVIHSQH	se57-1 [235,254]	13	1671	LLANHFRVISRPQWVAYKYN	PIWIL3 [127,146]
2	279	KKHYRLRLLEALIRFGGFR	SLCO6A1 [46,65]	13	1672	QYDITVSDLNQ PMLVSLKK	PIWIL4 [343,362]
2	280	SEPHIKRPMNAFMVWAKDER	SOX-6 [617,636]	13	1673	RRLWGSIQSRYISMSVWTSP	PRAME [4,23]
2	281	KEEVA AVKIQA AFRGHIARE	SP17 [113,132]	13	1674	VTQLEGRPFNAEKRTSVKQ	PRSS55 [298,317]
2	282	YYTRISALPTVVAYNNRAQ	SPAG1 [231,250]	13	1675	RLQDFDKSNPIVLRMMNDQL	PSMA [649,668]
2	283	REEAQKMSSLLPTMWLGAQN	SPAG9 [959,978]	13	1676	KLKLSGVVRLSSYSSTPLQS	RAGE-1 [351,370]
2	284	NPLQMEEEEFMEIMVEIPAK	SPAN-Xc [78,97]	13	1677	NNQPQPSYDLSTVLPGLTYL	SAGE1 [542,561]
2	285	KGVGLPFLPITSSDIDVVES	SPATA19 [14,33]	13	1678	FRYSTSLEKHKLFISGLPFS	SART3 [792,811]
2	286	KSAQKFS LILKILSMIYKLV	SPO11 [106,125]	13	1679	MEKQKPFALFVPPRSSSSQV	SCP-1 [1,20]
2	287	EKISYVVMKRNKAMTKLGF	SSX-1 [44,63]	13	1680	LQQSRIVQSQR LKTIKQLYE	SCP3a [161,180]
2	288	EWEKMKASEKIFYVVMKRKY	SSX-2 [36,55]	13	1681	TGEGEFNFSEV FSPVEDHLD	SCRN1 [215,234]
2	289	EKIVYVVMKRYEAMTKLGF	SSX-3 [44,63]	13	1682	KQEDSKQLLQV NKLEKEQKL	se57-1 [148,167]
2	290	VERPQMTFGSLQRIFPKIMP	SSX-4 [94,113]	13	1683	LLPEALIRFGGFRKRKAKS	SLCO6A1 [53,72]
2	291	EKIIYVVMKRYEAMTKLGF	SSX-5 [44,63]	13	1684	AAASGLSPLQLQKHVSHQP	SOX-6 [315,334]
2	292	QPFLKDHRI STFKNWPFLEG	Survivin [11,30]	13	1685	LKNNLIEKDP SLYVQHLLYL	SPAG1 [857,876]
2	293	EPRVEVLINRINEVQQA KKK	SYCE1 [50,69]	13	1686	GQGENKMKNL PVPVYLRPLD	SPAG9 [660,679]
2	294	NLTLKNHFQSVLEQLLEQEK	TAF7L [424,443]	13	1687	MLKVSRRSLHILSTSKGLIA	SPO11 [160,179]
2	295	AEDTRLFAPSIKARFPAETY	TAG-1 [231,250]	13	1688	GQDTSSQKIEDLMEMVQKLQ	SYCE1 [25,44]
2	296	NLEPLVSRDPPASASLFQDT	TAG-2a [64,83]	13	1689	VWKHGITPPLKNVRKKRFRK	TAF7L [217,236]
2	297	WAERIMFSDLRSLQLKKTME	TDRD1 [246,265]	13	1690	NPVGTVVSREAILRFGFLQE	TAG-1 [115,134]
2	298	TLQEIFQAENTIMLLERSIM	TEKT5 [363,382]	13	1691	KVLLDAGFAVGEQSMVTDKP	TDRD1 [665,684]
2	299	NDKDSLSQFWEFSETTASTV	TEX101 [115,134]	13	1692	QEQMRKLAQRIDIQMRDNRD	TEKT5 [225,244]
2	300	KSDIYSFSMIMQEILTDDIP	TEX14 [436,455]	13	1693	QAKATQFNSALFTLSSHRQG	TEX14 [875,894]
2	301	TLVELQMMMETIQFIENKKR	TEX15 [1689,1708]	13	1694	PQAKEMFIDTVISSYNIETA	TEX15 [389,408]
2	302	VTKKVVASPRIISLAKPKVR	THEG [326,345]	13	1695	NEGYDRRPLASMSLPPPKAS	THEG [349,368]
2	303	RRTPTTSSDR TINLLEVL PW	TMEM31 [57,76]	13	1696	RQQYFSDLFNILD TAIIVIL	TPTE [150,169]
2	304	SKIKKIVHSIVSSFAFGLFG	TPTE [79,98]	13	1697	KSPKSTTAHAILRRVETERD	TSGA10 [87,106]
2	305	MWMGLIQLVEGVKRDQGF L	TRAG-3 [1,20]	13	1698	LSKADGMWPQFRTIQEKEVI	TSP50 [247,266]
2	306	RQNYSSNAYHMSSTMKPNTK	TSGA10 [650,669]	13	1699	ASAKEGTAFRMEAVQEGAAG	TSPY1 [32,51]
2	307	SSRPRLWQTPTTQTL PSTT	TSP50 [67,86]	13	1700	FVDSIFEQWLRRHRPLQEVY	TYR [392,411]
2	308	DEDEDMLSYMVSLEVGE EKH	TSPY1 [175,194]	13	1701	PPPHSFIKQEPSWGGAEPHE	WT1 [66,85]
2	309	HNALHIYMNGTMSQVQGSAN	TYR [363,382]	13	1702	SQSSNLSQHQRIHMRNLLM	ZNF165 [466,485]
2	310	VAKKGKAVRRGRRGKGAAT	VCX [38,57]	14	1703	THLES LHLLEDNALKVLHNGT	5T4 [258,277]

2	311	PSQASSGQARMFPNAPYLPS	WT1 [117,136]	14	1704	SPISPHFTVTERQTFQPWPE	ACRBP [151,170]
2	312	KKKNQQLKVGILHLGSRQKK	XAGE-1 [5,24]; XAGE-1b [5,24]; XAGE-1c [84,103]; XAGE-1d [5,24]	14	1705	GFTKRLFRELMGDHVSSTKA	ACTL8 [306,325]
2	313	PRRSLQPPELIGAMLEPTDE	XAGE-2 [13,32]	14	1706	DFAKYIEMHVIVEKQLYNHM	ADAM2 [175,194]
2	314	GRAFNLNSHLIRHQRIHTRE	ZNF165 [406,425]	14	1707	EDLYVIVNIIVDSILDVIGVK	ADAM29 [223,242]
3	315	DGRLRLARLALVLLGWVSSS	5T4 [13,32]	14	1708	KAPQLTSSELMAITRKMAAT	AFP [438,457]
3	316	RNQNPGLSLQLPHTTEALLVL	ACRBP [309,328]	14	1709	ERQLNEAVGNVTPQLLDWL	AKAP-3 [830,849]
3	317	DRKKMLEILFELLHVPSVLL	ACTL8 [110,129]	14	1710	QWKQNATDIMEAMLKRLVSA	AKAP-4 [414,433]
3	318	RRYIENIYHSPMRWPFPLF	ADAM2 [673,692]	14	1711	KIRSEFKRKYGKSLYYIQQ	ANXA2 [302,321]
3	319	EIKPLAFSTTFEHLVYKMDS	ADAM29 [135,154]	14	1712	KNGRLTNQLQYLQKVVLKDL	BRDT [24,43]
3	320	QKLGEYLYQNAFLVAYTKKA	AFP [420,439]	14	1713	LSGEAAEAVHSGTSVKSSSG	CABYR [451,470]
3	321	SVVSDMMVSIKMTLKIQVKD	AKAP-3 [291,310]	14	1714	SDTMNVSNLSQGVMLSHSPI	CAGE1 [33,52]
3	322	LDSQKMDMSNIVMLIQKLL	AKAP-4 [619,638]	14	1715	GFDIKKVHVILHFNKYHEN	CALR3 [138,157]
3	323	RDKVLIRIMVSRSEVDMLEKI	ANXA2 [284,303]	14	1716	SDLQFLNFNVENSQELIQMY	CCDC62 [294,313]
3	324	QARLMKEESPVSVWRLEPED	BAGE-1 [16,35]; BAGE-2 [16,35]; BAGE-3 [16,35]; BAGE-5 [16,35]	14	1717	TYMEFLWQYKSSADKMQLN	CDC41 [137,156]
3	325	FVQNTLTCLKDRRKMOTVQ	BAGE-2 [82,101]; BAGE-3 [82,101]	14	1718	TILSPKQIKTPFKILRDKD	CT46 [239,258]
3	326	LKDLWKHSFSWPFQRPVDAV	BRDT [40,59]	14	1719	QQKLKVMTELYQENEMKLYR	CTAGE2 [349,368]
3	327	QADIEVMSTVHISSVYNDVP	CABYR [282,301]	14	1720	SEQDELMAIDISKRIQLEDE	cTAGE5 [160,179]
3	328	SRLEKLLTQVRNLQFMSENE	CAGE1 [507,526]	14	1721	MSLLSIQQQEGVQVVVQPPG	CTCF [97,116]
3	329	HLTYLILRPDLSYDVKIDGQ	CALR3 [170,189]	14	1722	GPLKNTSDVINAAKKIAEAG	CTNNA2 [733,752]
3	330	NSPTSLLIYKDAPAFNEKAS	CCDC62 [600,619]	14	1723	HAIELNPSRTLLATGGDNPN	DCAF12 [144,163]
3	331	RETYMEFLWQYKSSADKMQQ	CDCA1 [135,154]	14	1724	TLSSHLQIDKMTDNKTGEVL	DKK1 [99,118]
3	332	GENLYMSSDPTSWSSAIQSW	CRISP2 [95,114]	14	1725	VKNSLRGLPGPYVPGQTGNQ	DMRT1 [253,272]
3	333	GQKYEKIFEMLEGVQGPTAV	CT45 [138,157]	14	1726	DVDIADVAYYFEKDVKGESL	EpCAM [206,225]
3	334	YQFKFKYTNNGLMDFISKV	CT46 [115,134]	14	1727	ERSVGPLTRKGFYLAQDIG	EPHA2 [167,186]
3	335	LGEEEGEQAAGLAAPVPRGGS	CT47 [61,80]	14	1728	KEKLSPDIMKDAYVQKLKVK	FAM46D [118,137]
3	336	QNFYLPQNYIDQFLTSFPT	CTAGE1 [27,46]	14	1729	FNVLEMEVMRRQLYAVNRRL	FATE1 [129,148]
3	337	LYVRREKKFAVALSGLIBEK	CTAGE2 [40,59]	14	1730	KFMNPYNAVLTKKFQVTMRG	FBXO39 [95,114]
3	338	TERLLKMKDWAAMLGEDITD	cTAGE5 [268,287]	14	1731	DIEDVTPVFPQLSRSIISKL	FSIP1 [433,452]
3	339	SEAVELQDMSLLSIQQQEGV	CTCF [89,108]	14	1732	LREEVSTWNSRILKRTAITI	GASZ [439,458]
3	340	SVKRGTMVRAARALLSAVTR	CTNNA2 [117,136]	14	1733	GSHTTASPWNLSPFKTSIH	GATA-3 [104,123]
3	341	SNSIYFSIAIVSEDFVPYKG	CXorf48 [129,148]	14	1734	KVKNLRLFLAELAYDLVDVDD	Glypican-3 [515,534]
3	342	IVFWKYRRFQRNTGEMSSNS	CXorf61 [16,35]	14	1735	PDASSIMSTESITGSLGPLL	gp100 [439,458]
3	343	DTKEDVFVHQTAIKRNNPRK	DBPC [114,133]	14	1736	HDVTHVYNFDFPRNIEEYVH	HAGE [554,573]
3	344	VKRSLVYYLKNREVRLQNET	DCAF12 [42,61]	14	1737	NLLNLYGLYRKMEIYRPHKA	HDAC1 [40,59]

3	345	GLTGLQSLQGFSLFLKGN	DKK1 [44,63]	14	1738	LNGLYRKMEIYRPHKATAE	HDAC2 [44,63]
3	346	MENRRHAMSSQYRMHSYYPPP	DMRT1 [278,297]	14	1739	FEYFAPDFTLHPDVSTRIEN	HDAC3 [329,348]
3	347	VDDEESVILTLVPVKDDANM	DPPA2 [18,37]	14	1740	PATNVSIFINNTQLSDTGT	IGFS11 [99,118]
3	348	VVAGIVVLVISRKKRMAKYE	EpCAM [279,298]	14	1741	QDLLDVSEFEDVELPQLAEM	JARID1B [891,910]
3	349	GIMGQFSHHNIIRLEGVISK	EPHA2 [665,684]	14	1742	RVPSFAAGRIVIGKGGKTVNE	KOC1 [493,512]
3	350	NRVAYMNPAMARWRGPTQS	FAM133A [6,25]	14	1743	SSKRDGAIANAATVLTNMAM	KU-CT-1 [408,427]
3	351	NGSVASYILASHNGISYKDL	FAM46D [64,83]	14	1744	RRVHPVSTMVKGLYGIKEEL	LDHC [268,287]
3	352	SAKRVMNMTATRPKMGSQL	FATE1 [63,82]	14	1745	SVKDSFRDLFIPRIETILMM	LIPI [49,68]
3	353	SPQFKKTMTSTFHNLSLNLN	FBXO39 [213,232]	14	1746	DLVGFLLLKYRAREPVTKE	MAGE-A1 [108,127]
3	354	RESLKMVRVKPFGLMLLSIW	FMR1NB [58,77]	14	1747	LYDGMELHIYGEPRKLLTQD	MAGE-A10 [255,274]
3	355	RPGSRSSNASLEVLSTPGS	FSIP1 [21,40]	14	1748	QAQEEDLGLVGAQALQAEQ	MAGE-A11 [127,146]
3	356	DDVALENFFRYFLRLSDDKM	FTHL17 [45,64]	14	1749	ELVHFLLLKYRAREPFTKE	MAGE-A12 [115,134]
3	357	RGRSTYYWPRRRYVQPPM	GAGE-7 [4,23]	14	1750	QSPQGASSLPTTMNYPLWSQ	MAGE-A3 [63,82]
3	358	DSGISVDSNFQYGTPLMYA	GASZ [67,86]	14	1751	AKELVTKAEMLERVIKNYKR	MAGE-A4 [127,146]
3	359	PGLSHSYMADAQYPLPEEVD	GATA-3 [29,48]	14	1752	DPPQSPQGASSLPTTMNYPL	MAGE-A6 [60,79]
3	360	EQLLQSASMEKFLIIQNAA	Glypican-3 [90,109]	14	1753	QENYLEYRQAPGSDPVRYEF	MAGE-A8 [255,274]
3	361	TLIGANASFSIALNFPQSQK	gp100 [76,95]	14	1754	VIFGKASEFMQVIFGTDVKE	MAGE-A9 [148,167]
3	362	DRQVTMTSATWPHSVHRLAQ	HAGE [420,439]	14	1755	VVDEKYKDHFTTEILNGASRR	MAGE-B1 [137,156]
3	363	EEAFYTTDRVMTVSFHKYGE	HDAC1 [184,203]; HDAC2 [185,204]	14	1756	KSGSLVQFLLYKYIKKSVT	MAGE-B2 [114,133]
3	364	SEYFEYFAPDFTLHPDVSTR	HDAC3 [326,345]	14	1757	NSNPARYEFLWGPRHAETS	MAGE-B3 [265,284]
3	365	ATQRDLIATQRDLIVTQRDL	HOM-TES-85 [261,280]	14	1758	AETSKMKVLEFLAKVNDTTP	MAGE-B4 [278,297]
3	366	NQPEQVILYQGGQMFDPGR	IGFS11 [68,87]	14	1759	EGILSGDNALPKSGLLMSLL	MAGE-B6 [273,292]
3	367	EGEDLSKKTLLRFLWPFGLFI	IL13RA2 [332,351]	14	1760	SDEQGMSONRLLILILSIIF	MAGE-C1 [989,1008]
3	368	TLDDLYPMNALKLRAESYN	JARID1B [737,756]	14	1761	ASSTLYLVFSPSSFSTSSSL	MAGE-C2 [42,61]
3	369	QHIKQLSRFAGASIKIAPAE	KOC1 [426,445]	14	1762	KQEFNLVQEYNHLLKVMGQY	MORC1 [414,433]
3	370	DPDFSMYVYEVTKSILPITN	KU-CT-1 [720,739]	14	1763	EQEKEEIASKSALLRQIKEV	MPHOSPH1 [207,226]
3	371	HITMPFSSPMEAEVRRILS	Lage-1 [91,110]	14	1764	GSGSSTTQGGQDVTLPATEP	MUC-1 [67,86]
3	372	TSGKDYSVSANSRIVIVTAG	LDHC [78,97]	14	1765	LLQEANFHIIDNVDLVVSAY	NLRP4 [572,591]
3	373	PSKGRRWAARAPSTRITYGT	LEMD1 [111,130]	14	1766	SPGSTLSSSRSVELNGFMAF	NR6A1 [191,210]
3	374	PDKTMDGFSFSLNQLGM	LIPI [367,386]	14	1767	NNKLYQLDGLSDITEKAPKV	NXF2 [279,298]
3	375	RALAETSYVKVLEYVIKUSA	MAGE-A1 [269,288]	14	1768	IPESIQKVMEINREVEEPP	NY-BR-1 [442,461]
3	376	DEKVTDLVQFLLFKYQMKEP	MAGE-A10 [135,154]	14	1769	GRGILIFSDFKDFIFDDMYI	NYD-TSPG [219,238]
3	377	DKIIDLVHLLLRKYRVKGLI	MAGE-A11 [224,243]	14	1770	KSQVMKTRLEADEVAAQLER	ODF2 [547,566]
3	378	PDLETSFQVALSRKMAELVH	MAGE-A12 [99,118]	14	1771	QPDQMRSAEQTRLMPEQRD	PASD1 [749,768]
3	379	PQGASSFTTINYTLWRQSD	MAGE-A2 [65,84]	14	1772	KRSPRGLSHSPWAVKKINPI	PBK [50,69]

3	380	LSRKVAELVHFLLLKYRARE	MAGE-A3 [109,128]	14	1773	GSILLPSFQIALLTSEDHIN	PEPP2 [212,231]
3	381	TTEEQEAAVSSSSPLVPGTL	MAGE-A4 [32,51]	14	1774	GSSGII VRLSTNHFRILTSRP	PIWIL1 [106,125]
3	382	TTEEQEAVSSSSPLVPGTLG	MAGE-A5 [32,51]	14	1775	KEITFLEYYSKNYGITVKEE	PIWIL2 [448,467]
3	383	QAALSRKVAKLVHFLLLKYR	MAGE-A6 [106,125]	14	1776	GTSLEIWLGYVTSVLQYENS	PIWIL3 [258,277]
3	384	EALDEKVAELVRFLLRKYQI	MAGE-A8 [110,129]	14	1777	VDSEATRNEWYDFYLISQVA	PIWIL4 [756,775]
3	385	VIKNYKRYFPVIFGKASEFM	MAGE-A9 [138,157]	14	1778	DSLFFLRGRDLQLLRHVMNP	PRAME [304,323]
3	386	NSDPTRYQFLWGPRAYAETT	MAGE-B1 [262,281]	14	1779	ENIKKFLYNFTQIPHLAGTE	PSMA [68,87]
3	387	FPEILKKAESGLSVVFGLEL	MAGE-B2 [149,168]	14	1780	IRGRRYPLSEKKIMHYMYQL	RAGE-1 [93,112]
3	388	YDGKHFIFGEPKRLITQDL	MAGE-B3 [233,252]	14	1781	GSMKVKRQFVEFTIKEARF	SAGE1 [854,873]
3	389	NSDPTRYQFLWGPRAHAETS	MAGE-B4 [262,281]	14	1782	PYEEALLQAEAPRLAEYQAY	SART3 [297,316]
3	390	GLYPHLYEDALIDEVERALR	MAGE-B6 [385,404]	14	1783	EETRQVYMDLNNNIEKMITA	SCP-1 [205,224]
3	391	EVDPDDSYVFNLTDLTSEG	MAGE-C1 [967,986]	14	1784	IEKRRKKRSSAGVVEDMGGE	SCP3a [50,69]
3	392	GREHFVYGEPRELLTKVWVQ	MAGE-C2 [261,280]	14	1785	SQSLTTKMDAEHPELRSYA	SCRN1 [189,208]
3	393	EDFPARWSFRAYTSVLYFNP	MORC1 [229,248]	14	1786	QDKRIENLREKVNILEAQNK	se57-1 [274,293]
3	394	ADIKKQAEIAHLYIASLPDP	MPHOSPH1 [687,706]	14	1787	TTIAFFIYKRLNENTDFPD	SLC06A1 [684,703]
3	395	STEKNAVSMTSSVLSHSPG	MUC-1 [48,67]	14	1788	QQEQEIARQQQLLQQQHKI	SOX-6 [232,251]
3	396	IWFQNRRYKTKRKQLSSELG	NKX3.1 [170,189]	14	1789	LADGNVKAFFRRALAHKGLK	SPAG1 [686,705]
3	397	QPERLLFVIDSFEELQGGLN	NLRP4 [222,241]	14	1790	EKKRSSIWQFFSRFLFSSSN	SPAG9 [546,565]
3	398	MKAINFLNQDIRGLTSASQL	NR6A1 [392,411]	14	1791	SLILKILSMIYKLVQSN TYA	SPO11 [112,131]
3	399	ASPQETQSAFIPVSTLSSS	NXF2 [544,563]	14	1792	PDVENEVKRLLRSDAEAVST	TAF7L [259,278]
3	400	HHIHEQIMEYIRKLSKNHQN	NY-BR-1 [195,214]	14	1793	NESVRPYTPFEVKIRSYNRR	TAG-1 [775,794]
3	401	SRHTPHKTLMPYASLFQSHS	NYD-TSPG [513,532]	14	1794	LMELNGSSSqliIMLLKNFM	TDRD1 [1060,1079]
3	402	EAELARRSLAQDAPPLPVP	NY-ESO-1 [101,120]	14	1795	DIPQLKLVNEVFTIDDTLQT	TEKT5 [409,428]
3	403	STNRSMQNYVQFLKSSYANV	ODF2 [788,807]	14	1796	AEQEHSSKL RHPYLLQLMAV	TEX14 [294,313]
3	404	SAPSHSISARTKAFRVDSTP	ODF3 [118,137]	14	1797	LRSLWYDETLYABELLGKPR	TEX15 [1716,1735]
3	405	RWPVDVSNRIHTSAHVMMSG	ODF4 [115,134]	14	1798	HVSDHNRLHLARPKAQSDK	THEG [293,312]
3	406	SRVTNNVLEAPFLVGIEGS	OIP5 [107,126]	14	1799	TTDKILIDVFDGLPLYDDVK	TPTE [458,477]
3	407	QAVPAFQGPDMFAQQELAL	PAGE2 [58,77]	14	1800	TVEKEMKSLARKAMDTESL	TSGA10 [174,193]
3	408	EPAAAAAAASDDQIDIAE	PASD1 [227,246]	14	1801	QMTQTASDVPVLQVIMHSRY	TSP50 [173,192]
3	409	EDPKDRPSAAHIVEALETDV	PBK [303,322]	14	1802	TPIEWYPDYEEVAYRRRHHN	TSPY1 [233,252]
3	410	PTPESSTIASYVTLRKTKKM	PEPP2 [856,875]	14	1803	SQVQGSANDPIFLHHA FVD	TYR [375,394]
3	411	QWALYQYHIDYNPLMEARRL	PIWIL1 [126,145]	14	1804	LESQPAIRNQGYSTVTFDGT	WT1 [138,157]
3	412	FYNVVRVRVMKLLDMKLVGR	PIWIL2 [322,341]	14	1805	LKPEIHTKEQILELLVLEQF	ZNF165 [78,97]
3	413	HYAHKLAYLVGQSIHQEPNR	PIWIL3 [854,873]	15	1806	ASNHFYLYLPDVLQAQLPSLR	5T4 [218,237]
3	414	FERKLLFSADVS YKVL RNET	PIWIL4 [253,272]	15	1807	ALSPGKSEDVVL RWSQEFST	ACRBP [517,536]
3	415	QEAQPLQPSHFLDISDWSL	PLAC1 [184,203]	15	1808	QNLGEALDFRERQQSALDES	ACT18 [216,235]
3	416	NLRRLLLSHIHASSYISPEK	PRAME [261,280]	15	1809	NFDSLVPQITVPEKIRSIK	ADAM2 [19,38]

3	417	KNSVKTDLMKAPMVIDWEE	PRSS55 [202,221]	15	1810	FRIVEIVVVIDNYLIYRER	ADAM29 [197,216]
3	418	TPLMYSLVHNLTKELKSPDE	PSMA [467,486]	15	1811	KWVESIFLI FLLNFTESTR	AFP [2,21]
3	419	EIQALRRNLNPHNIMLHEV	RAGE-1 [50,69]	15	1812	LGNGSSVDEVSYFANRLTNL	AKAP-3 [115,134]
3	420	MTPTIRKTQKIVIKKREPLN	RCA51 [98,117]	15	1813	YSVYADQVNIDYLMNRPQNL	AKAP-4 [156,175]
3	421	NGQAASDNVFSVPPAFINM	SAGE1 [589,608]	15	1814	LEKDIISDTSGDFRKL MVAL	ANXA2 [155,174]
3	422	KNPDFKVFYRSTSLKHKLF	SART3 [785,804]	15	1815	GDKLGRVVHIIQSREPSLSN	BRDT [527,546]
3	423	ASLEIELSNLKAELLSVKKQ	SCP-1 [747,766]	15	1816	KVSSIHSDDQSDVLMVDVATS	CABYR [182,201]
3	424	AKRKRLEMYTKASLKTSNQK	SCP3a [87,106]	15	1817	GAKLDKYHSLNEELDFLVT	CAGE1 [688,707]
3	425	RSIFKPFIFVDDVKLVPKTQ	SCRN1 [302,321]	15	1818	KVHVILHFKNKYHENKKLIR	CALR3 [143,162]
3	426	MEDNSALYESTSAHIIETE	se57-1 [16,35]	15	1819	ARNETLSNTLVLSAQVQGL	CCDC62 [133,152]
3	427	RVVPDKLRSLALGVSYVILR	SLCO6A1 [605,624]	15	1820	SQEIFLNLKTALEKYHDGIE	CDCA1 [419,438]
3	428	GSSLDILSSLNSPALFGDQD	SOX-6 [475,494]	15	1821	NVGEVSTPFHIFKVKVTTER	CT46 [211,230]
3	429	SSEEDKEKEEVA AVKIQAAF	SP17 [106,125]	15	1822	ATBELETYRKRAKDLKEFEK	CTAGE2 [394,413]
3	430	NRALELHPFSMKPLRRAMA	SPAG1 [511,530]	15	1823	ELYQENEMKLRKLTVEENY	CTAGE5 [387,406]
3	431	EDGRVQAFGWSLPQKYKQVT	SPAG9 [639,658]	15	1824	AFQDSVLEEEVELVLAPSEE	CTCF [55,74]
3	432	ESSTILVVRNRNVKRTSFE	SPAN-Xc [46,65]	15	1825	TVMPRF AEQVEVAIEALSAN	CTNNA2 [580,599]
3	433	EQVRSISRLTDVSAQDFSM	SPATA19 [141,160]	15	1826	HLGTLNKVFASQWLNHRQVV	DCAF12 [85,104]
3	434	QGIRNLVTDKFLVIVEKDA	SPO11 [208,227]	15	1827	KEALVPIQKATDSFHTLHP	DKKL1 [146,165]
3	435	WKMKYSEKISYVYMKRNYK	SSX-1 [37,56]	15	1828	ASGALVGAASGSSAGGSSRG	DMRT1 [34,53]
3	436	EKIFVYVYMKRYEAMTKLGF	SSX-2 [44,63]	15	1829	GDQDNWLR TNWVYRGEAERI	EPHA2 [75,94]
3	437	EWEKMKVSEKIVYVYMKRKY	SSX-3 [36,55]	15	1830	ASHNGISYKDLDFVIFGVLP	FAM46D [73,92]
3	438	EWEKMKSEKIVYVYMKLNY	SSX-4 [36,55]	15	1831	ERLARILLQEIPRSISLRS	FBXO39 [296,315]
3	439	EWEKMKASEKIIYVYMKRKY	SSX-5 [36,55]	15	1832	QGLEMRIKLWEEIKSAKYSE	FSIP1 [142,161]
3	440	TLPPAWQPFLLKDHRISTFKN	Survivin [5,24]	15	1833	YAASVANAE LVRVLLDRGAN	GASZ [85,104]
3	441	KNKQRQLRLAFEEQLEDLMG	SYCE1 [148,167]	15	1834	PLPD SMKLESSHSRGSM TAL	GATA-3 [189,208]
3	442	QRQKDLIMKVENLT LKNHFQ	TAF7L [413,432]	15	1835	IQNAAVFQEA FEI VVRHAKN	Glypican-3 [105,124]
3	443	DFSTKS VFSKFAQLNLAAED	TAG-1 [214,233]	15	1836	AFTITDQVPFSVSVS QL RAL	gp100 [206,225]
3	444	GGAESERGLPASTLSRLSNR	TAG-2a [29,48]	15	1837	FVNLKNITYLV LDEADKMLD	HAGE [384,403]
3	445	GDFYVQLYSSEVLEYMNQLS	TDRD1 [277,296]	15	1838	RPDNMSEYSKQMQRFN VGED	HDAC1 [80,99]; HDAC2 [81,100]
3	446	DQMRQFTDTNLAFNARISE	TEKT5 [329,348]	15	1839	PTATQDQVQGT VTI RNISAL	IGFS11 [189,208]
3	447	MTVEADPANMFNWTTEE VET	TEX101 [34,53]	15	1840	PYKYKLRYRTLD DLYPMMN	JARID1B [727,746]
3	448	QMAYLGSLPVIGEKEVIQAD	TEX14 [226,245]	15	1841	DQTPDENDQVVVKITGHFYA	KOC1 [526,545]
3	449	LKSKYFISTYIDFVPYIAS	TEX15 [2172,2191]	15	1842	FHPGGLMKLRSEADLYRFI	KU-CT-1 [853,872]
3	450	TERFLED TLTITVPAVSR	THEG [174,193]	15	1843	KDYSVSANSRIVIVTAGARQ	LDHC [81,100]
3	451	LYDDVKVQFFYSNLPTY YDN	TPTE [472,491]	15	1844	NDFVNISSIGLTYFQSSNLQ	LIPI [413,432]
3	452	DQVDWSRLRLDAGLVKMSRK	TRAG-3 [52,71]	15	1845	GREHSAYGEPRKLLTQDLVQ	MAGE-A1 [226,245]

3	453	MANERISMQNLEALLVANRD	TSGA10 [557,576]	15	1846	LLTQDWVQENYLEYRQVPGS	MAGE-A10 [270,289]; MAGE-A9 [244,263]
3	454	DNFYHNFTKIPTLVQIIKSQ	TSP50 [274,293]	15	1847	VGAQALQABEQEAAFFSSTL	MAGE-A11 [136,155]
3	455	LVNITEYRASHSTPIEWYPD	TSPY1 [221,240]	15	1848	SPQGASTLPTTINYTLWSQS	MAGE-A12 [64,83]
3	456	ADASQSSMHNLHIYMGTM	TYR [355,374]	15	1849	REPVTKAEMLGSVVGNWQYF	MAGE-A3 [127,146]; MAGE-A6 [127,146]
3	457	AVRRGRRGKGAATKMAAVT	VCX [44,63]	15	1850	WVQENYLEYRQVPGSNPARY	MAGE-A4 [251,270]
3	458	TWNQMNLGATLKGVAAGSSS	WT1 [237,256]	15	1851	DSIFGDPKLLTQYFVQENY	MAGE-A6 [236,255]
3	459	QTPGINLDLGSQVVKIIPK	XAGE-1 [46,65]; XAGE-1c [125,144]; XAGE-1b [46,65]	15	1852	QIKEPVTKAEMLESVIKNYK	MAGE-A8 [128,147]
3	460	QLKVGILHLGSRQKKIRIQL	XAGE-1d [10,29]	15	1853	DGEEHLIYGEPRKFITQDLV	MAGE-B1 [231,250]
3	461	TPDKREDDQGAABIQVDDL	XAGE-2 [47,66]	15	1854	VNPNHGHTYTFIDKVDLTDEE	MAGE-B2 [171,190]
3	462	KEQILELLVLEQFLTILPGD	ZNF165 [85,104]	15	1855	KMKKPIMKADMLKIVQKSHK	MAGE-B3 [127,146]
4	463	NSLVSLTYVSFRNLTHLESL	5T4 [244,263]	15	1856	LKIIISKYKEHFPEIFRKVS	MAGE-B4 [136,155]
4	464	EDVVLRWSEQEFSTLTGQFG	ACRBP [524,543]	15	1857	GSPDAVVSYSKSDVAANGQD	MAGE-B6 [71,90]
4	465	KTLEFAGQDLSAYLLKSLFK	ACT18 [171,190]	15	1858	LQIPVSRFSFSTLLSIFQSS	MAGE-C1 [198,217]
4	466	RTISLESILAVILAQLLSLSM	ADAM2 [300,319]	15	1859	YTLDEKVAELVEFLLKYEA	MAGE-C2 [139,158]
4	467	SENITPRMQHDTSHLFTTLG	ADAM29 [274,293]	15	1860	LYRPRKYLYVTSSFKGAFKD	MORC1 [268,287]
4	468	NFGTRTFQAITVTKLSQKFT	AFP [229,248]	15	1861	RKKWLEEKMLITQAKEAEN	MPHOSPH1 [1459,1478]
4	469	DLRSVFFNFIRNLLSETIFK	AKAP-3 [589,608]	15	1862	STLVHNGTSARATTTTPASKS	MUC-1 [970,989]
4	470	SDLQKYGALGFQHALSPSTST	AKAP-4 [116,135]	15	1863	QELLVANFEKARRAHWIFLG	NLRP4 [481,500]
4	471	QNKPLYFADRLYDSMKGKGT	ANXA2 [264,283]	15	1864	QDFTEYKYTHQPNRFPDLMM	NR6A1 [423,442]
4	472	SEILKEMLAKKHFSYAWPFY	BRDT [277,296]	15	1865	KLESASWELGKVKGLKLEELW	NXF2 [307,326]
4	473	AYFQELTMYRGNTTMDIKDL	CABYR [39,58]	15	1866	LQRKMNVDSSTIYNNEVLH	NY-BR-1 [1175,1194]
4	474	KITKQQVFIDVINKLENVE	CAGE1 [343,362]	15	1867	TIYVYQEGLVRFATEKFDLS	NYD-TSPG [269,288]
4	475	RVALATVYFQEEFLDGEHWR	CALR3 [15,34]	15	1868	DSLVERLHRQTAEYSAFKLE	ODF2 [488,507]
4	476	HPSNFIIIEAPGHMSDVEWMS	CCDC62 [517,536]	15	1869	LETPQDYIRLWQELSDSLGP	PASD1 [683,702]
4	477	QEKRGAVYERVTTINQEIQK	CDCA1 [381,400]	15	1870	EAVEENGVITDKADIFAFGL	PBK [216,235]
4	478	NKHNELRKAVSPPASNMLKM	CRISP2 [42,61]	15	1871	QTESAGIQRAQIQKELWRIQ	PEPP2 [747,766]
4	479	AGDSLIIAGSAMS KAKKLMTG	CT45 [42,61]	15	1872	LSTNHFRLT SRPQWALYQYH	PIWIL1 [114,133]
4	480	VGEVSTPFHIFKVKVTTTERE	CT46 [212,231]	15	1873	KSMRFGMLKDHQAVTGNVTA	PIWIL2 [254,273]
4	481	ENRQLSRLMVGPAAARNLW	CT47 [143,162]	15	1874	LKFDTNFLSVPGRVLKNANI	PIWIL3 [458,477]
4	482	LTERLLKMKDGVAMLEEDVT	CTAGE2 [237,256]	15	1875	WGLHFGSQISLTGRIVPSEK	PIWIL4 [434,453]
4	483	PSSETRAFLSPPTLLEGPLR	cTAGE5 [527,546]	15	1876	PSVSQLSVLSSLGVMMLTDVS	PRAME [346,365]
4	484	KSDLRVHMRNLHAYSAAELK	CTCFL [440,459]	15	1877	SVYETYELVEKFYDPMFKYH	PSMA [554,573]

4	485	ISDSFLETNVPLLVLEAAK	CTNNA2 [388,407]	15	1878	RLNPHPNILMLHEVVFDKRS	RAGE-1 [56,75]
4	486	RLRLALAFYGRTPAERQ	CXorf48 [3,22]	15	1879	TIKEAARFKKVLIQQLKA	SAGE1 [866,885]
4	487	PHSIARQKRILVNLMSVENK	CXorf61 [71,90]	15	1880	ELTKVRMARQKMSEIFPLTE	SART3 [127,146]
4	488	PARSQADKPVLAIQVLGTVK	DBPC [80,99]	15	1881	EELKGTEQELIGLLQAREKE	SCP-1 [458,477]
4	489	GSEWSVYAVGSQAHVSFLDP	DCAF12 [305,324]	15	1882	EGVGVDINKALLAKRKRLM	SCP3a [75,94]
4	490	SRLSPRKTHLLYLPRSRQL	DKKL1 [223,242]	15	1883	QEESITVQTMNTLRDKASG	SCRN1 [245,264]
4	491	SSQDSGLVSLSSSPISNKS	DMRT1 [328,347]	15	1884	IPPRDKMEDNSALYESTSAH	se57-1 [10,29]
4	492	ERAEETNTVEVITSAPGAML	DPPA2 [167,186]	15	1885	LKTIEKLALEKSYDISSGLV	SLCO6A1 [139,158]
4	493	QKEITTRYQLDPKFITSILY	EpCAM [167,186]	15	1886	TSPTQNLFPASKTSPVNLPN	SOX-6 [441,460]
4	494	PGHQKRIAYSLGLKQDVNT	EPHA2 [952,971]	15	1887	PGNVKALLRRATTYKHKQNK	SPAG1 [273,292]
4	495	RGPTQSVGPTIQDYLNRP	FAM133A [20,39]	15	1888	SIKLKDSILSIVHVKGIVLV	SPAG9 [996,1015]
4	496	LDPMDFYSDKNAKLTKEYS	FAM46D [180,199]	15	1889	LASSEVVLASIENIIQDIIT	SPO11 [41,60]
4	497	EEQGATWRHRETLIIAVLVS	FATE1 [152,171]	15	1890	QGHTSSEYDMLREMFSDSR	TAF7L [311,330]
4	498	WRNSIRSSFISLSFFLKMK	FBXO39 [141,160]	15	1891	LWSKGTBILVNSSRVTVTPD	TAG-1 [451,470]
4	499	RRSHRAMVAHLELATYELA	FMR1NB [13,32]	15	1892	IKIVDILEEEVVTFAVEVEL	TDRD1 [410,429]
4	500	EEEDTFSSVFHTQIPPEEYE	FSIP1 [191,210]	15	1893	DESTSTLRPTILPTLSAL	TEKT5 [66,85]
4	501	LSMAFYFNRDDVALENFFRY	FTHL17 [36,55]	15	1894	GEYFYSSTAQENLALETSSP	TEX14 [1088,1107]
4	502	WPRPRRYVQPEMIGPMRPE	GAGE-7 [11,30]	15	1895	LDKQRILTVDSFAASSTVPH	TEX15 [1354,1373]
4	503	LKERDITLRHLTMTREDEFT	GASZ [295,314]	15	1896	EDTTLTITVPAVSRRVVEELS	THEG [179,198]
4	504	FPKNSSFNPAALSRHMSSLS	GATA-3 [386,405]	15	1897	AYDPKHFNVRVIMIDHDN	TPTE [289,308]
4	505	SMELKFLIIQNAAVFQEAFF	Glypican-3 [97,116]	15	1898	SRDVAQFRNVVTQLEADLDI	TSGA10 [610,629]
4	506	AHSSSAFTITDQVPFSVSVS	gp100 [201,220]	15	1899	TTQTLPTSTMETQFPVSEK	TSP50 [78,97]
4	507	EEEKWSHMOTFLQSMSSDK	HAGE [470,489]	15	1900	LVERREEAQAQAVPGPGP	TSPY1 [83,102]
4	508	EKIKQRLFENLRMLPHAPGV	HDAC1 [360,379]; HDAC2 [361,380]	15	1901	KNGSTPMFNDINIYDLFVWM	TYR [160,179]
4	509	WTYETSLVVEEAISEELPYS	HDAC3 [307,326]	15	1902	QRKFSRSDHLKTHTRHTGK	WT1 [389,408]
4	510	PNHPSRKKNVFLDMSLDDII	HOM-TES-85 [15,34]	15	1903	ENSRSMFKLEIFEKIESQRI	ZNF165 [188,207]
4	511	SSDNNTLTSSNAYNSRYWSN	IGFS11 [305,324]	16	1904	HLPSLRQLDLSHNPLADLSP	5T4 [140,159]
4	512	GSETWTKTIIITKNLHYKDFD	IL13RA2 [77,96]	16	1905	KEGREAVSQLQTDSEPKFHS	ACRBP [239,258]
4	513	PYSAVEKAMARLQELLTVSE	JARID1B [950,969]	16	1906	TLEFAGQDL SAYLLKSLFKE	ACT18 [172,191]
4	514	EAQDIKFTBEIPLKILAHNN	KOC1 [267,286]	16	1907	QLYNHMGSDTTVVAQKVFQL	ADAM2 [189,208]
4	515	LLRELDVMNSVIAQLAPEEE	KU-CT-1 [103,122]	16	1908	VFTYTDQGAILEDQPPVQNN	ADAM29 [80,99]
4	516	AELVRRILSRDAAPLPRPGA	lage-1 [102,121]	16	1909	EYSRRHPQLAVSVILRVAKG	AFP [357,376]
4	517	NLDSARFRYLIGEKLGVHPT	LDHC [164,183]	16	1910	MDTSTDVPRVLSWLRRDLEK	AKAP-3 [32,51]
4	518	LQGNILSTESKSKLKKWPE	LEMD1 [74,93]	16	1911	SKIASEMAYEAVELTAAEMR	AKAP-4 [268,287]
4	519	GSIPLWLQNFVRILLNEEDM	LIPI [108,127]	16	1912	ETVILGLLKTPAQYDASELK	ANXA2 [96,115]
4	520	FPEIFGKASESLQLVFGIDV	MAGE-A1 [140,159]	16	1913	DKSKLWLLKDRDLARQKEQE	BRDT [900,919]
4	521	DGMEHLIYGEPKLLTQDWV	MAGE-A10 [257,276]	16	1914	PGTEQTEAVGGLSSKPATPK	CABYR [129,148]
4	522	EEQEAAFFSSTLNVGTLEEL	MAGE-A11 [144,163]	16	1915	PVQEDMALNEVLQKLKHTNR	CAGE1 [298,317]

4	523	QDFFPVIFSKASEYLQLVFG	MAGE-A12 [144,163]; MAGE-A2 [144,163]	16	1916	HKEKDKGLQTTQNGRFYAIS	CALR3 [59,78]
4	524	PDLESEFQAALSRKVAVLVH	MAGE-A3 [99,118]	16	1917	PTLSDEKQWHDVSVYLGLTN	CCDC62 [453,472]
4	525	NKVDELAHFLLRKYRAKELV	MAGE-A4 [112,131]	16	1918	DLSDNREKLASILKESLNLE	CDCA1 [302,321]
4	526	AIPTAIDFTLWRQSIKSSN	MAGE-A5 [70,89]	16	1919	ESSMLSTDTKKASILLIRKI	CT46 [138,157]
4	527	PDLESEFQAALSRKVAVLVH	MAGE-A6 [99,118]	16	1920	TEIEFKIKLLEKDPYGLDVP	CTAGE2 [458,477]
4	528	EEQKAASSSTLIMGTLEEV	MAGE-A8 [34,53]	16	1921	IEEKSKLLEKFSLVQKEYEG	cTAGE5 [86,105]
4	529	QGGASSSISVYYTLWSQFDE	MAGE-A9 [62,81]	16	1922	TSGELVRHRRYKHTHEKPFK	CTCF1 [324,343]
4	530	RTTATTFRARSRAPFSRSSH	MAGE-B1 [326,345]	16	1923	KKTRDLRRQLRKAVMDHISD	CTNNA2 [371,390]
4	531	PLTRKSGSLVQFLLYKYKIK	MAGE-B2 [110,129]	16	1924	PSLLKEREHFLGTLNKFAS	DCAF12 [76,95]
4	532	EERVQAAAMLNDGSSAMGRK	MAGE-B3 [315,334]	16	1925	EHQLGNNTLSSHQIDKMTD	DKK11 [92,111]
4	533	RVAARRGTTAMTSAYSRAIS	MAGE-B4 [320,339]	16	1926	GSSRGSGSGSGASDLGAGSK	DMRT1 [49,68]
4	534	VRREYKPYFPQILNRTSQHL	MAGE-B6 [225,244]	16	1927	LEGRSTTSLSVSWSIPPPQQ	EPHA2 [444,463]
4	535	ISRYTGYFPVIFRKAREFIE	MAGE-C1 [939,958]	16	1928	PTMEVKPKDIHVVKDQLIG	FAM46D [34,53]
4	536	VFSPSSFSTSSSLILGGPEE	MAGE-C2 [49,68]	16	1929	RPSRVHASEVESAVWYVKKF	FBXO39 [66,85]
4	537	TSVLYFNPWMRIFIQAKRVK	MORC1 [241,260]	16	1930	FIKRNIELAKESRNPVVMVD	FSIP1 [254,273]
4	538	KFSVWVSFFEIYNEYIYDLF	MPHOSPH1 [268,287]	16	1931	TQVVALLVAHGAEVNTQDEN	GASZ [162,181]
4	539	NGGSSLSYTNPAVAASANL	MUC-1 [1236,1255]	16	1932	KDNEISTFHNLGNVHSPCLK	Glypican-3 [545,564]
4	540	ELERKFSSHQKYLAPERAHL	NKX3.1 [138,157]	16	1933	DIVQGIESAEILQAVPSGEG	gp100 [488,507]
4	541	MQDPAFVKQAVNLLQEAHFH	NLRP4 [560,579]	16	1934	GSTDNNVVAGDRPLIDWDQI	HAGE [157,176]
4	542	SSRSVELNGFMFAFREQYMG	NR6A1 [198,217]	16	1935	GSVAGAVKLNRRQQTDMVNW	HDAC2 [117,136]
4	543	IFVNHSTAPYSVKNKLKPGQ	NXF2 [194,213]	16	1936	RGSSPQVMSRNSGVSRSKPR	IGFS11 [378,397]
4	544	EKNEEIFNYYNNHLKNRIYQY	NY-BR-1 [1312,1331]	16	1937	LPEIQELYQTLLAKPSPAQQ	JARID1B [1360,1379]
4	545	SNLQNNYAHLTNSSINKSGA	NYD-TSPG [288,307]	16	1938	SDLESIFKDAKIPVSGPFLV	KOC1 [16,35]
4	546	ILTIRLTAAHRLQLQLSISS	NY-ESO-1 [132,151]	16	1939	SPLRSANTVVQSKAALAVTA	KU-CT-1 [446,465]
4	547	EDSERLMEQQGALLKRLAEA	ODF2 [281,300]	16	1940	QHGSLLFFSTSKITSGKDYSV	LDHC [66,85]
4	548	KASQPSFSIKGRSKLGGFSD	ODF3 [155,174]	16	1941	PRLGYQAKLFGKVLKERMEG	LIP1 [319,338]
4	549	RITHSFRWMAQVLASELSLV	ODF4 [71,90]	16	1942	YRQVPDSDPARYEFLWGPRA	MAGE-A1 [251,270]
4	550	THNRLKSLMKILSEVTPDQS	OIP5 [206,225]	16	1943	YRQVPGSDPARYEFLWGPRA	MAGE-A10 [283,302]
4	551	DGPDVREGIMPTFDLTKVLE	PAGE2 [86,105]	16	1944	YEFLWGPRAHAETSMMKVLE	MAGE-A11 [382,401]
4	552	EVNPLYRADPVDLEFSVDQV	PASD1 [292,311]	16	1945	ILGDPKKLLTQHVFQENYLE	MAGE-A3 [238,257]
4	553	IILKVALNMARGLYLHQEK	PBK [142,161]	16	1946	ASESLKMIFGIDVKEVDPAS	MAGE-A4 [155,174]
4	554	DHINRKYAFKAAHPNMRTYY	PEPP2 [228,247]	16	1947	SVMGLYDGREHSVYWKLRKL	MAGE-A8 [229,248]
4	555	VTPAMGMQMRKAIMIEVDDR	PIWIL1 [518,537]	16	1948	YKMREPIMKADMLKVVDKEY	MAGE-B1 [123,142]
4	556	ESVGLVSMFRGLGIETVSKT	PIWIL2 [67,86]	16	1949	DGEHVSFVGEPWKLITKDLV	MAGE-B2 [234,253]
4	557	FGERHIFDGNLLSRPLKE	PIWIL3 [170,189]	16	1950	KVDSTKDSYVLVSKMDLPNN	MAGE-B3 [170,189]
4	558	ADVSYKVLNRNETVLEFMTAL	PIWIL4 [261,280]	16	1951	NPTTHSYILVSMLGPNDGNQ	MAGE-B4 [170,189]

4	559	HFLDISEDWSLHTDDMIGSM	PLAC1 [193,212]	16	1952	LDEKVDLARFLLKYQVKQ	MAGE-C1 [908,927]
4	560	YLGQMINLRLLLSHIHASS	PRAME [255,274]	16	1953	QATIDTADDATVMASELSV	MAGE-C2 [345,364]
4	561	DNDIALLLASFIKLDLKV	PRSS55 [154,173]	16	1954	FNQIQNTYMQVEKKIKRKL	MORC1 [866,885]
4	562	EMKTYSVSFDLSFSAVKNFT	PSMA [621,640]	16	1955	RTLDSVSQISNIDLNLRLD	MPHOSPH1 [993,1012]
4	563	ELMDMNIYELIRGRYPLSE	RAGE-1 [83,102]	16	1956	HNGTSARATTPASKSTPFS	MUC-1 [974,993]
4	564	EEEEDAAWQAEVLRQQKLA	RCAS1 [160,179]	16	1957	MAASFFSDFGLMWYLELKK	NLRP4 [1,20]
4	565	DQPQPNVNLSTVQPVIIYLT	SAGE1 [308,327]	16	1958	LQGMGNRKAIREDMPPGRN	NR6A1 [121,140]
4	566	TDYVEIWQAYLDYLRRLVDF	SART3 [415,434]	16	1959	DGYTRNWFVKTIPYGIKYDK	NXF2 [118,137]
4	567	DKKTQTFLETFEIIYWKLD	SCP-1 [793,812]	16	1960	IDIHFLERKMQHLLKEKNE	NY-BR-1 [1296,1315]
4	568	QNEFKKEMAMLQKKIMMETQ	SCP3a [201,220]	16	1961	RTTTPAFTLNIPEANHTEQ	NYD-TSPG [19,38]
4	569	HSFQSAYLIVDRDEAWVLET	SCRN1 [151,170]	16	1962	ITPPSSEKLVSMRLSDLST	ODF2 [91,110]
4	570	LQFVIHSQHQNLRSVIQEME	se57-1 [246,265]	16	1963	SSTVFLDTPESPALSQDF	PASD1 [268,287]
4	571	IIFTTIAFFIYKRRLENENTD	SLCO6A1 [681,700]	16	1964	KERPISMINASNYNVTSDY	PEPP2 [115,134]
4	572	IGEYKQLMRSRRQEMRQFFT	SOX-6 [707,726]	16	1965	PLDNWLLIYTRRNYEAANSL	PIWIL1 [492,511]
4	573	GSKVEDRFYNNHAFEEQEPF	SP17 [61,80]	16	1966	DRIETYVRTIQTSLGAEKGI	PIWIL2 [647,666]
4	574	SMKPLLRAMAYETLEQYGG	SPAG1 [520,539]	16	1967	DGDANSYIDTLRKYTRPTLQ	PIWIL3 [549,568]
4	575	RLDSTLRLYHAHTYQHLQDV	SPAG9 [1107,1126]	16	1968	GQLKTLIEYVPPQLSSVAE	PIWIL4 [698,717]
4	576	TILVVRYYRRNVKRTSPEELL	SPAN-Xc [49,68]	16	1969	TSPRRLVELAGQSLKDEAL	PRAME [21,40]
4	577	RWSHTRIFQVPSEMTEDIMR	SPATA19 [118,137]	16	1970	PHLAGTEQNFQALQIQSQW	PSMA [81,100]
4	578	ASIENIIQDIITSLARNEAP	SPO11 [49,68]	16	1971	NFDFPFKKGSGIPLLTNLS	RAGE-1 [236,255]
4	579	TFGRHLHRIIPKIMPKKPAED	SSX-1 [100,119]	16	1972	AMSSRDLYATITHSVREEKM	SAGE1 [474,493]
4	580	AWTHRLRERKQLVIYEEISD	SSX-2 [163,182]	16	1973	AATEAPKMSNADFAKLFLRK	SART3 [944,963]
4	581	AMTKLGFKAIFPSFMRNKR	SSX-3 [57,76]	16	1974	EVEKAKVIADAEVVKLQKEID	SCP-1 [681,700]
4	582	TFGSLQRIFPKIMPKKPAEE	SSX-4 [100,119]	16	1975	SGKPSVEDQFTRAYDFETED	SCP3a [12,31]
4	583	EAMTKLGFKATLPPFMRNKR	SSX-5 [56,75]	16	1976	EHPELRSYAQSQGWWTGE	SCRN1 [200,219]
4	584	TNNKKKEFEETAKKVRRAIE	Survivin [117,136]	16	1977	LKIKLQASREAGAAALRNVA	se57-1 [112,131]
4	585	RKAEELLAAAQRHQQLQKQ	SYCE1 [248,267]	16	1978	SGSQDEVSRGVEPLEAARAQ	SLCO6A1 [9,28]
4	586	LRTLDKKTFYKTADISQMLV	TAF7L [163,182]	16	1979	PERRKGSLADVVDTLKQKKL	SOX-6 [120,139]
4	587	WMDYEFRVIASNILGTGEPS	TAG-1 [678,697]	16	1980	DTFLLLIQSLKNNLIEKDPS	SPAG1 [848,867]
4	588	YRASVLAYASEESVLVGYVD	TDRD1 [559,578]	16	1981	NQYKERLMELQEA VRWTEMI	SPAG9 [516,535]
4	589	GFWKSELSYELDRLLTENQN	TEKT5 [149,168]	16	1982	VTDAKFVLI VEKDATFQRL	SPO11 [214,233]
4	590	QADDEPTFSFFSGPYVMVTN	TEX14 [243,262]	16	1983	DRGSETTYESSADIAGDEGT	TAF7L [36,55]
4	591	YIEIVMVSETIHFLKNSIAK	TEX15 [2062,2081]	16	1984	GGAPGELIVNWT PMSREYQN	TAG-1 [721,740]
4	592	MPMSEVSQVSRAAQMAVPSS	THEG [247,266]	16	1985	GDGSWYRALVKEILPNHVK	TDRD1 [775,794]
4	593	FIKHFIYSIPRYVRDLKIQ	TPTe [415,434]	16	1986	EEAEHLFETLSDQMWRQFTD	TEKT5 [318,337]
4	594	DAGLVKMSRKPRASSPLSNN	TRAG-3 [62,81]	16	1987	QAI IQGFSYDLKKIDSPQR	TEX14 [152,171]

4	595	LNAERSYKSQISTLHKSVVK	TSGA10 [470,489]	16	1988	LKKAHRRVHTSLQLITKVGE	TEX15 [1004,1023]
4	596	IWRDVIYSVRVGSPWIDQMT	TSP50 [156,175]	16	1989	TPVWPIFRSSLEYRASSRLK	THEG [214,233]
4	597	GEEAVLLDDIMAEVEVVAE	TSPY1 [60,79]	16	1990	RRILFIKHFIYISIPRYVRD	TPTE [411,430]
4	598	HYVSMDDALLGGSEIWRDID	TYR [180,199]	16	1991	LLYEQAQEEITRLRREMMKS	TSGA10 [66,85]
4	599	GAQYRIHTGVFRGIQDVRR	WT1 [283,302]	16	1992	IMHSRYRAQRFWSWVGQAND	TSP50 [187,206]
4	600	TAITREEGGPRSGGAQAKLG	XAGE-1c [13,32]	16	1993	AVQVELEPVNAQARKAFSRQ	TSPY1 [114,133]
4	601	EGGTDVKGKILPKAEHFKMP	XAGE-2 [83,102]	16	1994	HPTNPNLLSPASFFSSWQIV	TYR [256,275]
4	602	DLERGTDEAVLQVQAHEHGQ	ZNF165 [126,145]	16	1995	GHTPSHHAAQFPNHSFKHED	WT1 [161,180]
5	603	EVRAGAFEHLPSLRQLDLSH	5T4 [132,151]	16	1996	FAESSDLTRHRIHTGERPF	ZNF165 [381,400]
5	604	SPNTLKEIEASAEVSPPTMT	ACRBP [131,150]	17	1997	HMADMVTWLKETEVVQKDR	5T4 [301,320]
5	605	DQLQMSLYASGLLTGVVVD	ACTL8 [131,150]	17	1998	SQASYKIVIEGKPYTVNLMQ	ADAM2 [43,62]
5	606	SYLVLRPHDVAFLLVYREKS	ADAM2 [256,275]	17	1999	IWTNKNLIVDDVRKSVHLY	ADAM29 [250,269]
5	607	DSEKQFSTMRSGFMQNEIT	ADAM29 [153,172]	17	2000	ESRTLHRNEYGIASILDSYQ	AFP [17,36]
5	608	ASFVHEYSRRHPQLAVSVIL	AFP [352,371]	17	2001	VSDLIDSFLRNLHVSVTGLM	AKAP-3 [330,349]
5	609	DDFTASVSEGIMTYANSVVS	AKAP-3 [275,294]	17	2002	SIDDLISFYVNLSSLVIQMA	AKAP-4 [213,232]
5	610	QWIAASQFNVPMPLYFMGDKD	AKAP-4 [779,798]	17	2003	MKGKGRDKVLIRIMVSRSE	ANXA2 [278,297]
5	611	RKYGKSLYYIQQDTKGDYQ	ANXA2 [309,328]	17	2004	SATEKVFKQKEIPSVFPKTS	BRDT [166,185]
5	612	EPEDGTALDVHFVSTLEPLS	BAGE-2 [32,51]; BAGE-3 [32,51]	17	2005	PADPAQLAAQMLGKVSSIHS	CABYR [169,188]
5	613	VGTDIMTLQSDIMTMFENN	BRDT [927,946]	17	2006	ALIQPVDTISISSLRQFETV	CAGE1 [105,124]
5	614	DQSDVLMVDVATSMFVVIKE	CABYR [189,208]	17	2007	IDQKNLNGKSQYYIMFGPDI	CALR3 [117,136]
5	615	NNIENYSTNALIQPVDTSI	CAGE1 [96,115]	17	2008	AVHQQQLLSWEEDRQKVLTL	CCDC62 [49,68]
5	616	ESGSIEYDWNLTSLKKTSP	CALR3 [192,211]	17	2009	LQQSLNQDFHQKTIIVLQEGN	CDCA1 [190,209]
5	617	ELHKRTEIIRSLTKVKKALE	CCDC62 [78,97]	17	2010	LQESQKQLLQEAQVWKEQVS	CTAGE2 [188,207]
5	618	EREKLSQEIFLNLKTALEK	CDCA1 [413,432]	17	2011	EEPGVTFQPYLGLLLEELRR	CTAGE5 [2,21]
5	619	SPPASNMLKMEWSREVTTNA	CRISP2 [52,71]	17	2012	VLQFHALEENVMVASEDSKL	CTCFL [150,169]
5	620	TDKTEKVAVDPEVFKRPRE	CT45 [2,21]	17	2013	RDEMAAARGALKKNATMLYT	CTNNA2 [203,222]
5	621	PNKISTEHQSLVLVKRLAV	CT46 [17,36]	17	2014	QNETSYSRVLHGYYAAQQLPS	DCAF12 [58,77]
5	622	NDHILIENTRQLSRLMVGPHA	CT47 [137,156]	17	2015	RLFLKGNLLRGIDSLFSAPM	DKKL1 [57,76]
5	623	SKSLKSQVAEAKMTFKRFQA	CTAGE2 [150,169]	17	2016	NSYNVRRTEGFSVTLLDLAP	EPHA2 [480,499]
5	624	VGFFAVLFFLWRSFRSVRSR	CTAGE5 [50,69]	17	2017	FGVELPGNEEFQVVKDAVLD	FAM46D [87,106]
5	625	SAVFHERYALIQHQKTHKNE	CTCFL [464,483]	17	2018	LSKSNRLKSLSIQYLELDR	FBX039 [119,138]
5	626	KNLMNAVLTVKASYVASTK	CTNNA2 [870,889]	17	2019	QLAEIDIKLQELSAASPTIS	FSIP1 [319,338]
5	627	IDESIYFSSDVVTGNVPLKV	CXorf48 [53,72]	17	2020	TKLEISGDEFNLFLKLKLNKQ	GASZ [347,366]
5	628	KRILVNLMSMVENKLELEHT	CXorf61 [78,97]	17	2021	DKYWREYILSLEELVNGMYR	Glypican-3 [293,312]
5	629	NRRKSRRFIPRPPSVAPPPM	DBPC [176,195]	17	2022	RNQPLTFALQLHDPSTGLAE	gp100 [234,253]
5	630	EVRLQNETSYSRVLHGYYAAQ	DCAF12 [54,73]	17	2023	GTLDLVAVSSVKQNIIVTTE	HAGE [451,470]
5	631	LQGFSLFLKGNLLRGIDSL	DKKL1 [52,71]	17	2024	PHAPGVQMQAIPEDAVHEDS	HDAC2 [375,394]
5	632	NLIAERQVRMAAQVALRRQQ	DMRT1 [106,125]	17	2025	SSNAYNSRYWSNPKVHRNT	IGFS11 [313,332]

5	633	RKAVTKRRLQRSYEMNERA	DPPA2 [150,169]	17	2026	AKINKKSLVSFKALIEESE	JARID1B [768,787]
5	634	KTQNDVDIADVAYFEKDVK	EpCAM [202,221]	17	2027	NDIASMNLQAHLPGLNLNA	KOC1 [353,372]
5	635	GLVTSRSFRTASVSINQTEP	EPHA2 [420,439]	17	2028	LLGSENDGTKIAASQAISAM	KU-CT-1 [324,343]
5	636	KQLENKKTGSKALAEFEKEM	FAM133A [46,65]	17	2029	ETRLALVQRNVAIMKSIIPA	LDHC [104,123]
5	637	IVKDARLNGSVASYILASHN	FAM46D [57,76]	17	2030	LQNFVRILLNEEDMNVIVVD	LPI [114,133]
5	638	EFNVLEMEVMRRQLYAVNRR	FATE1 [128,147]	17	2031	QGASAFPTTINFTRQRQPSE	MAGE-A1 [59,78]
5	639	RKLFYFKIWAFLDVSFVERI	FBXO39 [366,385]	17	2032	ITKAEILESIRNYEDHFPL	MAGE-A10 [155,174]
5	640	KAKGRNRRSHRAMRVAHLEL	FMR1NB [7,26]	17	2033	FGEPKRLLTQNWVQEKYLVY	MAGE-A11 [352,371]
5	641	PVFPQLSRISIISKLNESET	FSIP1 [439,458]	17	2034	ASEEEIWEEELGVMGVYDGRE	MAGE-A4 [217,236]
5	642	KNVNQSLDLQLAVEKGDP	FTHL17 [109,128]	17	2035	KLVFHLLKRYRAREPVTKAE	MAGE-A6 [115,134]
5	643	GWEIGYLDRTSQKLRLLEPI	GASZ [24,43]	17	2036	MLLGQKSQRKAEGLQAQG	MAGE-A8 [1,20]
5	644	SSLSHISFSSHMLTTPT	GATA-3 [402,421]	17	2037	NLSNDWDFPRNGLMLPLLV	MAGE-B1 [188,207]
5	645	KHINQLLRTMSMPKGRVLDK	Glypican-3 [467,486]	17	2038	SLLSSWDFPRRKLMLPLLV	MAGE-B2 [191,210]
5	646	LNVSADTNSLAVVSTQLIM	gp100 [567,586]	17	2039	VDVSYKSKYGANSKIEKKQ	MAGE-B3 [75,94]
5	647	RNRPGMLVLTPTRELALQVE	HAGE [314,333]	17	2040	ARPRVAARRGTTAMTSAYS	MAGE-B4 [317,336]
5	648	FKPVMKVMEMFQPSAVVLQ	HDAC1 [241,260]	17	2041	PQSPLQGEEFQSSQLSPVSI	MAGE-C1 [612,631]
5	649	RQQTDMAVNWAGGLHHAKKS	HDAC2 [127,146]	17	2042	ASEEVIWEVLNAVGVYAGRE	MAGE-C2 [244,263]
5	650	QSYKHLFPVINQVVDVFP	HDAC3 [230,249]	17	2043	HESLSSFELSASRRGQKRNI	MORC1 [606,625]
5	651	SPSRQQSKAHRHRHRRGYSR	HOM-TES-85 [59,78]	17	2044	VKDLLKGQSRIFTYGLTNS	MPHOSPH1 [137,156]
5	652	LLSLHGVAAASLEVSESPGS	IGFS11 [12,31]	17	2045	PPLTSSNHSTSPQLSTGVSF	MUC-1 [1023,1042]
5	653	DGFDLNGIEAKIHTLLPWQ	IL13RA2 [93,112]	17	2046	EVLFPYQFDLKYLSFTLTCLS	NLRP4 [688,707]
5	654	EGDALRYMIERTVNWQHRAQ	JARID1B [1248,1267]	17	2047	KENFTGSETLKHLVLQFLQQ	NXF2 [379,398]
5	655	RNIPPHLQWEVLDSSLVQYG	KOC1 [86,105]	17	2048	QEKENKYFEDIKILKEKNAE	NY-BR-1 [1070,1089]
5	656	DVGYGRSISSSSLRRSSKE	KU-CT-1 [621,640]	17	2049	SWDVDDLLWKIHRMVILT	NYD-TSPG [333,352]
5	657	SRLQLHITMPFSSPMEABL	Lage-1 [85,104]	17	2050	EKSEYAEQLHVQLADKDLV	ODF2 [414,433]
5	658	LKGEMMDLQHGSLLFFSTSKI	LDHC [58,77]	17	2051	QKQPNTLRHVVIPDLQSSEA	PASD1 [410,429]
5	659	QTIESWREEGFPVGLKLAVL	LEMD1 [142,161]	17	2052	RGTEIGMIGSKPFSTVKYK	PEPP2 [779,798]
5	660	TYKIQRMLKSLTYPERPPL	LPI [437,456]	17	2053	KSIGRGYNPRLTVIVVKKRV	PIWIL1 [725,744]
5	661	QSPQGASAFPTTINFTRQRQ	MAGE-A1 [56,75]	17	2054	YHDPSRGMRSVGVFVASINL	PIWIL2 [747,766]
5	662	PRAHAEIRKMSLLKFLAKVN	MAGE-A10 [300,319]	17	2055	SPNNFTLAFIVVKKRINTRF	PIWIL3 [750,769]
5	663	EESFSPTAMDAIFGSLSDEG	MAGE-A11 [177,196]	17	2056	MSGRARVKARGIARSPSATE	PIWIL4 [1,20]
5	664	DGREDVSFAHPRKLLTQDLV	MAGE-A12 [232,251]	17	2057	DVLLAQEVRPRRWKLQVLDL	PRAME [105,124]
5	665	AISRKMVELVHFLLLKYRAR	MAGE-A2 [108,127]	17	2058	KFSGYPLYHSVYETYELVEK	PSMA [545,564]
5	666	KLLTQHVFQENYLEYRQVPG	MAGE-A3 [244,263]	17	2059	RSVYSKQPYTEYISTRWYRA	RAGE-1 [150,169]
5	667	LLIIVLGTIAMEGDSASEEE	MAGE-A4 [202,221]	17	2060	KMENVQPAPDNVLLTLRPRR	SAGE1 [210,229]

5	668	LDTQEEALGLVGVAATTEE	MAGE-A5 [16,35]	17	2061	LALWEAYREFESAIVEAARL	SART3 [225,244]
5	669	FPVIFSKASDSLQLVFGIEL	MAGE-A6 [147,166]	17	2062	TEKENKMKDLTFLEESRDK	SCP-1 [276,295]
5	670	QEALKLKVAVELVHFLHKKYR	MAGE-A9 [105,124]	17	2063	EYSQQFLTFLQQWDLDMQKA	SCP3a [124,143]
5	671	STESSVKDPVAWEAGMLMHF	MAGE-B1 [99,118]	17	2064	AHEWARAIIESDQEQQGRKLR	SCRN1 [350,369]
5	672	KIVGKRFREHFPEILKKASE	MAGE-B2 [139,158]	17	2065	QDLQREISILQEQISHLQFV	se57-1 [230,249]
5	673	TVPSAFQFWYEEALRDEEBER	MAGE-B3 [298,317]	17	2066	IKEGLITADAEGDFIDARPG	SLCO6A1 [550,569]
5	674	KEVNPTTHSYILVSM LGPND	MAGE-B4 [167,186]	17	2067	DQDTVMKAIQEARKMREQIQ	SOX-6 [492,511]
5	675	DEESVSASQKAIIFKRLSKD	MAGE-B6 [174,193]	17	2068	QLANDSVNRLSRILMELDGP	SPAG1 [555,574]
5	676	PVSPSFSTLVSLFQSSPER	MAGE-C1 [271,290]	17	2069	DVLQGELEAVKQAKLKLEEK	SPAG9 [446,465]
5	677	DSESSFTYTLDEKVAELVEF	MAGE-C2 [132,151]	17	2070	TAVAVPSNIQGIRNLVTDK	SPO11 [199,218]
5	678	STTHSFLFGALAEELDNARD	MORC1 [22,41]	17	2071	SEYLERQLQAEFIESGQYR	TAF7L [363,382]
5	679	SSKKTYSRLRSQASIIGVNLA	MPHOSPH1 [1703,1722]	17	2072	KWDPVVPFRNESAVTGYKML	TAG-1 [931,950]
5	680	LQRDISEMFLQIYKQGGFLG	MUC-1 [1069,1088]	17	2073	KYTSDDFWYRAVVLGTSDD	TDRD1 [1000,1019]
5	681	AETEPERHLGSYLLDSENTS	NKX3.1 [91,110]	17	2074	YRYLSNWRPSLFYKIANVQT	TEKT5 [44,63]
5	682	RNKSVRYLDLSANVLKDEGL	NLRP4 [805,824]	17	2075	TGLKRLSSFIGAGSPSLVKA	TEX14 [1283,1302]
5	683	STWQELILSLTVYSKQIF	NR6A1 [322,341]	17	2076	NDKNSKVLQMNAATYWNELP	TEX15 [2618,2637]
5	684	QMEMLKLTMNKRYNVSQAL	NXF2 [213,232]	17	2077	RKRRRRRLMELAEPKINWQ	THEG [120,139]
5	685	ITKRSEQIVEFLLIKNNAN	NY-BR-1 [124,143]	17	2078	QVKHLYNWNLP RRILFIKH	TPTE [399,418]
5	686	LVFRVDETTPAVVQSVLLER	NYD-TSPG [87,106]	17	2079	IKLDSSKELNLRQLVAKDQE	TSGA10 [516,535]
5	687	LELEIIVLNDRVTDLVNQQQ	ODF2 [458,477]	17	2080	ADGMWPQFRTIQEKEVILN	TSP50 [250,269]
5	688	SPGPRYNVNP KILRTGKDLG	ODF3 [65,84]	17	2081	FFNWFSDHNFAGSNKIAEIL	TSPY1 [257,276]
5	689	AFSKKWLDSLRS LFYQRWV	ODF4 [99,118]	17	2082	PWHRLFLRWEQEIQKLTGD	TYR [209,228]
5	690	YLLKTKAIVNASEMDIQNVP	OIP5 [172,191]	17	2083	LQPVETKAHFDSEPPQLLWD	ZNF165 [163,182]
5	691	ILRTQLLQQLYTSKAVSDEA	PASD1 [175,194]	18	2084	YLPRDVLAQLPSLRHLDLSN	5T4 [224,243]
5	692	VYQKRLMDEAKILKSLHHPN	PBK [77,96]	18	2085	SIIEGIESQASYKIVIEGK	ADAM2 [35,54]
5	693	WQQRQFYNKQSTLPRHSTLS	PEPP2 [506,525]	18	2086	KVLLFGLEIWTNKNLIVVDD	ADAM29 [242,261]
5	694	RRSIAGFVASINEGMTRWFS	PIWIL1 [641,660]	18	2087	EGLSPNLNRLGDRDFNQFS	AFP [324,343]
5	695	KWYSRVVFQMPHQEIVDSLK	PIWIL2 [770,789]	18	2088	AQDKAESYSLISMKMGDPK	AKAP-3 [397,416]
5	696	LHSWLILYSRSSHREMSLK	PIWIL3 [507,526]	18	2089	RNQSLEFSTMKAEKMRDKG	AKAP-4 [461,480]
5	697	QENPAAFVRAIQYVDPDVQ	PIWIL4 [526,545]	18	2090	AKGRRADGGSVIDYELIDQD	ANXA2 [175,194]
5	698	HQAGAQEAQPLQPSHFLDIS	PLAC1 [179,198]	18	2091	PSVFPKTSISPLNVVQGASV	BRDT [178,197]
5	699	SLLKDEALAI AALELLPREL	PRAME [33,52]	18	2092	YRGNTTMDIKDLVKQFHQIK	CABYR [47,66]
5	700	GDRSIFEGRTRYSRITGME	PRSS55 [54,73]	18	2093	ERPEIVSTWSSAGISWRSEA	CAGE1 [260,279]
5	701	STNEVTRIYNVIGTLRGAVE	PSMA [348,367]	18	2094	TQNGRFYAI SARFKPFSNKG	CALR3 [69,88]
5	702	VFYETIASLQPLFPGVNELDQ	RAGE-1 [191,210]	18	2095	QERTNSELHNLRIYVKQQS	CCDC62 [275,294]
5	703	QQRKKMEKAQRLMKKEQNK	RCA51 [188,207]	18	2096	YAKIDEKTAE LKRKMFKMST	CDCA1 [445,464]
5	704	QSRTDKVLSTAPPQLVHMAA	SAGE1 [121,140]	18	2097	BEKLSKVDEMISHATEELET	CTAGE2 [381,400]
5	705	NAKYANMWLEYNLERAHGD	SART3 [504,523]	18	2098	LLLEELRRVVAALPEGMRPD	CTAGE5 [14,33]

5	706	MEESNKARAAHSFVVTEFET	SCP-1 [363,382]	18	2099	QEGVQVVVQPGPGLLWLEE	CTCFL [105,124]
5	707	KILQQSRIVQSQRKTIKQL	SCP3a [159,178]	18	2100	PKSLEIRTLTVERLLEPLVT	CTNNA2 [14,33]
5	708	GETAKEALDIVVSLLEEHGQ	SCRN1 [120,139]	18	2101	NTLFVVVDVQTSQITKIPILK	DCAF12 [110,129]
5	709	IEETEFYVKIRTTLQKIRTQ	se57-1 [31,50]	18	2102	AAPIHDADAQESSLGLTGLQ	DKKL1 [30,49]
5	710	EKSYDISSGLVAIFIAFYGD	SLCO6A1 [148,167]	18	2103	GKIPIRWTAPEAISYRKFTS	EPHA2 [777,796]
5	711	SYNHKQIEQLYAAQLASMQV	SOX-6 [360,379]	18	2104	LKFVSSLRRQFEFSVDSFQI	FAM46D [159,178]
5	712	ISGKEETSVTILDSSEEDK	SP17 [92,111]	18	2105	AKLARQATNLKVNFFFERIM	FBXO39 [274,293]
5	713	SGDYEEAVMYYSRISALPT	SPAG1 [222,241]	18	2106	TQIPPEEYEMQMQLNKDFT	FSIP1 [202,221]
5	714	GREVENLILENTQLETKNA	SPAG9 [407,426]	18	2107	IAKRNXHHEIFNLLSFTLNP	GASZ [221,240]
5	715	IDVVESEAVSVLHHWLKTE	SPATA19 [28,47]	18	2108	NYTNAMFKNNYPSLTPQAFE	Glypican-3 [124,143]
5	716	YATKRDIYYTDSQLFGNQTV	SPO11 [130,149]	18	2109	VNNTIINGSQVWGGQPVYPQ	gp100 [105,124]
5	717	HRLRERKQLVIYEEISDPPE	SSX-1 [166,185]; SSX-2 [166,185]	18	2110	KTGKVRILIATDLASRGDLV	HAGE [534,553]
5	718	QIPEKIQKAFDDIAKYFSKE	SSX-2 [16,35]	18	2111	DVDKLHFTPRIQRNLBLEAQ	JARID1B [77,96]
5	719	PGKPTTSEKINMISGVLQRY	SSX-3 [142,161]	18	2112	GPPEAQFKAQGRIYGKIKEE	KOC1 [458,477]
5	720	GKHAWTHRLRERKQLVVYEE	SSX-4 [160,179]	18	2113	LANMSABYTSKVQIFEHGGL	KU-CT-1 [133,152]
5	721	ATLPPFMNRKRVADFGQND	SSX-5 [65,84]	18	2114	GTDSDEHWNKNIHKVQISA	LDHC [219,238]
5	722	AFLSVKKQFEELTLGEFLKL	Survivin [85,104]	18	2115	LEFSQLSVKDSFRDLFIPRI	LPI [43,62]
5	723	AEGPSTLDEGLFLRSQEAAA	SYCE1 [219,238]	18	2116	ALAETSYVKVLEYVIKVSAR	MAGE-A1 [270,289]
5	724	DEVPDEVENQFILRLPLEHA	TAF7L [92,111]	18	2117	ESVIRNYEDHFPLLFSEASE	MAGE-A10 [162,181]
5	725	NESAVTGYKMLYQNDLHLTP	TAG-1 [940,959]	18	2118	RAHAETSKMKVLEYIANANG	MAGE-A11 [389,408]
5	726	DKTIQANVLEIISPRLFYAL	TDRD1 [939,958]	18	2119	PDAESLFREALSNKVDELAH	MAGE-A4 [100,119]
5	727	DNIKHSQNMNRANSIQLREEA	TEKT5 [301,320]	18	2120	DLESEFQAALSRKVAKLVHF	MAGE-A6 [100,119]
5	728	QGFIHRSLSSYAVHIISPGE	TEX14 [370,389]	18	2121	EEIWKFMNVLGAYDGEHHLI	MAGE-B1 [218,237]
5	729	VTELEYNYNQFSTLLKNVMS	TEX15 [2198,2217]	18	2122	RGQKSKLRAREKRRKARDET	MAGE-B2 [3,22]
5	730	PKIRDNFWSMPMSEVSQVSR	THEG [238,257]	18	2123	EFLNKMRIYDGKKHFI FGEP	MAGE-B3 [225,244]
5	731	SFYFWLHTSFIENNRLYLFPK	TPTE [493,512]	18	2124	GEPRKLITQDLVQEKYLEYQ	MAGE-B4 [239,258]
5	732	VLGEAWRDQVDWSRLLRDAG	TRAG-3 [45,64]	18	2125	DDSTATESASSSVMSPSFSS	MAGE-C1 [1122,1141]
5	733	KARQSEADNNTLKLLELITAE	TSGA10 [430,449]	18	2126	LLVIYNLKLNLNGEPELDVK	MORC1 [197,216]
5	734	DPEAVARRWPMVSVVRANGT	TSP50 [116,135]	18	2127	LPRTLNVLFDSLQERLYTKM	MPHOSPH1 [172,191]
5	735	FWANVIANHPQMSALITDED	TSPY1 [158,177]	18	2128	LFEMQDPAFVKQAVNLLQEA	NLRP4 [557,576]
5	736	DSFQDYIKSYLEQASRIWSW	TYR [458,477]	18	2129	FFVQDASAASALKDVSYKIY	NXF2 [166,185]
5	737	GATLKGVAAGSSSVKWTEG	WT1 [244,263]	18	2130	KKEIAMLKLEIATLKHQYQE	NY-BR-1 [1052,1071]
5	738	WRGRSTYRPRRSLQPPPEL	XAGE-2 [3,22]	18	2131	LTFVMPNDYTKFVAEYFQER	NYD-TSPG [180,199]
5	739	GKTFRVSSHILRHFRHTGE	ZNF165 [434,453]	18	2132	EMDGAAAQVMALKDTIGK	ODF2 [215,234]
6	740	LQGLRRLELASNHFLYLPRD	5T4 [209,228]	18	2133	KDEVYQKIILKFPLLNSETH	PASD1 [86,105]
6	741	EDVRVSGWLQTEFLSQDGD	ACRBP [452,471]	18	2134	NLRDNPFRRTTQTRRRDDKEL	PEPP2 [940,959]
6	742	MQRVAPEMFFSPQVFEQPGP	ACTL8 [251,270]	18	2135	QETAQLVGSTASQQPGYIQP	PIWIL1 [16,35]

6	743	GLGGLRMSDNFDSLVPQITV	ADAM2 [10,29]	18	2136	AMDQARELVNMLEKIAGPIG	PIWIL2 [614,633]
6	744	LQINDFAYEIKPLAFSTTFF	ADAM29 [127,146]	18	2137	SHREAMSLKGHLQSVTAPMG	PIWIL3 [518,537]
6	745	DLATIFFAQFVQEATYKEVS	AFP [45,64]	18	2138	ARLVDNIQRNTNARFELETW	PIWIL4 [415,434]
6	746	NRNVNFAMKSETKLREKMY	AKAP-3 [417,436]	18	2139	SQLTTLSEFYGNISISALQS	PRAME [406,425]
6	747	SKGLMVYANQVASDMMVSLM	AKAP-4 [330,349]	18	2140	WNLLEHETDSAVATARRPRWL	PSMA [2,21]
6	748	SDTSGDFRKLMMVALAKGRRA	ANXA2 [161,180]	18	2141	GEGTFSEVMKMQSLRDGNYY	RAGE-1 [11,30]
6	749	VDAVKLQLPDYYTIIKNPMD	BRDT [56,75]	18	2142	MSTRDQYAAVTHNIREEKIN	SAGE1 [616,635]
6	750	SKPRLVVPYGLKTLLEGISR	CABYR [4,23]	18	2143	LDRQLKVKDLVLSVHNRAIR	SART3 [354,373]
6	751	YHSLNEELDFLVTSYEEIE	CAGE1 [694,713]	18	2144	QENRKIEAQKATQELQFG	SCP-1 [135,154]
6	752	AISARFKPFSNKGKTLVIQY	CALR3 [76,95]	18	2145	MFRQQQKILQQSRIVQSQRL	SCP3a [153,172]
6	753	DKELNDMVAHVQQQLLSWEE	CCDC62 [41,60]	18	2146	SLDLLMKKIKGKDLQLEMN	se57-1 [87,106]
6	754	LKTEENSFKRLMIVKKEKLA	CDCA1 [334,353]	18	2147	EPHMKRPMNAFMVWAKDERR	SOX-6 [618,637]
6	755	QLQVQREIVNKHNELRKAVS	CRISP2 [33,52]	18	2148	IEAKMELEEVTRLLNLKDK	SPAG1 [724,743]
6	756	AMSAKAKLMTGHAIPPSQLD	CT45 [51,70]	18	2149	SVTKAERSHLIVWQVMYGN	SPAG9 [1302,1321]
6	757	SNESMLSTDTKKASILLIR	CT46 [136,155]	18	2150	ITGKGVPDLNTRLVKKLWD	SPO11 [247,266]
6	758	EEGEQAAGLAAPVPRGSAEE	CT47 [64,83]	18	2151	PLKNVRKKRFRKTQKKVPDV	TAF7L [225,244]
6	759	TELYQENEMKLYRKLIIVEEK	CTAGE2 [356,375]	18	2152	SSSLSIKWDPVVPFRNESAV	TAG-1 [925,944]
6	760	SKSLKSQVAEAKMTFKIQM	cTAGE5 [180,199]	18	2153	QKKAHVLYIDYGNIEIPLN	TDRD1 [341,360]
6	761	NMAFVTSGELVRHRRYKHTH	CTCF1 [319,338]	18	2154	ELDRLLTENQNLTVKRRLE	TEKT5 [158,177]
6	762	RGSQKKHISPVALSEFKAM	CTNNA2 [931,950]	18	2155	FDDWDWQNGSLSSLPEST	TEX14 [696,715]
6	763	VTINEDNIYISNSIYFSIA	CXorf48 [118,137]	18	2156	QHSVEYEGNIHTSLAIAQKL	TEX15 [343,362]
6	764	NSTALALVRPSSGLINSNT	CXorf61 [34,53]	18	2157	AAQMAVPSSRILQLSKPKAP	THEG [258,277]
6	765	HQTAIKRNNPRKFLRSVGDG	DBPC [122,141]	18	2158	DIKLLRNI PRWTHLLRLLRL	TPTE [180,199]
6	766	SRVPVYAHITHKALKDIPKE	DCAF12 [227,246]	18	2159	EESNRQMMEQLRKANEDAE	TSGA10 [406,425]
6	767	STLVIPSAAPIDHADAQES	DKKL1 [22,41]	18	2160	SAKEGTAFRMEAVQEGAAGV	TSPY1 [33,52]
6	768	QSVPPQFFTFEDAPSYPEAR	DMRT1 [302,321]	18	2161	TERRLLVRRNIFDLSAFEKD	TYR [113,132]
6	769	GRLLSADTKGWRLQFHAGQ	DPPA2 [228,247]	18	2162	AQDEGFGKILTHKNTVRGEI	ZNF165 [250,269]
6	770	FITSILYENNVITIDLQNS	EpCAM [180,199]	19	2163	SSSAPFLASAVSAQPPLPDQ	5T4 [42,61]
6	771	AISYRKFTSASDVWSFGIVM	EPHA2 [788,807]	19	2164	GLRGVLQFENVSYGIEPLES	ADAM2 [113,132]
6	772	SVDSFQIVLDPMLDFYSDKN	FAM46D [172,191]	19	2165	EIPNMSDHTTVHVARFNDIM	ADAM29 [561,580]
6	773	PGTDAVAQTSLEEFNVLEME	FATE1 [116,135]	19	2166	VMKNFGTRTFQAITVTKLSQ	AFP [226,245]
6	774	MGKRLDYLNLKGARLTVEQG	FBXO39 [160,179]	19	2167	GRRDARSFVEAAGTTFNPAN	AKAP-3 [543,562]
6	775	KRKRKSEMLQKAARGREEHG	FMR1NB [234,253]	19	2168	NRLSSLVIQMAHKEIKEKLE	AKAP-4 [222,241]
6	776	KRPSFLDDPLYGISVLSSE	FSIP1 [533,552]	19	2169	LYYYIQQDTKGDYQKALLYL	ANXA2 [315,334]
6	777	HFLESHYLHEQVKTIKELGG	FTHL17 [132,151]	19	2170	SSDELNFQFRKAAIEKEVKA	BRDT [821,840]
6	778	HHEIFNLLSFTLNPLEGKLQ	GASZ [227,246]	19	2171	IKIGSEKSLHLEVEITSIVS	CABYR [409,428]
6	779	DQPRWVSHHHPAVLNGQHPD	GATA-3 [6,25]	19	2172	ESRNDKEMQLQKFKKIKANY	CAGE1 [398,417]

6	780	DMVNELFDSLFPVIYTQLMN	Glypican-3 [165,184]	19	2173	KIDGQSIESGSIEYDWNLT	CALR3 [185,204]
6	781	VLRYGSFSVTLDIVQGI	gp100 [476,495]	19	2174	NQKSLFKDQKFEAMLVQQNR	CCDC62 [348,367]
6	782	MSSTDKVIVFVSRKAVADHL	HAGE [484,503]	19	2175	AHQEALMKLERLDSVPVEEQ	CDCA1 [158,177]
6	783	ELLKYHQRVLYIDIDIHHGD	HDAC1 [162,181]; HDAC2 [163,182]	19	2176	SENQKLQKQLKVMTELYQEN	CTAGE2 [343,362]
6	784	FKPIISKVMEMYQPSAVVLQ	HDAC2 [242,261]	19	2177	MKLHRKLTVEENYRLEKEEK	CTAGE5 [394,413]
6	785	QNSRQYLDQIRQTIFENLKM	HDAC3 [349,368]	19	2178	SYASRDYKLRHMRTHSGE	CTCF [376,395]
6	786	GDLVDTQSDLIATQRDLIAT	HOM-TES-85 [236,255]	19	2179	QVEVAIEALSANVPQPFEEEN	CTNNA2 [588,607]
6	787	TGTMPATNVSIFINNTQLSD	IGF511 [95,114]	19	2180	KSDARHNVSVPVYAHITHK	DCAF12 [219,238]
6	788	EIKVNPPQDFEIVDPGYLGY	IL13RA2 [29,48]	19	2181	HTELHPRVAFWIIKLPRRRS	DKK1 [160,179]
6	789	IEEIPAYLPNGAALKDSVQR	JARID1B [997,1016]	19	2182	GTNFQKRLFTKIDTIAPDEI	EPHA2 [131,150]
6	790	LDKLNQFQLENFTLKVAIIP	KOC1 [136,155]	19	2183	KESYPVVVAESMYGDFQEAM	FAM46D [196,215]
6	791	KKNSYHFSAGFGSPIEDKSE	KU-CT-1 [643,662]	19	2184	NPYNAVLTKKQVQVTRGLLS	FBXO39 [98,117]
6	792	GARRPDSRLQLHITMPFSS	Lage-1 [79,98]	19	2185	AWQSKEEMENTKKFLSLTAV	FSIP1 [162,181]
6	793	SILKNLRVHPVSTMVKGly	LDHC [262,281]	19	2186	GAEVNTQDENGYTALTWAAR	GASZ [172,191]
6	794	LSTEKSKKLKWPEASTTKR	LEMD1 [80,99]	19	2187	KVFGNFPKLIMTQVSKSLQV	Glypican-3 [206,225]
6	795	SRGATTFIYNRAVKNTRKVA	LIPI [135,154]	19	2188	FSPQLPHSSSHWLRLPRIF	gp100 [625,644]
6	796	ITKKVADLVGFLLLKYRARE	MAGE-A1 [102,121]	19	2189	LKNITYLVLEADKMLDMGF	HAGE [387,406]
6	797	QDRIATDDTTAMASASSA	MAGE-A10 [342,361]	19	2190	QTRVKLNFLDQIAKYWELQG	JARID1B [96,115]
6	798	GSVIKNYEDYFPEIFREASV	MAGE-A11 [250,269]	19	2191	HSVPKRQRIRKLQIRNIPPH	KOC1 [72,91]
6	799	KASEYLQLVFGIEVVEVRI	MAGE-A12 [153,172]	19	2192	GSKDFNNQGIPLIQLLKS	KU-CT-1 [348,367]
6	800	SKASEYLQLVFGIEVVEVVP	MAGE-A2 [152,171]	19	2193	MSTVKEQLIEKLIEDDENSQ	LDHC [1,20]
6	801	EEQEAASSSSTLVEVTLGEV	MAGE-A3 [34,53]; MAGE-A6 [34,53]	19	2194	AKFVDVIHSDSNGLGIEPL	LIPI [224,243]
6	802	ATEEQEAASSSSTLVEVTLG	MAGE-A6 [32,51]	19	2195	HAEIRKMSLLKFLAKVNGSD	MAGE-A10 [303,322]
6	803	VRVNARVRISYPSLHEEALG	MAGE-A8 [294,313]	19	2196	VYAGREHFLFGEPKRLLTQN	MAGE-A11 [343,362]
6	804	VGKEHMFYGEPRKLLTQDWV	MAGE-A9 [231,250]	19	2197	KISGGPRISYPLLHEWALRE	MAGE-A6 [292,311]
6	805	MHFILRKYKMRPIMKADML	MAGE-B1 [116,135]	19	2198	RSSVRARRRTTATTFRARS	MAGE-B1 [318,337]
6	806	ESLLSSWDFPRKLLMPLLG	MAGE-B2 [190,209]	19	2199	VDLTDEESLSSWDFPRRKL	MAGE-B2 [184,203]
6	807	VQFLMEMYKMKPIMKADML	MAGE-B3 [119,138]	19	2200	RQQTQDHQGAQITATNKKV	MAGE-B3 [19,38]
6	808	FPEIFRKVSQRTLVFGLAL	MAGE-B4 [147,166]	19	2201	AEKEESPSSSSSVLRDTASS	MAGE-B4 [33,52]
6	809	DSSGESYTLVSKLGLPSEGI	MAGE-B6 [256,275]	19	2202	RTHSTFEGFPQSLLQIPMTS	MAGE-C1 [325,344]
6	810	EFLAMLKNTVPITFPSSYKD	MAGE-C1 [1086,1105]	19	2203	PMEDVNLSSGHIARVSVSGS	MORC1 [780,799]
6	811	PRELLTKVWVQGHYLEYREV	MAGE-C2 [270,289]	19	2204	ENNEGLRAFLLTIEENELKNE	MPHOSPH1 [882,901]
6	812	EKPLNSFYQRRQAMGIPFI	MORC1 [464,483]	19	2205	YQPDLYKLSFTLTCLSRDDI	NLRP4 [692,711]
6	813	RAKRKLYTSEISSPIDISGQ	MPHOSPH1 [1775,1794]	19	2206	TIPYGIKYDKAWLMNSIQSH	NXF2 [128,147]
6	814	TSPQLSTGVSFFFLSFHISN	MUC-1 [1032,1051]	19	2207	LQSKNMWLQQQLVHAHKKAD	NY-BR-1 [1270,1289]

6	815	TETQVKIWFQNNRYKTKRKQ	NKX3.1 [164,183]	19	2208	RGKAPDPQAGNFVLVFFPNE	NYD-TSPG [545,564]
6	816	STTSVYSSFVNLFTEPGAE	NLRP4 [367,386]	19	2209	HKA EVEAIMEQLKELKQKGD	ODF2 [377,396]
6	817	RSLD PQSYSLIHQLLSAEDL	NR6A1 [244,263]	19	2210	HDAIQNQNAL ELMMDHLQK	PASD1 [392,411]
6	818	DNEWNYTRAGQAFTMLQTEG	NXF2 [596,615]	19	2211	RSWTYGITRGGVFFINEEA	PEPP2 [14,33]
6	819	SSEIVGMLLQQNVDFVFAADI	NY-BR-1 [161,180]	19	2212	GLTDKMRNDFNVMKDLAVHT	PIWIL1 [391,410]
6	820	DDMYIVQKYISNPLLI GRYK	NYD-TSPG [234,253]	19	2213	ENYQPKMVV FVVQKKISTNL	PIWIL2 [841,860]
6	821	ATSAQNIEFLQVI AKREEAI	ODF2 [675,694]	19	2214	FRRTFKLLDFEQVGRNYYTK	PIWIL3 [229,248]
6	822	PAAYRQTDV RVTKFKAPQYT	ODF3 [182,201]	19	2215	SATEVGRIQASPLPRSDLS	PIWIL4 [17,36]
6	823	NIWIFELERNVSIPIGWSYF	ODF4 [165,184]	19	2216	MPMQDIKMILKMVLQDSIED	PRAME [218,237]
6	824	NNVVLEAPFLVGIEGSLKGS	OIP5 [111,130]	19	2217	FLDELKAENIKKFLYNFTQI	PSMA [61,80]
6	825	RADPVDLEFSVDQVSDVQE	PASD1 [298,317]	19	2218	TPAQKILTKFKQSRAMNDF	RAGE-1 [220,239]
6	826	FDDEAYYAALGTRPPINMEE	PBK [266,285]	19	2219	NNSQPAPGNILSTAPPWLRH	SAGE1 [635,654]
6	827	SQEIMHADNPAAIQT VVLQ	PEPP2 [674,693]	19	2220	ESDGDEYAMASSAESSPGEY	SART3 [64,83]
6	828	IYTRRNYEAA NSLIQNLFKV	PIWIL1 [499,518]	19	2221	ELEDIKVSLQRSVSTQKALE	SCP-1 [323,342]
6	829	AASIRRTDGGFLFLADVSHK	PIWIL2 [364,383]	19	2222	SILQEQISHLQFVIHSQHQN	se57-1 [237,256]
6	830	KKKAIQLYRHGTSLEIWLGY	PIWIL3 [248,267]	19	2223	EKQPYEEQARLSKI HLEKY	SOX-6 [666,685]
6	831	SNKAKAFD GAILFLS QKLEE	PIWIL4 [151,170]	19	2224	RALRKDKPAATAASFTAEW	SPAG1 [73,92]
6	832	QLTTL SFYGN SISISALQSL	PRAME [407,426]	19	2225	GVDGQWDL SNYHLDDLGRPH	SPAG9 [1028,1047]
6	833	EA EVGEFPWQVSIQARSEPF	PRSS55 [73,92]	19	2226	PMGPEASFFDVLDRHRESLL	SPO11 [5,24]
6	834	SFDSLFS AVKNFT EIA SKFS	PSMA [628,647]	19	2227	NEVKRLLRSDAEAVSTRWEV	TAF7L [263,282]
6	835	KRRGPAYVMELPKL KLSGVV	RAGE-1 [339,358]	19	2228	QTTFGPVFEDQPLSVLPPEE	TAG-1 [32,51]
6	836	IRKTQKIVIKKREPLNFGIP	RCAS1 [102,121]	19	2229	DYGNEEIIPLNRIYHLNRNI	TDRD1 [350,369]
6	837	PAPDNVLLTLRPRRINMTDT	SAGE1 [216,235]	19	2230	QTQLAKTLQE I FQAENTIML	TEKT5 [357,376]
6	838	APRLAEYQAYIDFEMKIGDP	SART3 [307,326]	19	2231	RITIGTLF SVLHERRSQFPV	TEX14 [328,347]
6	839	HDLEIQLTAITTS EQYYSKE	SCP-1 [479,498]	19	2232	REDNAVSAATALLESEDTI	TEX15 [544,563]
6	840	RLKTIKQLYEQFIKSMEELE	SCP3a [171,190]	19	2233	SKPKAPATLLEEWDPV PKPK	THEG [272,291]
6	841	NTREPAAEIEALLGMDLVRL	SCRN1 [96,115]	19	2234	FTKEVNEWMAQDL ENIVAIH	TPTE [318,337]
6	842	EAGAAALRNVAQRLFENYQT	se57-1 [121,140]	19	2235	ISMQNLEALLVANRDKEYQS	TSGA10 [562,581]
6	843	DFQKEYQLKTIEKL ALEKSY	SLC06A1 [132,151]	19	2236	VNITEYRASHSTPIEWYPDY	TSPY1 [222,241]
6	844	AAQLASMQVSPGAKMPSTPQ	SOX-6 [371,390]	19	2237	NFSFRNTLEGFASPLTGIAD	TYR [337,356]
6	845	SNTHYRIPQFGN LLEGLTR	SP17 [6,25]	19	2238	GTDEAVLQVQAHEHGQE IFQ	ZNF165 [130,149]
6	846	TPNNHFTLEDI QALKRQYEL	SPAG1 [907,926]	20	2239	AALLAGRALQGLRRLELASN	5T4 [201,220]
6	847	STAHSRIRKERPISLGIFPL	SPAG9 [190,209]	20	2240	ILSSLELWIDENKIATTGEA	ADAM2 [224,243]
6	848	HLKSDLLANQSQEVLEERT	SPATA19 [93,112]	20	2241	RDFNQFSSGEKNIFLASFVH	AFP [337,356]
6	849	RSSWENIKFEDSVGLQMVSH	SPO11 [75,94]	20	2242	AREGGRFFPRERKRFRGQER	AKAP-3 [254,273]
6	850	GKHAWTHRLRERKQLVIYEE	SSX-1 [160,179]	20	2243	GGGQSAKALSVKQLESHRAP	AKAP-4 [588,607]
6	851	GFKAILPSFMRNKRVTDFQG	SSX-3 [62,81]	20	2244	IQNKPLYFADRLYDSMKGKG	ANXA2 [263,282]
6	852	ISEKLKAFDDIAKYFSKKE	SSX-4 [17,36]	20	2245	YLQKVVLKDLWKHSFSWPFQ	BRDT [34,53]

6	853	HRVRERKQLVIYEEISDPQE	SSX-5 [166,185]	20	2246	TEKPEFQSQVYNYAKDNNIK	CAGE1 [138,157]
6	854	MGQHKDLWDFHMPERLAKEI	SYCE1 [166,185]	20	2247	QMVTDLLELSTLLPISHENLT	CCDC62 [643,662]
6	855	DADSSAQAAAQAPENFQEGK	TAF7L [66,85]	20	2248	PKAKRTSRFLSGIINFIHFR	CDCA1 [112,131]
6	856	AAVALVSSSAWSSALGSQTT	TAG-1 [15,34]	20	2249	KLLEKFSLVQKEYEGYEVEES	CTAGE2 [61,80]
6	857	IMLLKNFMLNQNVMLSVKGI	TDRD1 [1072,1091]	20	2250	RRVVAALPEGMRPDSNLYGF	cTAGE5 [20,39]
6	858	LVNEVFTIDDTLQTLKRLR	TEKT5 [415,434]	20	2251	EQFTKIKELELMPEKGLKEE	CTCFL [11,30]
6	859	LLQISDALRYLHFQGFHRS	TEX14 [357,376]	20	2252	PQVINAALTLAARPQSKVAQ	CTNNA2 [460,479]
6	860	KDLRRHKIYGRKRLTSQDS	TEX15 [933,952]	20	2253	VGSQAHVSLDPRQPSYNVK	DCAF12 [313,332]
6	861	EDIPEISRLSISQKLPSTTM	THEG [97,116]	20	2254	GERPYWELSNHEVMKAINDG	EPHA2 [814,833]
6	862	ERRQQYFSDLFNILDTAIIV	TPTE [148,167]	20	2255	LIGQGIIVKDARLNGSVASY	FAM46D [51,70]
6	863	SEIELLRSQMANERISMQNL	TSGA10 [548,567]	20	2256	ELDRLVWRNSIRSSFISLS	FBXO39 [135,154]
6	864	SDVPVLQVIMHSRYAQRFW	TSP50 [179,198]	20	2257	FLDDPLYGISVSLSSDQHL	FSIP1 [537,556]
6	865	DRRGAVIQSVPGFWANVIAN	TSPY1 [146,165]	20	2258	LDRGANASFEKDKQSILITA	GASZ [99,118]
6	866	EKDKFFAYLTLAKHTISSDY	TYR [130,149]	20	2259	YRIYDMENVLLGLFSTIHDS	Glypican-3 [311,330]
6	867	TGSQALLRTPYSSDNLYQM	WT1 [210,229]	20	2260	HRRGSRSYVPLAHSSSAFTI	gp100 [190,209]
6	868	GKAFRHSSKLARHQRIHTGE	ZNF165 [350,369]	20	2261	MGFEPQIMKILLDVRPDRQT	HAGE [404,423]
7	869	FSGSNASVSAPSPLVELILN	5T4 [162,181]	20	2262	KPPLEKILPLLASLQIRVR	JARID1B [1226,1245]
7	870	SQPVVILSPNTLKEIEASAE	ACRBP [124,143]	20	2263	DAKVRMVIITGPPEAQFKAQ	KOC1 [448,467]
7	871	IERGRILNWEGVQYLWSFVL	ACTL8 [67,86]	20	2264	RAKLQELNAIPPIIDLKSE	KU-CT-1 [184,203]
7	872	QDFAKYIEMHVIVEKQLYNH	ADAM2 [174,193]	20	2265	MIEEPRLYEKNKPFYKLQEV	LPI [386,405]
7	873	SKHLPVFVFTYTDQGAILEDQP	ADAM29 [75,94]	20	2266	FPTVRPADLTRVIMPLEQRS	MAGE-A11 [98,117]
7	874	YKEVSKMVKDALTAIEKPTG	AFP [60,79]	20	2267	REKRRKAREETQGLKVAHAT	MAGE-B1 [12,31]
7	875	KQLQAVLQWVAASELNVPIIL	AKAP-3 [771,790]	20	2268	WGPRAYAETSKMKVLEFLAK	MAGE-B2 [275,294]
7	876	KQLQAVLQWIAASQFNVPMML	AKAP-4 [772,791]	20	2269	ATEEKIWEFLNKMRIYDGKK	MAGE-B3 [218,237]
7	877	PKWISIMTERSVPPLQKVFD	ANXA2 [211,230]	20	2270	STSTERSLKDLSLRTKTKMLV	MAGE-B4 [98,117]
7	878	LKAVHQQLQVLSQVPFRKLN	BRDT [430,449]	20	2271	EVIKRVVEFLAMLKNTVPI	MAGE-C1 [1078,1097]
7	879	TMYRGNTTMDIKDLVKQFHQ	CABYR [45,64]	20	2272	RKLQSIYDSNTRGIHNEIS	MORC1 [883,902]
7	880	EKVSDIMLQKLKSLHLKKKT	CAGE1 [645,664]	20	2273	LDVQIQHVVEGKRALSELTO	MPHOSPH1 [1135,1154]
7	881	DSRFGHFRLSSGKFYGHKEK	CALR3 [43,62]	20	2274	RTGYTKTYQAHAKQKFSRLW	NLRP4 [92,111]
7	882	SRQMVTDLLELSTLLPISHEN	CCDC62 [641,660]	20	2275	KYFEDSRNMKTLKDPYLGKE	NXF2 [439,458]
7	883	KSSADKMQLNAAHQEALMK	CDCA1 [146,165]	20	2276	AFEPAIEMQKSVPNKALELK	NY-BR-1 [704,723]
7	884	PASNMLKMEWSREVTTNAQR	CRISP2 [54,73]	20	2277	GLNVKRIIQELQKLMNKQHS	NYD-TSPG [573,592]
7	885	SQIDDFTFGFSKDRMMQKPGS	CT45 [71,90]	20	2278	ANVFGDGPYSTFLTSSPIRS	ODF2 [805,824]
7	886	KKASILLIRKIYILMQNLGP	CT46 [147,166]	20	2279	KLNWIPSFPTYDYFNQVTLQ	PASD1 [20,39]
7	887	DSGPDSSDVVPAAEVVGVAG	CT47 [37,56]	20	2280	LPRNMPSHRAQIMARYPEGY	PEPP2 [439,458]
7	888	LEGERNQIYIQLSEVDKTKE	CTAGE2 [299,318]	20	2281	HAFDGTILFLPKRLQQKVTE	PIWIL1 [161,180]

7	889	LLEKDPYALDVPNTAFGREH	cTAGE5 [497,516]	20	2282	IEGRVLPMERINLKNTSFIT	PIWIL2 [563,582]
7	890	MSGDERSDEIVLTVSNSNVE	CTCFL [206,225]	20	2283	KDYSIVKELAKHTRLSPRRR	PIWIL3 [413,432]
7	891	FGKEMVKLNYYAARRQQELK	CTNNA2 [179,198]	20	2284	ILKKLSMYQIGRNFYNPSEP	PIWIL4 [213,232]
7	892	GYVPQVDDIVNVVMVESIQF	CXorf48 [208,227]	20	2285	PLQALLERASATLQDLVFDE	PRAME [368,387]
7	893	SMVENKLVLEHTLLSKGFR	CXorf61 [85,104]	20	2286	DSVELAHYDVLLSYPNKTHP	PSMA [106,125]
7	894	VLGTVKWFNVNRNGYGFNRN	DBPC [94,113]	20	2287	DERIAAHQALQHPYFQEQRK	RAGE-1 [271,290]
7	895	HKDWIFSIAWISDTMAVSGS	DCAF12 [183,202]	20	2288	QQQPDNILSTASTGLINVAG	SAGE1 [262,281]
7	896	VAFWI IKLPRRRSHQDALEG	DKKL1 [167,186]	20	2289	EYENESQASQAVMKMDGMTI	SART3 [847,866]
7	897	SSQYRMHSYYPPPSYLGQSV	DMRT1 [285,304]	20	2290	PSSLTTPGSTLKFGAIRKMR	SCP-1 [933,952]
7	898	QQLGLSTNGKKIEVYLRHR	DPPA2 [105,124]	20	2291	EKLEEKHSQITELNVLQRM	se57-1 [179,198]
7	899	VDEKAPEFSMQGLKAGVIAV	EpCAM [252,271]	20	2292	KDERRKILQAFPMHNSNIS	SOX-6 [633,652]
7	900	KETFNLYAASDLDYGTNFQ	EPHA2 [116,135]	20	2293	ETLEQYGGAYVDYKTVLQID	SPAG1 [532,551]
7	901	NLTWDQVITLDQVLDEVIPI	FAM46D [8,27]	20	2294	REAEKKKEYNALHQHRTMI	SPAG9 [148,167]
7	902	TRPKKMGSQLPKPRMLRESG	FATE1 [73,92]	20	2295	IYYTDSQLFGNQTVVDNI IN	SPO11 [136,155]
7	903	RKWNQMMYSAELWRYRTITF	FBXO39 [44,63]	20	2296	DGTKEIESQSGIPGFLISSG	TA7L [286,305]
7	904	RSLFWRSEPADDLQRQDNRV	FMR1NB [205,224]	20	2297	DIGDTTITQLSWSRGFDNHSP	TAG-1 [618,637]
7	905	AIQMKKKLDKILAKKQRREK	FSIP1 [118,137]	20	2298	VDVADKLVTFLAKNITPQR	TDRD1 [1109,1128]
7	906	LSDDKMEHAQKLMRLQNLRG	FTHL17 [59,78]	20	2299	LYHREKRIGIDLVDHNEKN	TEKT5 [194,213]
7	907	MAASALRGLPVAGGGESSES	GASZ [1,20]	20	2300	SVSTPLSPGVSASAQYKD	TEX14 [1209,1228]
7	908	GLYHKMNGQNRPLIKPKRRL	GATA-3 [289,308]	20	2301	HSNLLYSQYFTYFAGEPQAN	TEX15 [2705,2724]
7	909	VLLGLFSTIHDSIQYVQKNA	Glypican-3 [319,338]	20	2302	YVTERI IAMSFPSSGRQSFY	TPTE [241,260]
7	910	SQKRSFVYVWKTWGQYQVL	gp100 [144,163]	20	2303	LAMKEKTISGMKNIIAEMEQ	TSGA10 [291,310]
7	911	PKASTWVVASRRSSTVSRAP	HAGE [8,27]	20	2304	EAYRRRHNSSLNFFNWFSD	TSPY1 [244,263]
7	912	TKYHSDDYIKFLRSIRPDNM	HDAC1 [65,84]	20	2305	ASQSSMHNALHIYMNGTMSQ	TYR [357,376]
7	913	EMTKYHSDEYIKFLRSIRPD	HDAC2 [64,83]	20	2306	PGPALNVKLQPVETKAHFD	ZNF165 [155,174]
7	914	SEELPYSEYFEYFAPDFTLH	HDAC3 [320,339]	21	2307	VSLTYVSFRNLTHLESLHLE	ST4 [247,266]
7	915	PSQKPSGFKSGQHPLNGQPL	HOM-TES-85 [92,111]	21	2308	QSVEPQQDFAKYIEMHIVE	ADAM2 [168,187]
7	916	IALLILGAFYWRSKNKEBEE	IGFS11 [258,277]	21	2309	TKVNFTEIQKLVLDVAHVHE	AFP [248,267]
7	917	IREDDTTLVTATVENETYTL	IL13RA2 [276,295]	21	2310	KGTGSABAVLQNAIYQAIHNE	AKAP-3 [721,740]
7	918	ESYNEWALNVNEALEAKINK	JARID1B [753,772]	21	2311	GMKQANGQFIDKLVSVMKL	AKAP-4 [688,707]
7	919	QDTDKITISPLQBLTLYNP	KOC1 [304,323]	21	2312	KSYSPYDMLIESIRKEVKGDL	ANXA2 [233,252]
7	920	VIDLMFHPGGLMKLRSREAD	KU-CT-1 [848,867]	21	2313	AQALEKLFMQKLSQMPQEEQ	BRDT [119,138]
7	921	REGAGRMVRVVGWGLGSASPE	Lage-1 [142,161]	21	2314	QLKKELEKATASALDLLKRE	CAGE1 [457,476]
7	922	QSAYEIIKLGYSWAIGLS	LDHC [236,255]	21	2315	VGQLQAREQALTTMIKLDK	CCDC62 [149,168]
7	923	LGFSPGPILPSTRKLYEKKL	LEMD1 [19,38]	21	2316	IQESLTKI VDSPEKLNKYK	CDCA1 [236,255]
7	924	DLFIPRIETILMMYTRNNLN	LPI [56,75]	21	2317	KSLKSQVAEAKMTFKRFQAN	CTAGE2 [151,170]

7	925	VQAATSSSSPLVLGTLEEVF	MAGE-A1 [28,47]	21	2318	ISHEKKAHDNWLAAARNAERN	cTAGE5 [454,473]
7	926	KLLTQDWVQENYLEYRQVPG	MAGE-A10 [269,288]; MAGE-A4 [245,264]	21	2319	SPQEMEVQLQFHAAEENVMVA	CTCF [144,163]
7	927	VKGLITKAEMLGSVIKNYED	MAGE-A11 [239,258]	21	2320	TGIGELAAALNEFDNKIILD	CTNNA2 [271,290]
7	928	ETSFQVALSRKMAELVHFL	MAGE-A12 [102,121]	21	2321	VTGQGSLLFYDIRAQRFL	DCAF12 [355,374]
7	929	FAHPRKLLMQDLVQENYLEY	MAGE-A2 [239,258]	21	2322	RLEGVISKYKPMIITEYME	EPHA2 [677,696]
7	930	APEEKIWEELSVLEVFEGR	MAGE-A3 [216,235]; MAGE-A6 [216,235]	21	2323	NNRLKSLSIQYLELDRLVWR	FBXO39 [123,142]
7	931	PVIFGKASESLKMFIDVK	MAGE-A4 [149,168]	21	2324	EASKGYLTALKTGHNMSEA	FSIP1 [477,496]
7	932	GGPRISYPLLHEWALREGEE	MAGE-A6 [295,314]	21	2325	VSLVQELDSDGISVDSNFQY	GASZ [59,78]
7	933	LRKLLTQEWVQENYLEYRQA	MAGE-A8 [245,264]	21	2326	TLSSRRRELQKLSFISFY	Glypican-3 [383,402]
7	934	KLKVAELVHFLHXYRVKEP	MAGE-A9 [109,128]	21	2327	GVSRLRTKAWNRQLYPEWT	gp100 [34,53]
7	935	EERAQVRSSVRARRRTTATT	MAGE-B1 [312,331]	21	2328	PPIKKNFYKESTATSAMSKV	HAGE [192,211]
7	936	QRAPTTAAAAAGVSSTKSK	MAGE-B2 [63,82]	21	2329	WEEFADPFAPFIHKIRPIAEQ	JARID1B [39,58]
7	937	IEKKQSFSQGLSSTVQSRD	MAGE-B3 [90,109]	21	2330	GKTVNELQNLSSAEVVPRD	KOC1 [507,526]
7	938	NQSSAWTLPRNGLMPLLSV	MAGE-B4 [188,207]	21	2331	YSQTGYLSSSNIINDGFYDY	KU-CT-1 [556,575]
7	939	IYDILHSIYGDARKIITED	MAGE-B6 [316,335]	21	2332	LSVHIKNLLKHGASLDNFHF	LPI [157,176]
7	940	SLQIPMTSSFSSTLLSIFQ	MAGE-C1 [336,355]	21	2333	AQALQAEQEAAFFSSTLNV	MAGE-A11 [138,157]
7	941	MIVIKYKDYFPVILKRAREF	MAGE-C2 [169,188]	21	2334	LKGNSSATEEIIWKFMNVLGA	MAGE-B1 [210,229]
7	942	EEESLSEVVVPMPSWLIRTR	MORC1 [135,154]	21	2335	LITKDLVQEKYLEYKQVPSS	MAGE-B2 [247,266]
7	943	QKFGDFLQHSPIQSKAKK	MPHOSPH1 [1731,1750]	21	2336	FPEILKKASFNMEEVVGVDL	MAGE-B3 [149,168]
7	944	TSASGSASGSASTLVHNGTS	MUC-1 [959,978]	21	2337	DPPRYQFLWGPRHAETS KM	MAGE-B4 [264,283]
7	945	PTPSKPLTSFLIQDILRGA	NKX3.1 [20,39]	21	2338	DELARFLLKYQVQPIITKA	MAGE-C1 [913,932]
7	946	MMAWSDNKIFRDRFLYTFYF	NLRP4 [169,188]	21	2339	PEEASDIIYFGRSKKRLSTL	MORC1 [74,93]
7	947	RLADELLFRQIAWIKKLFFF	NR6A1 [289,308]	21	2340	DSDDTLTGSLTNSLNISEFE	MPHOSPH1 [231,250]
7	948	FPKLLRLDGRSAPVIVDI	NXF2 [350,369]	21	2341	MEKRPVQVLLSSLLRKKMLP	NLRP4 [252,271]
7	949	PKKPSAFKPAIEMQNSVPNK	NY-BR-1 [461,480]	21	2342	KWHSEDEIRITTWRNRKPPE	NXF2 [90,109]
7	950	PNDYTKFVAEYFQERQMLGT	NYD-TSPG [185,204]	21	2343	QIVEFLLIKNNANAVNKYK	NY-BR-1 [130,149]
7	951	KLVEAEMDGAAAKQVMALK	ODF2 [210,229]	21	2344	TEKFDLSNLQNNYAHLTNSS	NYD-TSPG [282,301]
7	952	MGPNTVGKASQFSFSIKGRS	ODF3 [148,167]	21	2345	VAEALSTLESWSRYNQVVK	ODF2 [434,453]
7	953	AFILLLVVAFSKKWLDSRS	ODF4 [91,110]	21	2346	RLWQELSDSLGPVVQVNTWS	PASD1 [691,710]
7	954	LKEKIVLTHNRLKSLMKILS	OIP5 [199,218]	21	2347	PKTMVNIISDQTMHSIPTSPS	PEPP2 [527,546]
7	955	EQLEERTWLLHDAIQNQNA	PASD1 [382,401]	21	2348	YHDMTAGRRSIAGFVASINE	PIWIL1 [634,653]
7	956	NMARGLYLHQEKLLHGD	PBK [149,168]	21	2349	KTPKDSFTMSDGKEITFLEY	PIWIL2 [436,455]
7	957	DLNLEWISLPRSWTYGITRG	PEPP2 [4,23]	21	2350	LLQLWDLKFDTNFLSVPGRV	PIWIL3 [452,471]
7	958	YNPLMEARRLSALLFQHED	PIWIL1 [136,155]	21	2351	ETQRGETIKMTITLKRELPS	PIWIL4 [178,197]
7	959	LVGNIVITRYNNRTYRIDDV	PIWIL2 [413,432]	21	2352	MLTDVSPEPLQALLERASAT	PRAME [360,379]
7	960	GSEGTVVQLLANHFRVISRP	PIWIL3 [119,138]	21	2353	TLRGAVEPDYVILGGHRDS	PSMA [361,380]

7	961	QYAHKLTLFLVAQSIHKEPSL	PIWIL4 [824,843]	21	2354	LQSVLGSGTNGRVFVLRPLK	RAGE-1 [368,387]
7	962	ETFKAVLDGLDVLLAQEVRP	PRAME [95,114]	21	2355	RSTRDLYATVIHDIQBEEME	SAGE1 [710,729]
7	963	FEGRTRYSRITGGMEAEVGE	PRSS55 [59,78]	21	2356	DGMTIKENIIKVAISNPPQR	SART3 [862,881]
7	964	KYADKIYSISMKHPQEMKTY	PSMA [606,625]	21	2357	DSSETDLLSMVSEETLKT	SCP-1 [893,912]
7	965	YDPDERIAAHQALQHPYFQE	RAGE-1 [268,287]	21	2358	KLLENKLLQLKSSATYGKS	se57-1 [209,228]
7	966	ISSTITRDLYVTATHSVHEE	SAGE1 [660,679]	21	2359	NEKERTRFENLGPQLTGKSN	SOX-6 [539,558]
7	967	EKVHSLFRRQLAIPLYDMEA	SART3 [245,264]	21	2360	PASVPLQAWHPAKEMISKQA	SPAG1 [587,606]
7	968	EQEQSSLRASLEIELSNLKA	SCP-1 [739,758]	21	2361	SIRLDSTLRLYHAHTYQHLQ	SPAG9 [1105,1124]
7	969	NLLTGAQNEFKKEMAMLQKK	SCP3a [195,214]	21	2362	KGVPDLNTRLRLVKKLWDTFH	SPO11 [250,269]
7	970	DQEQGRKLRLSTMLELQGL	SCRN1 [361,380]	21	2363	PDVKEMEKSSFTYIESPDV	TAF7L [242,261]
7	971	ERKLSLENKLLQLKSSATYG	se57-1 [207,226]	21	2364	VFSKFAQLNLAAEDTRLFAP	TAG-1 [220,239]
7	972	DRKKVIFWFVASSFLIGLGS	SICO6A1 [167,186]	21	2365	ESVLGVYVDYGNFEILSLMR	TDRD1 [570,589]
7	973	EDAEGSKAMNGSAAKLQYY	SOX-6 [574,593]	21	2366	IDDTLQTLKLRLRETQDTLQ	TEKT5 [422,441]
7	974	SIPFSNTHYRIPQGFNLE	SP17 [2,21]	21	2367	PEHSEAFQASDSTLVAVEKS	TEX14 [1042,1061]
7	975	EPAGSEIADDLSILYSNRAA	SPAG1 [476,495]	21	2368	NPETDVSLVPDASVLSKPIF	TEX15 [2497,2516]
7	976	DEEVVKELMPLVVAVLENLD	SPAG9 [43,62]	21	2369	ILADLIFTDSKLYIPLEYRS	TPTE [109,128]
7	977	EMTEDIMRDRIEQVRRSISR	SPATA19 [130,149]	21	2370	VANRDKEYQSQIALQEKES	TSGA10 [572,591]
7	978	PTGGSRLASSEVLASIENI	SPO11 [35,54]	21	2371	SANDPIFLLHHAFVDSIFEQ	TYR [380,399]
7	979	EKRKAFFDIATYFSKKEWK	SSX-1 [19,38]	22	2372	NRNLTEVPDLPAYVRNLFL	5T4 [79,98]
7	980	MNGDDAFARRPTVGAQIPEK	SSX-2 [1,20]	22	2373	LVLRPHDVAFLLVYREKSNY	ADAM2 [258,277]
7	981	MNGDDTFARRPTVGAQIPEK	SSX-3 [1,20]	22	2374	FQKLGEYYLQNAFLVAYTKK	AFP [419,438]
7	982	VTLPPFMRSKRAADFHGND	SSX-4 [65,84]	22	2375	SDSWAEDLIVSALLLIQYHL	AKAP-3 [520,539]
7	983	KYFSEKEWEKMKASEKIIYV	SSX-5 [30,49]	22	2376	MVYANQVASDMMVSLMKT	AKAP-4 [334,353]
7	984	VHLKEILSKKQETLRILRLH	SYCE1 [96,115]	22	2377	RIMVSRSEVDMLKIRSEFKR	ANXA2 [290,309]
7	985	NEGTSIVMEIQKQIEKKEK	TAF7L [384,403]	22	2378	DVFETHFSKIPVSESMPL	BRDT [367,386]
7	986	VSREAILRFGFLQEFSEKER	TAG-1 [121,140]	22	2379	QVFIDVINKLENVEELIED	CAGE1 [348,367]
7	987	LGVTKEIAIWAERIMFSDLR	TDRD1 [237,256]	22	2380	IYVKQQSDLQFLNFVENSQ	CCDC62 [288,307]
7	988	TILPTLRSALFSRYSPHDWD	TEKT5 [76,95]	22	2381	KMKDTVQKLKNARQEVVEKY	CDCA1 [257,276]
7	989	PPSLNYIPPVQLQSGGQKPD	TEX14 [796,815]	22	2382	ILHEKKAHDNWSAAWTAERN	CTAGE2 [423,442]
7	990	YGLEHIFDAAKNLVWKERT	TEX15 [1882,1901]	22	2383	LTETELKFELLEKDPYALDV	cTAGE5 [488,507]
7	991	RPKRFYLEYYNNRTTPVWP	THEG [199,218]	22	2384	KYASVEASKLRHVRSHSTGE	CTCFL [348,367]
7	992	IALFFLMDVLLRVFVERRQQ	TPTE [133,152]	22	2385	SNNEEGVKLVMAATQIDSL	CTNNA2 [439,458]
7	993	RRQLDETNDLAQIARERDI	TSGA10 [330,349]	22	2386	RHNVSrvPVYAHITHKALKD	DCAF12 [223,242]
7	994	KSEAPPIYLQVSSYQHWID	TSP50 [336,355]	22	2387	QSPEDVYFSKSEQLKPLKTY	EPHA2 [569,588]
7	995	HHNSSLNFFNWFSDHNFAGS	TSPY1 [250,269]	22	2388	QFKKTMSTFHNLSLNLN	FBXO39 [215,234]
7	996	KHTISSDYVIPIGTYGQMK	TYR [142,161]	22	2389	LREIDEKLMKMKENVLEST	FSIP1 [382,401]

7	997	IQDVRVPVPGVAPTLVRSASE	WT1 [297,316]	22	2390	LITAVQNVITELPVNSQKIT	GASZ [370,389]
7	998	FKWNSDFINHQIIYAGEKNH	ZNF165 [301,320]	22	2391	IHDSIQYVQKNAGKLTTTIG	Glypican-3 [327,346]
8	999	LRHLDLSNNSLVSLTYVSFR	ST4 [236,255]	22	2392	SGYLAEADLSYTWDFGDSSG	gp100 [248,267]
8	1000	PWPERLSNNVEELLQSSLSL	ACRBP [167,186]	22	2393	DLASRGLDVHDTVHVNFDF	HAGE [545,564]
8	1001	LYPGFTKRLFRELMGDHVSS	ACTL8 [303,322]	22	2394	DQIAKYWELQGSLTKIPHVE	JARID1B [105,124]
8	1002	IFVSFNITIISSLELWIDE	ADAM2 [215,234]	22	2395	LQELTLNPERTITVKGNGVE	KOC1 [315,334]
8	1003	QKQSSYVGWVHFRIVEIVV	ADAM29 [185,204]	22	2396	FSWELHISELKFQLKSNVIP	KU-CT-1 [767,786]
8	1004	KLSQKFTKVNFTIQKLVLD	AFP [242,261]	22	2397	KNKPFYKLQEVKILAQFYND	LPI [395,414]
8	1005	DAMLRLKLYNVMAFKVPEHV	AKAP-3 [375,394]	22	2398	SSVRARRRTTATFRARSRA	MAGE-B1 [319,338]
8	1006	MTDSDFVSAVKRNLFNQWKQ	AKAP-4 [398,417]	22	2399	TTAAAAAGVSSSTKSKKGA	MAGE-B2 [67,86]
8	1007	RYKSYSPYDMLESIRKEVKG	ANXA2 [231,250]	22	2400	GRSRALKKQQRALSTTTSV	MAGE-B3 [56,75]
8	1008	PSRQTAIIVNPPPEYINTK	BRDT [4,23]	22	2401	EEERAGARPRVAARRGTTAM	MAGE-B4 [311,330]
8	1009	EVPAQLLDAEGAIGISEKS	CABYR [397,416]	22	2402	FPSSTSSSLQSSPVSSFPS	MAGE-C1 [817,836]
8	1010	ADQRLAISHSQIAHLEERNK	CAGE1 [715,734]	22	2403	VVPMPSWLIRTRESVTDPPQ	MORC1 [143,162]
8	1011	TQYDLSEFENIGAIGLELWQ	CALR3 [287,306]	22	2404	QDVKGYSFIKDLQWIVQSDS	MPHOSPH1 [304,323]
8	1012	VEWMSIFKPSKMQRIVRLKS	CCDC62 [532,551]	22	2405	AAPITEIVSQPERLLFVIDS	NLRP4 [213,232]
8	1013	EKTKRLNELKLSVVSLEIKQ	CDCA1 [218,237]	22	2406	NKLKPGQMEMKLTMNKRYN	NXF2 [207,226]
8	1014	ALLARKQAGDSLIGSAMS	CT45 [34,53]	22	2407	ASLTPLLLSITKRSEQIVF	NY-BR-1 [115,134]
8	1015	ESPDLISHSQVEQLVNKTS	CT46 [306,325]	22	2408	NNYAHLTNSSINKSGASYEK	NYD-TSPG [292,311]
8	1016	LKEFEKTIHFYQKKIILHEK	CTAGE2 [408,427]	22	2409	LKRLAEADSEKARLLLLLQD	ODF2 [294,313]
8	1017	TLEGERNQIYIQLSEVDKTK	cTAGE5 [328,347]	22	2410	LVQQEQHLKEQQRLREQLQ	PASD1 [482,501]
8	1018	TLQTVHFTSEAVELQDMSLL	CTCF1 [81,100]	22	2411	SNSIKRNPAPVVRGWLYK	PEPP2 [159,178]
8	1019	LVYDGVDIRKAVLMIRTPE	CTNNA2 [615,634]	22	2412	MEARRLRSALLFQHEDLIGK	PIWIL1 [140,159]
8	1020	QQGLPQGDQTTLTVQGVVTS	CXorf48 [26,45]	22	2413	TIGQPTRLRSVAQKILLQIN	PIWIL2 [703,722]
8	1021	TDNNLAVYDLSDILNPFPH	CXorf61 [53,72]	22	2414	VGQSIHQEPNRSLSLRLFY	PIWIL3 [863,882]
8	1022	VPPPRFRPRYRPRFRPRRQ	DBPC [272,291]	22	2415	GLTDQATSDFQLMKAVAEKT	PIWIL4 [384,403]
8	1023	ERGSIGRSVSFYEHIIITVGT	DCAF12 [338,357]	22	2416	NSHQDFWTVWSGNRASLYSF	PRAME [127,146]
8	1024	PRMBEKEALVPIQKATDSFH	DKKL1 [141,160]	22	2417	SDIVPPFSAFSPQGMPEGDL	PSMA [155,174]
8	1025	ASEGRMVIQDIPAVTSRQHV	DMRT1 [178,197]	22	2418	LMKEVRRFGQNYERIFILLE	SAGE1 [831,850]
8	1026	KIEVYLRLHRHAYPEQRQDM	DPPA2 [115,134]	22	2419	FIQATDYVEIWQAYLDYLR	SART3 [411,430]
8	1027	TVNGEQLDLDPGQTLIYYVD	EpCAM [234,253]	22	2420	LSRVYSKLYKEAEKIKKWKV	SCP-1 [102,121]
8	1028	DLEPHMNYTFTVEARNGVSG	EPHA2 [401,420]	22	2421	ESTSAHIIETEVVKIRTT	se57-1 [24,43]
8	1029	AKLTKEYPVVVAESMYGDF	FAM46D [192,211]	22	2422	TQVKDEAAAQPLNLSSRPKT	SOX-6 [414,433]
8	1030	LQEYAGNFQGIRFHYDRNPG	FATE1 [98,117]	22	2423	EDYKEKTVIDKSHLSKIETR	SPAG1 [175,194]
8	1031	QILDLSYMRNENVISELNI	FBXO39 [181,200]	22	2424	QRHTEMIHNYMEHLERTKLH	SPAG9 [161,180]
8	1032	ESLKMVRVSKPFGMLMLSIWI	FMR1NB [59,78]	22	2425	MIYKLVQSNYATKRDIYYT	SPO11 [120,139]

8	1033	ILKQKSI IKLSSERKKEDIE	FSIP1 [416,435]	22	2426	EYLERQLQAEFIESGQYRAN	TAF7L [365,384]
8	1034	HEQVKTIKELGGYVSNLRKI	FTHL17 [140,159]	22	2427	QNRVEVLAGDLRFSLSLSD	TAG-1 [370,389]
8	1035	DENGYTALTWAARQGHKNIV	GASZ [179,198]	22	2428	MFSDLRLSLQLKKTMEIKGTV	TDRD1 [251,270]
8	1036	KLESSHSRGSMTALGGASSS	GATA-3 [195,214]	22	2429	ERRSQFPVLHMEVIVHLLLQ	TEX14 [340,359]
8	1037	YYPEDLFDKKVLKVAHVEH	Glypican-3 [361,380]	22	2430	ELDHLALEWQITPSFESLSQ	TEX15 [320,339]
8	1038	SYTWDFGDSSGTLISRALVV	gp100 [257,276]	22	2431	RLLRLIILLRIFHLFHQKRQ	TPTE [195,214]
8	1039	KALENFKTGKVRILIATDLA	HAGE [528,547]	22	2432	LAENKMAIQSRDVAQFRNVV	TSGA10 [601,620]
8	1040	QRLFENLRMLPHAPGVQMQA	HDAC1 [364,383]; HDAC2 [365,384]	22	2433	RNTLEGFASPLTGIADASQS	TYR [341,360]
8	1041	YGLYKMIIVFKPYQASQHDM	HDAC3 [39,58]	23	2434	LAQLPSLRHLDLNNSLVSL	5T4 [230,249]
8	1042	NHHSERSRNHLERSLSQSDR	HOM-TES-85 [156,175]	23	2435	VIEGKPYTVNLMQKNFLPHN	ADAM2 [50,69]
8	1043	RKPRPPHTHSYTISHATLER	IGFS11 [394,413]	23	2436	YLQNAFLVAYTKKAPQLTSS	AFP [426,445]
8	1044	TNGSEVQSSWAETTYWISPO	IL13RA2 [114,133]	23	2437	ERPLASSPPRLYEDDETPGA	AKAP-3 [630,649]
8	1045	GEARLREMEALQSLRLANEG	JARID1B [1146,1165]	23	2438	LIMAKYSNDGAALAELEEQA	AKAP-4 [709,728]
8	1046	QVNTDSETAVNVVYSSKDQ	KOC1 [112,131]	23	2439	DTTTPATSAVKASSEFSPTF	BRDT [216,235]
8	1047	THEDKIVRRNATMIFGILAS	KU-CT-1 [77,96]	23	2440	KFWHVEAFDDEMTEKPEFQS	CAGE1 [126,145]
8	1048	VLKDFTVSGNLLFMSVRDQD	Lage-1 [122,141]	23	2441	STIEKQRKELQLLIGELKDR	CCDC62 [21,40]
8	1049	GETRLALVQRNVAIMKSIIP	LDHC [103,122]	23	2442	SNSGRSLSGPAELRSFNMPSL	cTAGE5 [629,648]
8	1050	LDGAQDSDSEELNIIILQGN	LEMD1 [58,77]	23	2443	ATIIARKSDLRVHMRNLHAY	CTCF [434,453]
8	1051	DGSFSFKLLNQLGMIEEPRL	LIPI [373,392]	23	2444	FIDASRLVYDGVDIRKAVL	CTNNA2 [609,628]
8	1052	APEEEIWEELSVMEVYDGRE	MAGE-A1 [209,228]	23	2445	YGSEWSVYAVGSQAHVSFLD	DCAF12 [304,323]
8	1053	DPARYEFLWGPRAHAEIRKM	MAGE-A10 [290,309]	23	2446	IEKVVQMTNDIDIKRIGVRLP	EPHA2 [933,952]
8	1054	REDSGDFGLQVSTMFSEDDF	MAGE-A11 [23,42]	23	2447	MYSAEWLRYRTITFSGRPSR	FBXO39 [50,69]
8	1055	EEQETASSSSTLVEVTLREV	MAGE-A12 [34,53]	23	2448	DVERNESLIKSGKKPFSNTE	FSIP1 [223,242]
8	1056	EEQQTASSSSTLVEVTLGEV	MAGE-A2 [34,53]	23	2449	FTKNGITSKDQKILAAALKE	GASZ [313,332]
8	1057	SEFQAALSRKVAELVHFLLL	MAGE-A3 [103,122]	23	2450	LGSDINVDDMVNELFDSLFP	Glypican-3 [157,176]
8	1058	DGREHTVYGEPRKLLTQDWV	MAGE-A4 [233,252]	23	2451	ANASFSLALNFPQSQKVLDP	gp100 [80,99]
8	1059	GSDPVRYEFLWGPRALAETS	MAGE-A8 [266,285]	23	2452	QKPTPIQSQAWPVILQGIDL	HAGE [263,282]
8	1060	ETSYEKVINYLVMNLAREPI	MAGE-A9 [279,298]	23	2453	VPTELVEKEFWRLVSTIEED	JARID1B [401,420]
8	1061	PRAYAETTKMKVLEFLAKMN	MAGE-B1 [274,293]	23	2454	IDVHRKENAGAAEKSITILS	KOC1 [229,248]
8	1062	KASEGLSVVFGLELNKVNPN	MAGE-B2 [155,174]	23	2455	EENKTTLLELGAVEPLTKLL	KU-CT-1 [57,76]
8	1063	FWAKVNKTVPFAQFWYEEA	MAGE-B3 [291,310]	23	2456	GLDPAGFRFRSRKPPYSRLDY	LIPI [202,221]
8	1064	DTTPNNFPLLYEALRDEEE	MAGE-B4 [294,313]	23	2457	FSQGLSSTVQSRTDPLIMKT	MAGE-B3 [96,115]
8	1065	PHLYEDALIDEVERALRLRA	MAGE-B6 [388,407]	23	2458	VLRDTASSSLAFGIPQEPQR	MAGE-B4 [45,64]
8	1066	IESEPLFTYTLDEKVDLAR	MAGE-C1 [898,917]	23	2459	RELLTKVWVQEHYLEYREVP	MAGE-C1 [1041,1060]
8	1067	KKKVLEFLAKLNNTVPSSFP	MAGE-C2 [311,330]	23	2460	KISEDKLNLR IKLALLLQK	MORC1 [911,930]
8	1068	EKQRELKTARTLSLFYGVNV	MORC1 [341,360]	23	2461	KMKESDHQIIKRRLRTKTAK	MPHOSPH1 [1801,1820]
8	1069	KKI IETMSSSKLSNVEASKE	MPHOSPH1 [1749,1768]	23	2462	QSTTSVYSSFVFNLFTEPGA	NLRP4 [366,385]

8	1070	AASRYNLTISDVSVDVFPF	MUC-1 [1128,1147]	23	2463	NVSQQALDLQNLRFDPDLMG	NXF2 [226,245]
8	1071	BAFSRASLVSVNSYPYPY	NKX3.1 [203,222]	23	2464	NVDVSSTIYNNEVLHQPLSE	NY-BR-1 [1180,1199]
8	1072	KFKEHLKQMTLQLELKQIPW	NLRP4 [25,44]	23	2465	FELFGFDILIDDLNKPWLLE	NYD-TSPG [367,386]
8	1073	LLSSTWQELILSSSLTVYSK	NR6A1 [319,338]	23	2466	EKAQAKTASELSKSMESMRG	ODF2 [328,347]
8	1074	SETLKHLVLQFLQQYYSID	NXF2 [385,404]	23	2467	VAFNQQQLVQQEQHLKEQQR	PASD1 [475,494]
8	1075	AQRKSKSLKINLNYAGDALR	NY-BR-1 [1200,1219]	23	2468	RSMRDDTMWQLYEWQQRQFY	PEPP2 [493,512]
8	1076	LVKRKLVDHIDLIYLNGLR	NYD-TSPG [402,421]	23	2469	ADGSEVSFLEYRKYQYNQEI	PIWIL1 [335,354]
8	1077	SMQNYVQFLKSSYANVFGDG	ODF2 [792,811]	23	2470	RGPAQRESVGLVSMFRGLGI	PIWIL2 [61,80]
8	1078	SISARTKAFRVDSTPGPAA	ODF3 [123,142]	23	2471	RNEWYDFFIVSQSVQDGTVT	PIWIL3 [792,811]
8	1079	DLRSRLFYQRPVVDVSNRIH	ODF4 [106,125]	23	2472	NPAAFVRAIQYVDPDVQLV	PIWIL4 [528,547]
8	1080	SMEWDTQVVKSSPLGPAGL	OIP5 [36,55]	23	2473	SLFFLRGRDLQLLRHVMNPL	PRAME [305,324]
8	1081	SQGQRGHTSMKAVYVEPAAA	PASD1 [212,231]	23	2474	KLGSNDFFVFFQRLGIASG	PSMA [514,533]
8	1082	MQKLGFGTGVNVYLMKRSPR	PBK [35,54]	23	2475	YKPDSNEFAVGTKNYSVSAG	SAGE1 [777,796]
8	1083	LHKEYTLEQALLSASQEIE	PEPP2 [659,678]	23	2476	LQQLEKYKPYEEALLQAEAP	SART3 [289,308]
8	1084	VGQSIHREPNLSLNRLYYL	PIWIL1 [842,861]	23	2477	TPEIYWKLDKAVPSQTVSR	SCP-1 [803,822]
8	1085	HFWALFYPKRAMDQARELVN	PIWIL2 [604,623]	23	2478	VDGKKLRIGEYKQLMRSRRQ	SOX-6 [700,719]
8	1086	SREIRELPLLNAMPLHSLWI	PIWIL3 [493,512]	23	2479	LPTVVAYNNRAQAEIKLQNW	SPAG1 [239,258]
8	1087	QHKLSLWPGFAISVSYFERK	PIWIL4 [237,256]	23	2480	LMELQEAVRWTEIRASREN	SPAG9 [522,541]
8	1088	LQALYVDSLFFLRGRDLQLL	PRAME [298,317]	23	2481	LLPSDLKRLNVPKDSLPLT	SPO11 [313,332]
8	1089	LTSPSMEIKEVASIILHKDF	PRSS55 [129,148]	23	2482	LATSHMDFSTKSVFSKFAQL	TAG-1 [208,227]
8	1090	KRQIYVAAFTVQAAETLSE	PSMA [729,748]	23	2483	YPRIISDVLIDEHLVLKSAS	TDRD1 [880,899]
8	1091	NILMLHEVVFDKSGSLALI	RAGE-1 [62,81]	23	2484	WNSQEFIQTLSDDFISVRER	TEX14 [1245,1264]
8	1092	SQPTPDNVL SAVTPELINLA	SAGE1 [402,421]	23	2485	LSRKLDKAVVHLKKAHRRVH	TEX15 [993,1012]
8	1093	QVISVTFEKNAGFIQATD	SART3 [397,416]	23	2486	SVLDNITTDKILIDVFDGLP	TPE [452,471]
8	1094	KDKRDYLWTSKNTLSTPLP	SCP-1 [833,852]	23	2487	AVQELRRQNYSSNAYHMSST	TSGA10 [644,663]
8	1095	QEEKILNMFQQQKILQQSR	SCP3a [146,165]	23	2488	SPLTGIADASQSSMHNALHI	TYR [349,368]
8	1096	DRDEAWVLETIGKYWAAEKV	SCRN1 [161,180]	24	2489	RHLDSLNNLSLVSLTYVSFRN	5T4 [237,256]
8	1097	KKIRTTLQKIRTQMFKDEIR	se57-1 [38,57]	24	2490	IEPLESSVGFHVIYQVKHK	ADAM2 [127,146]
8	1098	DISSGLVAIFIAFYGDRKKV	SLCO6A1 [152,171]	24	2491	FQTKAATVTKELESSLLNQ	AFP [202,221]
8	1099	QEMRQFFTVGQQPQIPITG	SOX-6 [719,738]	24	2492	DDKSGDASRLTSAFPDSLVE	AKAP-3 [697,716]
8	1100	REILREQPDNIPAFAAAYFE	SP17 [25,44]	24	2493	SDMMVSLMKTCLKVHSSGKPI	AKAP-4 [342,361]
8	1101	YLSKAERFKMMLTLISKQK	SPAG1 [875,894]	24	2494	NYDEKRQLSLNINKLPGDKL	BRDT [511,530]
8	1102	AQRKRFTRVEMARVLMERNQ	SPAG9 [498,517]	24	2495	DQLGNEYFRQPPRSPPLIH	CAGE1 [176,195]
8	1103	EVLEERTRIQFIRWSHTRIF	SPATA19 [106,125]	24	2496	QTALQKTQLQLQEMAQKATH	CCDC62 [104,123]
8	1104	SSDYLSRVYLPNKLKFGGWI	SPO11 [377,396]	24	2497	KSLKSQVAEAKMTFKIFQMN	cTAGE5 [181,200]
8	1105	SYVYMKRNYKAMTKLGFKVT	SSX-1 [47,66]	24	2498	KKGRSKAHVLAASVEQATQ	CTNNA2 [50,69]

8	1106	WEKMKASEKIFYVYMKRKYE	SSX-2 [37,56]	24	2499	SRERGSIGIRSVSFYEHIITV	DCAF12 [336,355]
8	1107	FGRLQGIFPKIMPKKPAEEG	SSX-3 [101,120]	24	2500	LVLAVGVFFIHRRRKNQRRAR	EPHA2 [549,568]
8	1108	EVMTKLGFVKVTLPPFMRSKR	SSX-4 [56,75]	24	2501	KLARQATNLKVNFFFERIMK	FBXO39 [275,294]
8	1109	RGKHAWTHRVRERKQLVIYE	SSX-5 [159,178]	24	2502	LSAASPTISSFSRPLENRNN	FSIP1 [330,349]
8	1110	KERISALNLQIEEEKNKQRQ	SYCE1 [134,153]	24	2503	KFKKAMTIGDVSLVQELLD	GASZ [49,68]
8	1111	KQKNEKLISLQEQQLRFLKK	TAF7L [443,462]	24	2504	HQVRSFFQRLQPKLWVPET	Glypican-3 [36,55]
8	1112	QALAPDFRLNPVRRILPAAR	TAG-1 [413,432]	24	2505	PSGSWSQKRSFVYVWKTWGQ	gp100 [139,158]
8	1113	SEDDQWYRASVLAYASEESV	TDRD1 [553,572]	24	2506	STDKVIVFVSRKAVADHLSS	HAGE [486,505]
8	1114	IMLLERSIMAKEGPKVAQT	TEKT5 [374,393]	24	2507	DMRRLIDLGVGLAPYSAVEK	JARID1B [937,956]
8	1115	KDRTMNLQDIRYILKNDLKD	TEX14 [497,516]	24	2508	AIIGKQGQHIKQLSRFAGAS	KOC1 [419,438]
8	1116	ALKSRISWEGGLALDNGEME	TEX15 [712,731]	24	2509	ILETKEKLNLDLHIEALAVIAN	KU-CT-1 [240,259]
8	1117	KPKPHVSDHNRLLHLARPKA	THEG [289,308]	24	2510	AEPLFEQNNSLNVNFTQKK	LPI [77,96]
8	1118	DSKLYIPLEYRSISLAIALF	TPTE [117,136]	24	2511	DLVKLYLEYRQVPNSNPAR	MAGE-B3 [251,270]
8	1119	DDERMEQMSNMTLMKETIST	TSGA10 [155,174]	24	2512	NMLGIYDGKRHLIFGEPRKL	MAGE-B4 [225,244]
8	1120	RGQRPTAPSAPRAGALLLLL	TSP50 [10,29]	24	2513	PGSPSFSSTLLSLFQSSPER	MAGE-C1 [376,395]
8	1121	ESEQAALGEEAVLLDDIMA	TSPY1 [53,72]	24	2514	RLSTLKFQYQGNGLKSGSM	MORC1 [89,108]
8	1122	KSYLEQASRIWSWLLGAAMV	TYR [465,484]	24	2515	KSSGQMAQKFSFSKVFPGPAT	MPHOSPH1 [104,123]
8	1123	LLLRTPYSSDNLYQMTSQLE	WT1 [215,234]	24	2516	KQKFSRLWSSKSVTEIHLF	NLRP4 [104,123]
8	1124	KIESQRIISGRISGYISEAS	ZNF165 [201,220]	24	2517	NEWNYTRAGQAFTMLQTEGK	NXF2 [597,616]
9	1125	AYPEKMRNRVLLELNSADLD	5T4 [324,343]	24	2518	KEILEAEIESHHPRLASAVQ	NY-BR-1 [1132,1151]
9	1126	DENSYWRNQNGSLQLPHT	ACRBP [303,322]	24	2519	LMAEDEPSGALLKPLVFRVD	NYD-TSPG [73,92]
9	1127	HPDTFSYPIERGRILNWEGV	ACTL8 [59,78]	24	2520	DEMKNKEIAARRQFQSQLAD	ODF2 [576,595]
9	1128	DVAFLLVYREKSNYVGATFQ	ADAM2 [264,283]	24	2521	DSVDLGAAGASAPLQPSPP	PASD1 [345,364]
9	1129	LFGLEIWTNKNLIVDDVRK	ADAM29 [245,264]	24	2522	RRGWLYKQDSTGMKLWKKRW	PEPP2 [172,191]
9	1130	QLAVSVILRVAKGYQELLEK	AFP [364,383]	24	2523	WYDFFIVSQAVRSGSVSPH	PIWIL1 [774,793]
9	1131	LMTDTQFVSAVKRTVFSHGS	AKAP-3 [348,367]	24	2524	LLPELSFMTGIPEKMKKDFR	PIWIL2 [493,512]
9	1132	KEFADSISKGLMVYANQVAS	AKAP-4 [323,342]	24	2525	ALLDHEAKKMSTYLKTISPN	PIWIL3 [733,752]
9	1133	EVDMLKIRSEFKRKYGKSLY	ANXA2 [297,316]	24	2526	VAESSSNTSSRLSVIVVRKK	PIWIL4 [715,734]
9	1134	DEIEIDFETLKASTLRELEK	BRDT [550,569]	24	2527	LAKFSPYLQGMINLRRLLS	PRAME [249,268]
9	1135	EYSDKTTQFPSVYAVPGTEQ	CABYR [114,133]	24	2528	NDQLMFLERAFIDPLGLPDR	PSMA [665,684]
9	1136	KNKSVSQYLEMDKTLSSKKEE	CAGE1 [431,450]	24	2529	MPAMSTRDQHATIIHNLREE	SAGE1 [378,397]
9	1137	NIGAIGLELWQVRSGTIFDN	CALR3 [296,315]	24	2530	EEDEVKAARTRRKVLRAVA	SART3 [25,44]
9	1138	LHNLRLQIYVVKQSDQLFLNF	CCDC62 [282,301]	24	2531	RVQAENSRLMHFKLKEDYE	SCP-1 [229,248]
9	1139	KNDLYPNPKPEVLHMIYMRA	CDCA1 [33,52]	24	2532	QQPHGVDGKLSSINNMGLNS	SOX-6 [517,536]
9	1140	MMQKPGSNAPVGGNVTSSFS	CT45 [84,103]	24	2533	GTTKTFKIPIEHLDIFYIEK	SPAG1 [13,32]
9	1141	ISTEHQSLVLVKRLAVSVS	CT46 [20,39]	24	2534	EQKREQYRQVKAHVQKEDGR	SPAG9 [623,642]
9	1142	PPWEQDYRMFPFPGQSPD	CTAGE2 [566,585]	24	2535	ARNEAPAFITIDNRSSWENIK	SPO11 [63,82]

9	1143	SVRSRLYVGREKKLALMLSG	cTAGE5 [65,84]	24	2536	EPVQQDMNGILLGYEIRYWK	TAG-1 [834,853]
9	1144	DSKLAVSLAETTGLIKLEEE	CTCFL [166,185]	24	2537	LQKQVEKHEHILLFLLNNST	TDRD1 [1147,1166]
9	1145	NAVVLTVKASYVASTKYQKV	CTNNA2 [874,893]	24	2538	LEAQLHEYVKQGNVVKVKKI	TEX14 [23,42]
9	1146	FIWRAISITPVHKSSSGFQD	CXorf48 [229,248]	24	2539	LVELQMMMETIQFIENKKRH	TEX15 [1690,1709]
9	1147	LEHTLLSKGFRGASPHRKST	CXorf61 [94,113]	24	2540	AARVSPISSESVLARLSKFEV	TPTE [49,68]
9	1148	PQRPRNRPYFQRRRQAPGP	DBPC [316,335]	24	2541	EIQGNVKVLKSERDKIFLLY	TSGA10 [49,68]
9	1149	VVDVQTSQITKIPIKLDREP	DCAF12 [114,133]	25	2542	FLLVYREKSNYVGATFQGKM	ADAM2 [267,286]
9	1150	LEGGHWLSEKRHLQAIRDG	DKK1 [184,203]	25	2543	EKNIFLASFVHEYSRRHPQL	AFP [346,365]
9	1151	PPSYLGQSVPPQFFTFEDAPS	DMRT1 [296,315]	25	2544	FRQGERPDDFTASVSEGIMT	AKAP-3 [268,287]
9	1152	SRKRKAVTKRRLQRSYEMN	DPPA2 [147,166]	25	2545	SQKMDMSNIVLMLIQKLLNE	AKAP-4 [621,640]
9	1153	DSKSLRTALQKEITTRYQLD	EpCAM [158,177]	25	2546	RRRREAMVGTIDMTLQSDIM	BRDT [920,939]
9	1154	RARRPKFADIVSILDKLIRA	EPHA2 [858,877]	25	2547	LEKRVKELQMKITKQVVID	CAGE1 [333,352]
9	1155	SRFFIDFPHIEEQKKIESY	FAM46D [264,283]	25	2548	LHDELLFTVEREKRKDELLN	CCDC62 [250,269]
9	1156	LVIAEMMELGSRSGASQKK	FATE1 [32,51]	25	2549	SENGAYLDNPPKGALKKLIH	cTAGE5 [299,318]
9	1157	EDYFSHHLAVYNPQFKKTM	FBXO39 [201,220]	25	2550	LANRFKEFGKEMVKLNYVAA	CTNNA2 [172,191]
9	1158	EMENTKKFLSLTAVSEETVG	FSIP1 [168,187]	25	2551	NKNKELGAVSLDGYFHLWKA	DCAF12 [262,281]
9	1159	DKMEHAQKLMRLQNLRGGHI	FTHL17 [62,81]	25	2552	EKDGEFSLVLQVLGMLRGIAA	EPHA2 [706,725]
9	1160	GHLITAVQNVITELPVNSQK	GASZ [368,387]	25	2553	ALRVFKARIYTNRYETNEED	FBXO39 [395,414]
9	1161	QGNHVPPYPYGNVSRATVQRY	GATA-3 [56,75]	25	2554	KELDSQLQDAIQMKKLDKI	FSIP1 [109,128]
9	1162	KMEEKYQLTARLNMEQLLQS	Glypican-3 [76,95]	25	2555	QLLQSASMELKFLIIQNAAV	Glypican-3 [91,110]
9	1163	MEVTVYHRRGSRSYVPLAHS	gp100 [184,203]	25	2556	LADTNSLAVVSTQLIMPQGE	gp100 [571,590]
9	1164	LMPGFIHLVLQPSLKGQRNR	HAGE [297,316]	25	2557	PSLKGQRNRPGMLVLTPTRE	HAGE [308,327]
9	1165	PYNDYFEYFGPDFKLHISPS	HDAC1 [329,348]; HDAC2 [330,349]	25	2558	LTESKETASAMATLGEARLR	JARID1B [1132,1151]
9	1166	SPTNMQGFTKSLNAFNVGDD	HDAC3 [74,93]	25	2559	RIRKLQIRNIPPHLQWEVLD	KOC1 [79,98]
9	1167	EVSESPGSIQVARGQPAVLP	IGFS11 [24,43]	25	2560	DLRAVLLINSKSYVSPSSM	KU-CT-1 [597,616]
9	1168	TVEYELKYRNIGSETWKTI I	IL13RA2 [66,85]	25	2561	KNLLKHGASLDNFHFIGVSL	LPI [162,181]
9	1169	FKSDYFNMPVHVMVPTLVEK	JARID1B [389,408]	25	2562	ALSTTTSVDVSYKSKYGAN	MAGE-B3 [68,87]
9	1170	QFEQSETETVHLFIPALSVG	KOC1 [399,418]	25	2563	VAARRGTTAMTSAYSRTSS	MAGE-B4 [321,340]
9	1171	AAYNKLLNNLSLKYSQTGY	KU-CT-1 [542,561]	25	2564	DVQSPLQNPASSFFSALLS	MAGE-C1 [123,142]
9	1172	ITMPFSSPMEAEVRRILSR	Lage-1 [92,111]	25	2565	EVKKAEEAVKIAESILKEAQ	MORC1 [288,307]
9	1173	WKNHKKQVIQSAYEIIKLG	LDHC [227,246]	25	2566	YLAYDETLNVLKFSIAIQKV	MPHOSPH1 [460,479]
9	1174	AARAPSTRITYGTITKERDY	LEMD1 [118,137]	25	2567	GLRKTDFDEETQALLTAESE	NLRP4 [956,975]
9	1175	NFNTQKKTVWLIHGYPVGS	LPI [90,109]	25	2568	SLSALPKTQHDLSILVDVW	NXF2 [470,489]
9	1176	SDPARYEFLWGPRALAETSY	MAGE-A1 [257,276]	25	2569	VPNKAFELKNEQTLRADPMF	NY-BR-1 [477,496]
9	1177	GSDPRSFPWLWYEEALKDEEE	MAGE-A10 [320,339]	25	2570	DETPPAVVQSVLLERGWKNF	NYD-TSPG [92,111]
9	1178	LLTQNWVQEKYLVRQVPGT	MAGE-A11 [358,377]	25	2571	TVTKSHKRGMKGDTVNVRRS	ODF2 [39,58]

9	1179	AREPFTKAEMLGSVIRNFQD	MAGE-A12 [126,145]	25	2572	GASAQPLQPSSPVAydiISQ	PASD1 [353,372]
9	1180	APEEKIWEELSMLEVFEGRE	MAGE-A2 [216,235]	25	2573	YTLEQALLSASQEIEMHADN	PEPP2 [664,683]
9	1181	KASSSLQLVFGIELMEVDPI	MAGE-A3 [153,172]	25	2574	KSQGLQISAGFQELSLAERG	PIWIL1 [61,80]
9	1182	PRALAETSYVKVLEHVVRVN	MAGE-A4 [276,295]; MAGE-A8 [278,297]	25	2575	NFYDPTSAMVLQQHRLQIWP	PIWIL2 [342,361]
9	1183	RKVAKLVHFLLLKYRAREPV	MAGE-A6 [111,130]	25	2576	NKLIGSIVLTkYNNKTYRVD	PIWIL3 [316,335]
9	1184	VAELVRFLRLKYQIKPVTk	MAGE-A8 [116,135]	25	2577	ILPSNQKTYYSIKKYLSSD	PIWIL4 [550,569]
9	1185	NYKRYFPVIFGKASEFMQVI	MAGE-A9 [141,160]	25	2578	DELFSYLIKVKRKKNVLRL	PRAME [189,208]
9	1186	DHFTEILNGASRRLELVFGL	MAGE-B1 [144,163]	25	2579	YDVLLSYPNKTHPNYISIIIN	PSMA [113,132]
9	1187	TKGEMLKIVGKRFREHFPEI	MAGE-B2 [133,152]	25	2580	AFINMAATGVSSMSTRDQYA	SAGE1 [604,623]
9	1188	ILKKASFNMEEVVFVDLKKV	MAGE-B3 [152,171]	25	2581	YVEFKEEKSALQALEMDRKS	SART3 [750,769]
9	1189	EPTTKAEMLKIIISKYKEHF	MAGE-B4 [128,147]	25	2582	SEETLKTLYRNNPPASHL	SCP-1 [905,924]
9	1190	EYKPYFPQILNRTSQHLVVA	MAGE-B6 [228,247]	25	2583	KQIEQLYAAQLASMQVSPGA	SOX-6 [364,383]
9	1191	PVSSFSYTLTLSLFQSSPER	MAGE-C1 [446,465]	25	2584	RKDKPAATAASFTAEEWEKI	SPAG1 [76,95]
9	1192	EEPVTEAEMLMIVIKYDYF	MAGE-C2 [159,178]	25	2585	ESLFEELSSAGSLIGDVDE	SPAG9 [380,399]
9	1193	RAQLRLDFIHANSTHSLFL	MORC1 [10,29]	25	2586	IPLTKRDQMKLDSILRRPYV	SPO11 [329,348]
9	1194	EENIGILPRTLNVLFDSLQE	MPHOSPH1 [166,185]	25	2587	SPPATYRWKMGTEMKLEPG	TAG-1 [66,85]
9	1195	TDYYQELQRDISEMFLQIYK	MUC-1 [1063,1082]	25	2588	RPAKSKKLNLKLVENSLSISN	TDRD1 [135,154]
9	1196	HQKYLsAPERAhLAKNLKLT	NKX3.1 [145,164]	25	2589	QLYNWAAPEVILQKAATVKS	TEX14 [418,437]
9	1197	SFFSDFGLMWYLEELKKEEF	NLRP4 [4,23]	25	2590	ELQTYHDQLVELLEETKREK	TEX15 [1758,1777]
9	1198	SDEGMEVIERLIYLYHKFHQ	NR6A1 [362,381]	25	2591	FHNRVVRIMIDHDNVPTLHQ	TPTE [295,314]
9	1199	PSLSQEQQEMVQAFSAQSGM	NXF2 [566,585]	25	2592	KQKVQDTNLEVNKLKNILKS	TSGA10 [386,405]
9	1200	QLKVLIAENTMLTSLKKEKQ	NY-BR-1 [1111,1130]	26	2593	RVSGSSQSPPNLYKYKSTLKI	AKAP-3 [201,220]
9	1201	STQSQALGSLRTTTPAFTLN	NYD-TSPG [9,28]	26	2594	DEAVGKVARKQLLDWLLANL	AKAP-4 [835,854]
9	1202	KNYEGMIDNYKSQVMKTRLE	ODF2 [537,556]	26	2595	LQLPDYYTIIKNPMDLNTIK	BRDT [61,80]
9	1203	TKYVFDSAPSHSISARTKAF	ODF3 [112,131]	26	2596	NVEELIEDKYKIIIEKNDTK	CAGE1 [360,379]
9	1204	STLMLFPINIWI FELERNVS	ODF4 [157,176]	26	2597	DAPAFNEKASIVLPSQDDFS	CCDC62 [610,629]
9	1205	DQASFTTSMEDWTQVVKGSS	OIP5 [29,48]	26	2598	RANRDYVFKQVQEAIAGISN	CTNNA2 [237,256]
9	1206	TSNSEAISSSSIPQFPITSD	PASD1 [658,677]	26	2599	WVYRGEAERIFIELKFTVRD	EPHA2 [85,104]
9	1207	NDHYRSVYQKRLMDEAKILK	PBK [71,90]	26	2600	QRREKEIKKQGLEMRIKLWE	FSIP1 [133,152]
9	1208	RSVPAGLTQLSVSPQSLQGK	PEPP2 [595,614]	26	2601	ELKFLIIQNAAVFQEAFeIV	Glypican-3 [99,118]
9	1209	LQFYNIIFRRLKIMNLQQI	PIWIL1 [209,228]	26	2602	EKVPVSEVMGTTLAEMSTPE	gp100 [377,396]
9	1210	RTDGGFLFLADVSHKVIrND	PIWIL2 [369,388]	26	2603	GRTGRAGRTGVSITTLTRND	HAGE [576,595]
9	1211	KKMSTYLKTI SPNNFTLAFI	PIWIL3 [740,759]	26	2604	NLNNMPVMEQSVLAHITADI	JARID1B [460,479]
9	1212	VAGSMGFNVDPKIIKVQEN	PIWIL4 [509,528]	26	2605	VNTDSETAVNVVYSSKDQA	KOC1 [113,132]
9	1213	SISISALQSLQLHLIGLSNL	PRAME [417,436]	26	2606	KIPKEKLPDFSWELHISELK	KU-CT-1 [758,777]
9	1214	LYSEELFPEELSVVLGTNDL	PRSS55 [110,129]	26	2607	ERMGRPLRTTVFLDTSGTY	LIPI [334,353]

9	1215	RPFYRHVIYAPSSHNKYAGE	PSMA [684,703]	26	2608	RAGREHFAGFEPRELLTKVW	MAGE-C1 [1029,1048]
9	1216	VYSKQPYTEYISTRWYRAPE	RAGE-1 [152,171]	26	2609	PLNSFYQYRRQAMGIPFIIQ	MORC1 [466,485]
9	1217	NVLSGLINMAGASIPAMSSR	SAGE1 [459,478]	26	2610	VSLDSNSNSKILNVKRATIS	MPHOSPH1 [502,521]
9	1218	RTRRKVLSRAVAAATYKTMG	SART3 [33,52]	26	2611	FVKQAVNLLQEANFHIIDNV	NLRP4 [565,584]
9	1219	GAIRKMREDRWAVIAKMDRK	SCP-1 [946,965]	26	2612	VEMRDVHKDQQLRHTPYISIR	NXF2 [65,84]
9	1220	LQKKIMMETQQEIASVRKS	SCP3a [211,230]	26	2613	ELEVKKQLEQALRIQDIELK	NY-BR-1 [1006,1025]
9	1221	EIEALLGMDLVRLGLERGET	SCRN1 [103,122]	26	2614	STDVLVKRKLVDHIDIIDLIYL	NYD-TSPG [398,417]
9	1222	EKEKRTLLERKLSLENKLLQ	se57-1 [199,218]	26	2615	QLADLQQLPDILKITEAKLA	ODF2 [592,611]
9	1223	PGSTRIKARKRQLHFFDSR	SLCO6A1 [340,359]	26	2616	VAENISSLLGHLPAEIVGKK	PASD1 [57,76]
9	1224	EGSDQHVASHLPLHPIMHNK	SOX-6 [31,50]	26	2617	TLRKTKKMDLRTERPRSAV	PEPP2 [868,887]
9	1225	GKYSAAIALLFAGSEIADD	SPAG1 [466,485]	26	2618	NEYMPSRIVYRDGVGDGQL	PIWIL1 [690,709]
9	1226	KTRDGGSVVGASVFKDVAG	SPAG9 [699,718]	26	2619	RTLGRGSSDASLLPLGRAAG	PIWIL2 [142,161]
9	1227	QDIHVTRDVVKHLSKSDLL	SPATA19 [81,100]	26	2620	ERRIGGVFQDLVNVTRQDMK	PIWIL3 [92,111]
9	1228	ADSKMKAEIQALTFLSSDYL	SPO11 [362,381]	26	2621	QLYQYHVITYIPDLASRLRI	PIWIL4 [122,141]
9	1229	AFDDIATYFSKKEWKMKYS	SSX-1 [24,43]	26	2622	SRYISMSVWTSPPRLVELAG	PRAME [12,31]
9	1230	PNRGNQVERPQMTFGRLQGI	SSX-2 [88,107]	26	2623	LQDFDKSNPIVLRMMNDQLM	PSMA [650,669]
9	1231	AQIPEKIQKAFDDIAKYFSK	SSX-3 [15,34]	26	2624	GIPSMSTKDLATVTQNVHE	SAGE1 [518,537]
9	1232	WEKMKSSSEKIVVYMKLNYE	SSX-4 [37,56]	26	2625	NEQRMKAAEKEAALVQEEEE	SART3 [577,596]
9	1233	NGDDAFVRRPRVGSQIPEKM	SSX-5 [2,21]	26	2626	KMKDLTFLLEESRDKNVQLE	SCP-1 [281,300]
9	1234	KIEDLMEMVQKLQKVGSLP	SYCE1 [32,51]	26	2627	SLYSFRNTSTSPHKPDEGSR	SOX-6 [88,107]
9	1235	KDKLKIDLLPDGRHAVVEVE	TAF7L [126,145]	26	2628	RSQGFAEAAGKYSAAIALLE	SPAG1 [457,476]
9	1236	TDGRHFVSQTGNLYIARTN	TAG-1 [179,198]	26	2629	LMPLVVAVLENLDSVFAQDQ	SPAG9 [50,69]
9	1237	TADELRMISSTFLNLPFGGI	TDRD1 [807,826]	26	2630	SSSEVLASIENIIQDIITSL	SPO11 [43,62]
9	1238	LQVRGAEASRLWASRLTDDS	TEKT5 [100,119]	26	2631	FAFGNPVPRIKWRKVDGSLS	TAG-1 [262,281]
9	1239	LVYERITIGTLFVSLHERRS	TEX14 [324,343]	26	2632	NSGKLLDHVLIEMGYGLKPS	TDRD1 [431,450]
9	1240	KQRFGRMLWFDLSLLPELVQ	TEX15 [2085,2104]	26	2633	KAVVSGNYLEADVRLPKPY	TEX14 [466,485]
9	1241	PSTTMTKARKRRRRRLMEL	THEG [112,131]	26	2634	NIHTSLAIAQKLMELKLGKI	TEX15 [351,370]
9	1242	MDVLLRVFVERRQQYFSDLF	TPTE [139,158]	26	2635	IYSIPRYVRDLKIQIEMEKK	TPTE [421,440]
9	1243	DKKSENIASLGESLAMKEKT	TSGA10 [278,297]	26	2636	RMEQMSNMTLMKETISTVEK	TSGA10 [158,177]
9	1244	IDQMTQTASDVPLQVIMHS	TSP50 [171,190]	27	2637	KDTTIATILLKKVLLKHAKE	AKAP-3 [309,328]
9	1245	TPESAPELLAVQVELEPVN	TSPY1 [104,123]	27	2638	MMAYSDTTMMSDDIDWLRS	AKAP-4 [1,20]
9	1246	FLHHAFVDSIFEQWLRHR	TYR [386,405]	27	2639	GLHNYDVVKNPMDLGTIKE	BRDT [305,324]
9	1247	ELVRHHNMHQNMKLQAL	WT1 [430,449]	27	2640	KKTLQNLEEVLANQKHLQE	CAGE1 [379,398]
9	1248	GRAFSQSSNLSQHQRIMHRE	ZNF165 [462,481]	27	2641	ITLSSIFTKDLVEKHNLPS	CCDC62 [393,412]
10	1249	AFARRPPLAELAAALNLGSR	ST4 [110,129]	27	2642	STKYQKVYGTAAVNSPVVSW	CTNNA2 [887,906]
10	1250	LQNETYSALSPGKSEDEVVLR	ACRBP [510,529]	27	2643	VMWEVMTYGERPYWELSNHE	EPHA2 [806,825]
10	1251	SNTYQLPDGSRVELTPMQRV	ACTL8 [235,254]	27	2644	EGDQSGWVVPVKGYELAVTQ	FSIP1 [297,316]

10	1252	VILAQLLSLSMGITYDDINK	ADAM2 [309,328]	27	2645	VIYQQLMNPGLPDSALDINE	Glypican-3 [177,196]
10	1253	PFGGQKHIHIKVKKLLFSK	ADAM29 [57,76]	27	2646	PDGQVIWVNNTIINGSQVWG	gp100 [98,117]
10	1254	LQTMKQEFLLNLVKQKPQIT	AFP [545,564]	27	2647	PEELVSMARFKAHQQKREM	HAGE [614,633]
10	1255	YSDSWAEDLIVSALLLIQY	AKAP-3 [518,537]	27	2648	HVERKILDLFQLNKLVAEEG	JARID1B [122,141]
10	1256	DIMEAMLKRLVSALIGEEKE	AKAP-4 [421,440]	27	2649	PKDVFDPLMIESKKAATVVL	KU-CT-1 [13,32]
10	1257	AQRQDIAFAYQRRTKKELAS	ANXA2 [66,85]	27	2650	ATTFIYNRAVKNTRKVAVSL	LIPI [138,157]
10	1258	PNHHQLAFNYQEHLQTVK	BRDT [732,751]	27	2651	SVLQIPVSAASSSTLVSIFQ	MAGE-C1 [161,180]
10	1259	PAQLAAQMLGKVSSIHSQS	CABYR [172,191]	27	2652	GVNVNRSQAGMFIYSNNRL	MORC1 [357,376]
10	1260	SDEAKSIRDVPTLLGAKLDK	CAGE1 [674,693]	27	2653	ILQIEDSEMSRVIRVSELSL	MPHOSPH1 [359,378]
10	1261	QDWEKHFLDASTSKQSDWNG	CALR3 [226,245]	27	2654	LKKEEFKFKFHEHLKQMTLQL	NLRP4 [18,37]
10	1262	TSKLQRLLAESRQMVTDLLEL	CCDC62 [631,650]	27	2655	LSDITEKAPKVKTLNLNLSKNK	NXF2 [288,307]
10	1263	MIVKKEKLATAQFKINKKHE	CDCA1 [345,364]	27	2656	AFKPAIEMQNSVPNKAFELK	NY-BR-1 [466,485]
10	1264	AQLQRTFMSALVFPNKISTE	CT46 [4,23]	27	2657	YNEDDSVVEKAVSVRPEAAP	NYD-TSPG [465,484]
10	1265	VAEAKMTFKRFQANEERLEI	CTAGE2 [157,176]	27	2658	HELAETEHEHTVLRHNIERM	ODF2 [167,186]
10	1266	MAATEISVLSEQFTKIKELE	CTCF1 [1,20]	27	2659	DKVNPQSSQRKLNWIPSFPT	PASD1 [10,29]
10	1267	ADMADVMRLLSHLKIVEEAL	CTNNA2 [141,160]	27	2660	EEETRGVISYQTLFRNMPSH	PEPP2 [427,446]
10	1268	VEEDKPHYGLRAIKVDVVR	CXorf48 [80,99]	27	2661	IDVEVTRPEWYDFFIVSQAV	PIWIL1 [765,784]
10	1269	SGLINSNTDNNLAVYDLSDR	CXorf61 [46,65]	27	2662	AFDGSILYLPVKLQQVLELK	PIWIL2 [273,292]
10	1270	VPVKGSRYPAPNRRKRRFIP	DBPC [166,185]	27	2663	GSKITYIDYRQKHKEIVTV	PIWIL3 [352,371]
10	1271	FHLWKAENTLSKLLSTKLPY	DCAF12 [276,295]	27	2664	LKKKRNDNSEAQLAHLIPEL	PIWIL4 [360,379]
10	1272	KMTDNKTGEVLISENVVASI	DKKL1 [108,127]	27	2665	PMQDIKMILKMVQLDSIEDL	PRAME [219,238]
10	1273	TYYSFYQPSLFPYNNLYN	DMRT1 [208,227]	27	2666	FSTQKVKMHIHSTNEVTRIY	PSMA [337,356]
10	1274	VRTYWIIEELKHKAREKPYD	EpCAM [139,158]	27	2667	PPEELHAAAYVFTNDGQQMR	SAGE1 [13,32]
10	1275	PPQQRVWVKYEVTRYRKKGDS	EPHA2 [460,479]	27	2668	RQKMSEIFPLTEELWLEWLH	SART3 [135,154]
10	1276	EQQKKIESYLNHFIEGEMT	FAM46D [275,294]	27	2669	ESKKKRKMAFEFDINSDSSE	SCP-1 [877,896]
10	1277	PNTKAEMEMSLAEELNHGRQ	FATE1 [6,25]	27	2670	SKDWKEKMERLNTSELLGEI	SOX-6 [158,177]
10	1278	FERIMKYERLARILLQEIP	FBXO39 [289,308]	27	2671	HPFSMKPLLRAMAYETLEQ	SPAG1 [517,536]
10	1279	PVKGYELAVTQHQLAEIDI	FSIP1 [306,325]	27	2672	NEQLITQYEREKALRKHAEE	SPAG9 [82,101]
10	1280	EAGLAEYLFDKLTLGGRVKE	FTHL17 [163,182]	27	2673	AVPSNIQGIIRNLVTDKQFVL	SPO11 [202,221]
10	1281	EKDHFSSYTAFGDLEVLFLH	GASZ [265,284]	27	2674	STGILSVRDATKITLAPSSA	TAG-1 [499,518]
10	1282	SSFNPAALSRHMSSLSHISP	GATA-3 [390,409]	27	2675	KEILPNGHVKVHFVDYGNIE	TDRD1 [785,804]
10	1283	ARRDLKVFGNFPKLIMTVQS	Glypican-3 [201,220]	27	2676	PPPSQELDDIELLKQQQGS	TEX14 [1331,1350]
10	1284	SLIYRRRLMKQDFSVPQLPH	gp100 [613,632]	27	2677	ENQIDTAFLSSTSKYEKLEK	TEX15 [1188,1207]
10	1285	IKNIQSTNTTTIQQEQPE	HAGE [90,109]	27	2678	KQKARRIYPSDFAVEILFGE	TPTE [520,539]
10	1286	TYETAVALDTEIPNELPYND	HDAC1 [313,332]	27	2679	QSQIALQEKESIEQLLKEHL	TSGA10 [580,599]
10	1287	LDQIRQTI FENLKMNLHAPS	HDAC3 [355,374]	28	2680	VFSHGSQKATDIMDAMLRKL	AKAP-3 [362,381]
10	1288	LGQSFSFHSNGANIPSIYAN	IGFS11 [341,360]	28	2681	NSSDDSEDERVKRLAKLQEQ	BRDT [410,429]

10	1289	VNGSSENKPIRSSYFTFQLQ	IL13RA2 [214,233]	28	2682	NIENYSTNALIQPVDTSIS	CAGE1 [97,116]
10	1290	SIPVHLNSLPRLETLVAEVQ	JARID1B [1048,1067]	28	2683	ELNDMVAHVHQQLLSWEEDR	CCDC62 [43,62]
10	1291	EEVKLEAHIRVPSFAAGRVI	KOC1 [484,503]	28	2684	NEFDNKIILDPMTFSEARFR	CTNNA2 [281,300]
10	1292	LQEPSDLRAVLLINSKSYVS	KU-CT-1 [592,611]	28	2685	IVSILDKLIRAPDSLKTLD	EPHA2 [867,886]
10	1293	EALFKKSAETLWNIQKDLIF	LDHC [313,332]	28	2686	GSRSSNASLEVLSTPGSFK	FSIP1 [23,42]
10	1294	LQEVKILAQFYNDVFNISII	LIPI [402,421]	28	2687	FTDVSLYILGSDINVDMMVN	Glypican-3 [149,168]
10	1295	AREPVTKAEMLESVIKNYKH	MAGE-A1 [119,138]	28	2688	RSYVPLAHSSSAFTITDQVP	gp100 [195,214]
10	1296	LVQFLLFKYQMKEPITKAEI	MAGE-A10 [141,160]	28	2689	LLMEAQQLQVSLPEIQELYQ	JARID1B [1349,1368]
10	1297	TVRPADLTRVIMPLEQRSQH	MAGE-A11 [100,119]	28	2690	PVIQLLALKTLGVIANDKES	KU-CT-1 [205,224]
10	1298	PRKLLTQDLQVQENYLEYRQV	MAGE-A12 [242,261]	28	2691	FSFKLLNQLGMIEEPRLYEK	LIPI [376,395]
10	1299	BEGPRMFPDLESEFQAISR	MAGE-A2 [92,111]	28	2692	QSPPEGENTHSPLQIVPSLP	MAGE-C1 [518,537]
10	1300	GSVVGWQYFFPVIFSKASS	MAGE-A3 [137,156]	28	2693	EGDLEQTDITYLEALLKEDNL	MORC1 [937,956]
10	1301	GSNPARYEFLWGPRLAETS	MAGE-A4 [264,283]	28	2694	NMANSIKFSVWVSFFEIYNE	MPHOSPH1 [262,281]
10	1302	KASDSLQLVFGIELMEVDPI	MAGE-A6 [153,172]	28	2695	HYEEQQAWNITLRIQKMDR	NLRP4 [62,81]
10	1303	AEMLESVIKNYKRYFPVIFG	MAGE-A9 [132,151]	28	2696	LLRRTKRDIVDSLALPKTQ	NXF2 [459,478]
10	1304	LNGASRRLELVFGLDLKEDN	MAGE-B1 [150,169]	28	2697	ANILIDSGADINLVDVYGNT	NY-BR-1 [66,85]
10	1305	NSATEEEIWEFLNMLGVYDG	MAGE-B2 [216,235]	28	2698	TDINTLTRQKELLQKLSTF	ODF2 [244,263]
10	1306	EPRKLITQDLVKLKYLEYRQ	MAGE-B3 [243,262]	28	2699	TQLLQQLYTSKAVSDEAVLT	PASD1 [178,197]
10	1307	LNMLGIYDGKRHLIFGEPRK	MAGE-B4 [224,243]	28	2700	KQDSTGMKLWKKRWFVLSDL	PEPP2 [178,197]
10	1308	ARKIITEDLVQDKYVYRQV	MAGE-B6 [328,347]	28	2701	LFLPKRLQQKVTVEFSKTRN	PIWIL1 [168,187]
10	1309	KQPITKAEMLTNVISRYTGY	MAGE-C1 [926,945]	28	2702	HRPSEQDNHGMILLKGEILL	PIWIL2 [474,493]
10	1310	PHSSPPYYEFLWGPRAHSES	MAGE-C2 [290,309]	28	2703	PMGITMKPAEMIEVDGDANS	PIWIL3 [535,554]
10	1311	LKSGSMRIGKDFILFTKKEE	MORC1 [103,122]	28	2704	ASRRRLRIALLYSHSELSNKA	PIWIL4 [135,154]
10	1312	QKWREERDQLVALEIQLKA	MPHOSPH1 [1516,1535]	28	2705	RLSEGDMHLSQSFSVSQLS	PRAME [333,352]
10	1313	DNRPALGSTAPPVHNVTAS	MUC-1 [943,962]	28	2706	SGKIVIARYGKVFGRGNKVK	PSMA [197,216]
10	1314	AFSHTQVIELERKFSHQKYL	NKX3.1 [130,149]	28	2707	RHSSSKRRKSMSSWLDKQED	SAGE1 [55,74]
10	1315	FKDPKRAMEAFNLVRESEQL	NLRP4 [315,334]	28	2708	YVEIWQAYLDYLRRRVDFKQ	SART3 [417,436]
10	1316	PSPGSTLSSRSVELNGFMA	NR6A1 [190,209]	28	2709	AVPSQTVSRNFTSVDHGISK	SCP-1 [814,833]
10	1317	TMNKRYNVSQALDLQNLRF	NXF2 [220,239]	28	2710	IGGSLGRGSSLDILSSLNSP	SOX-6 [468,487]
10	1318	IEVHNKASLTPLLSITKRS	NY-BR-1 [109,128]	28	2711	NWREKLSPIPAVPASVPLQA	SPAG1 [575,594]
10	1319	SDFKDFIFDDMYIVQKYISN	NYD-TSPG [226,245]	28	2712	AATSPSTNGASPVMDKPEM	SPAG9 [855,874]
10	1320	FKLENERLKASFAPMEDKLN	ODF2 [504,523]	28	2713	RKEMEIMADSKMAEIQALT	SPO11 [355,374]
10	1321	RTGKDLGPAYSILGRYQTKT	ODF3 [78,97]	28	2714	LVSSSAWSSALGSQTTFGPV	TAG-1 [19,38]
10	1322	YFNHKSFWSLILSHPSGAVS	ODF4 [201,220]	28	2715	YGNIEEVTADLRMISSFTL	TDRD1 [800,819]
10	1323	IVNASEMDIQNVPLSEKIAE	OIP5 [179,198]	28	2716	RVQRYGLHPDVNVYLGTLSE	TEX14 [530,549]
10	1324	SIPQFPITSDSTISTLETPO	PASD1 [668,687]	28	2717	DSQSDLTLHSEIAYISKPGI	TEX15 [1550,1569]

10	1325	MDEAKILKSLHHPNIVGYRA	PBK [83,102]	28	2718	GVKTPSQKRYVAYFAQVKHL	TPTE [384,403]
10	1326	YNVTSYAVHPMSPVGRTSR	PEPP2 [128,147]	29	2719	VSALLLIQYHLAQGGRRDAR	AKAP-3 [529,548]
10	1327	RDWGLSFDNLLSFSGRILQ	PIWIL1 [439,458]	29	2720	KPGDDIVLMAQALEKLFMQK	BRDT [110,129]
10	1328	RINLKNTSFITSQELNWKVE	PIWIL2 [572,591]	29	2721	EERNKHLEDLIRKPREKARK	CAGE1 [730,749]
10	1329	DVSHKLLRIETAYDFIKRTS	PIWIL3 [283,302]	29	2722	NHPKVDIKREKNQKSLFKDQ	CCDC62 [337,356]
10	1330	PGFAISVSYFERKLLFSADV	PIWIL4 [244,263]	29	2723	DGVRDIRKAVLMIRTPEELE	CTNNA2 [618,637]
10	1331	KLPTLAKFSPYLGQMINLRR	PRAME [245,264]	29	2724	KEVPVAIKTLKAGYTEKQRV	EPHA2 [639,658]
10	1332	LVNYNLWIEKVTLQEGRPFN	PRSS55 [288,307]	29	2725	VVMVDREKKRLVELLKDLE	FSIP1 [269,288]
10	1333	LKKEGWRPRRTILFASWDAE	PSMA [405,424]	29	2726	YQLTARLNMEQLLQSASMEL	Glypican-3 [81,100]
10	1334	YVMELPKLKLSGVVRLSSYS	RAGE-1 [345,364]	29	2727	PSAAELQDLLDVSEFDFVEL	JARID1B [885,904]
10	1335	FGQNYERIFILLEEVQSGMK	SAGE1 [838,857]	29	2728	LVRGEYGRAWNEVMLQNSR	KU-CT-1 [815,834]
10	1336	EKALNAGFIQATDYVEIWQA	SART3 [404,423]	29	2729	SLTDSSESLIESEPLFTYTLD	MAGE-C1 [890,909]
10	1337	ESKQLNVYIEIKVKNKLELE	SCP-1 [632,651]	29	2730	MKRSSSLPSWKSLLNVPMED	MORC1 [764,783]
10	1338	GEVQNMLEGVGVNDINKALLA	SCP3a [68,87]	29	2731	LKLGIXHQSVAFTKLNNASS	MPHOSPH1 [330,349]
10	1339	FTGTPDPSRSIFKPFIFVDD	SCRN1 [294,313]	29	2732	DLRRNGVVDADIPALLGTKI	NLRP4 [418,437]
10	1340	YESTSAHIEETEVVKKIRT	se57-1 [23,42]	29	2733	PPEKPSAFEPAIEMQKSVPN	NY-BR-1 [698,717]
10	1341	RKRKQLHFFDSRLKDLKLG	SLCO6A1 [348,367]	29	2734	EQLHVQLADKDLVVAELST	ODF2 [421,440]
10	1342	TGGATVAEAVRYRDARGRAS	SOX-6 [597,616]	29	2735	VEQYGPQENVHMFVDSSTY	PASD1 [247,266]
10	1343	IAKPNNAYEFGQIINALSTR	SPAG1 [800,819]	29	2736	DRPLTKINSVKLNSLPSEYE	PEPP2 [335,354]
10	1344	GYRNKIYVVQPKAMKIEKSF	SPAG9 [1063,1082]	29	2737	GVGDGQLKTLVNYEVPQFLD	PIWIL1 [703,722]
10	1345	DIMRDRIEQVRRSISRLTDV	SPATA19 [134,153]	29	2738	SINLTLTKWYSRVVFQMPHQ	PIWIL2 [763,782]
10	1346	DVLDHRHRESLLAALRRGGRE	SPO11 [14,33]	29	2739	LAFIVVKKRINTRFFLKHGS	PIWIL3 [756,775]
10	1347	DNDHNRRIQVEHPQMTFGR	SSX-1 [85,104]	29	2740	ASSSNGFLGTSRISTNDKYG	PIWIL4 [40,59]
10	1348	PNRGNQVQRPQMTFGR	SSX-3 [88,107]	29	2741	SLSGVMLTDVSPPEPLQALLE	PRAME [355,374]
10	1349	HRLRERKQLVVYEEISDP	SSX-4 [166,185]	29	2742	MPEGDLVYVNYARTEDFFKL	PSMA [169,188]
10	1350	QIPEKMQAFDDIAKYFSEK	SSX-5 [16,35]	29	2743	TNDGQQMRSDEVNLVATGHQ	SAGE1 [25,44]
10	1351	LQIEEEKNKQRLRLAFEEQ	SYCE1 [142,161]	29	2744	AHGTVKDLRLVTNRAGKPKG	SART3 [823,842]
10	1352	GSIPGFLISSGMSSHKQGHT	TAF7L [295,314]	29	2745	ESNKARAHSFVVTEFETTV	SCP-1 [365,384]
10	1353	GLSYRWLLNEFPNFIPTDGR	TAG-1 [163,182]	29	2746	LNSPALFGDQDTVMKAIQEA	SOX-6 [484,503]
10	1354	IISDVLIDEHLVLKSASPHK	TDRD1 [883,902]	29	2747	LAITAPKDLPMFLSNKLEGD	SPAG1 [829,848]
10	1355	FQAENTIMLLERSIMAKEGP	TEKT5 [368,387]	29	2748	MSERVSLAGSIYREFERLI	SPAG9 [20,39]
10	1356	WKRLGWSESSRIIVLDQSDL	TEX14 [1476,1495]	29	2749	SGPSSKIRTREAAPSVAPSG	TAG-1 [697,716]
10	1357	TKREKNSYYVFLKYKRVNE	TEX15 [1773,1792]	29	2750	EIIPLNRIYHLNRNIDLFPP	TDRD1 [355,374]
10	1358	RSSLEYRASSRLKELAAPKI	THEG [221,240]	29	2751	DIPWKGLDGSVVKKAVVSGN	TEX14 [453,472]
10	1359	QKRYVAYFAQVKHLYNWNLP	TPTE [390,409]	29	2752	TPKKVEMQRSPLGSLLEN	TEX15 [2384,2403]
10	1360	ENELDSAHSEIELLSQMAN	TSGA10 [540,559]	29	2753	HLFHQKRQLEKLIRRRVSEN	TPTE [207,226]

10	1361	DIGLLKLKQELKYSNYVRPI	TSP50 [206,225]	30	2754	SFYANRLTNLVIAMARKEIN	AKAP-3 [125,144]
10	1362	SNPYFQNKVITKEYLVNITE	TSPY1 [207,226]	30	2755	SVFPKTSISPLNVVQGASVN	BRDT [179,198]
10	1363	PAFLPWHLRLLRWQEIQK	TYR [205,224]	30	2756	LSKKEEEVERLQQLKKELEK	CAGE1 [445,464]
10	1364	AQYRIHTHGVFRGIQDVRRV	WT1 [284,303]	30	2757	QAFLRHPDVAATRANRDYVF	CTNNA2 [225,244]
10	1365	EHGQEIFQKKVSPPGPALNV	ZNF165 [142,161]	30	2758	LDDLAPDTTYLVQVQALTQE	EPHA2 [494,513]
11	1366	DERQNRSEFGMVVAALLAGR	ST4 [188,207]	30	2759	LEMRIKLWEEIKSAKYSEAW	FSIP1 [144,163]
11	1367	TPTAKAWKYMEEEEILGFGKS	ACRBP [340,359]	30	2760	NNYPSLTPQAFEFVGEFFTD	Glypican-3 [132,151]
11	1368	WEGSNRNFVWLGLASVVAHL	ACTL8 [328,347]	30	2761	PDDWDNRSTSYLHSPFSTGRS	JARID1B [1316,1335]
11	1369	VLIAIMVKVNFQRKKWRTED	ADAM2 [701,720]	30	2762	ISELKFKLKSNNVPIGHVKK	KU-CT-1 [773,792]
11	1370	ERNDSKILLEDLYVIVNIIVDS	ADAM29 [215,234]	30	2763	ERTQSTFEGFAQSFLQIPVS	MAGE-C1 [219,238]
11	1371	QITBEQLEAVIADFSGLLEK	AFP [562,581]	30	2764	LPSIPLGTMTISFSPKNEKE	MORC1 [529,548]
11	1372	IDGHMSGQMVEHLMNSVMKL	AKAP-3 [661,680]	30	2765	NASSRSHSIFTVKILQIEDS	MPHOSPH1 [346,365]
11	1373	QVASDMMVSLMKTLLKVHSSG	AKAP-4 [339,358]	30	2766	FFKDPKRAMEAFNLVRESEQ	NLRP4 [314,333]
11	1374	KELASALKSALSGHLETIVIL	ANXA2 [81,100]	30	2767	VIEVHNKASLTPLLSITKR	NY-BR-1 [108,127]
11	1375	ELEHLQTVKNISPLQILPPS	BRDT [743,762]	30	2768	APMEDKLNQAHLEVQQLKAS	ODF2 [516,535]
11	1376	AQLEENAKYSSVYMEAEATA	CABYR [366,385]	30	2769	LELMDHLQKQPNTLRHVVI	PASD1 [402,421]
11	1377	SGEMLKFTEKSLAKSIKES	CAGE1 [197,216]	30	2770	PAQTVHYRPINLSSSENKIV	PEPP2 [360,379]
11	1378	GTIFDNFLITDDEYADNFG	CALR3 [310,329]	30	2771	FRLTSRPQWALYQYHIDYNP	PIWIL1 [119,138]
11	1379	NFNVENSQELIQMYDSKMEE	CCDC62 [300,319]	30	2772	LVSFMRGLGIETVSKTPLKR	PIWIL2 [71,90]
11	1380	NYKEKMKDVTQKLKNARQEV	CDCA1 [253,272]	30	2773	LLNAMPLHSLWILYSSRSHR	PIWIL3 [501,520]
11	1381	TERERMEIDSTILSPKQIK	CT46 [228,247]	30	2774	EKQLIGLIVLTRYNNRTYSI	PIWIL4 [294,313]
11	1382	HSEQNELMADISKRIQSLED	CTAGE2 [129,148]	30	2775	KYAGESFPGIYDALFDIESK	PSMA [699,718]
11	1383	EELERTIHSYQQQIISHEKK	cTAGE5 [440,459]	30	2776	INDDIKYQLMKEVRRFGQNY	SAGE1 [823,842]
11	1384	EESEKYILTQLTVHFTSEAV	CTCF1 [73,92]	30	2777	HVDLIRLLRLEGELTKVRMA	SART3 [115,134]
11	1385	SLEERLESIIISGAALMADSS	CTNNA2 [302,321]	30	2778	GSTLKFGAIRMREDRWAVI	SCP-1 [940,959]
11	1386	SIYFSSDVVTGNVPLKVGQK	CXorf48 [56,75]	30	2779	GATVAEARVYRDARGRASSE	SOX-6 [599,618]
11	1387	ALIVFWKYRRFQRNTGEMSS	CXorf61 [14,33]	30	2780	GLQLANDSVNRLSRILMELD	SPAG1 [553,572]
11	1388	NPATAVSGTPAPPARSQADK	DBPC [68,87]	30	2781	ILENTQLETKNALNIVKND	SPAG9 [414,433]
11	1389	ETWRNYFSIDIFFPNAVYTH	DCAF12 [405,424]	30	2782	EYQNGDGFYLLSFRQGST	TAG-1 [737,756]
11	1390	EVLISENVVASIQPAEGSFE	DKKL1 [116,135]	30	2783	SIKIVDILEEEVVTFAVEVE	TDRD1 [409,428]
11	1391	PQYSMALAADSASGEVGNPL	DMRT1 [229,248]	30	2784	SSTAQENLALETSSPIEDF	TEX14 [1093,1112]
11	1392	HKAREKPYDSKSLRTALQKE	EpCAM [150,169]	30	2785	SYGENIVELSSSDSSLLKLD	TEX15 [1421,1440]
11	1393	MAAGYTAIEKVVMQNTDDIK	EPHA2 [926,945]	30	2786	VFDGLPLYDDVKVQFFYSNL	TPTE [466,485]

Table 25B - Hotspot Sequences and corresponding TAA

Cycle	SEQ ID NO	Sequence	Source Antigen(s) [AA position in Antigen]	Cycle	SEQ ID NO	Sequence	Source Antigen(s) [AA position in Antigen]
28	5432	SVYADQVNIDYLMNRPQNLR	AKAP4 [157,176]	11	5682	SQVAGRLLIIRAEELAQMWKV	Ropporin-1A [77-96]
24	5433	FTSSRMSSFNRHMKTHITSEK	CTCF [264,283]	11	5683	YPPEIVRYSPGYSDTLQQR	SPAG6 [481-500]
31	5434	KQQVFIDVINKLKENVEELI	CAGE1 [346,365]	11	5684	ESTEGSRSRSLDIQPSSE	SPAG8 [5-24]
10	5435	KKIEVYLRHRHAYPEQRQD	DPPA2 [114,133]	11	5685	KSLPNENFQSLYNKELPVHI	TDRD4 [903-922]
15	5436	GSKLGRRRAKPEGALQNNLGL	EpCAM [75,94]	11	5686	FQQQQHQILATPLQNLQVLA	TTK [491-510]
31	5437	SDTKDYFMSKTLGIGRLKRP	FSIP1 [516,535]	11	5687	ASAAARGFPLRTLNDWFSSM	WBP2NL [133-152]
16	5438	KLHNINRPLTMKKEGIQTRN	GATA-3 [347,366]	11	5688	RTYLSQKSLQAHIKRRHKRA	ZNF645 [122-141]
20	5439	SVMDLVGSILKNLRRVHPVS	LDHC [255,274]	12	5689	KWVGESERQLRLFLDQAYQM	ATAD2 [504-523]
22	5440	QEESFSPTAMDAIFGSLSDE	MAGE-A11 [176,195]	12	5690	KVFTHQGKVALYGLVQSAQ	CASC5 [2009-2028]
14	5441	EDSVFAHPRKLLMQDLVQEN	MAGE-A2 [235,254]	12	5691	KQHREDEVDVSVLLSASKIL	CCDC110 [5-24]
18	5442	REALDEKVAELVRFLRKYQ	MAGE-A8 [109,128]	12	5692	ATYLWVWNNQSLPVSPRLQL	CEA [174-193]
31	5443	LQRPVSSFFSYTLASLLQSS	MAGE-C1 [775,794]	12	5693	LLKQQEEQTRVALLEQQMQA	CEP55 [339-358]
31	5444	ESLVEKTPDEAASLVEGTSD	NY-BR-1 [262,281]	12	5694	SDLDFPTQVIFLKTNAVAS	EZH2 [87-106]
28	5445	DWNLVWRTSSFRMTEHNSVK	NYD-TSPG [120,139]	12	5695	SYGERHLDDLKILREDKK	HORMAD2 [57-76]
3	5446	SARVRSRGRGDGEAPDV	PAGE4 [2,21]	12	5696	LRDAVVIEQSSSLNEASSGL	hTERT [786-805]
31	5447	YLTGLTDKMRNDFNVMKDLA	PIWIL1 [388,407]	12	5697	PPMQLGFPSLHSHFKEHSLQ	KIF20A [511-530]
31	5448	ENPAMQEKKRSSIWQFFSRL	SPAG9 [540,559]	12	5698	SLQARLFPGLAIKIQRNGL	MCAK [6-25]
32	5449	NEQDLVREEAQKMSLLPTM	SPAG9 [953,972]	12	5699	TRFFSRITKANVDLLPRGAP	MSLN [138-157]
18	5450	GFSYEQDPTLRDPEAVARRW	TSP50 [105,124]	12	5700	MWKVVNLPTDLFNSVMNVGR	Ropporin-1A [93-112]
1	5451	RQLRLLFDQAYQMRPSIIF	ATAD2 [511-530]	12	5701	AVTNTLPVLLSLYMSTESSE	SPAG6 [375-394]
1	5452	GVVFLALSAQLLQARLMKEE	BAGE-3 [4-23]	12	5702	YWPLRGKREAMLEMLLQHQI	SPAG8 [342-361]
1	5453	RLLFSSSAFAKFEITLFLS	CASC5 [2266-2285]	12	5703	KFEDGIWYRAKVIGLPGHQE	TDRD4 [736-755]
1	5454	QQLESFQALRMQTLQNVSMV	CCDC110 [61-80]	12	5704	EDLSGRELTIDSIMNKVRDI	TTK [4-23]
1	5455	AQNTTYLWVWNGQSLPVSPR	CEA [527-546]	12	5705	NEGPPAGYRASPAGSGARPQ	WBP2NL [266-285]
1	5456	KKRSEELLSQVQFLYTSLLK	CEP55 [322-341]	12	5706	RDHLSYIPPEQHTMVSLPSV	ZNF645 [174-193]
1	5457	HPLLGVSATLNSVLNSNAIK	DKK1 [24-43]	13	5707	VLRMTRARRSQVEQQQLITV	ATAD2 [1293-1312]
1	5458	TGEELFFDYRYSQADALKYV	EZH2 [718-737]	13	5708	TIREFFILLQVHILIQKPRQ	CASC5 [1895-1914]
1	5459	MSWRGRSTYRPRPRRYVEPP	GAGE-2 [1-20]	13	5709	AKIQYLQNYLKESVQIQKKV	CCDC110 [426-445]
1	5460	EKRYLRMAVLTLYTDPMGSE	HORMAD2 [95-114]	13	5710	TPIISPDPSSYLSGANLNL	CEA [595-614]
1	5461	AERNRVATMPVRLRLRDPAA	HSPB9 [24-43]	13	5711	KLDRQHVQHQLHVILKELRK	CEP55 [367-386]
1	5462	SFFYVTETTFQKNRLFFYRK	hTERT [559-578]	13	5712	KVMMVNGDHRIGIFAKRAIQ	EZH2 [698-717]
1	5463	ANIRFSIWSFFEIYNELLY	KIF20A [295-314]	13	5713	GFHSMKVVMTEATKVIDLE	HORMAD2 [226-245]
1	5464	KAQNASKGIYAMASRDVFL	MCAK [365-384]	13	5714	DTDPRRLVQLLRQHSSPWQV	hTERT [442-461]

1	5465	SQQNVSMDLATFMKLRTDAV	MSLN [520-539]	13	5715	VGQASFFNLTVKEMVKDVLK	KIF20A [131-150]
1	5466	DEERELEKLFQLGPPSPVKM	PTTG-1 [150-169]	13	5716	FQIILRAKGRMHGKFSLVDL	MCAK [474-493]
1	5467	STFQFLYTYIAKVDGEISAS	Ropporin-1A [159-178]	13	5717	DVLYPKARLAFQNMNGSEYF	MSLN [482-501]
1	5468	QNIETLQNAGVMSLLRLLLL	SPAG6 [32-51]	13	5718	EDFDPGVKEAAAWALRYIAR	SPAG6 [135-154]
1	5469	FRHGHRGLLTMQLKSPMPSS	SPAG8 [309-328]	13	5719	ATAVNTRQRYYPMAGYIKED	TDRD4 [77-96]
1	5470	KMKSLEKISYVYMKRKYEAM	SSX-7 [39-58]	13	5720	VSDEKSSELIITDSITLKNK	TTK [340-359]
1	5471	GERVDVSKYLIKGLALRER	TDRD4 [1087-1106]	13	5721	PQRSEGSNVFSGRKTGTFL	WBP2NL [34-53]
1	5472	KKFAFVHISFAQFELSQGNV	TTK [140-159]	13	5722	IKRRHKRARKQVTSASLEKV	ZNF645 [134-153]
1	5473	PKPEEKRFLLLEPMPFFYLK	URLC10 [95-114]	14	5723	ASLADVDPMLDSSVRFDSV	ATAD2 [409-428]
1	5474	RTLNDWFSSMGIYVITGEGN	WBP2NL [143-162]	14	5724	EITGMNTLLSAPIHTQMQQK	CASC5 [131-150]
1	5475	IPPEQHTMVSLPSVQHMLQE	ZNF645 [180-199]	14	5725	KDKERQFFLVKQGSIISENE	CCDC110 [393-412]
2	5476	SRQDQIHSSIVSTLLALMDG	ATAD2 [542-561]	14	5726	ERVDGNRQIIGYVIGTQQAT	CEA [71-90]
2	5477	TALDVHFVSTLEPLSNAVKR	BAGE-3 [37-56]	14	5727	EKVAASPKSPTAALNESLVE	CEP55 [420-439]
2	5478	WEQSLFSTTKPLFSSGQFSM	CASC5 [717-736]	14	5728	EWSGAEASMFRLVIGTYIDN	EZH2 [431-450]
2	5479	LKFHSRVPRYTLSTFLDQTKH	CCDC110 [371-390]	14	5729	VKVMTEATKVIDLENNLFRE	HORMAD2 [232-251]
2	5480	AQYSWFVNGTFQQSTQELFI	CEA [267-286]	14	5730	EHRLREEILAKFLHWMMSVY	hTERT [533-552]
2	5481	LTDKERHRLLEKIRVLEAEK	CEP55 [51-70]	14	5731	ERGIGQATHRFTFSQIFGPE	KIF20A [111-130]
2	5482	STLDGYSRRTTLSSKMYHTK	DKK1 [163-182]	14	5732	EYTLNTRLRYADRVKELSPHS	MCAK [573-592]
2	5483	PRKFPSDKIFEAISSMFPDK	EZH2 [215-234]	14	5733	EDIRKWNVTSLLETKALLEV	MSLN [382-401]
2	5484	KEPINVQVGFVSTGFHSMKV	HORMAD2 [213-232]	14	5734	AWALRYIARHNAELSQAQVVD	SPAG6 [146-165]
2	5485	EELVVQVDGQWLMVTGQQQL	HSPB9 [66-85]	14	5735	LERSASTDKTLLNSSAVMLD	TDRD4 [125-144]
2	5486	QQVWKNPTFFLRVISDTASL	hTERT [1023-1042]	14	5736	ELRNLSVQNSHFKEPLVSD	TTK [323-342]
2	5487	DSMEKVKVYLVRPLLPSEL	KIF20A [60-79]	14	5737	ESTAAQAPENEASLPSASSS	WBP2NL [286-305]
2	5488	ETASNEVVYRFTARPLVQTI	MCAK [317-336]	14	5738	PIQWETVSIIFTRKHGNLTV	ZNF645 [222-241]
2	5489	DLPGRFVAESAEBVLLPRLVS	MSLN [191-210]	15	5739	YQMRPSIIFDEIDGLAPVR	ATAD2 [521-540]
2	5490	ESNLLQSPSSILSTLDVELP	PTTG-1 [175-194]	15	5740	KNDMDITKSYTIEINHRPLL	CASC5 [895-914]
2	5491	IRVQPQDLIQWAADYFEALS	Ropporin-1A [26-45]	15	5741	RPLASDLKGYFKVKDRTLKH	CCDC110 [813-832]
2	5492	VKEAAAWALRYIARHNAELS	SPAG6 [141-160]	15	5742	GIQNELSVSDHSDPVILNVLY	CEA [394-413]
2	5493	MQDGSESEFFRHHGHRGLLTM	SPAG8 [300-319]	15	5743	KSETTLEKLKGEIAHLKTSV	CEP55 [22-41]
2	5494	RLQRIFPKIMPKKPAEEGND	SSX-7 [103-122]	15	5744	VEDETVLHNI PYMGDEVLDQ	EZH2 [122-141]
2	5495	LNAAMNIARALQLSPSLRTY	TDRD4 [237-256]	15	5745	ITYLRGLFPESYGERHLDD	HORMAD2 [46-65]
2	5496	LYYMTYGKTPFQQIINQISK	TTK [724-743]	15	5746	REKRAERLTSRVKALFSVLN	hTERT [647-666]
2	5497	LVVALPRVWTDANLTARQRD	URLC10 [8-27]	15	5747	KLNILKESLTSFYQEEIQER	KIF20A [625-644]
2	5498	KLVRFRNGDAIEFAQLMVKAA	WBP2NL [114-133]	15	5748	ESALAQQAQKHSALRDVIKA	MCAK [684-703]
2	5499	ELSLSLPFPPIQWETVSIIFTR	ZNF645 [214-233]	15	5749	EDLKALSQQNVSMDLATFMK	MSLN [514-533]

3	5500	KKSQNYNIFQLENLYAVISQ	ATAD2 [1342-1361]	15	5750	PPNILKHVVQGFSKVLPHDS	SPAG6 [425-444]
3	5501	FVQNTLTCLKKDRRKMQTVQ	BAGE-3 [82-101]	15	5751	KLAYIEPYKRTMQWSKEAKE	TDRD4 [792-811]
3	5502	EHTTGQLTTMNRQIAVKVEK	CASC5 [814-833]	15	5752	SGTVNQIMMANNPEDWLSL	TTK [49-68]
3	5503	SIEMEAMKTNILLIQDEKEM	CCDC110 [568-587]	16	5753	KEERTKFFEDLILKQAAKPP	ATAD2 [926-945]
3	5504	AYSGREIYPNASLLIQNI I	CEA [94-113]	16	5754	QAPPSSLLVHKLI FQYVEEK	CASC5 [2190-2209]
3	5505	LRDQLKARYSTTTLEQLEE	CEP55 [87-106]	16	5755	NLKSMMKPLIFTTQSLIQKV	CCDC110 [454-473]
3	5506	LNSVLNSNAIKNLPPLGGA	DKK1 [33-52]	16	5756	FVSNLATGRNNSIVKSITVS	CEA [656-675]
3	5507	KTLNAVASVPIMYSWSPLQQ	EZH2 [99-118]	16	5757	RDQLKARYSTTTLEQLEET	CEP55 [88-107]
3	5508	LIRKLYILMQDLEPLPNVV	HORMAD2 [160-179]	16	5758	SFLFNLNDFVVDATRKGNK	EZH2 [664-683]
3	5509	RVSYRMSQKVHRKMLPSNLS	HSPB9 [92-111]	16	5759	VTEMYQFKFKYTKEGATMDF	HORMAD2 [116-135]
3	5510	RVKALFVSLNYERARRPGLL	hTERT [657-676]	16	5760	FQKNRLLFFYRKSVMKLSQSI	hTERT [568-587]
3	5511	STYDETLHVAKFSAIASQLV	KIF20A [489-508]	16	5761	KQIRQEBEMKLSLLNGGLQE	KIF20A [215-234]
3	5512	ILRAKGRMHGKFSVLVDLAGN	MCAK [477-496]	16	5762	RAKGRMHGKFSVLVDLAGNER	MCAK [479-498]
3	5513	LAFQNMNGSEYFVKIQSFLG	MSLN [490-509]	16	5763	TVAEVQKLLGPHVEGLKAAE	MSLN [543-562]
3	5514	DAYPEIEKFFPNPLDFESF	PTTG-1 [109-128]	16	5764	LNPDAKLKHQILSALSQVSK	SPAG6 [219-238]
3	5515	GEISASHVSRMLNYMEQEV I	Ropporin-1A [173-192]	16	5765	SDILELGARIFVSSIKNGMW	TDRD4 [461-480]
3	5516	SLAEQNRFYKAAAFVLRAV	SPAG6 [91-110]	16	5766	TYGKTPFQQI INQISKLHAI	TTK [728-747]
3	5517	IPPGFRNLVADRVPNYTSWS	SPAG8 [213-232]	17	5767	LHNHSAASATGSLDLSSDFL	ATAD2 [10-29]
3	5518	KHAWTHRLRERKQLVIYEEI	SSX-7 [161-180]	17	5768	SFADTIKVQFTESHMKIVRK	CASC5 [60-79]
3	5519	NPWEKLSIHLYFDGMSLSYF	TDRD4 [1330-1349]	17	5769	TLEFEMRHLQREYLSLSDKI	CCDC110 [759-778]
3	5520	NQTLDSYRNEIAYLNKLQQH	TTK [562-581]	17	5770	QHTQELFISNITEKNSGLYT	CEA [457-476]
3	5521	KAASAAARGFPLRTLNDWFS	WBP2NL [131-150]	17	5771	IAELESKTNTLRLSQTVPAPN	CEP55 [139-158]
3	5522	QDVVTPNSVRSQVPALTTY	ZNF645 [301-320]	17	5772	VYEFVRVKESSI IAPAPAEDV	EZH2 [466-485]
4	5523	VEKALAILSQPTPSLVVDHE	ATAD2 [1312-1331]	17	5773	RTLEVQSDYSSYARTSIRAS	hTERT [938-957]
4	5524	AQLLQARLMKEESPVVSWRL	BAGE-3 [12-31]	17	5774	QATHRFTFQSIFGPEVGQAS	KIF20A [116-135]
4	5525	PVQNDLAYANDFASEYYLES	CASC5 [1360-1379]	17	5775	QPDYDLET FVNKAESALAQQ	MCAK [671-690]
4	5526	NSDILKNYNNFYRFLPTAPP	CCDC110 [190-209]	17	5776	GVLANPPNISSLSPRQLLGF	MSLN [50-69]
4	5527	TQDATYLWWVNQSLPVSPR	CEA [171-190]	17	5777	VAELATRPQNIETLQNAGVM	SPAG6 [24-43]
4	5528	LESKQLHEFAITEPLVTFQ	CEP55 [394-413]	17	5778	QLIEGLDILFLKTIIEFYK	TDRD4 [696-715]
4	5529	SFGNDHSTLDGYSRRTTLSS	DKK1 [157-176]	17	5779	DPKQRISIPPELLAHYPVQIQ	TTK [775-794]
4	5530	FRRADEVKSMFSSNRQKILE	EZH2 [32-51]	18	5780	RRSQVEQQQLITVEKALAIL	ATAD2 [1300-1319]
4	5531	KEGVNSHFLFLDKEPINVQV	HORMAD2 [201-220]	18	5781	YSQDLGEMTKLNSKRVSFKL	CASC5 [1432-1451]
4	5532	EDNDHARDGFQMKLDAHGFA	HSPB9 [45-64]	18	5782	NENNRMSIEMEAMKTNILLI	CCDC110 [562-581]
4	5533	EAFTTSVRSYLPNTVTDALR	hTERT [113-132]	18	5783	NGNRTLTLFNVTRNDARAYV	CEA [551-570]
4	5534	FPSLHSLFIKEHSLQVSPSLE	KIF20A [517-536]	18	5784	RHRLLKIRVLEAEKEKNAY	CEP55 [56-75]
4	5535	MAMSSSLQARLFPGLAIKIQ	MCAK [1-20]	18	5785	NAVASVPIMYSWSPLQQNFM	EZH2 [102-121]

4	5536	ATQMDRVNAIPFTYEQLDVL	MSLN [333-352]	18	5786	RAVRSLLRSHYREVLPATF	hTERT [8-27]
4	5537	QIAHLPLSGVPLMILDEERE	PTTG-1 [135-154]	18	5787	KDVLKGQNWLIYTYGVNSG	KIF20A [146-165]
4	5538	IRABELAQMWKVNLPTDLF	Ropporin-1A [85-104]	18	5788	QEHLVNSADDVIKIMDMGSA	MCAK [435-454]
4	5539	DILPQLVYSLAEQNRIFYKKA	SPAG6 [83-102]	18	5789	QNVSMDLATFMKLRDTAVLP	MSLN [522-541]
4	5540	DYRQEQPETFWIQRAPQLPV	SPAG8 [403-422]	18	5790	VVGQFSKVLPHDSKARRLFV	SPAG6 [432-451]
4	5541	ISYVYMKRKYEAMTKLGFKK	SSX-7 [46-65]	18	5791	SVIKILEDNVLLVELFDSL	TDRD4 [825-844]
4	5542	WEEEAKEVFLKMNKAVSM	TDRD4 [590-609]	18	5792	SVVKDSQVGTVNYMPEAIK	TTK [677-696]
4	5543	PYVQIQTHPVNQMAKGTTEE	TTK [789-808]	19	5793	QNIPSFAPVLLLATSDKPHS	ATAD2 [882-901]
4	5544	NGDAIEFAQLMVKAASAAAR	WBP2NL [119-138]	19	5794	VQEIAEKQALAVGNKIVLHT	CASC5 [1234-1253]
4	5545	EYNKEGKYSGVKLVRRKKK	ZNF645 [12-31]	19	5795	LPTAPPNVMSQADTVILDKS	CCDC110 [204-223]
5	5546	GSSVKEVETYHRTRALRSLR	ATAD2 [59-78]	19	5796	SWRINGIPQQTQVLFIAKI	CEA [626-645]
5	5547	EPEDGTALDVHFVSTLEPLS	BAGE-3 [32-51]	19	5797	LKDALEKNQQLVYDQQREV	CEP55 [174-193]
5	5548	EWSDDQAVFTFVYDTIQLTI	CASC5 [2139-2158]	19	5798	FVVDAIRKGNKIRFANHSVN	EZH2 [673-692]
5	5549	NPQFSSEKNLVFGTRIEKDL	CCDC110 [97-116]	19	5799	IPQDRLTEVIASIIKPQNTY	hTERT [720-739]
5	5550	DDPTISPSYTYRPGVNLSSL	CEA [416-435]	19	5800	QDQTLAELQNNMVLVKLDLR	KIF20A [785-804]
5	5551	QQWLVYDQQREVYVKGLLAK	CEP55 [182-201]	19	5801	IKIQRSNGLIHSANVRTVNL	MCAK [17-36]
5	5552	GFINDEIFVELVNALGQYND	EZH2 [164-183]	19	5802	PIIRSIPOGIVAARQRSSR	MSLN [258-277]
5	5553	EKVTEMYQFKFKYTKEGATM	HORMAD2 [114-133]	19	5803	MSQRQVLQVFEQYQKARTQF	SPAG6 [1-20]
5	5554	ERNRVATMPVRLLRDSPAQ	HSPB9 [25-44]	19	5804	SLPSPGELYAVQVHVSPN	TDRD4 [1406-1425]
5	5555	TLTDLQPYMRQFVAHLQETS	hTERT [765-784]	19	5805	AKGTTEEMKYVVLGQVLGNS	TTK [802-821]
5	5556	IAEQYHTVLKLGQVSAKKR	KIF20A [810-829]	20	5806	VRFDSVGGLSNHIAALKEMV	ATAD2 [423-442]
5	5557	EVYVTFFEIYNGKLFDLLNK	MCAK [396-415]	20	5807	FPFLDKRYRKIVDVNFQSLL	CASC5 [2167-2186]
5	5558	YPESVIQHLGLFLKMSPED	MSLN [364-383]	20	5808	TAEENFLQEIKNKASEASII	CCDC110 [671-690]
5	5559	GLKLGSGPSIKALDGRSQVS	PTTG-1 [23-42]	20	5809	VNEEATGQFRVPELPKPSI	CEA [130-149]
5	5560	LHSQVAGRLIIRAEELAQMW	Ropporin-1A [75-94]	20	5810	IFELEKKTETAAHSLPQQT	CEP55 [202-221]
5	5561	AHSENLAMAVIISKGVPLS	SPAG6 [322-341]	20	5811	YMRLRQLKRFRRADDEVKSMF	EZH2 [23-42]
5	5562	SSDDSPRSALAAATAAAAAA	SPAG8 [35-54]	20	5812	YVVELLRSFYVVTETTFQKN	hTERT [552-571]
5	5563	PEKIQKSFDDIAKYFSKKEW	SSX-7 [18-37]	20	5813	MSQGILSPAGLLSDDDVVV	KIF20A [1-20]
5	5564	VVEKQFDQLLAFDSSRKKNL	TDRD4 [189-208]	20	5814	LLLVHEPKLVKDLTKYLENQ	MCAK [288-307]
5	5565	WERKSYWKNMLEAVHTIHQH	TTK [622-641]	20	5815	SRDPSWRQPRTILRPRFR	MSLN [276-295]
5	5566	SNVFSGRKTGTFLTSYRVI	WBP2NL [40-59]	20	5816	SKHSVDLAEMVVEAEIFPVV	SPAG6 [237-256]
5	5567	KRTYLSQKSLQAHIKRRHKK	ZNF645 [121-140]	20	5817	SILVQFVDYGSTAKTLNRL	TDRD4 [1510-1529]
6	5568	PASPARPRYLSSAGPRSPY	ATAD2 [325-344]	20	5818	VERGAVPLEMLEIALRNLL	TTK [170-189]
6	5569	LQARLMKEESPVSWRLEPE	BAGE-3 [15-34]	21	5819	RKIRKSNWYLGTIKKRRKI	ATAD2 [1164-1183]
6	5570	NQDARILAMTPESIYSNPSI	CASC5 [429-448]	21	5820	AGKLNLSPSQYINEENLPVY	CASC5 [1726-1745]
6	5571	LEALVKLLLPFRETYSKFHV	CCDC110 [315-334]	21	5821	ELKKHSQENIKFENSISRLT	CCDC110 [721-740]

6	5572	SASGHSRTTVKTI TVSAELP	CEA [482-501]	21	5822	QQSTQELFIPNITVNNSGSY	CEA [278-297]
6	5573	BEKDLVKQQLSAATSRIABL	CEP55 [123-142]	21	5823	LKELRKARNQITQLESKQL	CEP55 [381-400]
6	5574	LQQNFMVEDETVLHNI PYMG	EZH2 [116-135]	21	5824	FLFNLNNDVFVDATRKGNKI	EZH2 [665-684]
6	5575	QDLEPLPNNVLTMLHYYN	HORMAD2 [169-188]	21	5825	LWGSRHNERRFLRNTKKFIS	hTERT [477-496]
6	5576	VVQVDGQWLMVTGQQQLDVR	HSPB9 [69-88]	21	5826	LNGGLQEEELSTSLKRSVYI	KIF20A [228-247]
6	5577	LGLDDIHRAWRTFVLRVRAQ	hTERT [681-700]	21	5827	SLRSRSTRMSTVSELRIQA	MCAK [106-125]
6	5578	ILIKQDQTLAELQNNMVLVK	KIF20A [781-800]	21	5828	SGKKAREIDESLIFYKKWEL	MSLN [304-323]
6	5579	FVNKAESALAQKAKHFSALR	MCAK [679-698]	21	5829	ALALGRLANYNDDLAEEAVVK	SPAG6 [62-81]
6	5580	LSTERVRELAVALAKNVKL	MSLN [77-96]	21	5830	SLYLTGAVATI ILQVDSEEN	TDRD4 [1051-1070]
6	5581	NLLQSPSSILSTLDVELPPV	PTTG-1 [177-196]	21	5831	SEEEKKNLSASTVLTQAQESF	TTK [196-215]
6	5582	NRBELTPELLKILHSQVAGR	Ropporin-1A [63-82]	22	5832	EIVVIGATNRLDSIDPALRR	ATAD2 [567-586]
6	5583	LQVFEQYQKARTQFVQMAE	SPAG6 [7-26]	22	5833	ADGTSLDFSTYRSQMESQF	CASC5 [1856-1875]
6	5584	PQKQPPWEFLQVLEPGARGL	SPAG8 [239-258]	22	5834	STDNLSSNII IHPSSENSDIL	CCDC110 [175-194]
6	5585	THRLRERKQLVIYEEISDPE	SSX-7 [165-184]	22	5835	PNASLLIQNI IQNDTGIFYTL	CEA [103-122]
6	5586	VPKLSFELIKMTNEIQSNL	TDRD4 [1199-1218]	22	5836	GETENREKVAASPKSPTAAL	CEP55 [414-433]
6	5587	GQNESFARIQVRFAELKAIQ	TTK [104-123]	22	5837	MFSSNRQKILERTEILNQEW	EZH2 [41-60]
6	5588	GWEGQATFKLVFRNGDAIEF	WBP2NL [106-125]	22	5838	RNTKKFISLGKHAHLSLQEL	hTERT [489-508]
6	5589	SLSLFFPIQWETVSIFTRKH	ZNF645 [216-235]	22	5839	SPMFESTAADLGSVVRKNLL	KIF20A [21-40]
7	5590	REDKVIPTVTRSLRARNIVQS	ATAD2 [122-141]	22	5840	EEQVHSIRGSSSANPVNSVR	MCAK [170-189]
7	5591	TPEDLMLSQYVYRPKIQIYR	CASC5 [1928-1947]	22	5841	GLKAEERHRPVRDWILRQRQ	MSLN [557-576]
7	5592	FHSRVPRYTLSTFLDQTKHEM	CCDC110 [373-392]	22	5842	QEIKABPGSLLQEYINSINS	SPAG6 [460-479]
7	5593	IIQNDTGFIYTLHVIKSDLVN	CEA [112-131]	22	5843	HFYIRKYSQIKDAKVLEKKV	TDRD4 [429-448]
7	5594	VERQTITQLSFELSEFRKY	CEP55 [250-269]	22	5844	LNKLQHQSDKI IRLYDYEIT	TTK [575-594]
7	5595	WRKRVKSEYMRRLQLKRFR	EZH2 [15-34]	23	5845	KEMVVFFLLYPEVFEKFKIQ	ATAD2 [439-458]
7	5596	DYQPLGFKGCVNSHFLFLDK	HORMAD2 [194-213]	23	5846	EENMDITKSHTVAIDNQIFK	CASC5 [507-526]
7	5597	QQQLDVRDPERVSYRMSQKV	HSPB9 [82-101]	23	5847	NSISRLTEDKILLENYVRSI	CCDC110 [734-753]
7	5598	DYSSYARTSIRASLTFNRGF	hTERT [945-964]	23	5848	EPEIQNTTYLWVNNQSLPV	CEA [346-365]
7	5599	SPYARILRSRRSPLKSGPF	KIF20A [867-886]	23	5849	IPYMGDEVLDQDGTFFIELI	EZH2 [131-150]
7	5600	PKESLRSRSTRMSTVSELRI	MCAK [103-122]	23	5850	HVRKAFKSHVSTLTDLQPYM	hTERT [754-773]
7	5601	DRVNAIPFTYEQLDVLKHKL	MSLN [337-356]	23	5851	DLKPLLSNEVIWLDSKQIRQ	KIF20A [200-219]
7	5602	PALPKATRKALGTVNRATEK	PTTG-1 [54-73]	23	5852	KAHTPFRESKLTQVLRDSFI	MCAK [534-553]
7	5603	SVMNVGRFTEEIEWLKFLAL	Ropporin-1A [106-125]	23	5853	RELAVALAQKNVLSLQELR	MSLN [83-102]
7	5604	PTIQQTAAALGRLANYND	SPAG6 [55-74]	23	5854	VRYYSPGYSDTLQQRVDSYQ	SPAG6 [486-505]
7	5605	GSEFFFRHGRGLTMQLK	SPAG8 [303-322]	23	5855	KFKSQSLRSHFEKNTTLHYH	TDRD4 [650-669]
7	5606	SGPKRGKHAWTHRLRERKQL	SSX-7 [155-174]	23	5856	NPEDWLSLLKLEKNSVPLS	TTK [61-80]

7	5607	KIVAIKEFNPLSILVQFVDY	TDRD4 [1499-1518]	24	5857	ISAKDFEVAMQKMIPASQRA	ATAD2 [674-693]
7	5608	LSDALLNKLIGRYSQAIEAL	TTK [79-98]	24	5858	LLPNEIAIRPMDKTVLFTDN	CASC5 [1167-1186]
7	5609	ALIPNGESLLKRSPNVELSF	WBP2NL [14-33]	24	5859	DEVDSVLLSASKILNSSEGV	CCDC110 [11-30]
7	5610	DIQAPPPPELSSLFPPIQWE	ZNF645 [207-226]	24	5860	EPETQDATYLLWVNNQSLPV	CEA [168-187]
8	5611	KRYYLQRKATVYYQAPLEK	ATAD2 [292-311]	24	5861	RQVYEFVRKESSIIAPAPAE	EZH2 [464-483]
8	5612	PHVSKERIQQLSNPLSISL	CASC5 [566-585]	24	5862	DGLRPIVNMDYVVGARTFRR	hTERT [628-647]
8	5613	LKEFKKIISKYNVLQGGNKT	CCDC110 [505-524]	24	5863	DISMYGKEELLQVVEAMKTL	KIF20A [554-573]
8	5614	PRLQLSNDNRTLTLSSVTRN	CEA [367-386]	24	5864	DDVAAINPELLQLLPLHPKD	MCAK [59-78]
8	5615	HQLHVILKELRKARNQITQL	CEP55 [375-394]	24	5865	LDQDQQEAARAALQGGGPPY	MSLN [215-234]
8	5616	GPNAKSVQREQSLHSFHTLF	EZH2 [266-285]	24	5866	REIAKHTPELSQLVNVAGGV	SPAG6 [276-295]
8	5617	STGFHSMKVKVMTEATKVID	HORMAD2 [224-243]	24	5867	NVWQPDALIEVLQQLSKRQV	TDRD4 [1301-1320]
8	5618	YRMSQKVHRKMLPSNLSPTA	HSPB9 [95-114]	24	5868	NESFARIQVRFAELKAIQEP	TTK [106-125]
8	5619	RLPRLPQRYWQMRPLFLELL	hTERT [378-397]	25	5869	LSLEHIGRRRLRSAGAAQKK	ATAD2 [29-48]
8	5620	DGGILPRSLALIFNSLQGQL	KIF20A [176-195]	25	5870	NLNNLNGKTGEFLAFQTVHL	CASC5 [1586-1605]
8	5621	DSSFPNWEFARMIKEFRATL	MCAK [224-243]	25	5871	EKNIQLSLEKQQMMEALDQL	CCDC110 [527-546]
8	5622	LLATQMDRVNAIPFTYEQLD	MSLN [331-350]	25	5872	RNNSIVKSITVSASGTSPGL	CEA [664-683]
8	5623	KMTEKTVKAKSSVPASDDAY	PTTG-1 [92-111]	25	5873	QRGSKKHLALLAPSDVAGWGI	EZH2 [607-626]
8	5624	KMLKEFAKAAIRVQPQDLIQ	Ropporin-1A [16-35]	25	5874	TYVPLLGLSLRTAQTLRKL	hTERT [1088-1107]
8	5625	IQEPEIALKRIAASALSDIA	SPAG6 [176-195]	25	5875	QNLVPFRDSKLTRVFQGGFT	KIF20A [454-473]
8	5626	RKLFEVESVTHHDYRMELAQ	SPAG8 [373-392]	25	5876	KREEKKAQNSEMRMKRAQY	MCAK [204-223]
8	5627	MNGDDAFARRPRAGAIPEK	SSX-7 [1-20]	25	5877	PQAPRRPLPQVATLIDRFVK	MSLN [409-428]
8	5628	RRGQIIRMVDTLVEVLLYD	TDRD4 [980-999]	25	5878	LSEEPEDHIKAAAALWALGQI	SPAG6 [344-363]
8	5629	KIIRLYDYEITDQYIYMVME	TTK [584-603]	25	5879	EEFARTTDDYLSNLIKAKSY	TDRD4 [210-229]
8	5630	HTENRRGALIPNGESLLKRS	WBP2NL [7-26]	25	5880	DSRGQTTKARFLYGENMPPQ	TTK [230-249]
8	5631	TTYDPSSGYIIVKVPPDMNS	ZNF645 [318-337]	26	5881	SEKLQLDLSSINISAKDFEV	ATAD2 [662-681]
9	5632	SSSKYAPSYHYVMPKQNSTL	ATAD2 [1114-1133]	26	5882	RNKKNSRRVSFADTIKVFQT	CASC5 [51-70]
9	5633	QLNNRDRNVDFTSSTHATAV	CASC5 [1302-1321]	26	5883	DLPTENQEENLSMEKSHHFE	CCDC110 [115-134]
9	5634	MSQADTVILDKSKITVPFLK	CCDC110 [212-231]	26	5884	TVYAEPKPFITSNNSNPVE	CEA [317-336]
9	5635	QQHTQVLFIAKITPNNGTY	CEA [634-653]	26	5885	VVDATRGKNKIRFANHSVNP	EZH2 [674-693]
9	5636	VYDQQREVYVKGLLAKIFEL	CEP55 [186-205]	26	5886	SLLRSHYREVLPATFVRRL	hTERT [12-31]
9	5637	YQHLEGAKEFAAALTAERIK	EZH2 [325-344]	26	5887	QGTIKDGGILPRSLALIFNS	KIF20A [171-190]
9	5638	IKKASVLLIRKLYILMQDLE	HORMAD2 [153-172]	26	5888	IRALGQNKHAHTPFRESKLTQ	MCAK [527-546]
9	5639	RSLLRSHYREVLPATFVRRL	hTERT [11-30]	26	5889	LFSLGWVQPSRTLAGEGTGQE	MSLN [25-44]
9	5640	LNQNSSRSHSIFIRILHLQ	KIF20A [373-392]	26	5890	TNTLPVLLSLYMSTESSEDL	SPAG6 [377-396]
9	5641	AKHFSALRDVIKALRLAMQL	MCAK [691-710]	26	5891	ISPEKIYVQWLLTENLLNSL	TDRD4 [926-945]
9	5642	RQLDVLYPKARLAFQNMNGS	MSLN [479-498]	26	5892	ISVKGRIYSILKQIGSGGSS	TTK [518-537]

9	5643	SQVSTPRFGKTFDAPPALPK	PTTG-1 [39-58]	27	5893	KIDLHKYLTVKDYLRDIDLI	ATAD2 [1037-1056]
9	5644	PELLKILHSQVAGRLIIRAE	Ropporin-1A [69-88]	27	5894	QDLIKDPRNLLANQTLVYSQ	CASC5 [1415-1434]
9	5645	LKDKDEYVKKNASTLIREIA	SPAG6 [260-279]	27	5895	IKNAKSEASIYKNSLSEIGK	CCDC110 [680-699]
9	5646	FEVESVTHHDYRMELAQAGT	SPAG8 [376-395]	27	5896	ETQNPVSARRSDSVILNVLY	CEA [216-235]
9	5647	DIKYFYSKKEWEKMSLEKI	SSX-7 [27-46]	27	5897	IFAKRAIQTGEELFFDYRYS	EZH2 [710-729]
9	5648	RSHFEKNTTLHYHPILPKE	TDRD4 [657-676]	27	5898	TDALRGSGAWGLLLRRVGDD	hTERT [128-147]
9	5649	IGSGGSSKVFQVLNEKKQIY	TTK [531-550]	27	5899	PVPANIRFSIWISFFEIYNE	KIF20A [292-311]
9	5650	GGWEGQATFKLVFRNGDAIE	WBP2NL [105-124]	27	5900	ETGQEAAPLDGVLANPPNIS	MSLN [40-59]
9	5651	SASEFASHHYNLNLPQFTE	ZNF645 [351-370]	27	5901	YYSFGYSDTLLQQRVDSYQPL	SPAG6 [488-507]
10	5652	QEEDTFRELRIFLRNVTTRL	ATAD2 [981-1000]	27	5902	YDDGLWYRAKIIVAIKEFNPL	TDRD4 [1490-1509]
10	5653	RPMDKTVVFDNVHVELEMT	CASC5 [963-982]	27	5903	QVLNEKKQIYAIKYVNLEEA	TTK [541-560]
10	5654	LQNVSMVQSEISEILNKSII	CCDC110 [74-93]	28	5904	SLDLSSDFLSLEHIGRRRLR	ATAD2 [21-40]
10	5655	PPAQYSWLIDGNIQHTQEL	CEA [443-462]	28	5905	FQDLSINSADKIHTTRSHIM	CASC5 [398-417]
10	5656	EVHNLNQLLYSQRRADVQHL	CEP55 [275-294]	28	5906	SKMKPLIFTTQSLIQKVETY	CCDC110 [457-476]
10	5657	EWKQRRIQPVHILTSVSSLR	EZH2 [59-78]	28	5907	TYLWWVNGQSLPVSPLQLS	CEA [531-550]
10	5658	KRYLRMAVLTLTYTDPMGSEK	HORMAD2 [96-115]	28	5908	YRYSQADALKYVGIEREMEI	EZH2 [726-745]
10	5659	GLLLDTRTLEVQSDYSSYAR	hTERT [932-951]	28	5909	SVWSKLQSIGIRQHLKRVQL	hTERT [579-598]
10	5660	TVKEMVKVDVLKGQNWLIYTY	KIF20A [140-159]	28	5910	FRDSKLTRVFGGFTTGRGRS	KIF20A [459-478]
10	5661	EELSSQMSSFNEAMTQIREL	MCAK [625-644]	28	5911	VIQHLGYLFLKMSPEDIRKW	MSLN [368-387]
10	5662	QGGIPNGYLVLDLSMQEALS	MSLN [587-606]	28	5912	AVSMKVFREDEGVLIVDLQK	TDRD4 [606-625]
10	5663	AHLPLSGVPLMILDEERELE	PTTG-1 [137-156]	28	5913	LNKLIGRYSQAIEALPPDKY	TTK [84-103]
10	5664	GPDGIITVNDFTQNPRVQLE	Ropporin-1A [193-212]	29	5914	RIRSRYSGVNQSMFLDKLIT	ATAD2 [159-178]
10	5665	LPHDSKARRLFTVTSGLKKV	SPAG6 [440-459]	29	5915	EKLQDGRITIREFFILLQVH	CASC5 [1887-1906]
10	5666	SYQPPGNVYWPLRGKREAML	SPAG8 [334-353]	29	5916	IAESENQIQPQSALKVLQQQ	CCDC110 [43-62]
10	5667	SSDMPVSLRDALVFMELAKF	TDRD4 [632-651]	29	5917	NGIPQQHTQVLFIKITPNN	CEA [630-649]
10	5668	KAVERGAVPLEMLEIALRNL	TTK [168-187]	29	5918	FSVLNYERARRPGLLGASVL	hTERT [662-681]
10	5669	WEGQATFKLVFRNGDAIEFA	WBP2NL [107-126]	29	5919	PRSLALIFNSLQGQLHPTPD	KIF20A [181-200]
10	5670	PQFTQTDAMDHRRWPAWKRL	ZNF645 [377-396]	29	5920	SLSPBELSSVPPSSIWAVRP	MSLN [451-470]
11	5671	AVLQKMDMKMKMRQRMREL	ATAD2 [183-202]	29	5921	QDKNQWRRGQIIRMVTDTLV	TDRD4 [974-993]
11	5672	EKSTKIDTTSFLANLKLHTE	CASC5 [198-217]	29	5922	ITDSITLKNKTESLLAKLE	TTK [350-369]
11	5673	LKNYNFYRFLPTAPPNVMS	CCDC110 [194-213]	30	5923	IYKDRMKIGASLADVDPMQL	ATAD2 [400-419]
11	5674	NGNRTLTLFNVTRNDTASYK	CEA [195-214]	30	5924	RLLGEBIEYLKRWGPNNYLM	CASC5 [2237-2256]
11	5675	FNSSINNIHEMEIQLKDALE	CEP55 [160-179]	30	5925	LHSVEEKLSGDSVNSLPQSV	CCDC110 [139-158]
11	5676	NGDHRIGIFAKRAIQTGEEL	EZH2 [703-722]	30	5926	VHNLPHQLFGYSWYKGERVD	CEA [55-74]
11	5677	ITNEHESLKMVKKLFATSSIS	HORMAD2 [25-44]	30	5927	AFKSHVSTLTDLQPYMRQFV	hTERT [758-777]
11	5678	DKEQLRPSFLLSSLRPSLTG	hTERT [337-356]	30	5928	RILRSRRSPLLKSGPFGKKY	KIF20A [871-890]

11	5679	SELALRRSQRLAASASTQQL	KIF20A [670-689]	30	5929	RITKANVDLLPRGAPERQRL	MSLN [143-162]
11	5680	ITAQENDMEVELPAAANSRK	MCAK [122-141]	30	5930	VGDDGTIFVVPKLSEFELIK	TDRD4 [1190-1209]
11	5681	EDLDALPLDLLLFLNPDAFS	MSLN [113-132]	30	5931	VQNSHFKEPLVSDEKSSELI	TTK [330-349]

Example 17 – Personalised selection of peptides to treat cancer

Effective immunotherapy for cancer patients stimulates T cell responses (ideally CD4+ and CD8+ T cell responses) that target TAA expressed by the cancer cells of the specific patient.

- 5 For treatment of a specific cancer patient, peptides comprising one or more of the 3286 hotspot amino acid sequences can be selected based on (i) cancer type (select peptides comprising hotspot sequences that are fragments of TSAs that are associated with the patient's cancer); (ii) TSA expression or TSA expression rate (sample patient's cancer cells and select peptides comprising hotspot sequences that are fragments of a TSA in fact expressed in the patient's cancer cells; or select peptides comprising hotspot sequences that are fragments of TSAs that are most frequently expressed in the patient's type of cancer); (iii) patient HLA genotype (select peptides comprising fragments of TSAs that comprise an amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I alleles of the patient (HLA class I-binding PEPI3+) (and ideally also comprise an amino acid sequence that is a T cell epitope capable of binding to multiple HLA class II alleles of the patient (HLA class II-binding PEPI2/3/4/5+)).

- 20 To illustrate the options for selecting peptides comprising hotspot amino acid sequences to treat individual patients, HLA class I-binding PEPI3+ were identified in the hotspot sequences for three colorectal cancer patients, one ovarian cancer patient and three breast cancer patients with known HLA genotypes. Only hotspot sequences that are fragments of TSA associated with the corresponding cancer (colorectal, ovarian, breast, Table 24) were considered. The number of hotspots sequences containing such a PEPI3+ and the number of antigens that could be targeted using selected peptides comprising a hotspot amino acid sequence are shown in Table 26. As expected, more hotspots containing PEPI3+ were identified and more TSA could be targeted using the hotspot sequences identified following a greater number of cycles of the method described in Example 16.

- 30 Table 26 – Number of selectable peptides matching to the patient HLA background) from antigens related to the indication. In case of MaxCycle=1, each antigen has only one potential peptide, therefore the peptide and antigen are selected together. The MaxCycle >1 means that

more than one peptides are related to a single antigen and hopefully more than one is matching to the patient's HLA set, therefore #peptides >= #antigens.

Indication max(#AG)	Patient ID	MaxCycle=1		MaxCycle=3		MaxCycle=5		MaxCycle=30	
		#Peptides	#AG	#Peptides	#AG	#Peptides	#AG	#Peptides	#AG
Colorectal (70 AGs)	CRC_P1	16	16	32	24	36	25	63	27
	CRC_P2	13	13	29	15	34	27	54	28
	CRC_P3	14	14	36	31	48	37	98	43
Ovarian (54 AGs)	OC_P1	10	10	17	14	28	20	51	22
Breast (70 AGs)	BRC_P1	27	17	45	31	60	34	99	35
	BRC_P2	23	13	43	35	48	36	86	36
	BRC_P3	13	13	26	19	33	23	60	28

Table 27 shows the peptide/hotspot amino acid sequences that are fragments of the breast cancer-associated TSA identified just in the first cycle of the method described in Example 16 that are expected to induce T cell responses in the three breast cancer patients of Table 26.

Table 27 – Options for peptide selection for breast cancer patients. Sequences are fragments of known breast cancer-associated CTAs and were identified in first cycle of method described in Exmpl X. “+” indicates peptide comprises subject-matched HLA class I-binding PEPI3+

SEQ ID NO	Sequence	BRC_P1	BRC_P2	BRC_P3
4	PHNFRVYSYSGTGIMKPLDQ	-	-	-
7	DEVSFYANRLTNLVIAMARK	+	+	-
8	IDDLSFYVNRLSSLVIQMAH	-	+	+
10	ARAVFLALSAQLLQARLMKE	-	-	-
16	QTTQNGRFYAISARFKPFSN	-	-	-
19	EGKDPAFTALLTTQLQVQRE	-	-	-
20	QGPTAVRKRFFESIIEAAR	-	-	-
21	ATAQLQRTPMSALVFPNKIS	-	+	-
22	LDMVHSLHRLSHNDHILIE	+	-	-
26	HTRFTQSGTMKIHLQKHGE	+	-	-
29	NTGEMSSNSTALALVRPSSS	-	-	-
32	NLLRGIDSLFSAPMDFRGLP	-	+	-
35	SERVRTYWIIELKHKAREK	+	+	-
40	EHLEVKFMNPYNAVLTKKFQ	+	+	-
41	SGSSYFVLANGHILPNSENA	-	-	-
42	ISDTKDYFMSKTLGIGRLKR	+	-	-
44	EEMRSHYVAQTGILWLLMNN	-	-	-
45	SRGKSTYYWPRPRRYVQPPE	-	-	-
46	WRGRSTYYWPRPRRYVQPPE	-	-	-
48	ALSRHMSSLSHISPFSSSH	-	+	-

51	RLNDLQMSNFVNKNITYLV	-	+	-
54	KKVNFLDMSLDDIIHYKELE	-	-	+
57	KLRYRYTLDDLYPMMNALKL	+	+	+
60	PDSRLQLHITMPFSSPMEA	+	+	-
61	QRNVAIMKSIIPAIVHYSPD	+	-	-
62	SEELNIIQGNILSTEKSK	-	-	-
64	VKVLEYVIKVSARVRFFPS	-	+	+
65	DDTTAMASASSSATGSFSYP	-	-	-
66	DPTSHSYVLVTSLNLSYDGI	+	+	-
67	ALSRKMAELVHFLLLKYRAR	+	+	-
68	GREDSVFAHPRKLLMQDLVQ	+	-	+
69	FPVIFSKASSSLQLVFGIEL	-	-	-
70	VNARVRIAYPSLREAALLEE	-	-	-
71	KSPQGASAIPTAIDFTLWRQ	-	-	-
72	KKLLTQYFVQENYLEYRQVP	-	-	+
73	RAPEEAIWEALSVMGLYDGR	-	+	-
74	PAQLEFMFQEALKLVAELV	+	+	+
80	RPVSSFFSYTLASLLQSSHE	-	-	+
81	ATVMASELSVMSSNVSFSE	+	-	-
83	RSQAGMFTYSNNRLIKMHEK	+	-	+
87	EEAFSRASLVSVYNSYPYP	+	-	-
90	QSQGSVLAFTRTFIATPGSS	-	+	-
91	KRASQYSGQLKVLIAENTML	+	-	-
93	KEFTVSGNILTIRLTAADHR	-	-	-
96	EKSTKYVFDSAPSHSISART	-	-	-
97	NSPLPFQWRITHSFRWMAQV	-	+	+
105	KEMELWMKAMLDAAALVQTEP	+	-	-
106	QYAHKLAFLVGQSIHREPNI	+	-	-
107	RSVVGFBASINLTITKWYSR	+	+	+
110	KAVSQDMVIYSTEIHYSSKG	-	-	-
111	RLDQLLRHVMNPLETSLITN	-	+	-
116	PPAFINMAATGVSSMSTRDQ	+	-	-
118	NNNIEKMITAFEELRVQAEN	-	+	-
122	QSSGISFQSKYLSFFILGQT	-	-	-
124	PDNIPAFAAAYFESLLEKRE	+	+	-
126	RDAVKFFVAVPGQVISQSS	+	-	-
127	KKMKTSESSTILVVRYYRNV	-	-	+
129	AEIQALTLFLSSDYLSRVYLP	-	-	-
130	RIQVEHPQMTFGRLHRIIPK	+	-	+
131	VERPQMTFGRLQGIFPKIMP	+	-	-
132	QRPQMTFGRLQGIFPKIMP	+	-	-
133	SEKIVYVYMKLNYEVMTKLG	-	+	-
134	NQVEHPQMTFGRLQGIFPKI	-	-	-
135	EFEETAKKVRRAIEQLAAMD	-	-	-
142	LSQFWEFSETTASTVSTTLH	-	-	-
149	EELQKVQFEKVSALADLSST	+	+	-
155	VGILHLGSRQKKIRIQLRSQ	-	-	-

Example 18 - Selection of polynucleic acids for treatment of cancer

Some peptides that are difficult to manufacture and use as peptide vaccines can still be used in vaccines and immunotherapy if delivered to patients as peptide-encoding polynucleic acids or vectors. To optimally design a set of peptides for treating cancer to be encoded by a nucleic acid or vector for administration to patients, the method of Example 16 was repeated but without eliminating hotspot sequences that did not meet the peptide manufacturing feasibility requirements. Table 28 shows the hotspot sequences identified in the first 20 cycles and the TSA of which they are a fragment.

Table 28 - Hotspot Sequences and corresponding TAA

Cycle	SEQ ID NO	AA Sequence	Source antigen(s) and AA position	Cycle	SEQ ID NO	AA Sequence	Source antigen(s) and AA position
1	2787	AGDGRRLRLALVLLGWVS	5T4 [11-30]	19	4110	PFKCSMCKYASVEASKLKRH	CTCFL [341-360]
1	2788	ELLHTFLRWKTSYLVLRPHD	ADAM2 [245-264]	19	4111	DSLCPQVINAALTLAARQS	CTNNA2 [456-475]
1	2789	NKTLGTFSTIAVAHHLGHNLG	ADAM29 [320-339]	19	4112	FYEHIITVGTGGSGLLFYDI	DCAF12 [348-367]
1	2790	IARRHPFLYAPTILLWAARY	AFP [166-185]	19	4113	HGRLLSADTKGWVRLQFHAG	DPPA2 [227-246]
1	2791	MAARAVFLALSAQLLQARLM	BAGE-1 [1-20]	19	4114	NRQCQCTSVGAQNTVICSKL	EPCAM [43-62]
1	2792	MAAGVVFLALSAQLLQARLM	BAGE-2 [1-20]; BAGE-3 [1-20]	19	4115	CSPGFFKFEASESPLECPE	EPHA2 [276-295]
1	2793	MAAGAVFLALSAQLLQARLM	BAGE-5 [1-20]	19	4116	GDFQEAMTHLQHKLICTRKP	FAM46D [209-228]
1	2794	YKDAYKFAADVRLFMNICYK	BRDT [331-350]	19	4117	PQDQSCWAFPLDLCLCRVFW	FBXO39 [10-29]
1	2795	ASQLASKMHSLALMVGLLT	CAGE1 [610-629]	19	4118	EQLKCLLDECILKQKSIKIL	FSIP1 [406-425]
1	2796	WAICMLRVALATVYFQEEFL	CALR3 [9-28]	19	4119	HEIFNLLSFTLNPLEGKLQQ	GASZ [228-247]
1	2797	PEVLHMIYMRALQIVYGIRL	CDCA1 [42-61]	19	4120	FSHSSHMLTTPMPHPPSSL	GATA-3 [410-429]
1	2798	PCEYYFRVYHSLCPISWVES	COX6B2 [55-74]	19	4121	SSRRRELIQKLKSFISFYSA	Glypican-3 [385-404]
1	2799	EAARCMRRDFVKHLKKLKR	CT45 [168-187]	19	4122	LHDPSGYLAEDLSYTWDFG	gp100 [244-263]
1	2800	LIRKIYILMQNLGPLNDVC	CT46 [153-172]	19	4123	CYVNDIVLAILELLKYHQRV	HDAC1 [151-170]
1	2801	HFVLLDMVHSLHRLSHNDH	CT47 [120-139]	19	4124	YGAGHPMKPHRLALTHSLVL	HDAC3 [18-37]
1	2802	NYIDQFLTSFPTFTSVGVL	CTAGE1 [34-53]	19	4125	IGTGAVIIIFCIALILGAFF	IGFS11 [247-266]
1	2803	FFAVLFLWRSFRSVTSRLYV	CTAGE2 [23-42]	19	4126	CTNGSEVQSSWAETTYWISP	IL13RA2 [113-132]
1	2804	HCDVCMFTSSRMSSFNRMK	CTCFL [258-277]	19	4127	MPKTGFLIIVLVMIAEGGH	MAGE-A1 [189-208]
1	2805	MNFYLLASSILCALIVFWK	CXorf61 [1-20]	19	4128	NMMGLYDGMELIYGEPRKL	MAGE-A10 [251-270]
1	2806	AATVPATAAGVVAVVVPVPA	DBPC [15-34]	19	4129	LGLVGAQALQAEQEAAFFS	MAGE-A11 [133-152]
1	2807	WVPTTHRRMISLFLLPACIF	DPPA2 [249-268]	19	4130	FTKAEMLGSVIRNFQDFFPV	MAGE-A12 [130-149]
1	2808	CSERVRTYWIIELEKHKARE	EPCAM [135-154]	19	4131	LLGDNQVMPKTGLLIIVLAI	MAGE-A2 [189-208]
1	2809	QYTEHFMAAGYTAIEKVVMQ	EPHA2 [920-939]	19	4132	LVHFLLKRYRAREPVTKAEM	MAGE-A3 [116-135]

1	2810	YQPAPYFAAEARYPIYVPE	FAM46D [349-368]	19	4133	LLGDNQIMPKTGFLIIILAI	MAGE-A6 [189-208]
1	2811	ETLIIIAVLVSASIANLWLWM	FATE1 [162-181]	19	4134	HAETSYEKVINYLVMNLARE	MAGE-A9 [277-296]
1	2812	CSGSSYFVLANGHILPNSN	FMR1NB [91-110]	19	4135	DPPRFQFLWGPAYAEATSKM	MAGE-B2 [267-286]
1	2813	TLLEYTSYLYLSMAFYFNRD	FTHL17 [26-45]	19	4136	DGNQSSAWTLPRNGLLMPLL	MAGE-B4 [186-205]
1	2814	TGILWLLMNNCFNLSPRKP	GAGE-1 [119-138]	19	4137	SILKADMLKCVRRYKPYFP	MAGE-B6 [215-234]
1	2815	SVDSNFQYGTPLMYAASVA	GASZ [71-90]	19	4138	DYFPVILKRAREFMELLFGL	MAGE-C2 [176-195]
1	2816	FEFVGEFFTDVSLYILGSDI	Glypican-3 [142-161]	19	4139	GSAATWGQDVTSPVTRPAL	MUC-1 [89-108]
1	2817	GKTLCYLMPGFHVLQPSL	HAGE [291-310]	19	4140	NVSCNQLDGTGPLLCEALCS	NLRP4 [757-776]
1	2818	AKCVEFVKSFNPLMLLGGG	HDAC1 [282-301]	19	4141	PLGTPMLIEDGYAVTQAEFL	NR6A1 [265-284]
1	2819	EASGFCYVNDIVLAILELLK	HDAC2 [147-166]	19	4142	AVTCGFHHIHEQIMEYIRKL	NY-BR-1 [189-208]
1	2820	GECVEYVKSFNIPLLVLGGG	HDAC3 [277-296]	19	4143	AEMDGAATAKQVMALKDTIG	ODF2 [214-233]
1	2821	ALINLNVIMVMTPLSNANQP	IGFS11 [51-70]	19	4144	PMVMGPNTVGKASQPSFSIK	ODF3 [145-164]
1	2822	GYLGYLYLQWQPPLSLDHFK	IL13RA2 [44-63]	19	4145	AVFQCAQCHAVLADSVHLAW	OIP5 [76-95]
1	2823	CDDSYHTFCLIPPLHDPKG	JARID1B [330-349]	19	4146	GFMITLSTDGVIICVAENIS	PASD1 [43-62]
1	2824	DDAAPRVEGVPVAVHKHALH	KAAG1 [3-22]	19	4147	ADIFAFGLTLWEMMTLSIPH	PBK [228-247]
1	2825	CPDESWALKAEALSGKIEL	KOC1 [44-63]	19	4148	TFKLCHMYWNWPGTIRVPAP	PIWIL2 [924-943]
1	2826	GIFIIIVFVYLTVENKSLFG	LEMD1 [162-181]	19	4149	NNFTLAFIVVKRINTRFFL	PIWIL3 [752-771]
1	2827	KYSAHAFQFSPRNVLWLLV	LIP1 [13-32]	19	4150	IPQHKLSLWPGFAISVSFE	PIWIL4 [235-254]
1	2828	VDPTGHSFVLVTSGLTYDG	MAGE-A10 [194-213]	19	4151	FDECGITDDQLLALLPSLSH	PRAME [385-404]
1	2829	VALSRKMAELVHFLLLKYRA	MAGE-A12 [107-126]	19	4152	AMNFDFFPKKSGIPLLTN	RAGE-1 [234-253]
1	2830	FRAALSKKVADLIHFLLLKY	MAGE-A5 [105-124]	19	4153	LEEDLQIATKTCQLTEEKE	SCP-1 [341-360]
1	2831	VKDPVAWEAGMLMHFILRKY	MAGE-B1 [104-123]	19	4154	SCHSFQSAAYLIVDRDEAWVL	SCRN1 [149-168]
1	2832	WTLPRNGLLMPLLSVIFLNG	MAGE-B4 [193-212]	19	4155	CCSLDLMLKKIKGKDLQLE	se57-1 [85-104]
1	2833	FLWGPAYAEATTMRVLRVL	MAGE-B6 [357-376]	19	4156	KATEYLVIIIGASEFLPIYLE	SLCO6A1 [392-411]
1	2834	RRRNGYRALMDKSLHVGTC	MART1 [49-68]	19	4157	GSDQHVASHLPLHPIMHNKP	SOX-6 [32-51]
1	2835	PARWSFRAYTSVLYFNPWMR	MORC1 [232-251]	19	4158	GDTFLLLIQSLKNNLIEKDP	SPAG1 [847-866]
1	2836	VFCLTVVCWTWVPLRGFSSP	NA17-A [12-31]	19	4159	KSDSPKSAQKFSILKILSM	SPO11 [101-120]
1	2837	NQKICIFVNHSTAPYSVKNK	NXF2 [189-208]	19	4160	NQEKLCMLTAEALLEYCNAPK	TDRD1 [965-984]
1	2838	NTALHYAVYSEILSVVAKLL	NY-BR-1 [84-103]	19	4161	PVWGLQLLPLLLPSFIHFS	TEX101 [230-249]
1	2839	MVILTILAIAPSPVFAANCF	NYD-TSPG [348-367]	19	4162	LKRLSSFIGAGSPSLVKACD	TEX14 [1285-1304]
1	2840	SRLLFYLAMPFATPMEAEEL	NY-ESO-1 [85-104]	19	4163	LSKPIFCFVKDVHPDLEMND	TEX15 [2511-2530]
1	2841	CLCDYKLYCLRPSLRLERK	ODF1 [74-93]	19	4164	SRAAQMAVPSSRILQLSKPK	THEG [256-275]
1	2842	LRAPAYSFRGAPMLLAENCS	ODF3 [46-65]	19	4165	IALQEKESIEIQLLKEHLCLA	TSGA10 [583-602]
1	2843	IPVGPHLYSTHAALALRGH	OIP5 [142-161]	19	4166	AGCQKSEAPPIYLQVSSYQH	TSP50 [332-351]

1	2844	FPTYDYFNQVTLQLLDGFMI	PASD1 [27-46]	19	4167	ALLAGLVSLLCRHKKQLPE	TYR [490-509]
1	2845	ASQDPFPAAIILKVALNMAR	PBK [133-152]	19	4168	PVETKAHFDSSPQLLWDCD	ZNF165 [165-184]
1	2846	EMELWMKAMLDAAALVQTEPV	PEPP2 [255-274]	20	4169	PILPPSLQTSYVFLGIVLAL	ST4 [346-365]
1	2847	PAPCQYAHKLAFLVGQSIHR	PIWIL1 [829-848]	20	4170	FESFCQFTHYRCSNHVYYAK	ACRBP [100-119]
1	2848	MRSVVGFFVASINLTITKWYS	PIWIL2 [754-773]	20	4171	CDRCLFQLETVAVTQMKNK	ACTL8 [193-212]
1	2849	PAPCHYAHKLAYLVGQSIHQ	PIWIL3 [850-869]	20	4172	KMCDANYAGGVVLHPRTISL	ADAM2 [285-304]
1	2850	LNKQGMMSIATKIAMQMT	PIWIL4 [582-601]	20	4173	CSQPRCIMHEGNPPITKFSN	ADAM29 [349-368]
1	2851	LCSIDWFMVTVHPFMLNNDV	PLAC1 [29-48]	20	4174	TLHRNEYGIASILDSYQCTA	AFP [20-39]
1	2852	HLERLAYLHARLRELLCELG	PRAME [456-475]	20	4175	DILCPKAKRTSRFLSGIINF	CDCA1 [108-127]
1	2853	NASGAHALQAAAAILALLPA	PSCA [84-103]	20	4176	APPWEQDYRMFPFPGQSYP	CTAGE2 [565-584]
1	2854	EKKIMHYMYQLCKSLDHIHR	RAGE-1 [102-121]	20	4177	KGAGTFFHCDVCMFTSSRMS	CTCFL [251-270]
1	2855	PTGLINMAATPIPAMSARDL	SAGE1 [179-198]	20	4178	PHCRDEMAAARGALKKNATM	CTNNA2 [200-219]
1	2856	KRCQHAKIAEMVALMEKHKHQ	SCP-1 [701-720]	20	4179	TKCNTLFVVDVQTSQITKIP	DCAF12 [107-126]
1	2857	QVPRTYAIMISRPALWGAE	SCRN1 [61-80]	20	4180	KVCRDTRLRWDQCQLGLSTNG	DPPA2 [94-113]
1	2858	YKLPLFIAFIFSTLIFSGFS	SLCO6A1 [576-595]	20	4181	SKLAAKCLVMKAEMNGSKLG	EpCAM [60-79]
1	2859	EEAVMYTTRSISALPTVVAY	SPAG1 [226-245]	20	4182	ERYMCSRFFIDFPHIEBQQK	FAM46D [259-278]
1	2860	TGKLGFSFVRITAMVSCNR	SPAG9 [1138-1157]	20	4183	WASPQNFTSVCEELVNNVED	GASZ [392-411]
1	2861	VEHPQMTFGRHLRIIPKIMP	SSX-1 [94-113]	20	4184	IDKYWREYILSLEELVNGMY	Glypican-3 [292-311]
1	2862	EKIVVYVMKLNVEVMTKLG	SSX-4 [44-63]	20	4185	GTATLRLVKRQVPLDCVLYR	gp100 [460-479]
1	2863	EHPQMTFGRHQGIFPKITPE	SSX-5 [95-114]	20	4186	HYGLYKKMIVFKPYQASQHD	HDAC3 [38-57]
1	2864	PHPGTVISHSVAMLILIGSL	TAG-1 [1019-1038]	20	4187	GRQCVEHYRLHRYCVFSDH	JARID1B [611-630]
1	2865	LPASTLSRLSNRLLRLLECN	TAG-2a [37-56]	20	4188	TGAVGMACAISILLKDLADE	LDHC [28-47]
1	2866	YLPGRYRLNSWRPSLFYKIA	TEKT5 [40-59]	20	4189	GASLDNFHFIGVSLGAHISG	LIPI [168-187]
1	2867	AMIGCRMLSGILAVGPMFVR	TEX101 [187-206]	20	4190	LESFRAVITKKVADLVGFL	MAGE-A1 [94-113]
1	2868	LTGATQMAVGLSPLVIGEKE	TEX14 [221-240]	20	4191	AQIACSSPSVVASLPLDQSD	MAGE-A10 [87-106]
1	2869	TLYFYKFFLPTILSLSFFIL	TMEM31 [132-151]	20	4192	LGDNQIVPKTGLLIIVLAI	MAGE-A12 [190-209]
1	2870	GFLEKEFYHKTNIKMRCEFL	TRAG-3 [18-37]	20	4193	YLQLVFGIEVVVVPISHLY	MAGE-A2 [157-176]
1	2871	APSRTLLALLPLSLALLAAL	TSP50 [366-385]	20	4194	IGHLYIFATCLGLSYDGLLG	MAGE-A3 [172-191]
1	2872	HLCKIMLFFRSNPFQNKVI	TSPY1 [197-216]	20	4195	IWKFMNVLGAYDGEHLIYG	MAGE-B1 [220-239]
1	2873	KGAATKMAAVTAPEAESAPA	VCX [53-72]	20	4196	CATEEKIWEFLNKMRIYDGK	MAGE-B3 [217-236]
1	2874	DVRDLNALLPAVPSLGGGGG	WT1 [4-23]	20	4197	RLSKDAVKKKACTLAQFLQK	MAGE-B6 [189-208]
1	2875	SRQKKIRIQLRSQCATWKVI	XAGE-1 [20-39]; XAGE-1b [20-39]	20	4198	RYTGYPVIFRKAREFIBIL	MAGE-C1 [941-960]
1	2876	CKECGRAFNLNSHLIRHQRI	ZNF165 [402-421]	20	4199	ARWSFRAYTSVLYFNPWMRI	MORC1 [233-252]
2	2877	PTSSASSFSSAPFLASAVS	ST4 [34-53]	20	4200	QSGAGVPGWGIALLVLCVL	MUC-1 [1151-1170]
2	2878	SVWLGASVVAHLSTYQSEWM	ACTL8 [336-355]	20	4201	LVANFEKARRAHWIFLGCF	NLRP4 [484-503]

2	2879	VFQLIGLTNAIFVSFNITII	ADAM2 [205-224]	20	4202	QLNKRYWYICQDFTEYKYTH	NR6A1 [413-432]
2	2880	ETFMNKFIYEIARRHPFLYA	AFP [156-175]	20	4203	DQSAYVSAIRDCFPKLLRLD	NXF2 [338-357]
2	2881	SGQMVEHLMNSVMKLCVIA	AKAP-3 [666-685]	20	4204	TRKDCLAKHLKHMRRMYGTS	NYD-TSPG [154-173]
2	2882	AVLQWIAASQFNVPMLYFMG	AKAP-4 [776-795]	20	4205	IDTSNSEAISSSSIQFPIT	PASD1 [656-675]
2	2883	RCIIILVLQEPTAFRISVTS	BAGE-2 [60-79]	20	4206	KELTPTSPDCRLRYNLFRR	PIWIL3 [212-231]
2	2884	SVTSSCFVQNTLTLLKDDR	BAGE-3 [76-95]; BAGE-2 [76-95]	20	4207	LETWGLHFGSQISLTGRIVP	PIWIL4 [431-450]
2	2885	MLAKKHFSYAWPFYNPVDVN	BRDT [283-302]	20	4208	VLPGLAYLATADMPAMSTRD	SAGE1 [366-385]
2	2886	CKVDGFTHLYTLILRPDLSY	CALR3 [163-182]	20	4209	MIGYALGYVLGAPLVKVPEN	SLC06A1 [275-294]
2	2887	CCHPSNFIEAPGHMSDVEW	CCDC62 [515-534]	20	4210	FVRITALMVSNRLVWGTGN	SPAG9 [1145-1164]
2	2888	IRLEHFYMPFVNSEVMYPHL	CDCA1 [59-78]	20	4211	KKLWDTFHVVPVFTLVADDPH	SPO11 [262-281]
2	2889	NCYQNFLDYHRCCLKTRTRRG	COX6B2 [31-50]	20	4212	EDVPLAAKLVDLPCVIESLR	TAFTL [145-164]
2	2890	VGHYTLVWYSTYQVCGIA	CRISP2 [134-153]	20	4213	GYVDYGNFEILSLMRLCPII	TDRD1 [575-594]
2	2891	PTAVRKRFESIIKEARCM	CT45 [154-173]	20	4214	QDTLQLLVMTKCRLEHELAI	TEKT5 [437-456]
2	2892	HAAARNLWGNLPPLLPQRL	CT47 [155-174]	20	4215	AFCELQTYHDQLVELLEETK	TEX15 [1755-1774]
2	2893	MFVILSLHNCVVISFVLF	CTAGE1 [1-20]	20	4216	IKLLRNIPRWTHLLRLRLI	TPTE [181-200]
2	2894	VRREKKFAVALSGLIEEKCK	CTAGE2 [42-61]	20	4217	WVLTVAHCLIRWDVIVSRV	TSP50 [147-166]
2	2895	HICHTRTQSGTMKIHLQK	CTCFL [401-420]	20	4218	STPMFNDINIYDLFVWMHY	TYR [163-182]
2	2896	HISDSFLETNVPLLVIEAA	CTNNA2 [387-406]	20	4219	PFMCAYPGCNKRYFKLSHLQ	WT1 [322-341]
2	2897	MLRLLRLALAFYGRADPAE	CXorf48 [1-20]	20	4220	HDGCERRLNLSNEFTHQKS	ZNF165 [272-291]
2	2898	RWCPPFFYRRRFVRGRPP	DBPC [222-241]	1	4221	VESTPMIMENIQELIRSAQE	ACRBP [275-294]
2	2899	VLAFLGLLLAAATATFAAAQE	EpCAM [6-25]	1	4222	LNWEGVQYLWSFVLENHRRE	ACTL8 [73-92]
2	2900	WDLMQNIMNDMPIYMSVCN	EPHA2 [52-71]	1	4223	DEVSFYANRLTNLVIAMARK	AKAP-3 [122-141]
2	2901	VPKQMMQMFGLGAISLILVC	FMR1NB [180-199]	1	4224	IDDLSFYVNRSLSLVIQMAH	AKAP-4 [214-233]
2	2902	ACGLYYKLHNINRPLTMKKE	GATA-3 [341-360]	1	4225	RTKKELASALKSALSGHLET	ANXA2 [78-97]
2	2903	IQKLKSFISFYALPGYICS	Glypican-3 [392-411]	1	4226	PSNINQFAAAYFQELTMYRG	CABYR [30-49]
2	2904	LLVLMVAVLASLIYRRRLMK	gp100 [603-622]	1	4227	SPASELIAIQDSHSLGSSKS	CCDC62 [566-585]
2	2905	NDLQMSNFVNLKNITYLVLD	HAGE [377-396]	1	4228	BGKDPAFALTTLTQLQVQRE	CRISP2 [20-39]
2	2906	ASGFCYVNDIVLAILELLKY	HDAC1 [147-166]	1	4229	FAVLFFLWRSFRSVRSRLVY	CTAGE5 [53-72]
2	2907	GAESGRYYCLNVPLRDGIDD	HDAC3 [210-229]	1	4230	KKNATMLYTASQAFLRHPDV	CTNNA2 [214-233]
2	2908	TVTIRNISALSSGLYQCVAS	IGFS11 [199-218]	1	4231	NEDNIYISNSIYFSIAIVSE	CXorf48 [122-141]
2	2909	YKLRYYRTLDDLYPMMNALK	JARID1B [730-749]	1	4232	SRVLHGYYAAQQLPSLLKERE	DCAF12 [64-83]
2	2910	LHDGLRQVAGPGAAAHLPR	KAAG1 [21-40]	1	4233	NLLRGIDSLFSAPMDFRGLP	DKKL1 [63-82]
2	2911	GTGAVGMACAISILLKDLAD	LDHC [27-46]	1	4234	IAERQVRMAAQVALRRQQAQ	DMRT1 [108-127]
2	2912	STRKLYBKLVQLLVSPPCA	LEMD1 [29-48]	1	4235	KRDNRVAYMNPAMARWRGP	FAM133A [3-22]

2	2913	DYFPEIFREASVCMQLLFGI	MAGE-A11 [258-277]	1	4236	EHLEVKFMNPYNAVLTKKFQ	FBXO39 [90-109]
2	2914	FQDFFPVIFSKASEYLQLVF	MAGE-A12 [143-162]	1	4237	ISDTKDYFMSKTLGIGRLKR	FSIP1 [515-534]
2	2915	PPQSPQGASALPTTISFTCW	MAGE-A4 [62-81]	1	4238	MSWRGRSTYRPRRRYVEPP	GAGE-2 [1-20]; GAGE-1 [1-20]; GAGE-8 [1-20]
2	2916	LKSPQGASAIPTAIDFTLWR	MAGE-A5 [62-81]	1	4239	SRGKSTYYWPRRRYVQPPE	GAGE-3 [4-23]
2	2917	FLWGPRAYAETSKMKVLEFL	MAGE-B2 [273-292]	1	4240	WRGRSTYYWPRRRYVQPPE	GAGE-6 [3-22]; GAGE-7 [3-22]
2	2918	PREDAHFIYGYPKKGHGSY	MART1 [2-21]	1	4241	ALSRHMSSLSHISPFSSSH	GATA-3 [396-415]
2	2919	KFRPGSVVVQLTLAFREGTI	MUC-1 [1093-1112]	1	4242	DGKNKHFLRNQPLTFALQLH	gp100 [226-245]
2	2920	MVLPDVFIRCVVFLTVVCW	NA17-A [1-20]	1	4243	KKVNFDMSLDDIIYKELE	HOM-TES-85 [21-40]
2	2921	QYIPHLFSYSGHSPLLPQQA	NR6A1 [224-243]	1	4244	IQNHDIMHAISPLRSANTV	KU-CT-1 [435-454]
2	2922	GQSQGSVLAFTRTFIATPGS	NXF2 [509-528]	1	4245	PDSRLQLHITMPFSSPMEA	Lage-1 [83-102]
2	2923	LLKEFTVSGNILTIRLTAAD	NY-ESO-1 [122-141]	1	4246	QRNVAIMKSIIPAIHVHSPD	LDHC [111-130]
2	2924	EKDVTYSYGLGSCVKIESPC	ODF1 [183-202]	1	4247	VKVLEYVIKVSARVRFFFPS	MAGE-A1 [277-296]
2	2925	PPTTGMKHTPTKLRAAYS	ODF3 [33-52]	1	4248	DPTSHSYVLVTSNLNSYDGI	MAGE-A11 [283-302]
2	2926	SNRIHTSAHVMSGLLHFYK	ODF4 [121-140]	1	4249	GREDSVFAHPRKLLMQDLVQ	MAGE-A2 [233-252]
2	2927	SLGAVVFSRVTNVLEAPF	OIP5 [100-119]	1	4250	FPVIFSKASSSLQLVFGIEL	MAGE-A3 [147-166]
2	2928	DGPDTRKRVCLRNEEQMKLPA	PAGE1 [77-96]	1	4251	VNARVRIAYPSLREAALEE	MAGE-A4 [294-313]
2	2929	GLTLWEMMTLSIPHINLSND	PBK [234-253]	1	4252	KKLLTQYFVQENYLEYRQVP	MAGE-A6 [243-262]
2	2930	NRKYAFKAAHPNMRTYYFCT	PEPP2 [231-250]	1	4253	RAPEEAIWEALSVMGLYDGR	MAGE-A8 [218-237]
2	2931	GKQQTVMIAIKIALQMNCCK	PIWIL1 [592-611]	1	4254	PAQLEFMFQEALKKVAELV	MAGE-A9 [97-116]
2	2932	CLRYYNILFRRTFKLLDFEQ	PIWIL3 [221-240]	1	4255	SSDPFRFQFLWGPRAYETS	MAGE-B2 [265-284]
2	2933	YFERKLLFSADVSQVLRNE	PIWIL4 [252-271]	1	4256	LIMKTNMLVQFLMEMYKMKK	MAGE-B3 [111-130]
2	2934	FKFIGLMILTSAFSAGSGQ	PLAC1 [4-23]	1	4257	RPVSSFFSYTLASLLQSSHE	MAGE-C1 [777-796]
2	2935	RHSQTLKAMVQAWPFTCLPL	PRAME [64-83]	1	4258	ATVMASESLSVSSNVSFSE	MAGE-C2 [354-373]
2	2936	PGSPRWLLLCPLSHVLFRA	PRSS55 [330-349]	1	4259	EIYNEYIYDLFVPVSSKFQK	MPHOSPH1 [277-296]
2	2937	MAGLALQPGTALLCYSCKAQ	PSCA [1-20]	1	4260	GVSFFFLSFHISNLQFNSSL	MUC-1 [1039-1058]
2	2938	QVRGGMVFELANSIVLPFDC	PSMA [578-597]	1	4261	EEAFSRASLVSVNSYPYYP	NKX3.1 [202-221]
2	2939	AASDNVSTVPPAFINMAAT	SAGE1 [592-611]	1	4262	SLLRKKMLPEASLLIAIKPV	NLRP4 [263-282]
2	2940	EDANSCHSFQSAYLIVDRDE	SCRN1 [145-164]	1	4263	IERLIYLYHKFHQLKVSNEE	NR6A1 [369-388]
2	2941	LWTWWINFLFAAVVAWCTLI	SLCO6A1 [311-330]	1	4264	ADKDLYVAEALSTLESWSR	ODF2 [428-447]
2	2942	QFIPSTMAAAAAGLSPLQL	SOX-6 [306-325]	1	4265	NSPLPFQWRITHSFRWMAQV	ODF4 [63-82]
2	2943	KGIVLVALADGTLAIFHRGV	SPAG9 [1010-1029]	1	4266	MGFLRLRIYRRRPMIYVESS	PAGE1 [1-20]
2	2944	MIITTWIVYILARKGVGLPF	SPATA19 [1-20]	1	4267	GPDMEAFQQELALLKIEDEP	PAGE2 [65-84]
2	2945	DSILRRPYVTCQPFWRKEME	SPO11 [340-359]	1	4268	RGDQGEAPDVVAFVAPGESQ	PAGE4 [12-31]

2	2946	FLKDHRISTFKNWPFLEGCA	Survivin [13-32]	1	4269	GTDVEAFQQELALLKIEDAP	PAGE5 [84-103]
2	2947	VTGYKMLYQNDLHLTPTLHL	TAG-1 [944-963]	1	4270	KNTPGIYTSLVNYNLWIEKV	PRSS55 [279-298]
2	2948	ECNVVIAHCNLEPLVSRDP	TAG-2a [54-73]	1	4271	SNPIVLRMMNDQLMFLERAF	PSMA [656-675]
2	2949	IPVWGLQLLLPLLLPSFIHF	TEX101 [229-248]	1	4272	GSTGFSSRLAATQDLFPFIHQ	RCAS1 [123-142]
2	2950	EPTFSFFSGPYMVMTNLVWN	TEX14 [247-266]	1	4273	KDSITVFVSNLPYSMQEPDT	SART3 [701-720]
2	2951	GLPIILHLFALSTLYFYKFF	TMEM31 [120-139]	1	4274	KLNQEYSQQFLTLFQQWDL	SCP3a [120-139]
2	2952	KIKKIVHSIVSSFAFLFGV	TPTE [80-99]	1	4275	TSELKTEGVSPYLMILRLRK	se57-1 [316-335]
2	2953	IKMRCEFLACWPAFTVLGEA	TRAG-3 [30-49]	1	4276	KERQLSTMITQLISLREQLL	SOX-6 [187-206]
2	2954	QNYSSNAYHMSSTMKPNTKC	TSGA10 [651-670]	1	4277	PDNIPAFAAAYFESLLEKRE	SP17 [32-51]
2	2955	IWRDIDFAHEAPAFLPWHRL	TYR [194-213]	1	4278	KKMKTSESSTILVVYRRNV	SPAN-Xc [40-59]
2	2956	ASSGQARMFPNAPYLPSCLE	WT1 [120-139]	1	4279	TRIQFIRWSHTRIFQVPSEM	SPATA19 [112-131]
2	2957	KKIRIQLRSQCATWKVICKS	XAGE-1c [102-121]	1	4280	AEIQALTFLSSDYLSRVLYP	SPO11 [368-387]
3	2958	LRRLELASNHFLYLPRDVL	5T4 [212-231]	1	4281	VERPQMTFGRLLQGISKIMP	SSX-2 [94-113]
3	2959	CDTDYIQYPNYCSFKSQCL	ACRBP [477-496]	1	4282	QRPQMTFGRLLQGIFPKIMP	SSX-3 [95-114]
3	2960	WNEPQMVFPNIVNYLPCKEN	ACTL8 [22-41]	1	4283	EFEETAKKVRRAIEQLAAMD	Survivin [123-142]
3	2961	RYIENIYHSPMRWPFLLFI	ADAM2 [674-693]	1	4284	LFLRSQEAATVQLFQEEHR	SYCE1 [229-248]
3	2962	PRCIIILVLQEPTPFRISVT	BAGE-3 [59-78]	1	4285	ESGQYRANEGTSSIVMEIQK	TAF7L [377-396]
3	2963	ECIEDFNTMFSNLYLNKPG	BRDT [93-112]	1	4286	SSEVLEYMNQLSASLKETYA	TDRD1 [285-304]
3	2964	EACRETYMEFLWQYKSSADK	CDCA1 [132-151]	1	4287	GKINQNYASIIIEAFKPKD	TEX15 [368-387]
3	2965	TRRGKSTQPCYYFRVYHSL	COX6B2 [47-66]	1	4288	VSRAAQMAVPSSRILQLSKP	THEG [255-274]
3	2966	NQDSLKYVVCYCPAGNNM	CRISP2 [157-176]	1	4289	DLDLTYVTERI IAMSFPSSG	TPTE [236-255]
3	2967	ECYQKFVKYTNNGPLMDFIS	CT46 [113-132]	1	4290	BELQKVQFEKVSALADLSST	TSGA10 [492-511]
3	2968	VVARRYPASGIHFVLLDMVH	CT47 [109-128]	1	4291	HNRESYMPFFIPLYRNGDFF	TYR [420-439]
3	2969	WELVIRAAVAGFFAVLFLWR	CTAGE2 [12-31]	1	4292	QTPGINLDLGSVKVKIIPK	XAGE-1c [125-144]; XAGE-1 [46-65]; XAGE-1b [46-65]
3	2970	CNDCNMAFVTSGLVLRHRY	CTCF [315-334]	1	4293	SRQKKIRIQLRSQVLGREMR	XAGE-1d [20-39]
3	2971	SSILCALIVFWKYRRFQRNT	CXorf61 [9-28]	1	4294	MSWRGRSTYRPRRSLQPP	XAGE-2 [1-20]
3	2972	ADKPVLAIQVLGTWKFNVR	DBPC [85-104]	1	4295	MIWRGRSTYRPRRSPVPP	XAGE-3 [1-20]
3	2973	VLLLLLSTLVIPSAAPIDH	DKKL1 [16-35]	2	4296	SHKTPFVSPLLASQSLSIGN	ACRBP [399-418]
3	2974	CKKCNLIAERQVMAAQVAL	DMRT1 [102-121]	2	4297	RIVEIVVIDNYLYIRYERN	ADAM29 [198-217]
3	2975	TNTVEVITSAPGAMLASWAR	DPPA2 [172-191]	2	4298	STPPSAYGSVKAYTNFDAER	ANXA2 [18-37]
3	2976	MNDMPIMYSVCNVMMSGDQD	EPHA2 [59-78]	2	4299	QLLQARLMKEESPVVSRL	BAGE-1 [13-32]; BAGE-2 [13-32]; BAGE-3 [13-32]; BAGE-5 [13-32]
3	2977	IWILLFVCYYLSYYLCSGSS	FMR1NB [76-95]	2	4300	AKYSSVYMEAEATALLSDTS	CABYR [372-391]

3	2978	YYWPRRRYVQPPMIGPMR	GAGE-7 [9-28]	2	4301	ENHPKSMTMPALFKENRND	CAGE1 [756-775]
3	2979	HHPGLSHSYMDAAQYPLPEE	GATA-3 [27-46]	2	4302	ATAQLQRTFMSALVFNKIS	CT46 [2-21]
3	2980	GECKYYSYKGLRSVCVYGGG	HAGE [334-353]	2	4303	ALKKLIHAAKLNASLKTLEG	cTAGE5 [312-331]; CTAGE2 [282-301]
3	2981	ISKVMEMYQPSAVVLQCGAD	HDAC2 [246-265]	2	4304	NTGEMSSNSTALALVRPSSS	CXorf61 [27-46]
3	2982	KPHRLALTHSLVLHYGLYKK	HDAC3 [25-44]	2	4305	GQGSLLFYDIRAQRFLERL	DCAF12 [358-377]
3	2983	AVLPCTFTTSAALINLNVIW	IGFS11 [40-59]	2	4306	TELHPRVAFWIIKLPRRRSH	DKKL1 [161-180]
3	2984	QDMDCVYVNWQYLLCSWKPG	IL13RA2 [141-160]	2	4307	SDSTYYSSFYQPSLFPYYNN	DMRT1 [205-224]
3	2985	QCAGEFVITFPRAVHSGFNQ	JARID1B [573-592]	2	4308	GKKIEVYLRRLHRHAYPEQRQ	DPPA2 [113-132]
3	2986	GVFPAVHKHALHDGLRQVAG	KAAG1 [11-30]	2	4309	EKEKDVRSLSKRKKSYPDD	FAM133A [168-187]
3	2987	PVSGPFLVKTGYAFVDCPDE	KOC1 [28-47]	2	4310	RRQFEFSVDSFQIVLDPMLD	FAM46D [166-185]
3	2988	PDFSMYVYEVTKSILPITNI	KU-CT-1 [721-740]	2	4311	EVMRRQLYAVNRRRLALEEQ	FATB1 [135-154]
3	2989	LHITMPFSSPMEAEVLRIL	Lage-1 [90-109]	2	4312	NLKVNF FERIMKYERLARI	FBXO39 [282-301]
3	2990	PRIETILMMYTRNNLCAEP	LPI [60-79]	2	4313	KLQELSAASPTISSFSRLE	FSIP1 [326-345]
3	2991	DPACYEFLWGPRALVETSYV	MAGE-A3 [265-284]	2	4314	GWESGLVAMESAFHLEKNVN	FTHL17 [93-112]
3	2992	PDPEFVFRALSKKVADLIH	MAGE-A5 [99-118]	2	4315	BEMRSHYVAQTGILWLLMNN	GAGE-1 [109-128]
3	2993	AALSRLVAKLVHFLLLKYRA	MAGE-A6 [107-126]	2	4316	MNLSRGKSTYYWPRRRYVQ	GAGE-3 [1-20]
3	2994	DPAGHSYILVTALGLSCDSM	MAGE-A9 [169-188]	2	4317	MSWRGRSTYYWPRRRYVQP	GAGE-6 [1-20]; GAGE-7 [1-20]
3	2995	ALPKSGLLMSLLVIFMNGN	MAGE-B6 [281-300]	2	4318	EKFKA MTIGDVS LVQELLD	GAS2 [48-67]
3	2996	KVVEFLAMLKNTVPITFPSS	MAGE-C1 [1083-1102]	2	4319	KPHRIRMTNLLNLYGLYRK	HDAC2 [32-51]; HDAC1 [31-50]
3	2997	AGREHFVYGEPRELLTKVWV	MAGE-C2 [260-279]	2	4320	MASFRKLTSEKVPNHPSR	HOM-TES-85 [1-20]
3	2998	IGCWYCRRRNGYRALMDKSL	MART1 [43-62]	2	4321	PIRSSYFTFQLQNIKPLPP	IL13RA2 [222-241]
3	2999	AYTSVLYFNPMRIFIQAKR	MORC1 [239-258]	2	4322	YENDIASMNLQAHLIPGLNL	KOC1 [351-370]
3	3000	LVALAIVYLIALAVCQRRK	MUC-1 [1170-1189]	2	4323	ATVLTNMAMQEPLRLNIQNH	KU-CT-1 [419-438]
3	3001	GSYRKWMCFSSESQVPTQKQ	NA17-A [32-51]	2	4324	GAVLKDFTVSGNLLFMSVRD	Lage-1 [120-139]
3	3002	SLVSVYNSYPYPYLCVGS	NKX3.1 [209-228]	2	4325	AQFYNDFVNISIGLTYFQS	LPI [409-428]
3	3003	ESSYVFLHVCIQEFCAALFY	NLRP4 [445-464]	2	4326	VSARVRFFPSLREAAALREE	MAGE-A1 [286-305]
3	3004	AFREQYMGMSVPPHYQYIPH	NR6A1 [209-228]	2	4327	ESVIRNYEDHFLFLFSEASE	MAGE-A10 [162-181]
3	3005	HTPHKTLMPYASLFQSHSCK	NYD-TSPG [515-534]	2	4328	PDLESEFQAAISRKMVELVH	MAGE-A2 [99-118]
3	3006	LQQLSLLMWITQCFLPVFLA	NY-ESO-1 [153-172]	2	4329	VVGWQYFFPVI FSKASSSL	MAGE-A3 [139-158]
3	3007	CDLHPYPYCLCYSKRSRSCG	ODF1 [47-66]	2	4330	VVGWQYFFPVI FSKASDSL	MAGE-A6 [139-158]
3	3008	RGPIMALYSSPGKYLIPTT	ODF3 [16-35]	2	4331	DGREHSVYWKLRKLLTQEWV	MAGE-A8 [235-254]
3	3009	QCHAVLADSVHLAWDLRSRL	OIP5 [82-101]	2	4332	AHAETSYEKVINYL VMLNAR	MAGE-A9 [276-295]
3	3010	QEDRLYLGVNVCILRTQLLQ	PASD1 [163-182]	2	4333	TEEEIWKFMNVLGAYDGEH	MAGE-B1 [216-235]

3	3011	GFTTSILQYENSIMLCTDVS	PIWIL1 [251-270]	2	4334	TNKKKVSFSSPLILGATIQK	MAGE-B3 [33-52]
3	3012	CIPFYNVVFRVMKLLDMKL	PIWIL2 [319-338]	2	4335	VAARRGTTAMTSAYSRRATSS	MAGE-B4 [321-340]
3	3013	NHVQPHAYQFTYRVTECGIR	PLAC1 [64-83]	2	4336	PQILNRTSQHLVVAFGVELK	MAGE-B6 [234-253]
3	3014	LQHLIGLSNLTHVLYPVPLE	PRAME [427-446]	2	4337	NPASSFFSSALLSIFQSSPE	MAGE-C1 [130-149]
3	3015	CWTARIRAVGLLTVISKGCS	PSCA [39-58]	2	4338	SSASSTLYLVFSPSSFSTSS	MAGE-C2 [40-59]
3	3016	SAGCVFYEIASLQPLFGVN	RAGE-1 [187-206]	2	4339	RSQAGMFIYSNNRLIKMHEK	MORC1 [363-382]
3	3017	MAITQFRLKFCTCLATVFS	RCAS1 [1-20]	2	4340	YEQANLNMANSIKFSVWVSF	MPHOSPH1 [256-275]
3	3018	PNNVLSTVQPVIIYLTATGI	SAGE1 [312-331]	2	4341	PQKRSRAAFSHTQVIELERK	NKX3.1 [123-142]
3	3019	CKALMRFIMVTSVISLILLV	SLCO6A1 [451-470]	2	4342	GINNVVSFGSQSVLLFEVLFY	NLRP4 [673-692]
3	3020	RALELHPFSMKPLLRAMAY	SPAG1 [512-531]	2	4343	KRASQYSQQLKVLIAENTML	NY-BR-1 [1103-1122]
3	3021	SAQKFSILILKILSMIYKLVQ	SPO11 [107-126]	2	4344	WTLRFRFYSYLRSDVDDLLL	NYD-TSPG [322-341]
3	3022	TSEKINMISGVLQRYCRFGS	SSX-3 [147-166]	2	4345	GDGPYSTFLTSSPIRSRSP	ODF2 [809-828]
3	3023	MGAPTLPPAQPFKLDHRIS	Survivin [1-20]	2	4346	NDQESSQPVGSVIVQEPTTE	PAGE2 [16-35]
3	3024	DKKTFYKTADISQMLVCTAD	TAF7L [167-186]	2	4347	MSARVRSRSGRGDQGEAPD	PAGE4 [1-20]
3	3025	LSNRLLLRLCNCVVIHAHCN	TAG-2a [45-64]	2	4348	RGNDQESSQPVGPVIVQQPT	PAGE5 [33-52]
3	3026	ECYQPYLPGYRLNSWRPS	TEKT5 [34-53]	2	4349	NHPVRFLQAQPIVPVQRAAE	PASD1 [599-618]
3	3027	YWTERFLEDITLTITVPAVS	THEG [172-191]	2	4350	LVGRNFYDPTSAMVLQQHRL	PIWIL2 [338-357]
3	3028	PYRLPALFELYPEFLLVFKE	TMEM31 [84-103]	2	4351	TKFKQSRAMNDFPFKKGSG	RAGE-1 [227-246]
3	3029	DVKVQFFYSNLPTYDNCSE	TPTE [475-494]	2	4352	QLEPDYFKDMTPTIRKTQKI	RCAS1 [89-108]
3	3030	ICAGTIIASQWVLTVAHCLI	TSP50 [137-156]	2	4353	KELEELRAAFTRALEYLQKE	SART3 [440-459]
3	3031	LFVWMHYVVSMDALLGGSEI	TYR [175-194]	2	4354	NNNIEKMITAFEELRVQAEN	SCP-1 [215-234]
3	3032	GCNKRYFKLSHLQMHSRKHT	WT1 [329-348]	2	4355	METQQQEIASVRKSLQSMLE	SCP3a [217-236]
3	3033	VICKSCISQTPGINLDLGG	XAGE-1c [117-136]	2	4356	EISILQEIQISHLQFVHSQH	se57-1 [235-254]
3	3034	QILELLVLEQFLTILPGDLQ	ZNF165 [87-106]	2	4357	KEEVAAVKIQAAFRGHIARE	SP17 [113-132]
4	3035	HYRCSNHVYAKRVLCSQPV	ACRBP [108-127]	2	4358	EKDPSLVYQHLLYLKSAERF	SPAG1 [863-882]
4	3036	HVPSVLLADQLQMSLYASGL	ACTL8 [123-142]	2	4359	NPLQMEEBEFMEIMVEIPAK	SPAN-Xc [78-97]
4	3037	CAIVTFMNKTLGTFSIAVAH	ADAM29 [313-332]	2	4360	EKISYVYMKRNYKAMTKLGF	SSX-1 [44-63]
4	3038	LNEELDFLVTSYEEIECAD	CAGE1 [697-716]	2	4361	EWKMKASEKIFYVYMKRKY	SSX-2 [36-55]
4	3039	MARALVQLWAICMLRVALAT	CALR3 [1-20]	2	4362	EKIVYVYMKRKYEAMTKLGF	SSX-3 [44-63]
4	3040	EVMPHLMGFLPFSNLVTH	CDCA1 [72-91]	2	4363	VERPQMTFGSLQRIFPKIMP	SSX-4 [94-113]
4	3041	RVYHSLCPISWVESWNEQIK	COX6B2 [61-80]	2	4364	EKIIYVYMKRKYEAMTKLGF	SSX-5 [44-63]
4	3042	SSDPTSWSSAIQSWYDEILD	CRISP2 [101-120]	2	4365	EPRVEVLINRINEVQAKKK	SYCE1 [50-69]
4	3043	DSPSYQKRQRMALLARKQGA	CT45 [23-42]	2	4366	NLTLKNHFQSVLEQLBELQEK	TAF7L [424-443]
4	3044	VKRLLAHSVSCITYLRGIFP	CT46 [30-49]	2	4367	WAERIMFSDRLSLQLKKTME	TDRD1 [246-265]
4	3045	VISFVLFLFGNNFIQNFYL	CTAGE1 [12-31]	2	4368	TLQEIFQAENTIMLLERSIM	TEKT5 [363-382]

4	3046	SHPYGFFWELVIRAAVAGFF	CTAGE2 [5-24]	2	4369	TLVELQMMMETIQFIENKKR	TEX15 [1689-1708]
4	3047	RPDSNLYGFFWELVICAAV	cTAGE5 [31-50]	2	4370	VTKKVVASPRIISLAKPKVR	THEG [326-345]
4	3048	SPAPARRHLLVLLLLLSTL	DKKL1 [5-24]	2	4371	VIMHSRYRAQRFWSVWGQAN	TSP50 [186-205]
4	3049	SQDSGLVSLSSSSPISNKST	DMRT1 [329-348]	2	4372	DEDEDMLSYMVSLEVGEKHX	TSPY1 [175-194]
4	3050	TSAPGAMLASWARIAARAVQ	DPPA2 [179-198]	2	4373	VAKKGKAVRRGRRGKGAAT	VCX [38-57]
4	3051	ECVCENYKLAVNCFVNNRQ	EpCAM [26-45]	2	4374	KKKNQQLKVGILHLGSRQKK	XAGE-1 [5-24]; XAGE-1b [5-24]; XAGE-1d [5-24]; XAGE-1c [84-103]
4	3052	ESTVCLMSYERRQILHLITM	FAM46D [308-327]	2	4375	PRRSLQPPELIGAMLEPTDE	XAGE-2 [13-32]
4	3053	SHYVAQTGILWLLMNNCFLN	GAGE-1 [113-132]	2	4376	KSFKSPKLAKHAAVFSGDKT	ZNF165 [324-343]
4	3054	LLKERDITLRHLLTMREDEF	GASZ [294-313]	3	4377	IKVKKLLFSKHLPVFTYTDQ	ADAM29 [67-86]
4	3055	SHISPFSSHMLTTPTPMH	GATA-3 [405-424]	3	4378	SGEKNI FLASFVHEYSRRHP	AFP [344-363]
4	3056	ATWPHSVHRLAQSYLKEPMI	HAGE [428-447]	3	4379	SEGIMTYANSVSDMMVSIM	AKAP-3 [282-301]
4	3057	NVARCWTYETAVALDCEIPN	HDAC2 [308-327]	3	4380	DQVNIDYLMNRPQNLRLMT	AKAP-4 [161-180]
4	3058	NVARCWTYETSLVVEAISE	HDAC3 [302-321]	3	4381	RDKVLIRIMVSRSEVDMLKI	ANXA2 [284-303]
4	3059	RQQSKAHRHRHRRGYSRCRS	HOM-TES-85 [62-81]	3	4382	QARLMKEESPVVSWRLEPED	BAGE-1 [16-35]; BAGE-5 [16-35]; BAGE-2 [16-35]; BAGE-3 [16-35]
4	3060	APLLLLSLHGVAASLEVSES	IGFS11 [9-28]	3	4383	QADIEVMSTVHISSVYNDVP	CABYR [282-301]
4	3061	LAIGCLYTFLISTTFGCTSS	IL13RA2 [6-25]	3	4384	SRLEKLLTQVRNLQFMSENE	CAGE1 [507-526]
4	3062	AVHKHALHDGLRQVAGPGAA	KAAG1 [15-34]	3	4385	QTTQNGRFYAI SARFKPFSN	CALR3 [67-86]
4	3063	HVKKGIFYHRALLFKALADR	KU-CT-1 [789-808]	3	4386	TVFGKSVITLSSI FTKDLV	CCDC62 [385-404]
4	3064	WREEGFPVGLKLAVLGIFII	LEMD1 [147-166]	3	4387	GQKYEKI FEMLEGVQGPTAV	CT45 [138-157]
4	3065	PEEVIWEALNMMGLYDGMH	MAGE-A10 [242-261]	3	4388	GNNFIQNFYLPQNYIDQFLL	CTAGE1 [22-41]
4	3066	KIIDLVHLLLRKYRVKGLIT	MAGE-A11 [225-244]	3	4389	TERLLKMKDWAAMLGEDITD	cTAGE5 [268-287]
4	3067	PACYEFLWGPRALVETSYVK	MAGE-A12 [266-285]	3	4390	SVKRGTMVRAARALLSAVTR	CTNNA2 [117-136]
4	3068	DPIGHLYIFATCLGLSYDGL	MAGE-A3 [170-189]	3	4391	RNGVIDYTIFFTLDSVKLPD	CXorf48 [188-207]
4	3069	PACYEFLWGPRALIETSYVK	MAGE-A6 [266-285]; MAGE-A2 [266-285]	3	4392	VKRSLVYYLKNREVRQLNET	DCAF12 [42-61]
4	3070	RVQAAAMLNDGSSAMGRKCS	MAGE-B3 [317-336]	3	4393	PGQTLIYYVDEKAPEFSMQG	EpCAM [244-263]
4	3071	KCVREYKPYFPQILNRTSQ	MAGE-B6 [223-242]	3	4394	NRVAYMNPAMARWRGPTQS	FAM133A [6-25]
4	3072	HSYTTABEAAAGIGILTIVILG	MART1 [19-38]	3	4395	KNLELKVFSSLRQFEFSVD	FAM46D [155-174]
4	3073	GKGKICMIVNISQCYLAYDE	MPHOSPH1 [44-465]	3	4396	GENQEHLVIAEMMELGSRSR	FATE1 [26-45]
4	3074	WSDNKIFRDRFLTYFYCCR	NLRP4 [172-191]	3	4397	SPQFKKTMTFHNLSLNLN	FBXO39 [213-232]
4	3075	RFTPVDFHYVRNACFFVQD	NXF2 [151-170]	3	4398	RPGSRSSNASLEVLSTPGS	FSIP1 [21-40]

4	3076	ILSVVAKLLSHGAVIEVHNK	NY-BR-1 [95-114]	3	4399	DDVALENFFRYFLRLSDDKM	FTHL17 [45-64]
4	3077	AEDWNLYWRTSSFRMTEHNS	NYD-TSPG [118-137]	3	4400	EKDHFSSYTAFGDLEVLH	GASZ [265-284]
4	3078	AADHRQLQLSISSCLQQLSL	NY-ESO-1 [139-158]	3	4401	BQLLQSASMELKFLIIQNAA	Glypican-3 [90-109]
4	3079	LGSKKYSYMNICKEFSLPPC	ODF1 [161-180]	3	4402	TLIGANASFISIALNFPQSQK	gp100 [76-95]
4	3080	ENGKVTFFISTLMLFPINIW	ODF4 [148-167]	3	4403	ATQRDLIATQRDLIVTQRDL	HOM-TES-85 [261-280]
4	3081	GDGPDVREGIMPTFDLTKVL	PAGE2 [85-104]	3	4404	WAIGLSVMDLVGSILKNLRR	LDHC [250-269]
4	3082	NEFPVVFSGFLFSSHLCADFA	PASD1 [139-158]	3	4405	SEELNIIILQGNIIILSTESK	LEM1 [67-86]
4	3083	ILTI PMHFALFYPKRAMDQ	PIWIL2 [598-617]	3	4406	RALABTSYVKVLEYVIKUSA	MAGE-A1 [269-288]
4	3084	YVTSVLQYENSITLCADVSH	PIWIL3 [267-286]	3	4407	DGMEHLIYGEPRKLLTQDWW	MAGE-A10 [257-276]
4	3085	PAPCQYAHKLTFLVAQSIHK	PIWIL4 [820-839]	3	4408	YAGREHFLFGEPRKLLTQNW	MAGE-A11 [344-363]
4	3086	MVTVHPFMLNNDVCVHFHEL	PLAC1 [36-55]	3	4409	PDLETSFQVALSRKMAELVH	MAGE-A12 [99-118]
4	3087	EKEEQYIAQFTSQFLSLQCL	PRAME [279-298]	3	4410	PQGASSFSTTINYTLWRQSD	MAGE-A2 [65-84]
4	3088	SILNKWWILTAACHLYSEEL	PRSS55 [96-115]	3	4411	ETSYVKVLEHVVRVNARVRI	MAGE-A4 [281-300]; MAGE-A8 [283-302]
4	3089	LQPAAILLALLPALGLLLWG	PSCA [91-110]	3	4412	EALDEKVAELVRFLLRKYQI	MAGE-A8 [110-129]
4	3090	VDCTPLMYSLVHNLTKELKS	PSMA [464-483]	3	4413	NSDPTRYQFLWGPAYATT	MAGE-B1 [262-281]
4	3091	ALICELMDMNIYELIRGRY	RAGE-1 [79-98]	3	4414	FPEILKKASEGLSVVGLLEL	MAGE-B2 [149-168]
4	3092	FKFCTCLATVFSFLKRLICR	RCAS1 [9-28]	3	4415	YDGKKHFIFGEPRKLITQDL	MAGE-B3 [233-252]
4	3093	GDPSCVIMQNWARIEARLCN	SART3 [468-487]	3	4416	SSSVLRDTASSSLAFGIPQE	MAGE-B4 [42-61]
4	3094	LLVFIIIFVRCNPVQFAGINE	SLCO6A1 [468-487]	3	4417	ADIKKQABIAHLYIASLPDP	MPHOSPH1 [687-706]
4	3095	NKECAIYTNRALCYLKCQF	SPAG1 [654-673]	3	4418	ASPQETQSAFISIPVSTLSSS	NXF2 [544-563]
4	3096	IRWSHTRIFQVPSEMTEDIM	SPATA19 [117-136]	3	4419	HHIHEQIMEYIRKLSKNHQN	NY-BR-1 [195-214]
4	3097	SWENIKFEDSVGLQMVSHCT	SPO11 [77-96]	3	4420	STNRSMQNYVQFLKSSYANV	ODF2 [788-807]
4	3098	AMTKLGFKVTLPPFMCNKQA	SSX-1 [57-76]	3	4421	LGQDGRLLSSTLSLSSNRSL	ODF4 [39-58]
4	3099	AMTKLGFKATLPPFMCNKRA	SSX-2 [57-76]	3	4422	QAVPAFQGPDMFAFQOELAL	PAGE2 [58-77]
4	3100	AMTKLGFKATLPPFMRNKRV	SSX-5 [57-76]	3	4423	EDPKDRPSAAHIVEALETDV	PBK [303-322]
4	3101	KHSSGCAFLSVKKQFEELTL	Survivin [79-98]	3	4424	GWEEAYTFEGARYYINHNER	PEPP2 [61-80]
4	3102	KAEELAAAAQRHQQLQKQC	SYCE1 [249-268]	3	4425	QKSIAGFVASTNAELTKWYS	PIWIL3 [663-682]
4	3103	PASASLFQDTCAGCASLLHG	TAG-2a [74-93]	3	4426	YIPDLASRRRLRIALLYSHSE	PIWIL4 [130-149]
4	3104	WYRASVLAYASEESVLVGYV	TDRD1 [558-577]	3	4427	DFKRAMDNDIALLLASPI	PRSS55 [147-166]
4	3105	LRPPTILPTLRSALFSRYSP	TEKT5 [72-91]	3	4428	QSGAAVVHEIVRSFGTLKKE	PSMA [389-408]
4	3106	VEVKGCTAMIGCRMMSGILA	TEX101 [180-199]	3	4429	KNPDFKVFYRSTSLKHKLF	SART3 [785-804]
4	3107	IYSFGFGKAMPWFQFYLTGA	TEX14 [205-224]	3	4430	ASLEIELSNLKAELLSVKKQ	SCP-1 [747-766]
4	3108	CGKGYAWISPCMSLHFCLC	THEG [148-167]	3	4431	AKRKRLEMYTKASLTSNQK	SCP3a [87-106]
4	3109	WPTEWIFNRYLPALFELYP	TMEM31 [76-95]	3	4432	DSEFFLTASGVSVLPQNRS	SCRN1 [268-287]

4	3110	LFIKHFIIYSIPRYVRDLKI	TPTE [414-433]	3	4433	MEDNSALYESTSAHIEETE	se57-1 [16-35]
4	3111	NGQALALPAPSRLLLLALPL	TSP50 [358-377]	3	4434	SEPHIKRPMNAFMVWAKDER	SOX-6 [617-636]
4	3112	LLGAAMVGAVLTALLAGLVS	TYR [478-497]	3	4435	SSEEDKEKEEVAAVKIQAAF	SP17 [106-125]
4	3113	EEQCLSAFTVHFSGQFTGTA	WT1 [85-104]	3	4436	REEAQKMSSLLPTMWLGAQN	SPAG9 [959-978]
4	3114	WKVICKSCISQTPGINLDLG	XAGE-1 [36-55]; XAGE-1b [36-55]	3	4437	ESSTILVVRYRRNVKRTSPE	SPAN-Xc [46-65]
4	3115	LHLGSRQKKIRIQLRSQCAT	XAGE-1c [95-114]	3	4438	KGVGLPFLPITSSDIDVVES	SPATA19 [14-33]
4	3116	CEGGTDVKGKILPKAEHFKM	XAGE-2 [82-101]	3	4439	WKKMKYSEKISYVVMKRNYK	SSX-1 [37-56]
4	3117	SECGKTFRVSSHILIRHFRIH	ZNF165 [431-450]	3	4440	EKIFYVVMKRKYEAMTKLGF	SSX-2 [44-63]
5	3118	PTEYERFFALLTPTWKAETT	ACRBP [40-59]	3	4441	EWEKMKSEKIVYVVMKLNLY	SSX-4 [36-55]
5	3119	KMLEILFELLHVPSVLLADQ	ACTL8 [113-132]	3	4442	EWEKMKASEKIIYVVMKRKY	SSX-5 [36-55]
5	3120	ESLAVILAQLLSLSMGITYD	ADAM2 [305-324]	3	4443	KNKQRQLRLAFEEQLEDLMG	SYCE1 [148-167]
5	3121	NITPRMQHDTSHLFTTLGLR	ADAM29 [276-295]	3	4444	GADAQYFVYSNESVRPYTPF	TAG-1 [765-784]
5	3122	EPTAFRISVTSSCFVQNTLT	BAGE-2 [69-88]	3	4445	GDFYVQLYSSEVLEYMNQLS	TDRD1 [277-296]
5	3123	EPTPFRISVTSSCFVQNTLT	BAGE-3 [69-88]	3	4446	LSQFWEFSETTASTVSTTLH	TEX101 [120-139]
5	3124	PSQNQIRNCYQNFLDYHRCL	COX6B2 [24-43]	3	4447	KSDIYSFSMIMQEILTDDIP	TEX14 [436-455]
5	3125	MALLPVLFLVTVLLPSLPAE	CRISP2 [1-20]	3	4448	LKSKYFISTYIDFVPYIAS	TEX15 [2172-2191]
5	3126	TQLVKWMLGCYDALQKKYLR	CT46 [76-95]	3	4449	DQVDWSRLLRDAGLVKMSRK	TRAG-3 [52-71]
5	3127	MVHSLHLRLSHNDHILIENR	CT47 [126-145]	3	4450	MANERISMQNLEALLVANRD	TSGA10 [557-576]
5	3128	LTSFPTFTSVGVLIIVLVLCS	CTAGE1 [41-60]	3	4451	LVNITEYRASHSTPIEWYPD	TSPY1 [221-240]
5	3129	RYCSAVFHERYALIQHKQTH	CTCFL [461-480]	3	4452	AVRRGRRGKGAATKMAAVT	VCX [44-63]
5	3130	AKNLMNAVVLTVKASYVAST	CTNNA2 [869-888]	3	4453	QLKVGILHLGSRQKKIRIQL	XAGE-1d [10-29]; XAGE-1 [10-29]; XAGE-1b [10-29]; XAGE-1c [89-108]
5	3131	VMVESIQFCFIWRAISITPV	CXorf48 [220-239]	3	4454	TPDQKREDDQGAETIQVDDL	XAGE-2 [47-66]
5	3132	MSEVEAAAGATAVPAATVPA	DBPC [1-20]	4	4455	EVRAGAFEHLPSLRQLDLSH	5T4 [132-151]
5	3133	HAMSSQYRMHSYPPPSYLG	DMRT1 [282-301]	4	4456	PHNFRVYSYSGTGIMKPLDQ	ADAM2 [67-86]
5	3134	AVVAGIVVLVISRKKRMAKY	EpCAM [278-297]	4	4457	QKLGEYYLQNAFLVAYTKKA	AFP [420-439]
5	3135	AARACFALLWGCALAAAAA	EPHA2 [5-24]	4	4458	DLRSVFFNFIRNLLSETIFK	AKAP-3 [589-608]
5	3136	GSVASYILASHNGISYKDLL	FAM46D [65-84]	4	4459	LDSQKMDMSNIVMLIQKLL	AKAP-4 [619-638]
5	3137	EQGATWRHRETLIIAIVLVA	FATE1 [153-172]	4	4460	QNKPLYFADRLYDSMKGKGT	ANXA2 [264-283]
5	3138	SCRKLFYFKIWAFLDVSFVE	FBXO39 [364-383]	4	4461	TALDVHVFVSTLEPLSNAVKR	BAGE-2 [37-56]; BAGE-3 [37-56]
5	3139	LEALLNFFFPPTCNLRENQV	FMR1NB [122-141]	4	4462	SEILKEMLAKKHFSYAWPFY	BRDT [277-296]
5	3140	AAINSHITLELYTSYLYLSM	FTHL17 [19-38]	4	4463	AYFQELTMYRGNTTMDIKDL	CABYR [39-58]
5	3141	GPVTAQVVLQAAIPLTSCGS	gp100 [284-303]	4	4464	NSPTSLLIYKDAPAFNEKAS	CCDC62 [600-619]
5	3142	NVARCWTYETAVALDTEIPN	HDAC1 [307-326]	4	4465	BEGNEAANFDLAVVARRYPA	CT47 [97-116]

5	3143	ASGFCYVNDIVIGILELLKY	HDAC3 [141-160]	4	4466	SEAVELQDMSLLSIQQEGV	CTCFL [89-108]
5	3144	KPGIGVLLDTNLYFYWYEG	IL13RA2 [158-177]	4	4467	SSDSSMLDSATSLIQAANKL	CTNNA2 [853-872]
5	3145	LDLLKSEYPVQLLALKTLG	KU-CT-1 [197-216]	4	4468	SNSIYFSSIAIVSEDFVPYKG	CXorf48 [129-148]
5	3146	AQGDGCRGVAFNVMFSAPI	Lage-1 [191-210]	4	4469	PHSIARQKRILVNLMSVENK	CXorf61 [71-90]
5	3147	CTYKIQRMLKSLTYPERPP	LIP1 [436-455]	4	4470	DTKEDVFVHQTAIKRNNPRK	DBPC [114-133]
5	3148	GLVCVQAATSSSSPLVLGTL	MAGE-A1 [24-43]	4	4471	GSEWSVYAVGSQAHVSFLDP	DCAF12 [305-324]
5	3149	AAISRKMVELVHFLLLKYRA	MAGE-A2 [107-126]	4	4472	GIMQFSSHNIIRLEGVISK	EPHA2 [665-684]
5	3150	KTGLLIIVLGTIAMEGDSAS	MAGE-A4 [199-218]	4	4473	RGPTQSVGPTIQDYLNRP	FAM133A [20-39]
5	3151	GGASSSISVYTLWSQFDEG	MAGE-A9 [63-82]	4	4474	SAKRVMNMTATRPKMGSQL	FATE1 [63-82]
5	3152	SWDFPRRKLMLPLLVIFLN	MAGE-B2 [195-214]	4	4475	WRNSIRSSFISLSFLLKMM	FBXO39 [141-160]
5	3153	PGLYPHLYEDALIDEVERAL	MAGE-B6 [384-403]	4	4476	RESLKMVRVKPFGMLMSIW	FMR1NB [58-77]
5	3154	GIGILTVILGVLLIGCWYC	MART1 [29-48]	4	4477	BEEDTFSSVFHTQIPPEEYE	FSIP1 [191-210]
5	3155	NSYPYPYLYCVGSWSPAFW	NKX3.1 [215-234]	4	4478	LSMAFYFNRRDDVALENFFRY	FTHL17 [36-55]
5	3156	AIFYCLFEMQDPAFVKQAVN	NLRP4 [552-571]	4	4479	SMELKFLIIQNAAVFQEAFA	Glypican-3 [97-116]
5	3157	KDYTCLLSSTWQELILLSSL	NR6A1 [314-333]	4	4480	AHSSSAFTITDQVPFVSVS	gp100 [201-220]
5	3158	IDIILNRRNCMAATLKIIE	NXF2 [248-267]	4	4481	GAGKGKYYAVNYPLRDGIDD	HDAC1 [215-234]
5	3159	MYGTSLYQFIPLTFVMPNDY	NYD-TSPG [169-188]	4	4482	RGHYERILNPYNLFLSGDSL	JARID1B [172-191]
5	3160	KRELAKLRRTTNRIASSCC	ODF1 [102-121]	4	4483	QHIKQLSRFAGASIKIAPAE	KOC1 [426-445]
5	3161	SSPGPKYLIPPTTGFMKHTP	ODF3 [24-43]	4	4484	AELVRRILSRDAAPLPRPGA	Lage-1 [102-121]
5	3162	THSFRWMAQVLASELSLVAF	ODF4 [73-92]	4	4485	NLDSARFRYLIGELGVHPT	LDHC [164-183]
5	3163	LRGHFCLSSDKMVCYLKTK	OIP5 [158-177]	4	4486	PDKTMMDGSFSFKLLNQLGM	LIP1 [367-386]
5	3164	GNVCILRTQLLQQLYTSKAV	PASD1 [171-190]	4	4487	FPEIFGKASESLQLVFGIDV	MAGE-A1 [140-159]
5	3165	LWKKRWFVLSDLCLFYRDE	PEPP2 [186-205]	4	4488	QDFFPVIIFSASEYLQLVFG	MAGE-A2 [144-163]
5	3166	VTGNVTAFDGSILYLPVKLQ	PIWIL2 [267-286]	4	4489	NKVDELAHFLLRKYRAKELV	MAGE-A4 [112-131]
5	3167	RELPLLNAMPLHSWLILYSR	PIWIL3 [497-516]	4	4490	TTEEQEAUVSSSSPLVPGTLG	MAGE-A5 [32-51]
5	3168	DVSYKVLNRNETVLEFMTALC	PIWIL4 [262-281]	4	4491	BEQKAASSSSTLIMGTLEEV	MAGE-A8 [34-53]
5	3169	GTPSKFVIPVSCAAPQKSPW	PLAC1 [104-123]	4	4492	VIKNYKRYFPVIFGKASEFM	MAGE-A9 [138-157]
5	3170	RAVGLLTVISKGCSLNCVDD	PSCA [45-64]	4	4493	DNPSGHTYTLVSKLNLTDG	MAGE-B1 [168-187]
5	3171	PSNALSTVLPGLAYLATADM	SAGE1 [359-378]	4	4494	PLTRKSGSLVQFLLYKYKIK	MAGE-B2 [110-129]
5	3172	GNAKYANMWLEYNLERAHG	SART3 [503-522]	4	4495	SLTRKTKMLVQFLLYKYKMK	MAGE-B4 [108-127]
5	3173	VPDKLRSLALGVSYVILRIF	SLCO6A1 [607-626]	4	4496	PVSPFSSTLVSLFQSSPER	MAGE-C1 [271-290]
5	3174	MSIPFSNTHYRIPQGFNLL	SP17 [1-20]	4	4497	VFSPSSFSTSSSLILGGPEE	MAGE-C2 [49-68]
5	3175	IEQVRRSISRLTDVSAQDFS	SPATA19 [140-159]	4	4498	DDPQKFAMELSIIYKYSFPK	MORC1 [159-178]
5	3176	MCYIKYGSMSFEAHLTV	SPO11 [286-305]	4	4499	STEKNAVSMTSSVLSHSPG	MUC-1 [48-67]
5	3177	EHAWTHRLRERKQLVIYEEI	SSX-2 [161-180]	4	4500	VQPTQKQKHLRFHWQANSE	NA17-A [45-64]

5	3178	HKDLWDFHMPERLAKEICAL	SYCE1 [169-188]	4	4501	IWFQNRRYKTKRKQLSSELG	NKX3.1 [170-189]
5	3179	PDEVENQFILRLPLEHACTV	TAF7L [95-114]	4	4502	MKAINFLNQDIRGLTSASQL	NR6A1 [392-411]
5	3180	AQDAGVYQCLASNPVGTVVS	TAG-1 [103-122]	4	4503	EDSERLMEQQGALLKRLAEA	ODF2 [281-300]
5	3181	CNLEPLVSRDPPASASLFQD	TAG-2a [63-82]	4	4504	EKSTKYVFDSPAPSHSISART	ODF3 [109-128]
5	3182	TIQANVLEIISPRLFYALPK	TDRD1 [941-960]	4	4505	SRVTNNVVLEAPFLVGIEGS	OIP5 [107-126]
5	3183	EEAITIVQHSSPPGLIVTSY	TEX101 [86-105]	4	4506	VYQKRLMDEAKILKSLHHPN	PBK [77-96]
5	3184	LLKAGVISAQNIYSFGFGKA	TEX14 [194-213]	4	4507	PTPESSTIASYVTLRKTCKM	PEPP2 [856-875]
5	3185	TSSDRITINLLEVLWPTEWI	TMEM31 [62-81]	4	4508	QWALYQYHIDYNPLMEARRL	PIWIL1 [126-145]
5	3186	YDNCSFYFWLHTSFIENNRL	TPTE [489-508]	4	4509	RQFVEFTIKEAARFKKVLI	SAGE1 [860-879]
5	3187	VQELRRQNYSSNAYHMSSTM	TSGA10 [645-664]	4	4510	DKKTQTFLLTEPEIYWKLD	SCP-1 [793-812]
5	3188	ECDNFYHNFTKIPTLVQIIK	TSP50 [272-291]	4	4511	QNEFKKEMAMLKQKIMMETQ	SCP3a [201-220]
5	3189	ECMTWNQMNLGATLKGVAAG	WT1 [234-253]	4	4512	RSIFKPFIFVDDVKLVPKTQ	SCRN1 [302-321]
5	3190	NECGKAFRHSSKLARHQRIH	ZNF165 [347-366]	4	4513	LQFVIHSQHQLRSVIQEME	se57-1 [246-265]
6	3191	LYGGLHMDFWCARLATKGCE	ACRBP [433-452]	4	4514	GSSLDILSSLNSPALFGDQD	SOX-6 [475-494]
6	3192	VVDSGYGLTRVQPFHQGRPL	ACTL8 [147-166]	4	4515	GSKVEDRFYNNHAFEEQEP	SP17 [61-80]
6	3193	KTSYLVLRLPHDVAFLVYRE	ADAM2 [254-273]	4	4516	RDAVKFFVAVPGQVISQSS	SPAG9 [1223-1242]
6	3194	FTTLGLRGLSGIGAFRGMCT	ADAM29 [289-308]	4	4517	TILVVYRRNVKRTSPEELL	SPAN-Xc [49-68]
6	3195	ISLADLATIFFAQFVQEATY	AFP [41-60]	4	4518	EWEKMKVSEKIVYVYMKRKY	SSX-3 [36-55]
6	3196	FLNLVQCIONKPLYFADRLY	ANXA2 [256-275]	4	4519	TFGSLQRIFPKIMPKKPAEE	SSX-4 [100-119]
6	3197	ALQIVYGRLEHFMMPVNS	CDCA1 [52-71]	4	4520	QRQKDLIMKENLTLKNHFQ	TAF7L [413-432]
6	3198	KSPNAVVGHYTQLVWYSTYQ	CRISP2 [128-147]	4	4521	AEDTRLFAPSISKARFPAETY	TAG-1 [231-250]
6	3199	DKTEKVAVDPETVFKRPREC	CT45 [3-22]	4	4522	YIEIVMVSETIHFKNLSIAK	TEX15 [2062-2081]
6	3200	NFYLPQNYIDQFLTSFPTF	CTAGE1 [28-47]	4	4523	MWMGLIQLVEGVKRDQGF	TRAG-3 [1-20]
6	3201	PQRQDRFYSNCARLSGPAEL	CTAGE2 [590-609]	4	4524	LNAERSYKSQISTLHKSVMK	TSGA10 [470-489]
6	3202	AAVVGFFAVLFFLWRSFRSV	CTAGE5 [47-66]	4	4525	GEEAVLLDDIMAEVEVVAE	TSPY1 [60-79]
6	3203	CHLCLKTFRVTLLRNHVNT	CTCFL [287-306]	5	4526	NSLVSLTYVSFRNLTHLES	ST4 [244-263]
6	3204	VFWKYRRFQRNTGEMSSNST	CXorf61 [17-36]	5	4527	NFGTRTFQAITVTKLSQKFT	AFP [229-248]
6	3205	VSRVPVYAHITHKALDIPK	DCAF12 [226-245]	5	4528	SVVSDMMVSIMKTLKIQVKD	AKAP-3 [291-310]
6	3206	CPDCAKRNKMMKRLMTVEK	DPPA2 [279-298]	5	4529	SDLQKYALGFQHALSPSTST	AKAP-4 [116-135]
6	3207	DVWSFGIVMWEVMTYGERPY	EPHA2 [799-818]	5	4530	RKYGKSLYYYIQDQTKGDYQ	ANXA2 [309-328]
6	3208	IKNLERYMCSRFFIDFPHE	FAM46D [255-274]	5	4531	LKDLWKHSFSWPFQRPVDAV	BRDT [40-59]
6	3209	SMRPTLIDLPTFRHTLQKL	FBXO39 [324-343]	5	4532	DQSDVLMVDVATSMVPVVIKE	CABYR [189-208]
6	3210	SSGTTSFKCFAPFRDVPKQM	FMR1NB [165-184]	5	4533	KITKQQVFIDVINKLKENVE	CAGE1 [343-362]
6	3211	DPNVACRRLMTPIMYAARDG	GASZ [141-160]	5	4534	FSNKGKTLVIQYTVKHEQKM	CALR3 [84-103]
6	3212	ADQPRVSHHHPAVLNGQHP	GATA-3 [5-24]	5	4535	ELHKRTEIIRSLTKKVKALE	CCDC62 [78-97]
6	3213	HSPLKLLTSMASVVCFFFL	Glypican-3 [559-578]	5	4536	AKRTSRFLSGIINFIFREA	CDCA1 [114-133]

6	3214	SSGTLISRALVVTHTYLEPG	gp100 [265-284]	5	4537	AGDSLIIAGSAMS KAKKLMTG	CT45 [42-61]
6	3215	MSKVMEMFQPSAVVLQCGSD	HDAC1 [245-264]	5	4538	PSSETRAFSLSPPTLLEGPLR	cTAGE5 [527-546]
6	3216	GVEEAFYTTDRVMTVSFHKY	HDAC2 [183-202]; HDAC1 [182-201]	5	4539	DLSRDILNPNFPHSIARQKRI	CXorf61 [61-80]
6	3217	GVQEAFYLTDRVMTVSFHKY	HDAC3 [176-195]	5	4540	EVRLQNETSYSRVLHGYYAQ	DCAF12 [54-73]
6	3218	PPHTHSYTI SHATLERIGAV	IGFS11 [398-417]	5	4541	GLTGLQSL LQGFSRLFLKGN	DKKL1 [44-63]
6	3219	FQLQNIVKLPVPVYLTF TRE	IL13RA2 [230-249]	5	4542	VDDEESVILTLVPVKDDANM	DPPA2 [18-37]
6	3220	SETETVHFLFIPALSVGAII G	KOC1 [403-422]	5	4543	KQLENKKTGSKALAEFE EK M	FAM133A [46-65]
6	3221	HEFASLCLANMSAEYTSKVQ	KU-CT-1 [126-145]	5	4544	PVFPQLSR SIISKLLNESET	FSIP1 [439-458]
6	3222	GTYPFCTYYFVLSI IVPDKT	LPII [351-370]	5	4545	GWEIGYLDRTSQKLRLLPI	GASZ [24-43]
6	3223	CILES LFRAVITKKVADLVG	MAGE-A1 [92-111]	5	4546	FPKNSSFNPAALSRHMSSLS	GATA-3 [386-405]
6	3224	EKVTDLVQFL LFKYQMKEPI	MAGE-A10 [136-155]	5	4547	KHINQLLRTMSMPKGRVLDK	Glypican-3 [467-486]
6	3225	EVVEVVRIGHLYILV TCLGL	MAGE-A12 [165-184]	5	4548	DRQTVMTSATWPHSVHRLAQ	HAGE [420-439]
6	3226	SRKVAELVHFL LKYLREREP	MAGE-A3 [110-129]	5	4549	GAGKGKYYAVNFPMDGIDD	HDAC2 [216-235]
6	3227	EFLWGPRLAETS YVKVLEH	MAGE-A4 [271-290]; MAGE-A8 [273-292]	5	4550	PNHPSRKKVNF LDMSLDDII	HOM-TES-85 [15-34]
6	3228	GLDTQEEALGLVGVQAATTE	MAGE-A5 [15-34]	5	4551	SSDNNTLTSSNAYNSRYWSN	IGFS11 [305-324]
6	3229	EALKLKV AELVHFL LHKYRV	MAGE-A9 [106-125]	5	4552	TLDDLYPMNALKLRAESYN	JARID1B [737-756]
6	3230	EVNPTTHSYILVSMLGPN DG	MAGE-B4 [168-187]	5	4553	EAQDIKFTEIPLKILAHNN	KOC1 [267-286]
6	3231	DPDDSYVFVNTLDTSEGCL	MAGE-C1 [969-988]	5	4554	TSGKDYSVSANSRIIVTAG	LDHC [78-97]
6	3232	EKNCEPVVPNAPPAYEKL SA	MART1 [90-109]	5	4555	PSKGRRWAARAPSTRITYGT	LEMD1 [111-130]
6	3233	IELERKF SHQKYL SAPERAH	NKX3.1 [137-156]	5	4556	DDTTAMASASSATGSFSYP	MAGE-A10 [349-368]
6	3234	LIEDGYAVTQAE L FALLCRL	NR6A1 [271-290]	5	4557	BEQEAAFFSSTLNVGTLEEL	MAGE-A11 [144-163]
6	3235	LKPLVFRVDETT PAVVQSVL	NYD-TSPG [84-103]	5	4558	DGREDSVF AHPRKLLTQDLV	MAGE-A12 [232-251]
6	3236	NILTIRLTAADHRQLQLSIS	NY-ESO-1 [131-150]	5	4559	PDLESEFQAALSRKV AELVH	MAGE-A3 [99-118]
6	3237	VDRELRLQRCIDEFSTRCLC	ODF1 [18-37]	5	4560	AIPTAIDFTLWRQSIKGSSN	MAGE-A5 [70-89]
6	3238	YDKKIDSLMNAV GCLKSEVK	ODF2 [123-142]	5	4561	FPVIFSKASDSLQLVFGIEL	MAGE-A6 [147-166]
6	3239	DSTPGPAAYMLPMVMGPNTV	ODF3 [134-153]	5	4562	RTTATTFRARSRAPFSRSSH	MAGE-B1 [326-345]
6	3240	SIPIGWSYFIGWLVLILYFT	ODF4 [176-195]	5	4563	TVPSAFQFWYEEALRDEEER	MAGE-B3 [298-317]
6	3241	QVTLQLLDGFMITLSTDGVI	PASD1 [35-54]	5	4564	NSDPTRYQFLWGPRAHAETS	MAGE-B4 [262-281]
6	3242	PICNDHYRSVYQKRLMDEAK	PBK [68-87]	5	4565	ISRYTGYFPVIFRKAREFIE	MAGE-C1 [939-958]
6	3243	PDHIQRLTYKLCHIYNNWPG	PIWIL1 [805-824]	5	4566	DSESSFTYTLDEKVAELVEF	MAGE-C2 [132-151]
6	3244	KYTRPTLQMGMSCLLVFKVI	PIWIL3 [561-580]	5	4567	STTHSFLFGALAE LLDNARD	MORC1 [22-41]
6	3245	LDQLLRHV MNPLETLSITNC	PRAME [313-332]	5	4568	SSKKTYSLSRQASIIGVNLA	MPHOSPH1 [1703-1722]

6	3246	NCVDDSDQDYVVGKKNITCCD	PSCA [60-79]	5	4569	LQRDISEMFLQIYKQGGFLG	MUC-1 [1069-1088]
6	3247	YELVEKFYDFPMFKYHLTVAQ	PSMA [559-578]	5	4570	HRLFHWQANSERADIPASLR	NA17-A [54-73]
6	3248	SRTDKVLSTAPPQLVHMAAA	SAGE1 [122-141]	5	4571	EKNBEIFNYYNNHLKNRIYQY	NY-BR-1 [1312-1331]
6	3249	GKKHRYLRLLPEALIRFGGF	SLCO6A1 [45-64]	5	4572	AMPFATPMEAEALARRSLAQD	NY-ESO-1 [93-112]
6	3250	TTGTGVVYPGAITMATTTPS	SOX-6 [736-755]	5	4573	LELEIIIVLNDRVTDLVNQQQ	ODF2 [458-477]
6	3251	AEAAGKYSAAIALLEPAGSE	SPAG1 [462-481]	5	4574	IILKVALNMARGLYLHQEK	PBK [142-161]
6	3252	NILDSFTVCNSHVLCIASVP	SPAG9 [780-799]	5	4575	VTPAMGMQMRKAIMEVDDR	PIWLL1 [518-537]
6	3253	RLRERKQLVIYEEISDPED	SSX-2 [167-186]	5	4576	ETFKAVLDGLDVLQAQVVRP	PRAME [95-114]
6	3254	PPAWQPFLKDHRISTFKNWP	Survivin [7-26]	5	4577	KNSVKTDLMKAPMVIDWEE	PRSS55 [202-221]
6	3255	QECKERISALNLQIEEEKNK	SYCE1 [131-150]	5	4578	STNEVTRIYNVIGTLRGAVE	PSMA [348-367]
6	3256	REEKCVWKHGITPPLKNVRK	TAF7L [212-231]	5	4579	VVRLSSYSSTPLQSVLGSST	RAGE-1 [357-376]
6	3257	RLLLRLECNAVIIAHCNLEP	TAG-2a [48-67]	5	4580	MTPTIRKTQKIVIKKREPLN	RCAS1 [98-117]
6	3258	TSGLELYCQKGLSMTVEADP	TEX101 [21-40]	5	4581	HDLEIQLTAITTSQYYSKE	SCP-1 [479-498]
6	3259	IVHLLQLISDALRYLHFQGF	TEX14 [353-372]	5	4582	KILQQSRIVQSRLKTIKQL	SCP3a [159-178]
6	3260	TISFFLCQMLYNRRKILQLK	TEX15 [2250-2269]	5	4583	RRHELYKAHEWARAIIESDQ	SCRN1 [343-362]
6	3261	FYKFFLPTILSLSFILLVL	TMEM31 [135-154]	5	4584	IEETEYVKKIRTTLQKIRTQ	se57-1 [31-50]
6	3262	YIPLEYSISLAIALLFLMD	TPTE [121-140]	5	4585	IGEYKQLMRSRRQEMRQFFT	SOX-6 [707-726]
6	3263	FYHKTNIKMRCEFLACWPAF	TRAG-3 [24-43]	5	4586	SMKPLLRAMAYETLEQYQK	SPAG1 [520-539]
6	3264	TRELCLKLDSSKELNLRQLV	TSGA10 [511-530]	5	4587	EDGRVQAFGWSLPQYKQVT	SPAG9 [639-658]
6	3265	GEPLVCSMEGTWYLVGLVSW	TSP50 [311-330]	5	4588	HRLRERKQLVIYEEISDPED	SSX-1 [166-185]
6	3266	LDRRGAVIQSVPGFWANVIA	TSPY1 [145-164]	5	4589	AMTKLGFKAILPSFMRNKR	SSX-3 [57-76]
6	3267	LCAQYRIHHTGVFRGIQDV	WT1 [281-300]	5	4590	GKHAWTHRLRERKQLVYEE	SSX-4 [160-179]
6	3268	MRCHAHGPSCLVTAITREEG	XAGE-1c [1-20]	5	4591	ATLPPFMRNKRVDQFGNDF	SSX-5 [65-84]
7	3269	YVRNLFITGNQLAVLPAGAF	5T4 [92-111]	5	4592	TNNKKKEFEETAKKVRRAIE	Survivin [117-136]
7	3270	NPGSLLQLPHTEALLVLCYS	ACRBP [312-331]	5	4593	DQMWRQFTDTNLAFNARISE	TEKT5 [329-348]
7	3271	QLQMSLYASGLLTGVVVDG	ACTL8 [132-151]	5	4594	VTELEYNNQFSTLLKNVMS	TEX15 [2198-2217]
7	3272	DRKVICFVDVSTLNVEDKDY	AKAP-4 [38-57]	5	4595	MPMSEVSQVSRAAQMAVPSS	THEG [247-266]
7	3273	EPLSNAVKNRNVPRCIIILVL	BAGE-2 [48-67]; BAGE-3 [48-67]	5	4596	DAGLVKMSRKPRASSPLSNN	TRAG-3 [62-81]
7	3274	ISISSLRQFETVCKFHWEA	CAGE1 [113-132]	5	4597	FWANVIANHPQMSALITDED	TSPY1 [158-177]
7	3275	THLYTLILRPDLSYDVKIDG	CALR3 [169-188]	5	4598	ADASQSSMHNALHIYMGTM	TYR [355-374]
7	3276	SSAIQSWYDEILDVYGVGP	CRISP2 [108-127]	5	4599	WRGRSTYRPRRRSLQPPEL	XAGE-2 [3-22]
7	3277	HILIEENRQLSRLMVGPHAAA	CT47 [139-158]	6	4600	FSGSNASVSAPSPLVELILN	5T4 [162-181]
7	3278	LIVLVLCSAFLLWQGBGVN	CTAGE1 [53-72]	6	4601	NRNVNFAMKSETKLREKMYS	AKAP-3 [417-436]
7	3279	IGCVTSINEDNIYISNSIYF	CXorf48 [115-134]	6	4602	SKGLMVYANQVASDMMVSLM	AKAP-4 [330-349]
7	3280	NPNSLAIYRLPTLDVPCVGD	DCAF12 [161-180]	6	4603	VGTIDMTLQSDIMTMFENNF	BRDT [927-946]

7	3281	VSVEAFMQASGVRWCVVHG	DPPA2 [209-228]	6	4604	SKPRLVVPYGLKTLLEGISR	CABYR [4-23]
7	3282	NTVICSCLKAACLVMKAEMN	EpCAM [55-74]	6	4605	NNIENYSTNALIQPVDTISI	CAGE1 [96-115]
7	3283	VCRKWNQMMYSABLWRYRTI	FBXO39 [42-61]	6	4606	ESGSIEYDWNLTSLKKETSP	CALR3 [192-211]
7	3284	RNRSSHRAAMRVHAHLELATYE	FMR1NB [11-30]	6	4607	DKELNDMVAHVHQQQLLSWEE	CCDC62 [41-60]
7	3285	NKHHEIFNLLSFTLNPLEGK	GASZ [225-244]	6	4608	VEGVSTPFPHIFKVKVTTTTERE	CT46 [212-231]
7	3286	ACGLYHKMNGQNRPLIKPKR	GATA-3 [287-306]	6	4609	LGEEEGEQAAAGLAAVPRGGS	CT47 [61-80]
7	3287	VNGMYRIYDMENVLLGLFST	Glypican-3 [307-326]	6	4610	RGSQKKHISPVQALSEFKAM	CTNNA2 [931-950]
7	3288	LSIGTGRAMLGTHTMEVTVY	gp100 [170-189]	6	4611	IDESIYFSSDVVTGNVPLKV	CXorf48 [53-72]
7	3289	TEEEKWSHMQTFLQSMSSTD	HAGE [469-488]	6	4612	HQTAIKRNNPRKFLRSVGDG	DBPC [122-141]
7	3290	AILELLKYHQRVLYIDIDIH	HDAC1 [159-178]; HDAC2 [160-179]	6	4613	SRLSPRKTHLLYILRPSRQL	DKKL1 [223-242]
7	3291	ALSSGLYQCVASNAIGTSTC	IGFS11 [207-226]	6	4614	QSVPPQFFTFEDAPSYPEARA	DMRT1 [302-321]
7	3292	NIPPHLQWEVLDSELLVQYGV	KOC1 [87-106]	6	4615	QKEITTRYQLDPKFITSILY	EpCAM [167-186]
7	3293	PCGARRPDSRLQLHITMPF	Lage-1 [77-96]	6	4616	EFNVLEMEVMRRQLYAVNRR	FATE1 [128-147]
7	3294	IPAIVHYSPDCKILVVSNPV	LDHC [121-140]	6	4617	KRPSFLDDPLYGISVLSSE	FSIP1 [533-552]
7	3295	YEKKLVQLLVSPPCAPPVMN	LEMD1 [34-53]	6	4618	KNVNQSLDLQLAVEKGDP	FTHL17 [109-128]
7	3296	AVITKKVADLVGFLLLKYRA	MAGE-A1 [100-119]	6	4619	MSSTDKIVVFVSRKAVADHL	HAGE [484-503]
7	3297	LGSVIRNFQDFFPVIFSKAS	MAGE-A12 [136-155]	6	4620	GDLVDTQSDLIATQRDLIAT	HOM-TES-85 [236-255]
7	3298	GIEVVVVPISHLYILVTCL	MAGE-A2 [163-182]	6	4621	PYSAVEKAMARLQELLTVSE	JARID1B [950-969]
7	3299	ASNTYTLVTCLGLSYDGLLG	MAGE-A4 [173-192]	6	4622	ITMPFSSPMEAEVLRRILSR	Lage-1 [92-111]
7	3300	AGSPGPLKSPQGASAIPTAI	MAGE-A5 [56-75]	6	4623	LKGEMMDLQHGSLFFSTSKI	LDHC [58-77]
7	3301	DPIGHVYIFATCLGLSYDGL	MAGE-A6 [170-189]	6	4624	LQGNIIILSTEKSKKLKWPPE	LEMD1 [74-93]
7	3302	KVINYLVMNLNAREPICYPSL	MAGE-A9 [284-303]	6	4625	EESFSPTAMDAIFGSLSDEG	MAGE-A11 [177-196]
7	3303	PQRAPTAAAAAGVSSTKS	MAGE-B2 [62-81]	6	4626	PDLESEFQAALSRKVAKLH	MAGE-A6 [99-118]
7	3304	FLGLLGIYDGLHSIYGDAR	MAGE-B6 [310-329]	6	4627	VRVNRVRIISYPSLHHEALG	MAGE-A8 [294-313]
7	3305	LKRAREFMELLFGLALIEVG	MAGE-C2 [182-201]	6	4628	MHFILRKYKMREPIMKADML	MAGE-B1 [116-135]
7	3306	TTAEEAAGIGILTIVILGVLL	MART1 [22-41]	6	4629	KIVGKRFRHEHFEILKKASE	MAGE-B2 [139-158]
7	3307	LRLDIFIHANSTTHSFLFGAL	MORC1 [13-32]	6	4630	VQFLMEMYKMKPIMKADML	MAGE-B3 [119-138]
7	3308	SEGCVHILDSQTVVLEKEPQC	MPHOSPH1 [77-96]	6	4631	DEESVSASQKAIIFKRLSKD	MAGE-B6 [174-193]
7	3309	ELLFRQIAWIKKLPPFCELS	NR6A1 [293-312]	6	4632	PRELLTKVWVQGHYLEYREV	MAGE-C2 [270-289]
7	3310	KHLKHMRRMYGTSLYQFIPL	NYD-TSPG [161-180]	6	4633	EKPLNSFYQRRQAMGIPFI	MORC1 [464-483]
7	3311	LSISSCLQQLSLLMWITQCF	NY-ESO-1 [147-166]	6	4634	KFSVWVSFFEYIYNEIYDLF	MPHOSPH1 [268-287]
7	3312	ERENRYDCLGSKKYSYMNIC	ODF1 [153-172]	6	4635	NGGSSLSYTNPAVAAASANL	MUC-1 [1236-1255]
7	3313	KHTPTKLRAPAYSFRRGAPML	ODF3 [40-59]	6	4636	QPERLLFVIDSFEEQLGGGLN	NLRP4 [222-241]
7	3314	TDGVIIICVAENISSLLGHLP	PASD1 [50-69]	6	4637	QEMVQAFSAQSGMKLEWSQK	NXF2 [573-592]

7	3315	SEKKKSVLCSTPTINIPASP	PBK [14-33]	6	4638	ITKRSEQIVEFLLIKNNANAN	NY-BR-1 [124-143]
7	3316	YAASIRRTDGGFLFLADVSH	PIWIL2 [363-382]	6	4639	ADSVHLAWDLRSRLGAVVFS	OIP5 [88-107]
7	3317	MKVFKFIGLMILLTSAFSAG	PLAC1 [1-20]	6	4640	WQQRQFYNKQSTLPRHSTLS	PEPP2 [506-525]
7	3318	LSLQCLQALYVDSLFFLRGR	PRAME [293-312]	6	4641	ESVGLVSMFRGLGIETVSKT	PIWIL2 [67-86]
7	3319	PRSWLLCPLSHVLFRAILY	PRSS55 [333-352]	6	4642	QENPAAFVRAIQYVDPDVQ	PIWIL4 [526-545]
7	3320	NITCCDIDLNASGAHALQP	PSCA [74-93]	6	4643	KAVSQDMVIYSTEIHYSSKG	PLAC1 [85-104]
7	3321	LSPQCLSLHAMVAYDPDER	RAGE-1 [254-273]	6	4644	DNDIALLLASPIKLDLKV	PRSS55 [154-173]
7	3322	AAGISSTITRDLYVTATHSV	SAGE1 [657-676]	6	4645	EIQALRRLNPHPNILMLHEV	RAGE-1 [50-69]
7	3323	TREPAABIEALLGMDLVRLG	SCRN1 [97-116]	6	4646	BEEEDAAWQAEVLRQQLA	RCAS1 [160-179]
7	3324	IAECTSMIGYALGYVLGAPL	SLCO6A1 [269-288]	6	4647	FIQATDYVEIWQAYLDYLR	SART3 [411-430]
7	3325	EIADDLSILYSNRAACYLKE	SPAG1 [481-500]	6	4648	MEESNKARAAHSFVTEFET	SCP-1 [363-382]
7	3326	GVWVSIRLDSTLRLYHAHTY	SPAG9 [1101-1120]	6	4649	RLKTIKQLYEQFIKSMEELE	SCP3a [171-190]
7	3327	INMISGVLQRYCRFGSRPLQ	SSX-3 [151-170]	6	4650	GETAKEALDVIVSLLEEHGQ	SCRN1 [120-139]
7	3328	KLNYEVMTKLGFKVTLPPFM	SSX-4 [52-71]	6	4651	EAGAAALRNVAQRLFENYQT	se57-1 [121-140]
7	3329	FLEGCACTPERMAEAGFIHC	Survivin [27-46]	6	4652	ISGKEETSVTILDSSEEDK	SP17 [92-111]
7	3330	QSGRKLAEQASLSKYCDQL	TDRD1 [515-534]	6	4653	IDVVESEAVSVLHHWLKTE	SPATA19 [28-47]
7	3331	ILLVLGASLLTSGLELYCQK	TEX101 [11-30]	6	4654	QGIRNLVTDKAFVLIVEKDA	SPO11 [208-227]
7	3332	LHFQGFHRSLSYAVHIIS	TEX14 [367-386]	6	4655	EKRSKAFDDIATYFSKKEWK	SSX-1 [19-38]
7	3333	FELYPEFLLVFKEAFHDISH	TMEM31 [91-110]	6	4656	GFKAILPSFMRNKRVTDFQG	SSX-3 [62-81]
7	3334	LAIALFFLMDVLLRVFVERR	TPTE [131-150]	6	4657	ISEKLRKAFDDIAKYFSKKE	SSX-4 [17-36]
7	3335	LLKEHLCLAEKMAIQSRDV	TSGA10 [594-613]	6	4658	HRVRERKQLVYIEEISDPQE	SSX-5 [166-185]
7	3336	FRSNPYFQNKVITKEYLVNI	TSPY1 [205-224]	6	4659	QALAPDFRLNPVRRLI PAAR	TAG-1 [413-432]
7	3337	EQASRIWSWLGAAVGAFL	TYR [469-488]	6	4660	IMLLKNFMLNQNVMLSVKGI	TDRD1 [1072-1091]
7	3338	ALPVSAGAAQWAPVLDFAFPG	WT1 [25-44]	6	4661	DNIKHSQNMRSNIQLREEA	TEKT5 [301-320]
7	3339	EEGGPRSGGAQAKLGCCWGY	XAGE-1c [18-37]	6	4662	PKIRDNFWSMPMSEVSQVSR	THEG [238-257]
8	3340	LVPDGAVCNLPYASWFESF	ACRBP [84-103]	6	4663	HNALHIYMNGTMSQVQGSAN	TYR [363-382]
8	3341	YAGGVVLHPTISLES LAVI	ADAM2 [291-310]	6	4664	DLERGTDEAVLQVQAHEHGQ	ZNF165 [126-145]
8	3342	MCTPHRSCAIVTFMNKTLGT	ADAM29 [306-325]	7	4665	GLGGLRMDSNFDSLVPQITV	ADAM2 [10-29]
8	3343	DKLVESVMKLCLIMAKYSND	AKAP-4 [698-717]	7	4666	EIKPLAFSTTFEHLVYKMDS	ADAM29 [135-154]
8	3344	LEPEDGTALDVHFVSTLEPL	BAGE-2 [31-50]; BAGE-3 [31-50]	7	4667	ASFVHEYSRRHPQLAVSVIL	AFP [352-371]
8	3345	FAADVRLFMNMCYKYNPPDH	BRDT [337-356]	7	4668	DDFTASVSEGIMTYANSVVS	AKAP-3 [275-294]
8	3346	SGIINFIHFREACRETYMEF	CDCA1 [122-141]	7	4669	SDTSGDFRKLMLVALAKGRRA	ANXA2 [161-180]
8	3347	RCGENLYMSSDPTSWSAIIQ	CRISP2 [93-112]	7	4670	VDAVKLQLPDYTYTIKPNMD	BRDT [56-75]
8	3348	NESSMLSTDTKKASILLIRK	CT46 [137-156]	7	4671	TMYRGNTTMDIKDLVKQFHQ	CABYR [45-64]
8	3349	ANFDLAVVARRYPASGIHFV	CT47 [103-122]	7	4672	SRQMVTDLELSTLLPISHEN	CCDC62 [641-660]

8	3350	YIDQFLLTSPFTFTSVGVLI	CTAGE1 [35-54]	7	4673	TLSPFRYNVAEIVIHNRKI	CDCA1 [3-22]
8	3351	FAMRNVYLPRGFLPYRPPRP	CTAGE2 [717-736]	7	4674	AMSKAKKLMTGHAIPPSQLD	CT45 [51-70]
8	3352	PKYQCPHCATIIARKSDLRV	CTCFL [426-445]	7	4675	DALQKKYLRMVVLAVYTNPE	CT46 [87-106]
8	3353	VVLTVKASYVASTKYQKVYG	CTNNA2 [876-895]	7	4676	LTERLLKMKDGVAMLEEDVT	CTAGE2 [237-256]
8	3354	PQVDDIVNVVMVESIQFCFI	CXorf48 [211-230]	7	4677	SKSLKSQVAEAKMTFKIFQM	CTAGE5 [180-199]
8	3355	LGTVKWFNVNRNGYGFNRND	DBPC [95-114]	7	4678	KSDLRVHMRNLHAYSAAELK	CTCFL [440-459]
8	3356	SGIRSVSFYEHIITVTGQG	DCAF12 [341-360]	7	4679	FGKEMVKLNYYAARRQQLK	CTNNA2 [179-198]
8	3357	KNMENRHAMSSQYRMHSYYP	DMRT1 [276-295]	7	4680	KRILVNLMSVENKLVELEHT	CXorf61 [78-97]
8	3358	TKGWVRLQFHAGQAWVPTTH	DPPA2 [235-254]	7	4681	NRRKSRRFIPRPPSVAPPPM	DBPC [176-195]
8	3359	LAAATATFAAAQECCVCENY	EpCAM [13-32]	7	4682	LQGF SRLFLKGNLLRGIDSL	DKK1 [52-71]
8	3360	VSLVTSRSFRTASVSINQT	EPHA2 [418-437]	7	4683	ASEGRMVIQDIPAVTSRSHV	DMRT1 [178-197]
8	3361	EPPPVSFQPYHPLHFRGSNG	FAM46D [368-387]	7	4684	PGHQKRIAYSLGLKDQVNT	EPHA2 [952-971]
8	3362	GQSLEEDSALEALLNFFFT	FMR1NB [113-132]	7	4685	LDPMLDFYSDKNAKLTKESY	FAM46D [180-199]
8	3363	CILKQKSIKLSSEKKEI	FSIP1 [415-434]	7	4686	PGTDAVAQTSLEEFNVLEME	FATE1 [116-135]
8	3364	GWTPLMYAASVANAEVVRVL	GASZ [79-98]	7	4687	AIQMKKLDKILAKQRREK	FSIP1 [118-137]
8	3365	DCVLYRYGSFVTLDIVQGI	gp100 [474-493]	7	4688	HFLESHYLHEQVKTIKELGG	FTHL17 [132-151]
8	3366	HEELPLCFALKSHFVGAVIG	HAGE [65-84]	7	4689	EKIKQRLFENLRMLPHAPGV	HDAC2 [361-380]; HDAC1 [360-379]
8	3367	GILELLKYHPRVLYIDIDIH	HDAC3 [153-172]	7	4690	TIFENLKMLNHAPSQIHDV	HDAC3 [361-380]
8	3368	VGFTGTMPATNVISFINNTQ	IGFS11 [92-111]	7	4691	PSQKPSGFKSGQHPLNGQPL	HOM-TES-85 [92-111]
8	3369	LPPVYLTFRESSCEIKLKW	IL13RA2 [239-258]	7	4692	GSETWKTIITKNLHYKDFD	IL13RA2 [77-96]
8	3370	VDILTYIVWKISGLPVTRVI	LDHC [140-159]	7	4693	IEEIPAYLPNGAALKDSVQR	JARID1B [997-1016]
8	3371	DHFPLLFSEASECMLLVFGI	MAGE-A10 [170-189]	7	4694	DVGYGRSISSSSLRRSSKE	KU-CT-1 [621-640]
8	3372	EYLQLVFGIEVVEVVRIGHL	MAGE-A12 [156-175]	7	4695	SRGATTFIYNRAVKNTRKVA	LIPI [135-154]
8	3373	GPRALIETSYVKVLHHTLKI	MAGE-A2 [274-293]	7	4696	PRAHAEIRKMSLLKFLAKVN	MAGE-A10 [300-319]
8	3374	SSSSPLVPGTLGEVPAAGSP	MAGE-A5 [40-59]	7	4697	VKGLITKAEMLGSVIKNYED	MAGE-A11 [239-258]
8	3375	RALIETSYVKVLHMHVKISG	MAGE-A6 [276-295]	7	4698	EEQEAASSSTLVEVTLGEV	MAGE-A3 [34-53]; MAGE-A6 [34-53]
8	3376	AGHSYILVTCLGLSYDGLLG	MAGE-A8 [175-194]	7	4699	EERAQVRSSVRARRTTATT	MAGE-B1 [312-331]
8	3377	WGPRAYAEETTKMKVLEFLAK	MAGE-B1 [272-291]	7	4700	IEKKQSFSGQLSSTVQSRTD	MAGE-B3 [90-109]
8	3378	TDEESLLSSWDFPRRLLMP	MAGE-B2 [187-206]	7	4701	FPEIFRKVSQRTELVFGLAL	MAGE-B4 [147-166]
8	3379	SDPPCYEFLWGPAYAEETTK	MAGE-B6 [350-369]	7	4702	SLLQIPMTSSFSSTLLSIFQ	MAGE-C1 [336-355]
8	3380	IGILTIVILGVLIGCWYCR	MART1 [30-49]	7	4703	TSPQLSTGVSFFFLSFHISN	MUC-1 [1032-1051]
8	3381	EESLSEVVVPMPSWLIRTRE	MORC1 [136-155]	7	4704	TETQVKIWFQNRKYTKRKQ	NKX3.1 [164-183]
8	3382	NISQCYLAYDETNLVLFKFS	MPHOSPH1 [455-474]	7	4705	MQDPAFVKQAVNLQAEANFH	NLRP4 [560-579]

8	3383	SSLRKLCSFVQNVFKKEDEH	NLRP4 [597-616]	7	4706	QMEMLKLTMTNKRYNVSQQAL	NXF2 [213-232]
8	3384	QDNEWNYTRAGQAFTMLQTE	NXF2 [595-614]	7	4707	AQRKSKSLKINLNYAGDALR	NY-BR-1 [1200-1219]
8	3385	HEEVVTFVLDRKCQLDVLGD	NY-BR-1 [29-48]	7	4708	ATSAQNIEFLQVIKREBAI	ODF2 [675-694]
8	3386	CGARGPESRLLEFYLPMPFA	NY-ESO-1 [78-97]	7	4709	PINIWIFELEARNVSIPIGWS	ODF4 [163-182]
8	3387	LASSCCSSNILGSVNVCGFE	ODF1 [116-135]	7	4710	THNRLKSLMKILSEVTPDQS	OIP5 [206-225]
8	3388	DKMVCYLLKTKAIVNASEMD	OIP5 [167-186]	7	4711	SQEIMHADNPAAIQTVVLQ	PEPP2 [674-693]
8	3389	PEVNPLYRADPVDLEFSVDQ	PASD1 [291-310]	7	4712	YNPLMEARRLSALLFQHED	PIWIL1 [136-155]
8	3390	DKADIFAFGLTLWEMMTLSI	PBK [226-245]	7	4713	FGERHIFDGNLLLLSRPLKE	PIWIL3 [170-189]
8	3391	GLKPDHMQRLTFKLCHLYYN	PIWIL4 [793-812]	7	4714	SNKAKAFDGAILFLSQKLEE	PIWIL4 [151-170]
8	3392	VTECGIRAKAVSQDMVIYST	PLAC1 [77-96]	7	4715	LKKEGWRPRRTILFASWDAE	PSMA [405-424]
8	3393	EVGEFPWQVSIQARSEFFCG	PRSS55 [75-94]	7	4716	QQRKMEKEBAQRLMKKEQNK	RCAS1 [188-207]
8	3394	LHEVVVDRKSGSLALICELM	RAGE-1 [66-85]	7	4717	EKVHSLFRRQLAIPLYDMEA	SART3 [245-264]
8	3395	VFSFLKRLICRSGRGRKLSG	RCAS1 [18-37]	7	4718	EQEQSSLRASLEIELSNLKA	SCP-1 [739-758]
8	3396	SLEKHKLFISGLPFSCCTKEE	SART3 [797-816]	7	4719	NLLTGAQNEBFKEMAMLQKK	SCP3a [195-214]
8	3397	AEGSKAMNGSAAKLQQYYCW	SOX-6 [576-595]	7	4720	ERKLSLENKLLQLKSSATYG	se57-1 [207-226]
8	3398	MTFGRHLHRIIPKIMPKPAE	SSX-1 [99-118]	7	4721	SYNHKQIEQLYAAQLASMQV	SOX-6 [360-379]
8	3399	TENEPDLAQCFCEKELEGW	Survivin [48-67]	7	4722	REILREQPDNIPAFAAAYFE	SP17 [25-44]
8	3400	ACTVRNLARSQSVMKDKLK	TAF7L [111-130]	7	4723	HLSKSDLLANQSQEVLEERT	SPATA19 [93-112]
8	3401	SIKARFPAETYALVGQVTL	TAG-1 [240-259]	7	4724	ASIENI IQDIITSLARNEAP	SPO11 [49-68]
8	3402	PLVSRDPPASASLFQDTCAG	TAG-2a [67-86]	7	4725	GKHAWTHRLRERKQLVIYEE	SSX-1 [160-179]
8	3403	AVGPMFVREACPHQLLTQPR	TEX101 [199-218]	7	4726	QIPEKIQKAFDDIAKYFSKE	SSX-2 [16-35]
8	3404	VGPPSLNYIPVVLQLSGGQK	TEX14 [794-813]	7	4727	KYFSEKEWEKMKASEKIIYV	SSX-5 [30-49]
8	3405	KAQMEKIGLPILHLFALST	TMEM31 [113-132]	7	4728	AEGPSTLDEGLFLRSQEAAA	SYCE1 [219-238]
8	3406	YFWLHTSFIENNRLYLPKNE	TPTE [495-514]	7	4729	DADSSAQAAAQAPENFQEGK	TAF7L [66-85]
8	3407	EAPPIYLQVSSYQHVIWDCL	TSP50 [338-357]	7	4730	VSREAILRFGFLQEFKSKEER	TAG-1 [121-140]
8	3408	TLAKHTISSDYVIPITYGQ	TYR [139-158]	7	4731	GGAESERGLPASTLSRLSNR	TAG-2a [29-48]
8	3409	WAPVLDFAPPGASAYGSLGG	WT1 [34-53]	7	4732	GFWKSELSYELDRLLTENQN	TEKT5 [149-168]
8	3410	GGAQAKLGCCWGYPSRSTW	XAGE-1c [25-44]	7	4733	ALKSRISWEGLLALDNGEME	TEX15 [712-731]
8	3411	LKQELCRQLFRQFCYQDSPG	ZNF165 [43-62]	7	4734	RPKRFYLEYYNNRTPVWP	THEG [199-218]
9	3412	PAGAFARRPPLAELALNLS	5T4 [107-126]	7	4735	VLGEAWRDQVDSRLLRDAG	TRAG-3 [45-64]
9	3413	FKSQQCLMRNRNRKVS RMRC	ACRBP [490-509]	7	4736	SDVPVLQVIMHSRYRAQRFW	TSP50 [179-198]
9	3414	SVESCEISLRPLLVSVMAC	ACTL8 [279-298]	7	4737	FKWNSDFINHQIYYAGEKNH	ZNF165 [301-320]
9	3415	EELQKYIQESQALAKRSCGL	AFP [399-418]	8	4738	LRHLDSLNNLSLVSLTYVSFR	5T4 [236-255]
9	3416	AVSPEFAYVPADPAQLAAQM	CABYR [160-179]	8	4739	KTLEFAGQDLSAYLLKSLFK	ACTL8 [171-190]
9	3417	ECADQRLAISHSQIAHLEER	CAGE1 [713-732]	8	4740	YKEVSKMVKDALTAIEKPTG	AFP [60-79]

9	3418	REKLKSQEIFLNLKTALEKY	CDCA1 [414-433]	8	4741	LMTDTQFVSAVKRTVFSHGS	AKAP-3 [348-367]
9	3419	QLVWYSTYQVCGIAYCPNQ	CRISP2 [139-158]	8	4742	PKWISIMTERSVPHLQKVPD	ANXA2 [211-230]
9	3420	KRKLVKELRCVGQKYEKIFE	CT45 [127-146]	8	4743	EVPAQLLDAEGAIGSEKS	CABYR [397-416]
9	3421	NKISTEHQSLVLVKRLLAWS	CT46 [18-37]	8	4744	EKVSDIMLQKLKSLHLKKKT	CAGE1 [645-664]
9	3422	YLPRGFLPYRPPRPAFFPPA	CTAGE2 [723-742]	8	4745	DSRFGHFRLSSGKFYGHKEK	CALR3 [43-62]
9	3423	LPQGDQLTLTVQGVVTSFCG	CXorf48 [29-48]	8	4746	VEWMSIFKPSKMQRIVRLKS	CCDC62 [532-551]
9	3424	PPARSQADKPVLAIQVLGTV	DBPC [79-98]	8	4747	SQIDDFTFGSKDRMMQKPGS	CT45 [71-90]
9	3425	AENTLSKLLSTKLPYCENNV	DCAF12 [281-300]	8	4748	LLEKDPYALDVPNTAFGREH	cTAGE5 [497-516]
9	3426	PYYNNLYNCPQYSMALAADS	DMRT1 [220-239]	8	4749	NSTALALVRPSSSGLINSNT	CXorf61 [34-53]
9	3427	KALNSCSIPVSEAFMLQAS	DPPA2 [200-219]	8	4750	PRMEEKEALVPIQKATDSFH	DKKL1 [141-160]
9	3428	ALLSVRVVYKKCPQLLQGLA	EPHA2 [190-209]	8	4751	TRPKKMGSQLPKPRMLRESG	FATE1 [73-92]
9	3429	CQILDLSYMRNENVISLNL	FBXO39 [180-199]	8	4752	MGKRLDYLNKLGARLTVEQG	FBXO39 [160-179]
9	3430	CYYLSYYLCSGSSYFVLANG	FMR1NB [83-102]	8	4753	LSDDKMEHAQKLMRLQNLRG	FTHL17 [59-78]
9	3431	KYDTNCDAAINSHITLELYT	FTHL17 [12-31]	8	4754	KLESSHSRGSMTALGGASSS	GATA-3 [195-214]
9	3432	NGYTALTWAARQGHKNIVLK	GASZ [181-200]	8	4755	YYPEDLFIDKKVLKVAHVEH	Glypican-3 [361-380]
9	3433	HVPPYYGNSVRATVQRYPPT	GATA-3 [59-78]	8	4756	NHHSERSRNHLERSLSQSDR	HOM-TES-85 [156-175]
9	3434	RCLHLAVIGALLAVGATKV	gp100 [7-26]	8	4757	EGDALRYMIERTVNWQHRAQ	JARID1B [1248-1267]
9	3435	KCEVEVKTFFNLPLMLGGGG	HDAC2 [284-303]	8	4758	LDKLNQFQLENFTLKVAYIP	KOC1 [136-155]
9	3436	INQVDFYQPTCIVLQCGAD	HDAC3 [240-259]	8	4759	LLRELDVMNSVIAQLAPEEE	KU-CT-1 [103-122]
9	3437	SKKTLRLFWLPPFGFILILVI	IL13RA2 [337-356]	8	4760	REGAGMRVVGWGLGSASPE	Lage-1 [142-161]
9	3438	DLHLQVLTIMNPNTLMTHEV	JARID1B [547-566]	8	4761	LSTEKSKKLKKWPEASTTKR	LEMD1 [80-99]
9	3439	EAHIRVPSFAAGRVIGKGGK	KOC1 [489-508]	8	4762	GSIPLWLQNFVRILLNEEDM	LIP1 [108-127]
9	3440	IIKLKGYTWSAIGLSVMDLV	LDHC [241-260]	8	4763	QSPQGASAFPTTINFTRQRQ	MAGE-A1 [56-75]
9	3441	TTKRKAVDTYCLDYKPSKGR	LEMD1 [96-115]	8	4764	GSVIKNYEDYFPEIFREASV	MAGE-A11 [250-269]
9	3442	FIKCNHQRAVHFLMASLETN	LIP1 [269-288]	8	4765	KLLTQHFVQENYLEYRQVPG	MAGE-A3 [244-263]
9	3443	EEALEAQQEALGLVCVQAAT	MAGE-A1 [13-32]	8	4766	TTEEQEAASVSSSPLVPGTL	MAGE-A4 [32-51]
9	3444	GPITQIFPTVRPADLTRVIM	MAGE-A11 [92-111]	8	4767	VGKEHMFYGEPRKLLTQDQV	MAGE-A9 [231-250]
9	3445	ALVETSYVKVLHLLKISGG	MAGE-A12 [277-296]	8	4768	FWAKVNKTVPFAFQFWYEEA	MAGE-B3 [291-310]
9	3446	EYLQLVFGIEVVEVVPISHL	MAGE-A2 [156-175]	8	4769	EPTTKAEMLKII SKKYKEHF	MAGE-B4 [128-147]
9	3447	LERVIKNIYKRCFPVIFGKAS	MAGE-A4 [137-156]	8	4770	IESEPLFTYTLDEKVDLAR	MAGE-C1 [898-917]
9	3448	APEEVIWEALSVMGVYVGKE	MAGE-A9 [215-234]	8	4771	KKKVLEFLAKLNNTVPSSFP	MAGE-C2 [311-330]
9	3449	PITKAEMLTNVISRYTGYFP	MAGE-C1 [928-947]	8	4772	AASRYNLTISDVSVSDVPFP	MUC-1 [1128-1147]
9	3450	MPREDAHFYGYPKKGHGS	MART1 [1-20]	8	4773	PTPSKPLTSFLIQDILRDGA	NKX3.1 [20-39]
9	3451	IEDSEMSRVIRVSELSLCDL	MPHOSPH1 [362-381]	8	4774	SSRSVELNGFMAFREQYMG	NR6A1 [198-217]
9	3452	CFPKLLRLDGRELSAPVIVD	NXF2 [349-368]	8	4775	SNLQNNYAHLTNSSINKSGA	NYD-TSPG [288-307]

9	3453	SEIVGMLLQQNVDFVFAADIC	NY-BR-1 [162-181]	8	4776	KLVEAEMDGAAAAQVMALK	ODF2 [210-229]
9	3454	CIDEFSTRCLCDLYMHFYCC	ODF1 [27-46]	8	4777	SAPSHSISARTKAFVRDSTP	ODF3 [118-137]
9	3455	IWIFELERNVSIPIGWSYFI	ODF4 [166-185]	8	4778	AFSKKWLDSLRSIFYQRWV	ODF4 [99-118]
9	3456	ERCAVFQCAQCHAVLADSVH	OIP5 [73-92]	8	4779	DLNLEWISLPRSWTYGITRG	PEPP2 [4-23]
9	3457	AVYVEPAAAAAAAIISDDQI	PASD1 [223-242]	8	4780	NSLIQNLFKVTPAMGMQMRK	PIWIL1 [509-528]
9	3458	DFDDEAYYAALGTRPPINME	PBK [265-284]	8	4781	KWYSRVVFQMPHQEIVDSLK	PIWIL2 [770-789]
9	3459	KKAIQLYRHGTSLEIWLGYV	PIWIL3 [249-268]	8	4782	LHSWLILYSRSSHREAMSLK	PIWIL3 [507-526]
9	3460	TRNEWYDFYLISQVACRGTV	PIWIL4 [761-780]	8	4783	QLTTLSFYGNSISISALQSL	PRAME [407-426]
9	3461	LLTSAFSAGSGQSPMTVLC	PLAC1 [12-31]	8	4784	EMKTYSVSFDLSFSAVKNFT	PSMA [621-640]
9	3462	LLKDEALAIAALELLPRELF	PRAME [34-53]	8	4785	PAPDNVLLTLRPRINMTDT	SAGE1 [216-235]
9	3463	ECGDRSIFEGRTRYSRITGG	PRSS55 [52-71]	8	4786	KDKRDYLWTSAKNTLSTPLP	SCP-1 [833-852]
9	3464	YPANEYAYRRGIAEAVGLPS	PSMA [272-291]	8	4787	QEEKILNMFRQKQKILQSQSR	SCP3a [146-165]
9	3465	QPYTEYISTRWYRAPECLLT	RAGE-1 [156-175]	8	4788	DQEQGRKLRSMTLELEKQGL	SCRN1 [361-380]
9	3466	PPQLVHMAAGIPSMSTRDL	SAGE1 [132-151]	8	4789	KKIRTTLQKIRTQMFKDEIR	se57-1 [38-57]
9	3467	RRKVLGRAVAAATYKTMGPA	SART3 [35-54]	8	4790	QSSGISFQSKYLSFFILGQT	SLCO6A1 [218-237]
9	3468	AAPPSYCFVAFPPRAKDGLV	SCRN1 [3-22]	8	4791	TPNNHFTLEDIQAALKRQYEL	SPAG1 [907-926]
9	3469	LCTIIFTTIAFFIYKRLNE	SLCO6A1 [678-697]	8	4792	GYRNKIYVVPKAMKIEKSF	SPAG9 [1063-1082]
9	3470	YAAQLASMQVSPGAKMPSTP	SOX-6 [370-389]	8	4793	EMTEDIMRDRIEQVRSISR	SPATA19 [130-149]
9	3471	CEKHLQALAPESRALRKDKP	SPAG1 [61-80]	8	4794	YATKRDIYYTDSQLFGNQTV	SPO11 [130-149]
9	3472	TFIPYCSMAHAQLCFHGHRD	SPAG9 [1205-1224]	8	4795	MNGDDAFARRPTVGAQIPEK	SSX-2 [1-20]
9	3473	PPGKPTTSEKINMISGVLQR	SSX-3 [141-160]	8	4796	MNGDDTFARRPTVGAQIPEK	SSX-3 [1-20]
9	3474	FHMPERLAKEICALDSSKEQ	SYCE1 [175-194]	8	4797	VTLPPFMRSKRAADPHGNDF	SSX-4 [65-84]
9	3475	TLPLCRVQPITSSHLALPFQ	TDRD1 [1032-1051]	8	4798	RGKHAWTHRVRERKQLVIYE	SSX-5 [159-178]
9	3476	SSPPGLIVTSYSNYCEDSFC	TEX101 [95-114]	8	4799	VHLKEILSKKQETLRLRLH	SYCE1 [96-115]
9	3477	CKMSLHFCLCWPSVYWTERF	THEG [158-177]	8	4800	LGVTKEIAIWAERIMFSDLR	TDRD1 [237-256]
9	3478	FLLVFKEAFHDISHCLKAQM	TMEM31 [97-116]	8	4801	LVNEVFTIDDTLQTLKRLR	TEKT5 [415-434]
9	3479	DRGTMTVCAFLIASEICSTA	TPTE [343-362]	8	4802	YGLEHIFFDAKNLVWKERT	TEX15 [1882-1901]
9	3480	HCLIWRDVIYSVRVGSPWID	TSP50 [153-172]	8	4803	PSTMTKARKRRRRRLMEL	THEG [112-131]
9	3481	DSCTGSQALLRLTPYSSDNL	WT1 [207-226]	8	4804	KARQSEADNNTLKLELITAE	TSGA10 [430-449]
10	3482	LASNHFYLYLPRDVLAQLPSL	5T4 [217-236]	8	4805	HHNSSLNFFNWFSDHNFAGS	TSPY1 [250-269]
10	3483	RKPAAGFLPSLLKVLLPLA	ACRBP [2-21]	9	4806	QDFAKYIEMHVIVEKQLYNH	ADAM2 [174-193]
10	3484	ENPGPSYARRRVSLGIDICH	ACTL8 [40-59]	9	4807	DSEKQFSTMRSGFMQNEIT	ADAM29 [153-172]
10	3485	LTNAIFVSFNITIISSLEL	ADAM2 [211-230]	9	4808	KQLQAVLQWVAASELNVPI	AKAP-3 [771-790]
10	3486	ILQINDFAYEIKPLAFSTTF	ADAM29 [126-145]	9	4809	MTDSDFVSAVKRNLFNQWKQ	AKAP-4 [398-417]
10	3487	ENCYSVYADQVNIDYLMNRP	AKAP-4 [153-172]	9	4810	RYKSYSPYDMLIESIRKEVKG	ANXA2 [231-250]
10	3488	VSNLSQGVMLSHSPICMETT	CAGE1 [38-57]	9	4811	LKAVHQQLQVLSQVFPFRKLN	BRDT [430-449]

10	3489	AIGLELWQVRSGTIFDNFLI	CALR3 [299-318]	9	4812	AISARFKPFSNKGKTLVIQY	CALR3 [76-95]
10	3490	TKKASILLIRKIYILMQNLG	CT46 [146-165]	9	4813	LHNLRFQIYVKQSDLQFLNF	CCDC62 [282-301]
10	3491	QLSRLMVGPHAAARNLWGNL	CT47 [146-165]	9	4814	BEGBQAAGLAAPRGGSAAE	CT47 [64-83]
10	3492	ELYQENEMKLYRKILVEEKC	CTAGE2 [357-376]	9	4815	LSGPAELRSFNMPSLDKMDG	CTAGE5 [634-653]
10	3493	PPPAPFAMRNVPYPPRGFPY	CTAGE5 [743-762]	9	4816	MSGDERSDEIVLTVSNSNVE	CTCFL [206-225]
10	3494	ACKQDLLAYLQRIALYCHQL	CTNNA2 [770-789]	9	4817	LVYDGVDIRKAVLMIRTPE	CTNNA2 [615-634]
10	3495	GPSDSGTRVLIGCVTSINED	CXorf48 [105-124]	9	4818	LEHTLLSKGFRGASPHRKST	CXorf61 [94-113]
10	3496	SGQRPRRCPPPPFYRRRFV	DBPC [216-235]	9	4819	VAFWIIKLPRRRSHQDALEG	DKKL1 [167-186]
10	3497	DSSGTLKFVAGGPLPSGLHG	DCAF12 [427-446]	9	4820	KTQNDVDIADVAYYFEKDVK	EpCAM [202-221]
10	3498	YPPPSYLGQSVQFFTFEDA	DMRT1 [294-313]	9	4821	IVKDALRNGSVASYILASHN	FAM46D [57-76]
10	3499	LASWARIAARAVQPKALNSC	DPPA2 [186-205]	9	4822	LQEYAGNFQGIHFHYDRNPG	FATE1 [98-117]
10	3500	EKAPEFSMQGLKAGVIAVIV	EpCAM [254-273]	9	4823	EMENTKKFLSLTAVSEETVG	FSIP1 [168-187]
10	3501	SKETFNLYYAESDLGYGTN	EPHA2 [114-133]	9	4824	VLLGLFSTIHDSIQYVQKNA	Glypican-3 [319-338]
10	3502	LRHKCCFSSSGTTSFKCFAP	FMR1NB [157-176]	9	4825	PKASTWVVASRRSSTVSRAP	HAGE [8-27]
10	3503	AQKLMRLQNLRGGHICLHDI	FTHL17 [67-86]	9	4826	NQPEQVILYQGGQMFDAAPR	IGFS11 [68-87]
10	3504	TTYPPYVPEYSSGLFPSSL	GATA-3 [220-239]	9	4827	KKNSYHFSAGFGSPIEDKSE	KU-CT-1 [643-662]
10	3505	DDMVNELFDSLFPVIYTQLM	Glypican-3 [164-183]	9	4828	VLKDFTVSGNLLFMSVRDQD	Lage-1 [122-141]
10	3506	CLNVSLADTNSLAVVSTQLI	gp100 [566-585]	9	4829	KLLTQDWQENYLEYRQVPG	MAGE-A10 [269-288]; MAGE-A4 [245-264]
10	3507	KYHSDDYIKFLRSIRPDNMS	HDAC1 [66-85]	9	4830	APEEKIWEELSVEVFEGRE	MAGE-A3 [216-235]; MAGE-A6 [216-235]
10	3508	SYKHLFPQVINQVVDYQPT	HDAC3 [231-250]	9	4831	KSPQGASAIPTAIDFTLWRQ	MAGE-A5 [63-82]
10	3509	ISHATLERIGAVPVMVPAQS	IGFS11 [406-425]	9	4832	LRKLLTQEWVQENYLEYRQA	MAGE-A8 [245-264]
10	3510	PQDFEIVDPGYLYLYLQWQ	IL13RA2 [35-54]	9	4833	DHFTFELNGASRRLELVFGL	MAGE-B1 [144-163]
10	3511	MNPNTLMTHEVPVYRTNQCA	JARID1B [556-575]	9	4834	KASEGLSVVFGLELNKVNPN	MAGE-B2 [155-174]
10	3512	MYVIDLMFHPGGLMKLSRE	KU-CT-1 [846-865]	9	4835	ILKKASFNMVVFVGLDKKV	MAGE-B3 [152-171]
10	3513	ISSIGLTYFQSSNLQCSTCT	LIP1 [418-437]	9	4836	DTTPNNFPLLYEEALRDEEE	MAGE-B4 [294-313]
10	3514	TGHSYVLVTCGLSYDGLLG	MAGE-A1 [165-184]	9	4837	DSSGESYTLVSKLGLPSEGI	MAGE-B6 [256-275]
10	3515	AQDRIATTDDTTAMASASS	MAGE-A10 [341-360]	9	4838	MIVIKYKDYFPVILKRAREF	MAGE-C2 [169-188]
10	3516	EVLSIMGVYAGREHFLFGEP	MAGE-A11 [336-355]	9	4839	EKQRELKTARTLSLFYGVNV	MORC1 [341-360]
10	3517	MAELVHFLLLKYRAREPFTK	MAGE-A12 [113-132]	9	4840	TDYYQELQRDISEMFLQIYK	MUC-1 [1063-1082]
10	3518	SVLRNCQDFFPVIFSKASEY	MAGE-A2 [138-157]	9	4841	AETEPERHLGSLYLLDSENTS	NKX3.1 [91-110]
10	3519	ALVETSYVKVLHMHVKISGG	MAGE-A3 [277-296]	9	4842	RNKSVRYLDLSANVLKDEGL	NLRP4 [805-824]
10	3520	SGGPRISYPLLEHWEALREGE	MAGE-A6 [294-313]	9	4843	RSLDPQSYSLIHQLLSAEDL	NR6A1 [244-263]

10	3521	MLGDGHSMPKAALLIIVLGV	MAGE-A9 [188-207]	9	4844	PNDYTKFVAEYFQERQMLGT	NYD-TSPG [185-204]
10	3522	RNGLLMPLLGVIIFLKNSAT	MAGE-B1 [197-216]	9	4845	EAEARRSLAQDAPPLPVPV	NY-ESO-1 [101-120]
10	3523	SVTKGEMLKIVGKRFRHFHP	MAGE-B2 [131-150]	9	4846	SMQNYVQFLKSSYANVFGDG	ODF2 [792-811]
10	3524	FLNMLGIYDGKRHLIFGEPR	MAGE-B4 [223-242]	9	4847	DVRVTKFAPQYTMAARVEP	ODF3 [189-208]
10	3525	IITEDLVQDKYVVYRQVCNS	MAGE-B6 [331-350]	9	4848	LHKEKYTLEQALLSASQEIE	PEPP2 [659-678]
10	3526	PVTEAEMLMIVIKYDYFPV	MAGE-C2 [161-180]	9	4849	IYTRRNYEAANSLIQNLFKV	PIWIL1 [499-518]
10	3527	KLKMCFNQIQNTYMVQYEKK	MORC1 [861-880]	9	4850	LVGNIVITRYNNRTYRIDDV	PIWIL2 [413-432]
10	3528	SDVPFFPSAQSGAGVPGWGI	MUC-1 [1142-1161]	9	4851	IRKTQKIVIKKREPLNFGIP	RCAS1 [102-121]
10	3529	PLCSTFSDQSAYVSAIRDCF	NXF2 [331-350]	9	4852	GAIRKMRDRWAVIAKMDRK	SCP-1 [946-965]
10	3530	VLVKRKLVDIIDLILNGL	NYD-TSPG [401-420]	9	4853	LQKKIMMETQQEIASVRKS	SCP3a [211-230]
10	3531	SLLMWITQCFLPVFLAQPPS	NY-ESO-1 [157-176]	9	4854	EKEKRTLLERKLSLENKLLQ	se57-1 [199-218]
10	3532	PYPYCLCYSKRSRSCGLCDL	ODF1 [51-70]	9	4855	EVLEERTRIQFIRWSHTRIF	SPATA19 [106-125]
10	3533	VVTFGIKHSYMTPLLDVDE	ODF3 [235-254]	9	4856	PTGGSRLASSEVLASIENI	SPO11 [35-54]
10	3534	FTCAILCYFNHKSFWSLILS	ODF4 [194-213]	9	4857	AFDDIATYFSKKKWKMKYS	SSX-1 [24-43]
10	3535	VVLEAPFLVGIEGSLKGSTY	OIP5 [113-132]	9	4858	WEKMKASEKIFVYVMKRKYE	SSX-2 [37-56]
10	3536	EELDESQKVIELFSVCTNE	PBK [284-303]	9	4859	WEKMKSEKIVYVMKLNIE	SSX-4 [37-56]
10	3537	TDGGLFLLADVSHKVRINDC	PIWIL2 [370-389]	9	4860	NGDDAFVRRPRVGSQIPEKM	SSX-5 [2-21]
10	3538	WPGFAISVSYFERKLLFSAD	PIWIL4 [243-262]	9	4861	NEGTSIVMEIQKQIEKKEK	TAF7L [384-403]
10	3539	NNDVCVHFHELHLGLGCPPN	PLAC1 [45-64]	9	4862	AAVALVSSSAWSSALGSQTT	TAG-1 [15-34]
10	3540	SPYLGQMINLRRLLLSHIHA	PRAME [253-272]	9	4863	IMLLERSIMAKEGPLKVAQT	TEKT5 [374-393]
10	3541	GEVKRQIYVAAFTVQAAAE	PSMA [726-745]	9	4864	KDRTMNLQDIRYILKNDLKD	TEX14 [497-516]
10	3542	DMNIYELIRGRRYPLSEKKI	RAGE-1 [86-105]	9	4865	KDLRRHKIYGRKRRLTSQDS	TEX15 [933-952]
10	3543	PTPDNVLSAVTPELINLAGA	SAGE1 [404-423]	9	4866	SEIELLRSQMANERISMQNL	TSGA10 [548-567]
10	3544	VECTYISIDQVPRTYAIMIS	SCRN1 [52-71]	9	4867	ESEQAALGEEAVLLDDIMA	TSPY1 [53-72]
10	3545	LCAALWILMKNPVLICLALS	SLCO6A1 [372-391]	9	4868	DSFQDYIKSYLEQASRIWSW	TYR [458-477]
10	3546	DQRTLAAAAAQGGFLFPPG	SOX-6 [275-294]	9	4869	KIESQRIISGRISGYISEAS	ZNF165 [201-220]
10	3547	IFYVYMKRYEAMTKLGFKKA	SSX-2 [46-65]	10	4870	KLSQKFTKVNFTFIQKLVLD	AFP [242-261]
10	3548	DLPCVIESLRTLDDKTFYKT	TAF7L [155-174]	10	4871	DAMLRKLYNVMFAKKVPEHV	AKAP-3 [375-394]
10	3549	VTLECFAGNPVPRIKWRKV	TAG-1 [257-276]	10	4872	EVDMLKIRSEFKRKYGKSLY	ANXA2 [297-316]
10	3550	LVMTKCRLEHELAIKANTLC	TEKT5 [443-462]	10	4873	PSRQTAIIVNPPPEYINTK	BRDT [4-23]
10	3551	MGTPRIQHLLILVLGASLL	TEX101 [1-20]	10	4874	PAQLAAQMLGKVSSIHSDQS	CABYR [172-191]
10	3552	PKPHVSDHNRLHLARPKAQ	THEG [290-309]	10	4875	TSKLQRLLAESRQMVTDLLEL	CCDC62 [631-650]
10	3553	VFKEAFHDISHCLKAQMEKI	TMEM31 [100-119]	10	4876	LKTEENSFKRLMIVKKEKLA	CDCA1 [334-353]
10	3554	QYFSDLFNILDTAIVILL	TPTE [152-171]	10	4877	SPPASNMLKMEWSREVTNTA	CRISP2 [52-71]
10	3555	HREKFCYELTGEPLVCSMEG	TSP50 [301-320]	10	4878	ALLARKQGAGDSLIIAGSAMS	CT45 [34-53]

10	3556	PEKDKFFAYLTLAKHTISSD	TYR [129-148]	10	4879	TLQTVHFTSEAVELQDMSLL	CTCFL [81-100]
10	3557	PYSSDNLQMTSQLECMTNW	WT1 [220-239]	10	4880	TDNNLAVYDLSRDILNNFPH	CXorf61 [53-72]
10	3558	EIHTKEQILELLVLEQFLTI	ZNF165 [81-100]	10	4881	LEGGHWLSEKRLHRLQAIRDG	DKKL1 [184-203]
11	3559	VLCSQPVSILSPNTLKEIEA	ACRBP [121-140]	10	4882	SVDSFQIVLDPMLDFYSDKN	FAM46D [172-191]
11	3560	GSNRNFSVWLGASVVAHLST	ACTL8 [330-349]	10	4883	PNTKAEMEMSLAEELNHGRQ	FATE1 [6-25]
11	3561	HHCHCNLYWDPPNCLIKGYG	ADAM29 [640-659]	10	4884	FERIMKYERLARILLQEPI	FBXO39 [289-308]
11	3562	DEKQWHDVSVYLGLTNCPSS	CCDC62 [457-476]	10	4885	PVKGYELAVTQHQQLAIEDI	FSIP1 [306-325]
11	3563	SADKMQLLNAHQEALMKLE	CDCA1 [148-167]	10	4886	MAASALRGLPVAGGESSES	GASZ [1-20]
11	3564	ARCMRDFVKHLKKLKRMI	CT45 [170-189]	10	4887	RNRPGMLVLTPTRELALQVE	HAGE [314-333]
11	3565	CAYGTRYLDDLCKVILREDK	CT46 [51-70]	10	4888	EMTKYHSDEYIKFLRSIRPD	HDAC2 [64-83]
11	3566	GAGAAARAGEGLGLIQEAAS	CT47 [175-194]	10	4889	QVNTDSETAVVNVYSSKDQ	KOC1 [112-131]
11	3567	CEKLNRFNSELVHEILCLEK	CTAGE2 [101-120]	10	4890	SILKNLRRVHPVSTMVKGly	LDHC [262-281]
11	3568	LEERLESITSGAALMADSSC	CTNNA2 [303-322]	10	4891	LGFSPGPILPSTRKLYEKKL	LEMD1 [19-38]
11	3569	ESIQFCFIWRAISITPVHKS	CXorf48 [223-242]	10	4892	GSDPVRYEFLWGPRLAETS	MAGE-A8 [266-285]
11	3570	RPPSVAPPPMVAEIPSGTG	DBPC [186-205]	10	4893	EPRKLITQDLVKLYLEYRQ	MAGE-B3 [243-262]
11	3571	KATDSFHTELHPRVAFWIK	DKKL1 [154-173]	10	4894	PVSSSFSYTLLSLFQSSPER	MAGE-C1 [446-465]
11	3572	SSFYQPSLFFYYNNLYNCPQ	DMRT1 [211-230]	10	4895	NAPPAYEKLSAEQSPPPYSP	MART1 [99-118]
11	3573	QKARCKIPALPLPTILPPIN	DPPA2 [74-93]	10	4896	RAKRKLYTSEISSPIDISGQ	MPHOSPH1 [175-1794]
11	3574	IVVVVIAVVAGIVVLVISRK	EpCAM [272-291]	10	4897	AFSHTQVIELERKFHQKYL	NKX3.1 [130-149]
11	3575	QDIGACVALLSVRVYKKCP	EPHA2 [183-202]	10	4898	FKDPKRAEAFNLVRESEQL	NLRP4 [315-334]
11	3576	SYERRQILHLITMMALKVLG	FAM46D [315-334]	10	4899	STWQELILLSSLTVYSKQIF	NR6A1 [322-341]
11	3577	VSKPFGMLMLSIWILLFVCY	FMR1NB [65-84]	10	4900	PKKPSAFKPAIEMQNSVPNK	NY-BR-1 [461-480]
11	3578	QVKTIKELGGYVSNLRKICS	FTHL17 [142-161]	10	4901	KNYEGMIDNYKSQVMKTRLE	ODF2 [537-556]
11	3579	CGHLITAVQNVITELPVNSQ	GASZ [367-386]	10	4902	SIPQFPITSDSTISTLETPO	PASD1 [668-687]
11	3580	QDEKECLKYQVPLPDSMKLE	GATA-3 [178-197]	10	4903	RSVPAGLTLSVSPQSLQGK	PEPP2 [595-614]
11	3581	GSLGPLLDGTATLRLVKRQV	gp100 [452-471]	10	4904	RRSIAGFVASINEGMTRWFS	PIWIL1 [641-660]
11	3582	GDVGNYYYGQGHMPKPHRIR	HDAC1 [17-36]	10	4905	GSEGTVVQLLANHFRVISRP	PIWIL3 [119-138]
11	3583	GDIGNYYYGQGHMPKPHRIR	HDAC2 [18-37]	10	4906	FEGRTRYSRITGGMEAEVGE	PRSS55 [59-78]
11	3584	PDVGNFHYGAGHPMKPHRLA	HDAC3 [11-30]	10	4907	APRLAEYQAYIDFEMKIGDP	SART3 [307-326]
11	3585	MTSQRSP LAPLLLSLHGVA	IGFS11 [1-20]	10	4908	ESKQLNVYEIKVNKLELELE	SCP-1 [632-651]
11	3586	TNYNLFYWYEGLDHALQCVD	IL13RA2 [167-186]	10	4909	GEVQNMLEGVGDINKALLA	SCP3a [68-87]
11	3587	DAFKSDYFNPVHMPVTELV	JARID1B [387-406]	10	4910	YESTSAHIEETEVVKKIRT	se57-1 [23-42]
11	3588	SVPLWSGVNVAGVALKTLDP	LDHC [197-216]	10	4911	IAKPNNAYEFGQIINALSTR	SPAG1 [800-819]
11	3589	LLGDNQIMPKTGFLIIVLVM	MAGE-A1 [182-201]	10	4912	STAHSRIRKERPISLGIFPL	SPAG9 [190-209]
11	3590	GILILILSIIFIEGYCTPEE	MAGE-A10 [225-244]	10	4913	QDIHVTRDVVKHHLKSKDLL	SPATA19 [81-100]

11	3591	HPRKLLMQDLVQENYLEYRQ	MAGE-A2 [241-260]	10	4914	DVLDRHRESLLAALRRGGRE	SPO11 [14-33]
11	3592	VFGIELMEVDPIGHLYIFAT	MAGE-A3 [161-180]	10	4915	DNDHNRRIQVEHPQMTFGRL	SSX-1 [85-104]
11	3593	LLGNNQIFPKTGLLIIVLGT	MAGE-A4 [190-209]	10	4916	FGRLQGIFPKIMPKKPABEG	SSX-3 [101-120]
11	3594	FGIELMEVDPIGHVYIFATC	MAGE-A6 [162-181]	10	4917	HRLRERKQLVVYEEISDPPE	SSX-4 [166-185]
11	3595	RYFPVIFGKASEFMQVIFGT	MAGE-A9 [144-163]	10	4918	QIPEKMQKAFDDIAKYFSEK	SSX-5 [16-35]
11	3596	KSGLLMSLLVVI FMNGNCAT	MAGE-B6 [284-303]	10	4919	KIEDLMEMVQKLQKVGSLPE	SYCE1 [32-51]
11	3597	LQGEFQSSLSQSPVSISSS	MAGE-C1 [616-635]	10	4920	TADELRMISSTFLNLPFQGI	TDRD1 [807-826]
11	3598	KHLCYCLYRPRKYLYVTSSF	MORC1 [262-281]	10	4921	RITIGTLFSLVHERRSQFPV	TEX14 [328-347]
11	3599	LVLVCVLVALAIVYLIALAV	MUC-1 [1164-1183]	10	4922	FRQPIFSQYASHQPLPQATY	TEX15 [2742-2761]
11	3600	EVLAGLLTNNKLTLYLVNSC	NLRP4 [741-760]	10	4923	RRQLDETDELAQIARERDI	TSGA10 [330-349]
11	3601	DMYIVQKYISNPLLIGRYKC	NYD-TSPG [235-254]	10	4924	TPESAPEBELLAVQVELEPN	TSPY1 [104-123]
11	3602	DHRQLQLSISSCLQQLSLLM	NY-ESO-1 [141-160]	11	4925	AYPEKMNRNVLELNSADLD	5T4 [324-343]
11	3603	DPCNPCYPCGSRFSCRKMIL	ODF1 [231-250]	11	4926	DVAFLLVYREKSNYVGATFQ	ADAM2 [264-283]
11	3604	VMKTRLEADEVAQAQLERCDK	ODF2 [550-569]	11	4927	LQTMKQEFLLINLVKQKPQIT	AFP [545-564]
11	3605	CSPGPRYNVNPILRTGKDL	ODF3 [64-83]	11	4928	YSDSWAEDLIVSALLLIQY	AKAP-3 [518-537]
11	3606	TSAHVMSMGLLHFYKSRSCS	ODF4 [126-145]	11	4929	KEFADSIKGLMVYANQVAS	AKAP-4 [323-342]
11	3607	QQQRGHTSMKAVYVEPAAAA	PASD1 [213-232]	11	4930	AQRQDIAFAYQRTKKELAS	ANXA2 [66-85]
11	3608	VSHKVIRNDCVLDVMHAIYQ	PIWIL2 [380-399]	11	4931	YNPPDHEVVTMARMQLQDVFE	BRDT [351-370]
11	3609	DTVQRLTYCLCHMYNLPGI	PIWIL3 [827-846]	11	4932	EYSDKTTQFPSPVYAVPGTEQ	CABYR [114-133]
11	3610	SAGSGQSPMTVLCSIDWFMV	PLAC1 [18-37]	11	4933	KEAQEQEFLSLQEEFQKLEK	CAGE1 [477-496]
11	3611	LLFSVLLLLSLVTGTQLGPR	PRSS55 [2-21]	11	4934	TQYDLSEFENIGAIGLELWQ	CALR3 [287-306]
11	3612	STAPPWLRHMAAGISSTIT	SAGE1 [646-665]	11	4935	NKHNELRKAVSPPASNMLKM	CRISP2 [42-61]
11	3613	PAEVLGLFYDCVDTEIKFFK	SCRN1 [395-414]	11	4936	SVRSRLYVGREKKLALMLSG	cTAGE5 [65-84]
11	3614	PIYLENQFILTPTVATTLAG	SLCO6A1 [407-426]	11	4937	DSKLAVSLAETTGLIKLEEE	CTCFL [166-185]
11	3615	GDNPYPVQFIPSTMAAAASG	SOX-6 [300-319]	11	4938	SGLINSNTDNNLAVYDLSRD	CXorf61 [46-65]
11	3616	AQNGCLYVHSSVAQWRKCLH	SPAG9 [976-995]	11	4939	HKDWIFSIAWISDTMAVSGS	DCAF12 [183-202]
11	3617	NDISCMKVSRRLHILSTS	SPO11 [155-174]	11	4940	LVIAEMMELGSRSRGASQKK	FATE1 [32-51]
11	3618	ISYVYMKRNYKAMTKLGFKV	SSX-1 [46-65]	11	4941	EDYFSSHLLAVYNPQFKKTM	FBXO39 [201-220]
11	3619	VMTKLGFKVTLPPFMRSKRA	SSX-4 [57-76]	11	4942	STEPGSFKVDASNLNSGKE	FSIP1 [35-54]
11	3620	IIVYVYMKRYEAMTKLGFKFA	SSX-5 [46-65]	11	4943	KMEEKYQLTARLNMEQLLQS	Glypican-3 [76-95]
11	3621	EILSKKQETLRILRLHCQEK	SYCE1 [100-119]	11	4944	IPEELVMAERFKAHQKQKRE	HAGE [613-632]
11	3622	ISNPGLFTSLGPPLRSTTCH	TDRD1 [152-171]	11	4945	QDTDTKITISPLQELTLNYP	KOC1 [304-323]
11	3623	LI IKAGTETAILATKCIPE	TEX101 [65-84]	11	4946	AAYNKLLNNLSLKYSGTGY	KU-CT-1 [542-561]
11	3624	ATSREFTNAYKLPLAVGPPS	TEX14 [779-798]	11	4947	LDGAQSDSDSEELNII LQGN	LEMD1 [58-77]
11	3625	QRFRGMLWFDLSLLPELVQC	TEX15 [2086-2105]	11	4948	DGSFSFKLLNQLGMIEEPRL	LIPI [373-392]

11	3626	HLFALSTLYFYKFFLPTILS	TMEM31 [126-145]	11	4949	LLTQNWVQEKYLVRQVPGT	MAGE-A11 [358-377]
11	3627	PSSRPRLWQTPTTQTL PST	TSP50 [66-85]	11	4950	EEQETASSSSTLVEVTLREV	MAGE-A12 [34-53]
11	3628	NLNHLIRHQRIHTREKPYE	ZNF165 [410-429]	11	4951	VAELVRFLLRKYQIKEPVTK	MAGE-A8 [116-135]
12	3629	NRKVS MRCLQNETYSALSP	ACRBP [501-520]	11	4952	LNGASRRLELVFGLDLKEDN	MAGE-B1 [150-169]
12	3630	QRVAPEMFFSPQVFEQPGPS	ACTL8 [252-271]	11	4953	NSATEEEIWEFLNMLGVYDG	MAGE-B2 [216-235]
12	3631	YVGKFLQIPRATIIYANIS	ADAM2 [549-568]	11	4954	SKMKVLEFWAKVNKTVP SAF	MAGE-B3 [284-303]
12	3632	LLHCLGVFLSCSGHIQDEHP	ADAM29 [6-25]	11	4955	FRKVSQRTEL VFGLALKEVN	MAGE-B4 [151-170]
12	3633	LAVSVILRVAKGYQELLEKC	AFP [365-384]	11	4956	PHSSPPYYEF LWGPRAHSES	MAGE-C2 [290-309]
12	3634	CPGSTMGYMAQSTQYEKCGG	AKAP-4 [570-589]	11	4957	QKFGDFLQHSPSILQSKAKK	MPHOSPH1 [1731-1750]
12	3635	QQDTKGDYQKALLYLCGGDD	ANXA2 [320-339]	11	4958	HQKYL SAPERAH LAKNLKLT	NKX3.1 [145-164]
12	3636	MISSKPRLVVPYGLKTLLEG	CABYR [1-20]	11	4959	SDEGMEVIERLIYLYHKFHQ	NR6A1 [362-381]
12	3637	LIHCSGEMLKFTESLAKSI	CAGE1 [193-212]	11	4960	PSLSQEQQEMVQAFAQSGM	NXF2 [566-585]
12	3638	ILHFKNKYHENKKLIRCKVD	CALR3 [147-166]	11	4961	IEVHNKASLTPLLSITKRS	NY-BR-1 [109-128]
12	3639	LNFNVENSQELIQMYDSKME	CCDC62 [299-318]	11	4962	LKEKIVLTHNRLKSLMKILS	OIP5 [199-218]
12	3640	GDCEGVI FEGEPMYLNVEV	CT46 [196-215]	11	4963	MQKLGFGTGVNVYLMKRSFR	PBK [35-54]
12	3641	GFVPPPLAPIRGLLPVDTR	CTAGE2 [659-678]	11	4964	YNVTS DYAVHP MSPVGRTSR	PEPP2 [128-147]
12	3642	PGFVPPPLAPIRGPLFPVDA	CTAGE5 [689-708]	11	4965	VGQSIHREP NLSLNRLYYL	PIWIL1 [842-861]
12	3643	GCGIHAIELNPSRTLLATGG	DCAF12 [140-159]	11	4966	VAGSMGFNVDPKIIKVQEN	PIWIL4 [509-528]
12	3644	LQFHAGQAWVPTTHRRMISL	DPPA2 [241-260]	11	4967	NLRRLLLSHIHASSYISPEK	PRAME [261-280]
12	3645	KFITSILYENNVITIDL VQN	EpCAM [179-198]	11	4968	EENSRLQERG VAYINADSS	PSMA [436-455]
12	3646	TWDQVITLDQVLDEVIPIHG	FAM46D [10-29]	11	4969	KRRGPAYVMELPKLKLSGVV	RAGE-1 [339-358]
12	3647	YFKIWAFLDV SFVERILKSQ	FBXO39 [370-389]	11	4970	QVISVTFE KALNAGFIQATD	SART3 [397-416]
12	3648	ISLILVCLPIYCRSLFWRSE	FMR1NB [193-212]	11	4971	DSDPALQKVNFLPVLEQVGN	SCP-1 [63-82]
12	3649	SNLRKICSP EAGLA EYLFDK	FTHL17 [154-173]	11	4972	DVIEGKTAVIEKRRKKRSSA	SCP3a [41-60]
12	3650	AARDGHTQV VALLVAHAEV	GASZ [156-175]	11	4973	EAQNKELKTQVALSSETPRT	se57-1 [289-308]
12	3651	RDGTGHYLCNACGLYHKMNG	GATA-3 [277-296]	11	4974	DLNKVILLDPSIIEAKMELE	SPAG1 [713-732]
12	3652	RLAQSYLKEPMIYVVGTLDL	HAGE [436-455]	11	4975	DIMRDRIEQVRRSISRLTDV	SPATA19 [134-153]
12	3653	LPYSEYFEYFAPDFTLHPDV	HDAC3 [323-342]	11	4976	PNRGNQVERPQMTFGR LQGI	SSX-2 [88-107]
12	3654	IFCIALILGAFFYWR SKNKE	IGFS11 [255-274]	11	4977	AQIPEKIQKAFDDIAKYFSK	SSX-3 [15-34]
12	3655	DLNKGIEAKIHTLLPWQCTN	IL13RA2 [96-115]	11	4978	KDKLKIDLLPDGRHAVVEVE	TAF7L [126-145]
12	3656	LYALPCVLSQTPLLKDLLNR	JARID1B [849-868]	11	4979	DFSTKSVFSKFAQLNLAAED	TAG-1 [214-233]
12	3657	PCDLPLRLLVPTQFVGAIIG	KOC1 [193-212]	11	4980	LQVRGAEASRLWASRLTDDS	TEKT5 [100-119]
12	3658	WLIHGYPVGS IPLWLQN FV	LIP1 [99-118]	11	4981	EDIPEISRLSISQKLPSTTM	THEG [97-116]
12	3659	EEGPSTSCILESLFRAVITK	MAGE-A1 [85-104]	11	4982	MDVLLRVFVERRQQYFSDLF	TPTE [139-158]
12	3660	PQSAQIACSSPSVVASLPLD	MAGE-A10 [84-103]	11	4983	DDERMEQMSNMTLMKETIST	TSGA10 [155-174]

12	3661	CIPEEVMWEVLSIMGVYAGR	MAGE-A11 [328-347]	11	4984	YEVEAYRRHHNSSLNFFNW	TSPY1 [241-260]
12	3662	MVELVHFLLKLRAREPVT	MAGE-A2 [113-132]	11	4985	FLHHAFVDSIFEQWLRHR	TYR [386-405]
12	3663	EFQAALSRKVAELVHFLLK	MAGE-A3 [104-123]	11	4986	GATLKGVAAGSSSSVKWTEG	WT1 [244-263]
12	3664	FPDIFSKASECMQVIFGIDV	MAGE-A8 [150-169]	12	4987	DERQNRSFEGMVVAALLAGR	5T4 [188-207]
12	3665	RRKLLMPLLGVIPLNGNSAT	MAGE-B2 [200-219]	12	4988	QKATDIMDAMLRKLYNMF	AKAP-3 [368-387]
12	3666	NCAREEEIWEFLNMLGIYDG	MAGE-B4 [213-232]	12	4989	ELEHLQTVKNISPLQILPPS	BRDT [743-762]
12	3667	AYAETTKMRVLRVLADSSNT	MAGE-B6 [363-382]	12	4990	QEKRGAVYERVITINQEIQK	CDC1 [381-400]
12	3668	LGLSNIKFRPGSVVQLTLA	MUC-1 [1087-1106]	12	4991	QLQVQREIVNKHNLKRAVS	CRISP2 [33-52]
12	3669	DRFLYTFYFCCRELRELPT	NLRP4 [180-199]	12	4992	MMQKPGSNAPVGGNVTSSFS	CT45 [84-103]
12	3670	MSVPPHYQYIPHLFSYSGHS	NR6A1 [217-236]	12	4993	QLLAERTKEQLFFVETMSGD	CTCPL [190-209]
12	3671	LRHTPSYIRCCERMKWHSED	NXF2 [76-95]	12	4994	ADMADVMRLSLHLKIVEEAL	CTNNA2 [141-160]
12	3672	LLWKKIHRMVILTILAIAPS	NYD-TSPG [340-359]	12	4995	VEEDKPHYGLRAIKVDVVR	CXorf48 [80-99]
12	3673	RRDIKKVDRELRLRCIDEF	ODF1 [12-31]	12	4996	SMVENKLVELEHTLLSKGFR	CXorf61 [85-104]
12	3674	LPFQWRITHSFRWMAQVLAS	ODF4 [66-85]	12	4997	VPPFRFRPRYRRPFRPRRQ	DBPC [272-291]
12	3675	LQEPCEVAFNQQLVQEQHL	PASD1 [470-489]	12	4998	KMTDNKTGEVLISENVVASI	DKK1 [108-127]
12	3676	LSHSPWAVKKINPICNDHYR	PBK [56-75]	12	4999	PQYSMALAADSASGEVGNPL	DMRT1 [229-248]
12	3677	TYKLCHIYYNWPGVIRVPAP	PIWIL1 [812-831]	12	5000	GVPFRTVSEWLESIKMQQYT	EPHA2 [903-922]
12	3678	CKYAHKLAFLSGHIHHEPA	PIWIL2 [944-963]	12	5001	VAQTSLEEFNVLEMEVMRRQ	FATE1 [121-140]
12	3679	SEKILMQDHICQPVSAADWS	PIWIL4 [451-470]	12	5002	KHNQDFIKRNIELAKESRNP	FSIP1 [249-268]
12	3680	CKKLKIFAMPMQDIKMLKM	PRAME [210-229]	12	5003	ARRDLKVFGNPFKLIMTQVS	Glypican-3 [201-220]
12	3681	EGNYTLRVDCPTPLMSLVHN	PSMA [457-476]	12	5004	SYTWDFGDSSGTLISRALVV	gp100 [257-276]
12	3682	TVPPAFINMAATGVSSMSTR	SAGE1 [600-619]	12	5005	PYNDYFEYFGPDFKLHISPS	HDAC1 [329-348]; HDAC2 [330-349]
12	3683	RNCPWTVALWSRYLLAMERH	SART3 [373-392]	12	5006	RQQTDMAVNWAGGLHHAKKS	HDAC2 [127-146]
12	3684	GVRICISQLSLTTKMDAHP	SCRN1 [183-202]	12	5007	LQEPSDLRAVLLINSKSYVS	KU-CT-1 [592-611]
12	3685	TLIFSGFSGVPIVLAMTRVV	SLC6A1 [588-607]	12	5008	GETRLALVQRNVAIMKSIIP	LDHC [103-122]
12	3686	AAAQQGFLFPPGITYKPGDN	SOX-6 [283-302]	12	5009	AREPFTKAEMLGSVIRNFQD	MAGE-A12 [126-145]
12	3687	SKAERFKMMLTLISKGQKEL	SPAG1 [877-896]	12	5010	DGREHTVYGEPRKLLTQDWW	MAGE-A4 [233-252]
12	3688	RYDEEVVKELMPLVVAVLEN	SPAG9 [41-60]	12	5011	AEMLESVIKNYKRYFPVIFG	MAGE-A9 [132-151]
12	3689	SFEAHHLTPAIRWLGLLPS	SPO11 [297-316]	12	5012	ETTKMKVLEFLAKMNGATPR	MAGE-B1 [279-298]
12	3690	HNRRIQVEHPQMTFGR LHRI	SSX-1 [88-107]	12	5013	LKKPQRALSTTTSVDVSYKK	MAGE-B3 [62-81]
12	3691	PNRGNQVEHPQMTFGR LQGI	SSX-5 [88-107]	12	5014	LQIPVSPSSSTLLSLFQSF	MAGE-C1 [233-252]
12	3692	KDLGEARTICEALQKELDSL	SYCE1 [72-91]	12	5015	KDYFPVILKRAREFMELLFG	MAGE-C2 [175-194]
12	3693	TPWMDYEFVRIASNILGTGE	TAG-1 [676-695]	12	5016	LKSGSMRIGKDFILFTKKEE	MORC1 [103-122]
12	3694	LRLRETQDTLQLLVMTKCR	TEKT5 [431-450]	12	5017	BENIGILPRTLNVLFDSLQE	MPHOSPH1 [166-185]

12	3695	FCNDKDSLSQFWEFSETTAS	TEX101 [113-132]	12	5018	RAHLAKNLKLTETQVKIWFQ	NKX3.1 [154-173]
12	3696	EHSSKLRHPYLLQLMAVCLS	TEX14 [297-316]	12	5019	SLVEKTPDEAASLVEGTSKD	NY-BR-1 [263-282]
12	3697	QRILTVDSPAASSTVPHCEQ	TEX15 [1357-1376]	12	5020	FKLENERLKASFAPMEDKLN	ODF2 [504-523]
12	3698	IPRSSLEYRASSRLKELAAP	THEG [219-238]	12	5021	KASQPSFSIKGRSKLGGFSD	ODF3 [155-174]
12	3699	PTILSLSFFILLVLLLLLFI	TMEM31 [141-160]	12	5022	DQASFTTSMEDWTQVVKGSS	OIP5 [29-48]
12	3700	LVDVVYIFFDIKLLRNIPRW	TPTE [171-190]	12	5023	TEADRVIQRTNSMQLEQWI	PEPP2 [399-418]
12	3701	PEAVARRWPWMVSVRANGTH	TSP50 [117-136]	12	5024	DVSHKLLRIETAYDFIKRTS	PIWIL3 [283-302]
12	3702	QALVCASAKEGTAFRMEAVQ	TSPY1 [27-46]	12	5025	QEAQPLQPSHFLDISDWSL	PLAC1 [184-203]
12	3703	EAPAFLPWHRLFLLRWEQEI	TYR [203-222]	12	5026	LTSPSMEIKEVASIILHKDF	PRSS55 [129-148]
12	3704	RNQQYSTVTFDGTPSYGHTP	WT1 [145-164]	12	5027	YDPDERIAAHQALQHPYFQE	RAGE-1 [268-287]
12	3705	CSECGRAFSQSSNLSQHORI	ZNF165 [458-477]	12	5028	FVPPRSSSSQVSAVKPQTLG	SCP-1 [10-29]
13	3706	MNPEAIFHSGVKIFSNCSFE	ADAM2 [338-357]	12	5029	RKRLEMYTKASLKTSNQKIE	SCP3a [89-108]
13	3707	TMRSGFMQNEITCRMEFEEI	ADAM29 [161-180]	12	5030	NLVQRMEKEKRTLLEKRLSL	se57-1 [193-212]
13	3708	SILDSYQCTAEISLADLATI	AFP [30-49]	12	5031	EQVRRSISRLTDVSAQDFSM	SPATA19 [141-160]
13	3709	GDLEN AFLNLVQCIQNKPLY	ANXA2 [250-269]	12	5032	PNRGNQVQRPMQTFGRLLQGI	SSX-3 [88-107]
13	3710	LQCSNLYLEKRVKELQMKIT	CAGE1 [326-345]	12	5033	KQKNEKLISLQEQQLRFLKK	TAFTL [443-462]
13	3711	LYPNKPPEVLHMIYMRALQI	CDCA1 [36-55]	12	5034	IISDVLIDEHLVLKASAPHK	TDRD1 [883-902]
13	3712	CGIAYCPNQDSLKYVVCQY	CRISP2 [150-169]	12	5035	DKKSENIASLGESLAMKEKT	TSGA10 [278-297]
13	3713	VTSLRYVRREKKFAVALSGL	CTAGE2 [36-55]	13	5036	LADLSPFAFGSGNASVSAPS	5T4 [154-173]
13	3714	CFRQKQLLNAHFRKYHDANF	CTCFL [522-541]	13	5037	SPNTLKEIBASAEVSPTTMT	ACRBP [131-150]
13	3715	GVKLVRMAATQIDSLCPQVI	CTNNA2 [444-463]	13	5038	IERGRILNWEGVQYLWSFVL	ACTL8 [67-86]
13	3716	SFCGDYGMIDESIYFSSDVV	CXorf48 [45-64]	13	5039	PPSKKSFFYKEVFESRNGDY	AKAP-3 [234-253]
13	3717	ATVPATAAGVVAVVVPVAG	DBPC [16-35]	13	5040	DIMEAMLKRLVSALIGEEKE	AKAP-4 [421-440]
13	3718	VVHGRLLSADTKGWVRLQFH	DPPA2 [225-244]	13	5041	DEIEIDFETLKASTLRELEK	BRDT [550-569]
13	3719	MAPPQVLAFLGLLAAATATF	EpCAM [1-20]	13	5042	KTTSGMSKKSVESVKLAQLE	CABYR [350-369]
13	3720	GMTKYDYLMTHLGVVNESTV	FAM46D [292-311]	13	5043	QDWEKHFLDASTSKQSDWNG	CALR3 [226-245]
13	3721	VLTKKFQVTMRGLSCLSKS	FBXO39 [103-122]	13	5044	EKQDYKQKLKALKIEVNKLK	CCDC62 [204-223]
13	3722	RAMRVAHLELATYELAATES	FMR1NB [17-36]	13	5045	ESPDLSISHSQVEQLVNKTS	CT46 [306-325]
13	3723	PASSSSLSGGHASPFLFTFP	GATA-3 [135-154]	13	5046	TLEGERNQIYIQLSEVDKTK	cTAGE5 [328-347]
13	3724	LQVTRIFLQALNLGIEVINT	Glypican-3 [223-242]	13	5047	SRDILNFPFHSIARQKRILV	CXorf61 [63-82]
13	3725	FYTDDRVTVSFHKYGEYFP	HDAC1 [187-206]; HDAC2 [188-207]	13	5048	VVDVQTSQITKIPILKDREP	DCAF12 [114-133]
13	3726	NANIPSIYANGTHLVPGQHK	IGFS11 [351-370]	13	5049	EVLISENVVASIQPAEGSFE	DKKL1 [116-135]
13	3727	VIFVTGLLLRKPNTYPMIP	IL13RA2 [355-374]	13	5050	GISHPIPLPSAELLVKREN	DMRT1 [132-151]
13	3728	ENDQVVVKITGHFYACQVAQ	KOC1 [531-550]	13	5051	DLAPDTTYLVQVQALTQEGQ	EPHA2 [496-515]
13	3729	IQSAYEIIKLGYSWAIGL	LDHC [235-254]	13	5052	KAAGSASAKRVNMTATRPK	FATE1 [57-76]

13	3730	FNTQKKTVWLHGYRVPVGS	LIP1 [91-110]	13	5053	SKTLGIGRLKRPSFLDDPLY	FSIP1 [524-543]
13	3731	EALNMMGLYDGMHLYGEP	MAGE-A10 [248-267]	13	5054	EAGLAEYLFDKLTLGGRVKE	FTHL17 [163-182]
13	3732	KVLHLLKISGGPHISYPPL	MAGE-A12 [285-304]	13	5055	PVNSQKITLWASQPNTSV	GASZ [382-401]
13	3733	EQQTASSSSTLVEVTLGEVP	MAGE-A2 [35-54]	13	5056	MEVTVYHRRGSRSYVPLAHS	gp100 [184-203]
13	3734	AEMLGSVVGWQYFFPVIFS	MAGE-A3 [133-152]; MAGE-A6 [133-152]	13	5057	KALENFKTGKVRILIATDLA	HAGE [528-547]
13	3735	WEAGMLMHFILRKYKMREPI	MAGE-B1 [110-129]	13	5058	QNSRQYLDQIRQTIFENLKM	HDAC3 [349-368]
13	3736	VVFGLELNKVNPNGHTYTFI	MAGE-B2 [162-181]	13	5059	SIPVHLNSLPRLETVAEVQ	JARID1B [1048-1067]
13	3737	LCNDVLAMKRSSSLPSWKS	MORC1 [757-776]	13	5060	THEDKIVRRNATMIFGILAS	KU-CT-1 [77-96]
13	3738	MTPGTQSPFFLLLLLTVLTV	MUC-1 [1-20]	13	5061	APEEEIWEELSVMVEVDGRE	MAGE-A1 [209-228]
13	3739	AELFALLCRLADELLFRQIA	NR6A1 [281-300]	13	5062	TVRPADLTRVIMPLEQRSQH	MAGE-A11 [100-119]
13	3740	HENENYLLHENCMLKKEIAM	NY-BR-1 [1038-1057]	13	5063	PVIFGKASESLKMIFGIDVK	MAGE-A4 [149-168]
13	3741	SQALGSLRTTTPAFTLNIPS	NYD-TSPG [12-31]	13	5064	TKAEMLESVIKKNHFPDI	MAGE-A8 [134-153]
13	3742	ENRYDCLGSKKYSYMNICKE	ODF1 [155-174]	13	5065	EPRKLLTQDWVQENYLEYRQ	MAGE-A9 [240-259]
13	3743	RTKAFRVDSTPGPAAAYMLPM	ODF3 [127-146]	13	5066	QSRTDPLIMKTNMLVQFLME	MAGE-B3 [105-124]
13	3744	KVTFFISTLMLFPINIWIFE	ODF4 [151-170]	13	5067	TTAMTSAYSRSATSSSSSQPM	MAGE-B4 [327-346]
13	3745	KSSQRKLNWIPSFPTYDYFN	PASD1 [15-34]	13	5068	EYKPYFPQILNRTSQHLVVA	MAGE-B6 [228-247]
13	3746	MARGLYLHQEKLLHGDIC	PBK [150-169]	13	5069	PLQSPVISFSSSTSLSPFSE	MAGE-C1 [850-869]
13	3747	FVASINLTITKWYSRVVFQM	PIWIL2 [760-779]	13	5070	EEEEASSASSTLYLVFSPS	MAGE-C2 [34-53]
13	3748	MSLKGHLQSVTAPMGITMKP	PIWIL3 [523-542]	13	5071	KKIETMSSSKLSNVEASKE	MPHOSPH1 [1749-1768]
13	3749	PSLSHCSQLTTLSTFYGNSIS	PRAME [400-419]	13	5072	LSSELGDLEKHSSLPALKEE	NKX3.1 [184-203]
13	3750	VLPGLTYLTAVGIPAMSTRD	SAGE1 [554-573]	13	5073	KFKEHLKQMTLQLELKQIPW	NLRP4 [25-44]
13	3751	FIDENVATHSAGIYLGIAEC	SLCO6A1 [253-272]	13	5074	SETLKHLLVQLFQQYYSIYD	NXF2 [385-404]
13	3752	CWPTGGATVAEARVYRDARG	SOX-6 [594-613]	13	5075	ELSKSMESMRGHLQAQLRSK	ODF2 [337-356]
13	3753	KEACAHLLAITAPKDLPMFL	SPAG1 [822-841]	13	5076	IVNASEMDIQNVPLSEKIAE	OIP5 [179-198]
13	3754	AGSIYREFERLIGRYDEEVV	SPAG9 [28-47]	13	5077	YSPQRTYRSEVSSPIQRGDV	PEPP2 [556-575]
13	3755	YVYMKRKYEAMTKLGFKAIL	SSX-3 [48-67]	13	5078	LQFYNIIFRRLKIMNLQOI	PIWIL1 [209-228]
13	3756	IKATKPLLMQYCSIKIVDI	TDRD1 [396-415]	13	5079	DYPKIIKVQENPAFVRAIQ	PIWIL4 [518-537]
13	3757	KCCGLTSLPAVQAPVIECY	TEKT5 [17-36]	13	5080	LYSEELFPEELSVVLGTNDL	PRSS55 [110-129]
13	3758	EVKGCTAMIGCRMSGILAV	TEX101 [181-200]	13	5081	SFDSLFSVKNFTETASKFS	PSMA [628-647]
13	3759	ILKKGIIYDAVNSLGQTALF	TEX14 [42-61]	13	5082	YVMELPKLKLGGVRLSSYS	RAGE-1 [345-364]
13	3760	PTLRSLWYDETLYAELLGK	TEX15 [1714-1733]	13	5083	AIVEAARLEKVHSLFRRQLA	SART3 [237-256]
13	3761	KRYVAYFAQVKHLYNWNLP	TPTE [391-410]	13	5084	BETRQVYMDLNNNIEKMITA	SCP-1 [205-224]
13	3762	PRTSAPSRAGALLLLLLLLR	TSP50 [14-33]	13	5085	LQQSRIVQSRLKTIKQLYE	SCP3a [161-180]

13	3763	YRVPERLRQGFQGVGRAAQA	TSPY1 [9-28]	13	5086	DRDEAWVLETIGKYWAAEKV	SCRN1 [161-180]
13	3764	LAVLYCLLWSFQTSAGHFPR	TYR [3-22]	13	5087	KQEDSKQLLQVKNLEKEQKL	se57-1 [148-167]
14	3765	YASWFESFCQFTHYRCSNHV	ACRBP [96-115]	13	5088	FLPITSSDIDVVESEAVSVL	SPATA19 [20-39]
14	3766	MAARTVIDHGSGLKAGTA	ACTL8 [1-20]	13	5089	ADSKMKAEIQALTFLSSDYL	SPO11 [362-381]
14	3767	SKPMRWPFLLFIPFFIIFCV	ADAM2 [682-701]	13	5090	LQIEEEKNKQRQLRLAFEEQ	SYCE1 [142-161]
14	3768	NIVDSILDVIGVKVLLFGLLE	ADAM29 [230-249]	13	5091	GSIPGFLISSGMSSHKQGHT	TAF7L [295-314]
14	3769	LTSSSELMAITRKMAATAATC	AFP [442-461]	13	5092	TDGRHFVSQTTGNLYIARTN	TAG-1 [179-198]
14	3770	TNSLQKQLQAVLQWIAASQF	AKAP-4 [767-786]	13	5093	EDTTLTITVPAVSRVVEELS	THEG [179-198]
14	3771	ASALKSALSGHLETVILGLL	ANXA2 [84-103]	13	5094	ENELDSAHSIEILLRSQMAN	TSGA10 [540-559]
14	3772	NGKSQYYIMFGPDICGFDIK	CALR3 [123-142]	13	5095	IQDVRRVPGVAPTLLVRSASE	WT1 [297-316]
14	3773	KALESNQMECQTALQKTQLQ	CCDC62 [94-113]	13	5096	EHGQEIFQKKVSPPGPALNV	ZNF165 [142-161]
14	3774	PRYNVAEIVIHIRNKILTGA	CDCA1 [7-26]	14	5097	GYHYRYEINADPRLTNLSSN	5T4 [398-417]
14	3775	SREVTNTAQRWANKCTLQHS	CRISP2 [64-83]	14	5098	MDTSTDVPRVLSWLRRDLEK	AKAP-3 [32-51]
14	3776	EHQSLVLVKRLLAHSVSCIT	CT46 [23-42]	14	5099	PNHHQLAFNYQLEHLQTVK	BRDT [732-751]
14	3777	GTGVQSTFTTFYEVD CDVID	CTNNA2 [810-829]	14	5100	DQAPEVTLQADIEVMSTVHI	CABYR [274-293]
14	3778	IHTEEVCITSVHGRNGVIDY	CXorf48 [175-194]	14	5101	SDEAKSIRDVPTLLGAKLDK	CAGE1 [674-693]
14	3779	FYLLLASSILCALIVFWKYR	CXorf61 [3-22]	14	5102	SKSLKSQVAEAKMTFKRFQA	CTAGE2 [150-169]
14	3780	RNYFSDIDFFPNAVYTHCYD	DCAF12 [408-427]	14	5103	AEAKMTFKIFQMNEERLKIA	cTAGE5 [188-207]
14	3781	QASGVRWCVVHGRLLSADTK	DPPA2 [217-236]	14	5104	AFQDSVLEEEVELVLAPSEE	CTCFL [55-74]
14	3782	GIAAGMKYLANMNYVHRDLA	EPHA2 [722-741]	14	5105	PQRPRNRPYFQRRRQAPGP	DBPC [316-335]
14	3783	LHLITMALKVLGELNILPN	FAM46D [322-341]	14	5106	LFSAPMDFRGLPGNYHKEEN	DKK1 [71-90]
14	3784	LIIAVLVSASIANLWLWMNQ	FATE1 [164-183]	14	5107	VENTPDLVSDSTYYSSFYQP	DMRT1 [197-216]
14	3785	LPIYCRSLFWRSEPADDLQR	FMR1NB [200-219]	14	5108	TVNGEQDLDPGQTLIYYVD	EpCAM [234-253]
14	3786	YTSYLYLSMAFYFNRRDVAL	FTHL17 [30-49]	14	5109	KYRKLIIESELSYFVIVYSVM	FBXO39 [423-442]
14	3787	VSTWNSRILKRTAITICGFG	GASZ [443-462]	14	5110	DIEDVTPVFPQLSRSIISKL	FSIP1 [433-452]
14	3788	RAMLGHTMEVTVYHRRGSR	gp100 [176-195]	14	5111	SSFNPAALSRHMSSLSHISP	GATA-3 [390-409]
14	3789	KIKNIQSTNTTTIQIIEQEP	HAGE [89-108]	14	5112	EAFEIVVRHAKNYTNAMFKN	Glypican-3 [113-132]
14	3790	EAFKPVMSKVMEMFQPSAV	HDAC1 [238-257]	14	5113	GEARLREMEALQSLRLANEG	JARID1B [1146-1165]
14	3791	FCSRYTGASLQGATQLNNKI	HDAC3 [103-122]	14	5114	GGLKKLLSFAENSTIPDIQK	KU-CT-1 [274-293]
14	3792	MPATNVSIFINNTQLSDTGT	IGFS11 [98-117]	14	5115	GSDPRSFLWYEEALKDEEE	MAGE-A10 [320-339]
14	3793	WEGEDLSKKTLLRFWLPFGF	IL13RA2 [331-350]	14	5116	REDSGDFGLQVSTMFSEDDF	MAGE-A11 [23-42]
14	3794	SMNLQAHILPGLNLNALGLF	KOC1 [357-376]	14	5117	APEEKIWEELSMLEVFEGRE	MAGE-A2 [216-235]
14	3795	VIGSGCNLDSARFRYLIGEK	LDHC [158-177]	14	5118	KASSSLQLVFGIELMEVDPI	MAGE-A3 [153-172]
14	3796	LETNCNFISFPCRSYKDYKT	LIPI [285-304]	14	5119	AASSSSTLIMGTLEEVTDSG	MAGE-A8 [38-57]
14	3797	PARYEFLWGPRALAETSYVK	MAGE-A1 [259-278]	14	5120	EEPSSSVDPAQLEFMFQEAL	MAGE-A9 [89-108]

14	3798	CAPEEKIWEELSVLEASDGR	MAGE-A12 [215-234]	14	5121	GEPRKFITQDLVQEKYLKYE	MAGE-B1 [239-258]
14	3799	ELVTKAEMLERVIKKNYKRCF	MAGE-A4 [129-148]	14	5122	AETSKMKVLEFLAKVNGTTP	MAGE-B2 [281-300]
14	3800	VAKLVHFLLLKYRAREPVTK	MAGE-A6 [113-132]	14	5123	NSNPARYEFLWGPRAHAETS	MAGE-B3 [265-284]
14	3801	AGARPRVAARRGTTAMTSAY	MAGE-B4 [315-334]	14	5124	PHLYEDALIDEVERALRLRA	MAGE-B6 [388-407]
14	3802	EEVIWEVLNAVGVYAGREHF	MAGE-C2 [246-265]	14	5125	SDEQGMNQNRLLILILSIIF	MAGE-C1 [989-1008]
14	3803	KCGTLLVIYNLKLNLNGEPE	MORC1 [193-212]	14	5126	TSASGSASGSASTLVHNGTS	MUC-1 [959-978]
14	3804	TTQKEFFQGCIMQPVKDLLK	MPHOSPH1 [123-142]	14	5127	EAFSRASLVSVYNSYPYPY	NKX3.1 [203-222]
14	3805	NRFPDLMMLPEIRYIAGKM	NR6A1 [435-454]	14	5128	MAASFFSDFGLMWYLEELKK	NLRP4 [1-20]
14	3806	QTERMLCFSVNGVFKEVEGQ	NXF2 [491-510]	14	5129	RADPVDLEFSVDQVDSVDQE	PASD1 [298-317]
14	3807	INLVDVYGNTALHYAVYSEI	NY-BR-1 [76-95]	14	5130	SATEVGRIQASPLPRSVDL	PIWIL4 [17-36]
14	3808	FSDFKDFIFDDMYIVQKYIS	NYD-TSPG [225-244]	14	5131	KYADKIYSISMKHPQEMKTY	PSMA [606-625]
14	3809	IEAARRQFQSQLADLQQLPD	ODF2 [582-601]	14	5132	YVEIWQAYLDYLRRRVDFKQ	SART3 [417-436]
14	3810	TKPCAPVVTFGIKHSDYMT	ODF3 [229-248]	14	5133	MEKQKPFALFVPPRSSSSQV	SCP-1 [1-20]
14	3811	KSFWSLILSHPSGAVSCSSS	ODF4 [205-224]	14	5134	IEKRKRKRSSAGVVEDMGGE	SCP3a [50-69]
14	3812	PLGPAGLGAEPAAGPQLPS	OIP5 [49-68]	14	5135	QDKRIENLREKVNILEAQNK	se57-1 [274-293]
14	3813	GYRAFTEANDGSLCLAMEYG	PBK [99-118]	14	5136	LKNNLIEKDPSLVYQHLLYL	SPAG1 [857-876]
14	3814	GILGSILLPSFQIALLTSED	PEPP2 [209-228]	14	5137	KTRDGGSVVGASVFYKDVAG	SPAG9 [699-718]
14	3815	LRDWGLSFDNLLSFSGRIL	PIWIL1 [438-457]	14	5138	PDVENEVKRLLRSDAEAVST	TAF7L [259-278]
14	3816	TITSCWEVDFYLLAHHVRQG	PIWIL2 [880-899]	14	5139	WKRLGWESSRIIVLDQSDL	TEX14 [1476-1495]
14	3817	TYCLCHMYNLPGIIRVPAP	PIWIL3 [833-852]	14	5140	PSSRILQLSKPKAPATLLEE	THEG [264-283]
14	3818	TWKLPFLAKFSPYLGQMINL	PRAME [243-262]	14	5141	DLKIQIEMEKKVVFSTISLG	TPTE [430-449]
14	3819	SVLLLLSLVTGTQLGPRTP	PRSS55 [5-24]	14	5142	KVITKEYLVNITEYRASHST	TSPY1 [214-233]
14	3820	PLLTNNLSPQCLSLHAMVA	RAGE-1 [248-267]	14	5143	FINHQIYYAGEKNHQYKGSF	ZNF165 [307-326]
14	3821	RRFGQNYERIFILLEEVQGS	SAGE1 [836-855]	15	5144	EDVVLRWSEFSTLTGQFG	ACRBP [524-543]
14	3822	IHYFTGTPDPSRSIFKPFIF	SCRN1 [291-310]	15	5145	QKQSSYVGWWIHFRIVEIVV	ADAM29 [185-204]
14	3823	VIVSTLEMSCKALMRFIMVT	SLCO6A1 [442-461]	15	5146	ERQLNEAVGNVTPLQLLDWL	AKAP-3 [830-849]
14	3824	QIQVQGHMPLMIPIFPHDQ	SOX-6 [257-276]	15	5147	VPHLQKVFDTRYKSYSPYDML	ANXA2 [222-241]
14	3825	NCTCGATAVAVPSNIQGIN	SPO11 [193-212]	15	5148	KNGRLTNQLQYLQKVVLKDL	BRDT [24-43]
14	3826	AHRKHTMLQECCKERISALNL	SYCE1 [123-142]	15	5149	APGHMSDVEWMSIFKPSKMQ	CCDC62 [525-544]
14	3827	RNGGTSMVMENMAVRPAPHP	TAG-1 [1002-1021]	15	5150	LKEFEKTIHFYQKKIILHEK	CTAGE2 [408-427]
14	3828	VIYSPGEFYCHVLKEDALKK	TDRD1 [722-741]	15	5151	SIYFSSDVVTGNVPLKVGQK	CXorf48 [56-75]
14	3829	QAPVIQECYQPYLPGYRYL	TEKT5 [28-47]	15	5152	VPVKGSRYPNRRKSRRFIP	DBPC [166-185]
14	3830	ADPANMFNWTTEEVETCDKG	TEX101 [38-57]	15	5153	DAQESSLGLTGLQSLQGF	DKKL1 [37-56]
14	3831	LICREDNAVSAATALLESEE	TEX15 [541-560]	15	5154	AISYRKFTSASDVWSFGIVM	EPHA2 [788-807]

14	3832	EQAQEEITRLRREMMKSCSKS	TSGA10 [69-88]	15	5155	VESAVWYVKKFGRYLEHLEV	FBXO39 [75-94]
14	3833	KLKQELKYSNYVRPICLPGT	TSP50 [211-230]	15	5156	KRKRKSEMLQKAARGREEHG	FMR1NB [234-253]
14	3834	LYRNGDFFISSKDLGYDYSY	TYR [432-451]	15	5157	QGLEMRKILWEEIKSAKYSE	FSIP1 [142-161]
14	3835	SDNHTTPILCGAQYRIHTHG	WT1 [273-292]	15	5158	LENFFRYFLRLSDDKMEHAQ	FTHL17 [49-68]
15	3836	GLPHIRVFLDNNPWVCDCHM	5T4 [283-302]	15	5159	SKDQKILAAKELQVEETIQ	GASZ [320-339]
15	3837	TLYPGFTKRLFRELMGDHVS	ACTL8 [302-321]	15	5160	KVKNQLRFLAELAYDLVDVDD	Glypican-3 [515-534]
15	3838	PTISLES LAVILAQLLSLS	ADAM2 [299-318]	15	5161	SQKRSFVYVWKTWQYVQVL	gp100 [144-163]
15	3839	TSSYANRRPCFSSLVVDETY	AFP [502-521]	15	5162	NLLLNLYGLYRKMEIYRPHKA	HDAC1 [40-59] ; HDAC2 [41-60]
15	3840	PDGECSIDDL SFYVNLSSL	AKAP-4 [208-227]	15	5163	KKIRESYENDIASMNLQAH	KOC1 [345-364]
15	3841	PSSEAAEDVMVAAPLVCSGK	CABYR [210-229]	15	5164	EALFKKSAETLWNIQKDLIF	LDHC [313-332]
15	3842	FKKIKANYVCLQERYMTEMQ	CAGE1 [410-429]	15	5165	KPPYSRLDYTDKAFVDVIHS	LIP1 [213-232]
15	3843	SGTIFDNFLITDDEEYADNF	CALR3 [309-328]	15	5166	SFSQDILHDKIIDLVLHLR	MAGE-A11 [216-235]
15	3844	FLWQYKSSADKMQLNAAHQ	CDCA1 [141-160]	15	5167	PRKLLTQDLVQENYLEYRQV	MAGE-A12 [242-261]
15	3845	KGLCTNSCQYQDLLSNCDL	CRISP2 [198-217]	15	5168	GSNPARYEFLWGPRALAE	MAGE-A4 [264-283]
15	3846	KWMLGCYDALQKKYLRMVVL	CT46 [80-99]	15	5169	VVDEKYKDHFEILNGASRR	MAGE-B1 [137-156]
15	3847	AFLSPPTLLEGPLRLSPLLP	CTAGE5 [533-552]	15	5170	TKGEMLKIVGKRFRHFPEI	MAGE-B2 [133-152]
15	3848	RQSLQQCVAISIQQELYSPQ	CTCF1 [127-146]	15	5171	KMKKPIMKADMLKIVQKSHK	MAGE-B3 [127-146]
15	3849	RAARALLSAVTRLLILADMA	CTNNA2 [125-144]	15	5172	LKIIISKYKEHFPEIFRKVS	MAGE-B4 [136-155]
15	3850	ILCALIVFWKYRRFQRNTGE	CXorf61 [11-30]	15	5173	LQIPVSRFSSTLLSIFQSS	MAGE-C1 [198-217]
15	3851	AVSLDGYFHLWKAENTLSKL	DCAF12 [269-288]	15	5174	ASSTLYLVFSPSSFSTSSSL	MAGE-C2 [42-61]
15	3852	GGSPVKNSLRLPGPYVPGQ	DMRT1 [249-268]	15	5175	ERSQRSQIANITTVWRAQPT	MORC1 [668-687]
15	3853	RKRKAVTKRRLQRSYEMNE	DPPA2 [148-167]	15	5176	QKWREERDQLVAALIEQLKA	MPHOSPH1 [1516-1535]
15	3854	KDTEITCSERVRYWIIIEL	EpCAM [129-148]	15	5177	ETQFNQYKTEAASRYNLTIS	MUC-1 [1118-1137]
15	3855	TQKVTCFYQPAPYFAAEARY	FAM46D [342-361]	15	5178	EKLDAFFGFQLSQEIKQQIH	NLRP4 [513-532]
15	3856	GHASPHLFTFPPTPPKDVSP	GATA-3 [144-163]	15	5179	BQLEERTWLLHDAIQNQNA	PASD1 [382-401]
15	3857	KEPMIVYVGTLDLVAVSSVK	HAGE [443-462]	15	5180	RPRRINMTDTGISPMSTRDP	SAGE1 [226-245]
15	3858	RLFENLRMLPHAPGVQMQAI	HDAC2 [366-385] ; HDAC1 [365-384]	15	5181	PIPESVIQNYNKALQOLEKY	SART3 [276-295]
15	3859	DRVMTVSFHKYGNVFFPGTG	HDAC3 [185-204]	15	5182	EELKGTEQELIGLLQAREKE	SCP-1 [458-477]
15	3860	LYQGGQMFDGAPRFHGRVGF	IGFS11 [75-94]	15	5183	EGVGVDINKALLAKRKRLM	SCP3a [75-94]
15	3861	TRQLCFVVRSKVNIYCSDDG	IL13RA2 [301-320]	15	5184	EIEALLGMDLVRLGLERGET	SCRN1 [103-122]
15	3862	CDVDKLHFTPRIQRLNELEA	JARID1B [76-95]	15	5185	IPPRDKMEDNSALYESTSAH	se57-1 [10-29]
15	3863	NDGTKIAASQAI SAMCENS	KU-CT-1 [329-348]	15	5186	QAFPMHNSNISKILGSRWK	SOX-6 [641-660]
15	3864	VADLVGFLLKRYRAREPVTK	MAGE-A1 [106-125]	15	5187	PGNVKALLRRATTYKHQNK	SPAG1 [273-292]

15	3865	GMLSDVQSMPKTGILILILS	MAGE-A10 [213-232]	15	5188	QKVGSLPRVEVLINRINEV	SYCE1 [44-63]
15	3866	REDSVFAHPRKLLMQDLVQE	MAGE-A2 [234-253]	15	5189	KVLLDAGFAVGEQSMVTDKP	TDRD1 [665-684]
15	3867	KVLHHMVKISGGPHISYPPL	MAGE-A3 [285-304]	15	5190	QAKATQFNSALFTLSSHRQG	TEX14 [875-894]
15	3868	LHHMVKISGGPRISYPLLHE	MAGE-A6 [287-306]	15	5191	SRRVEELSRPKRFYLEYYNN	THEG [191-210]
15	3869	FLWGPRLAETSYVKVLEHV	MAGE-A8 [274-293]; MAGE-A4 [272-291]	15	5192	KVLKSERDKIFLLYEQAQEE	TSGA10 [55-74]
15	3870	LKVAELVHFLHKKYRVKEPV	MAGE-A9 [110-129]	16	5193	LIFLLNFTBSRTLHRNEYGI	AFP [9-28]
15	3871	YDGILHSIYGDARKIITEDL	MAGE-B6 [317-336]	16	5194	QVASDMMVSLMKTCLKVHSSG	AKAP-4 [339-358]
15	3872	KMVNVPLEQLPLLFKVVLS	NR6A1 [453-472]	16	5195	VNILTNRNAQRQDIAFAYQ	ANXA2 [57-76]
15	3873	TLKIIERNFPELLSLNLCNN	NXF2 [261-280]	16	5196	SGKINRHEHYFNQFHRRNEL	CALR3 [365-384]
15	3874	ACLQRKMNVDSSTIYNNEV	NY-BR-1 [1173-1192]	16	5197	LQQSLNQDFHQTIVLQEGN	CDCA1 [190-209]
15	3875	CKPAELSRGRGILIFSDFKD	NYD-TSPG [211-230]	16	5198	PASNLMKMEWSREVTNAQR	CRISP2 [54-73]
15	3876	DELERKLEATSAQNIEFLQV	ODF2 [667-686]	16	5199	EELERTIHSYQQQIISHEKK	cTAGE5 [440-459]
15	3877	GPAYSILGRYQTKMTLTPGP	ODF3 [84-103]	16	5200	MSLLSIQQQEGVQVVVQQPG	CTCFL [97-116]
15	3878	RWMAQVLASELSLVAFILL	ODF4 [77-96]	16	5201	QPFEENEFDASRLVYDGVR	CTNNA2 [602-621]
15	3879	STYNLLFCGSCGIPVGFHLY	OIP5 [130-149]	16	5202	GLINSNTDNNLAVYDLSDI	CXorf61 [47-66]
15	3880	CSTPTINIPASPFMQKLGFG	PBK [22-41]	16	5203	LHKRKLPPVKRSLVYYLKN	DCAF12 [33-52]
15	3881	VTGQPSQDNCIFVNEQTVA	PEPP2 [88-107]	16	5204	TLSSHLDIKMTDNKTGEVL	DKKL1 [99-118]
15	3882	AWNCSNEYMPRIIVYRDGV	PIWIL1 [685-704]	16	5205	DSKSLRTALQKEITTRYQLD	EpCAM [158-177]
15	3883	IAGPIGMRMSPPAWVELKDD	PIWIL2 [628-647]	16	5206	GDQDNWLRNTNWVYRGEAERI	EPHA2 [75-94]
15	3884	KMSTYLKTI SPNFTLAFIV	PIWIL3 [741-760]	16	5207	FIKRNIELAKESRNPVVMVD	FSIP1 [254-273]
15	3885	ADCLKVMTGALNKWKYKYNH	PIWIL4 [663-682]	16	5208	IQNAAVFQEA FEIVVRHAKN	Glypican-3 [105-124]
15	3886	ELFPPLFMAAFDGRHSQTLK	PRAME [51-70]	16	5209	QVSLKVSNDGPTLIGANASF	gp100 [65-84]
15	3887	VIMDWEBCKMFPKLTKNML	PRSS55 [215-234]	16	5210	SDEYIKFLRSIRPDNMSEYS	HDAC2 [70-89]
15	3888	FKYHLTVAQVRGMVFELAN	PSMA [570-589]	16	5211	RDYTLRTFGEMADAFKSDYF	JARID1B [375-394]
15	3889	APECLLTDGFYTYKMDLWSA	RAGE-1 [169-188]	16	5212	TSLGLTYDGMLSDVQSMPKT	MAGE-A10 [205-224]
15	3890	GRCWIYNKTKMAFLLVGICF	SLCO6A1 [655-674]	16	5213	LEHVVRVNARVRIAYPSLRE	MAGE-A4 [288-307]
15	3891	QKRFRTRVEMARVLMERNQY	SPAG9 [499-518]	16	5214	KASDSLQLVFGIELMEVDPI	MAGE-A6 [153-172]
15	3892	DADPHGIEIMCIYKGSMSM	SPO11 [277-296]	16	5215	QENYLEYRQAPGSDPVRYEF	MAGE-A8 [255-274]
15	3893	CSEELYERQLQAEFIESGQY	TAF7L [362-381]	16	5216	DGEEHLIYGEPRKFITQDLV	MAGE-B1 [231-250]
15	3894	PGLSYRWLLNEFPNFIPTDG	TAG-1 [162-181]	16	5217	GEPWKLITKDLVQEKYLEYK	MAGE-B2 [242-261]
15	3895	LECAANEVNCPLQVALECLY	TEKT5 [176-195]	16	5218	KVDSTKDSYVLVSKMDLPNN	MAGE-B3 [170-189]
15	3896	VREACHQLLTQPRKTENGA	TEX101 [205-224]	16	5219	AETSKMKVLEFLAKVNDTTP	MAGE-B4 [278-297]
15	3897	KREKNSYYVFLKYKRVNEC	TEX15 [1774-1793]	16	5220	DDSTATESASSSVMSPSFSS	MAGE-C1 [1122-1141]

15	3898	GLFGVFLVLLDVTILADLI	TPTE [95-114]	16	5221	YTLDEKVAELVEFLLKYEA	MAGE-C2 [139-158]
15	3899	LQVSSYQHVIWDCLNGQALA	TSP50 [344-363]	16	5222	BQEKEEIASKSALLRQIKEV	MPHOSPH1 [207-226]
15	3900	CGVGRAAQALVCASAKEGTA	TSPY1 [20-39]	16	5223	DSLVERLHRQTAEYSAFKLE	ODF2 [488-507]
15	3901	DINIYDLFVVMHYVVSMDAL	TYR [169-188]	16	5224	EHGDSSAYENVKFI VNV RDI	PASD1 [118-137]
15	3902	FKDCERRFSRSDQLKRHQRR	WT1 [357-376]	16	5225	MDEAKILKSLHHPNIVGYRA	PBK [83-102]
15	3903	ALSRLRELCCQWLKPEIHTK	ZNF165 [66-85]	16	5226	IPTSPSHGSIAAYQGYSPQR	PEPP2 [541-560]
16	3904	WVCDCHMADMVTLKETE VV	5T4 [296-315]	16	5227	HDIVNRQKSIAGFVASTNAE	PIWIL3 [657-676]
16	3905	QYPNYCSFKSQCLMRNRNR	ACRBP [483-502]	16	5228	ARLVDNIQRNTNARFELETW	PIWIL4 [415-434]
16	3906	SGLLTGVVVD SGYGLTRVQP	ACTL8 [140-159]	16	5229	SISISALQSLQLHLGLSNL	PRAME [417-436]
16	3907	TTGEANELLHTFLRWKTSYL	ADAM2 [239-258]	16	5230	PYEEALLQAEAPRLAEYQAY	SART3 [297-316]
16	3908	KHLPVFTYTDQGAILEDQPF	ADAM29 [76-95]	16	5231	EVEKAKVIADAEAVKLQKEID	SCP-1 [681-700]
16	3909	AEDLIVSALLLIQYHLAQGG	AKAP-3 [524-543]	16	5232	SGKPSVEDQFTRAYDFETED	SCP3a [12-31]
16	3910	YCVQDTSANTTLVHQTTPS	BRDT [708-727]	16	5233	LKIKLQASREAGAAALRNVA	se57-1 [112-131]
16	3911	QLPEQIVIPFTDQVACLKEN	CABYR [311-330]	16	5234	MITQLISLREQLLAHDEQK	SOX-6 [194-213]
16	3912	KSVSQYLEMDKTL SKKEEEV	CAGE1 [433-452]	16	5235	GQGENKMKNL PVPVYLRPLD	SPAG9 [660-679]
16	3913	QSDLQFLNFVNENSQELIQM	CCDC62 [293-312]	16	5236	QGHTSSEYDMLREMFSDSRS	TAFT7L [311-330]
16	3914	SVSCITYLRGIFPECAYGTR	CT46 [37-56]	16	5237	PGNISWTFSSSLSIKWDPV	TAG-1 [916-935]
16	3915	SLYPPTLLEGPLRLSPLLPR	CTAGE2 [503-522]	16	5238	PQAKEMFIDTVISSYNIETA	TEX15 [389-408]
16	3916	FCGDYGMIDESIYFSSDVVT	CXorf48 [46-65]	16	5239	TERDVAFTDLRMTTERDSL	TSGA10 [103-122]
16	3917	EAAAGATAVPAATVPATAAG	DBPC [5-24]	16	5240	TPIEWYPDYEV EAYRRRHNN	TSPY1 [233-252]
16	3918	CEPASEPSSFTVTPVIEEDE	DMRT1 [354-373]	17	5241	EDVRVSGWLQTEFLSFQDGD	ACRBP [452-471]
16	3919	ARAVQPKALNSCSIPVSVEA	DPPA2 [194-213]	17	5242	SNTYQLPDGSRVELTPMQRV	ACTL8 [235-254]
16	3920	PGNEEFQVVKDAVLDCLLDF	FAM46D [92-111]	17	5243	LFGLIEIWTNKNLIVDDVRK	ADAM29 [245-264]
16	3921	LLSCLSKSNRLKSLSIQYL	FBXO39 [115-134]	17	5244	KWVESIFLI FLNFTESRTL	AFP [2-21]
16	3922	RRKAKGRNRRSHRAMRVAHL	FMR1NB [5-24]	17	5245	LGNGSSVDEV SFYANRLTNL	AKAP-3 [115-134]
16	3923	GDPQLCHFLESHYLHEQVKT	FTHL17 [126-145]	17	5246	SSGKPIPASVVLKRVLLRHT	AKAP-4 [356-375]
16	3924	EISGDEFLN FLLKLNKQCGH	GASZ [350-369]	17	5247	KIRSEFKRKYGKSLYYIIQQ	ANXA2 [302-321]
16	3925	ANGDPVCNACGLYKLNHNIN	GATA-3 [333-352]	17	5248	PDSQQQYNNVKT VKVTEQLR	BRDT [255-274]
16	3926	TLCYLMPGFIHLVLQPSLKG	HAGE [293-312]	17	5249	AQLEENAKYSSVYMEAEATA	CABYR [366-385]
16	3927	CWTYETSLVVEEAI SEELPY	HDAC3 [306-325]	17	5250	KMKNTDYLTQYDLSEFENIG	CALR3 [279-298]
16	3928	SESPGSIQVARGQPAVL PCT	IGFS11 [26-45]	17	5251	ARNETLSNTLVLSAQVGQL	CCDC62 [133-152]
16	3929	ESSCEIKLWSIPLGPIPAR	IL13RA2 [249-268]	17	5252	SEQDELMADISKRIQSLEDE	cTAGE5 [160-179]
16	3930	TEEIPLKILAHNNFVGR LIG	KOC1 [274-293]	17	5253	EHQLGNNTLSSHLQIDKMTD	DKKL1 [92-111]
16	3931	PDVKKNSMECIYNLVQDFQC	KU-CT-1 [164-183]	17	5254	QQLGLSTNGKKIEVYLR LHR	DPPA2 [105-124]
16	3932	NSQCKITIVGTGAVGMACAI	LDHC [18-37]	17	5255	HKAREKPYDSKSLRTALQKE	BpCAM [150-169]
16	3933	KLQEVKILAQFYND FVNISS	LIP1 [401-420]	17	5256	BQQKKIESYLHNHF IEGGMT	FAM46D [275-294]

16	3934	LESVIKKNYKHCPEIFGKAS	MAGE-A1 [129-148]	17	5257	GPLSVYPPASSSSLSGGHAS	GATA-3 [128-147]
16	3935	WVQEKYLVYRQVPGTDPACY	MAGE-A11 [363-382]	17	5258	SLIYRRRLMKQDFSVPQLPH	gp100 [613-632]
16	3936	IGHLYILVTCLGLSYDGLLG	MAGE-A12 [172-191]	17	5259	QLSTGGSVASAVKLNKQQT	HDAC1 [111-130]
16	3937	ISHLYILVTCLGLSYDGLLG	MAGE-A2 [172-191]	17	5260	HNLLLNLYGLYRKMEIYRPHK	HDAC2 [40-59]
16	3938	LGDNQIMPAGLLIIVLAII	MAGE-A3 [190-209]	17	5261	IREDDTTLVTATVENETYTL	IL13RA2 [276-295]
16	3939	GTDVKEVDPAHSHYILVTAL	MAGE-A9 [162-181]	17	5262	QEGPSTFPDLETSFQVALSR	MAGE-A12 [92-111]
16	3940	CATEEEVWEFLGLGIYDGI	MAGE-B6 [301-320]	17	5263	EEGPRMFPDLESEFQAASR	MAGE-A2 [92-111]
16	3941	AGALEDFPARWSFRAYTSVL	MORC1 [225-244]	17	5264	VGNWQYFFPVIFSKASSSLQ	MAGE-A3 [140-159]
16	3942	KNYQQLDIFPARDTYHPMSE	MUC-1 [1189-1208]	17	5265	BEGVEAQEEALGLVGAQAPT	MAGE-A4 [13-32]
16	3943	TPQTQHQLKALCSLAAEGMW	NLRP4 [389-408]	17	5266	PAHLESFPREALDEKVAELV	MAGE-A8 [101-120]
16	3944	MCLPEIRYIAGKMVNVPLEQ	NR6A1 [442-461]	17	5267	YKMREPIMKADMLKVVDKEY	MAGE-B1 [123-142]
16	3945	RNWFKVTIPYGIKYDKAWLM	NXF2 [122-141]	17	5268	KSGSLVQFLLYKYIKKSVT	MAGE-B2 [114-133]
16	3946	IQDAQKRTALHWACVNGHEE	NY-BR-1 [12-31]	17	5269	VDVSYKSKYGANSKIEKKQ	MAGE-B3 [75-94]
16	3947	KPLTIYVYQEGLVRFATEKF	NYD-TSPG [266-285]	17	5270	SASQKAIIFKRLSKDAVKKK	MAGE-B6 [179-198]
16	3948	TWRPHRPRGPIMALYSSPGP	ODF3 [9-28]	17	5271	STFEGFAQSSSLQIPVSPSFS	MAGE-C1 [258-277]
16	3949	RSCSDLENGKVTIFISTLML	ODF4 [142-161]	17	5272	KLREILLYFFPEHQLPSELE	MORC1 [824-843]
16	3950	GHFCLSSDKMVCYLLKTKAI	OIP5 [160-179]	17	5273	QQHVPFRESKLTTHYFQSFFN	MPHOSPH1 [426-445]
16	3951	KMGELLRVDIPLKLVMIVG	PIWIL1 [611-630]	17	5274	QLKVLIAENTMLTSKLKEKQ	NY-BR-1 [1111-1130]
16	3952	DSLKLCLVGLSKKFYEVNHC	PIWIL2 [786-805]	17	5275	ITPPSSEKLVSMRLSDLST	ODF2 [91-110]
16	3953	SLVNYNLWIEKVTQLEGRPF	PRSS55 [287-306]	17	5276	SMEWDTQVVKGSSPLGPAGL	OIP5 [36-55]
16	3954	LHETDSAVATARRPRWLCAG	PSMA [5-24]	17	5277	GPPDPQAFQGPAAYPDQMR	PASD1 [735-754]
16	3955	PQCLSLHAMVAYDPDERIA	RAGE-1 [256-275]	17	5278	GTGVNVYLMKRSRPLGSHSP	PBK [41-60]
16	3956	PAPGNILSTAPPWLRHMAAA	SAGE1 [639-658]	17	5279	DVMHLSQSPSVSLSVLSLS	PRAME [338-357]
16	3957	WGAEMGANEHGVCIANEAIN	SCRN1 [77-96]	17	5280	IGEGTFSEVMKMQSLRDGNY	RAGE-1 [10-29]
16	3958	FLFAAVVAWCTLIPLSCFPN	SLCO6A1 [318-337]	17	5281	RKQDNVLSNVLSGLINMAGA	SAGE1 [451-470]
16	3959	YPSLWGFGTTKTFKPIEHL	SPAG1 [6-25]	17	5282	TEKENMKMDLTFLLEESRDK	SCP-1 [276-295]
16	3960	TVVDNIINDISCMKVSRRS	SPO11 [148-167]	17	5283	EYSQFLTLFQQWDLDMQKA	SCP3a [124-143]
16	3961	LKGERPGAHQAGPDVLIGQ	SYCE1 [312-331]	17	5284	VAFPPRAKDGLVVFVKNSAR	SCRN1 [11-30]
16	3962	QPITSSHLALPFQIIRCSLE	TDRD1 [1039-1058]	17	5285	IQDIITSLARNEAPFTIDN	SPO11 [55-74]
16	3963	EKCMGMRKTFPCTPRLVGHT	TEKT5 [466-485]	17	5286	GQDTSSQKIEDLMEMVQLQ	SYCE1 [25-44]
16	3964	IGCRLMSGILAVGPMFVREA	TEX101 [189-208]	17	5287	DRGSETTYESSADIAGDEGT	TAFL7L [36-55]
16	3965	PLPTQLYNWAAPEVILQKAA	TEX14 [414-433]	17	5288	LMELNGSSSQLIIMLLKNFM	TDRD1 [1060-1079]
16	3966	LCWPSVYWTERFLEDTLTI	THEG [166-185]	17	5289	SNAAIQIASATMPALSLNND	TEX15 [598-617]
16	3967	NLPPRRILFIKHFIISIPR	TPTE [407-426]	17	5290	NEGYYRRPLASMSLPPPKAS	THEG [349-368]

16	3968	DQMTQTASDVPVLQVIMHSR	TSP50 [172-191]	17	5291	SSGRQSFYRNPIKEVVRFLD	TPTE [253-272]
16	3969	NLLSPASFFSSWQIVCSRLE	TYR [261-280]	17	5292	ELVRHHNMHQRNMTKLQLAL	WT1 [430-449]
16	3970	KRPFCAYPGCNKRYFKLSH	WT1 [320-339]	17	5293	SQSSNLSQHQRIMHRENLLM	ZNF165 [466-485]
16	3971	GTCDQSFKWNDFINHQIYY	ZNF165 [295-314]	18	5294	PWPERLSNNVEELLQSSLSL	ACRBP [167-186]
17	3972	TGNQLAVLPAGAFARRPPLA	5T4 [99-118]	18	5295	LAKDLIVSALKLIQYHLTQQ	AKAP-4 [540-559]
17	3973	GSDDTVVAQKVFQILGLTNA	ADAM2 [195-214]	18	5296	LEKDIISDTSGDFRKLMLVAL	ANXA2 [155-174]
17	3974	RQFETVCKFHWVEAFDDEMT	CAGE1 [119-138]	18	5297	DKSKLWLLKDRDLARKEQE	BRDT [900-919]
17	3975	SEKTKRLNELKLSVVSLEKEI	CDCA1 [217-236]	18	5298	KVSSIHSDQSDVLMVDVATS	CABYR [182-201]
17	3976	SDPTSWSSAIQSWYDEILDF	CRISP2 [102-121]	18	5299	QERTNSELHNLRLQIYVKQQS	CCDC62 [275-294]
17	3977	FEGEPMYLNVGEVSTPFHIF	CT46 [203-222]	18	5300	AQLQRTPMASALVFPNKISTE	CT46 [4-23]
17	3978	PGPPRAPFAMRNVLPRGFL	CTAGE2 [710-729]	18	5301	ELYQENEMKLHRKLTVEENY	cTAGE5 [387-406]
17	3979	KTFRTVTLLRNHVNTHTGTR	CTCFL [292-311]	18	5302	GFLKNTSDVINAAKKIAEAG	CTNNA2 [733-752]
17	3980	AGAIRGRAARVIHIINAEME	CTNNA2 [540-559]	18	5303	RLFLKGNLLRGIDSLFSAPM	DKK1 [57-76]
17	3981	PSAPGSRTPGNPATAVSGTP	DBPC [58-77]	18	5304	VRTYWIIEELKHKAREKPYD	EPCAM [139-158]
17	3982	NVCLAYGSEWSVYAVGSQAH	DCAF12 [299-318]	18	5305	VLPDQQVIWVNNNTIINGSQV	gp100 [96-115]
17	3983	SFYQPSLFPPYNNLYNCPQY	DMRT1 [212-231]	18	5306	PARRAKMRRAEAMNIEPE	JARID1B [227-246]
17	3984	MELQAARACFALLWGICALAA	EPHA2 [1-20]	18	5307	LENFTLKVAYIPDEMAAQQN	KOC1 [144-163]
17	3985	RILLQEIPRISISLRSCYFS	FBXO39 [300-319]	18	5308	AAEADGIDPLINLLSSKRDG	KU-CT-1 [394-413]
17	3986	SLEEDSALEALLNFFFPPTTC	FMR1NB [115-134]	18	5309	WKNHKKQVIQSAYEIIKLG	LDHC [227-246]
17	3987	AENMKCLQFSKDVIIISDTKD	FSIP1 [501-520]	18	5310	VKNTRKVAVSLSVHIKNLLK	LIP1 [147-166]
17	3988	AINSHITELYTSYLYLSMA	FTHL17 [20-39]	18	5311	KVLEYVIKVSARVRFFPSL	MAGE-A1 [278-297]
17	3989	LLDSGISVDSNFQYGTPLM	GASZ [65-84]	18	5312	ASEEEIWBELGVMGVYDGRE	MAGE-A4 [217-236]
17	3990	RTACLVVAMLLSLDFPGQAQ	Glypican-3 [6-25]	18	5313	VGNWQYFFPVIFSKASDSLQ	MAGE-A6 [140-159]
17	3991	VHDVTHVYNFDFPRNIEEYV	HAGE [553-572]	18	5314	VNPNGHYTFIDKVDLTDEE	MAGE-B2 [171-190]
17	3992	NNKICDIANWAGGLHHAKK	HDAC3 [119-138]	18	5315	EFLNKMRIYDGKKHFI FGEP	MAGE-B3 [225-244]
17	3993	NIGLIAGAIGTGAVIIIFCI	IGFS11 [239-258]	18	5316	GEPRKLITQDLVQEKYLEYQ	MAGE-B4 [239-258]
17	3994	CAVNTFLTENSPYSLEVLVC	JARID1B [107-1091]	18	5317	RTSQHLVVAFGVELKEMDSS	MAGE-B6 [239-258]
17	3995	LIPGLNLNALGLFPPTSGMP	KOC1 [364-383]	18	5318	LDEKVDELARFLLKYQVKQ	MAGE-C1 [908-927]
17	3996	PEEEVVIHEFASCLANMSA	KU-CT-1 [119-138]	18	5319	AFTKLNNASSRSHSIFTVKI	MPHOSPH1 [340-359]
17	3997	YSPDCKILVVSNPVDILTYI	LDHC [127-146]	18	5320	PSPGSTLSSSRSELNGFMA	NR6A1 [190-209]
17	3998	NKRPCLEFSQLSVKDSFRDL	LIP1 [38-57]	18	5321	YKGBELLRRTKRDI VDSL SA	NXF2 [454-473]
17	3999	PVTKAEMLESVIKYNKCFP	MAGE-A1 [122-141]	18	5322	IDIHFLERKMQHLLKEKNE	NY-BR-1 [1296-1315]
17	4000	SDPARYEFLWGPRAHAEIRK	MAGE-A10 [289-308]	18	5323	EKSEYAEQLHVQLADKDLY	ODF2 [414-433]
17	4001	LVHLLLRKYRVKGLITKAEM	MAGE-A11 [229-248]	18	5324	QPDQMRSABQTRLMPEAQRD	PASD1 [749-768]

17	4002	MPKTGFLIIILAIIAKEGDC	MAGE-A6 [196-215]	18	5325	SNSIKRNPAPVVRGWLK	PEPP2 [159-178]
17	4003	GLSCDSMLGDGHSMKAAALL	MAGE-A9 [182-201]	18	5326	QETAQLVGSTASQQPGYIQP	PIWIL1 [16-35]
17	4004	RNGLLMPLLSVIFLNGNCAR	MAGE-B4 [197-216]	18	5327	MSGRARVKARGIARSPSATE	PIWIL4 [1-20]
17	4005	VTEAEMLMIVIKYKDYFPVI	MAGE-C2 [162-181]	18	5328	RRLWGSIQSRYISMSVWTSP	PRAME [4-23]
17	4006	SPGSGSSTTQGGQDVTLPAT	MUC-1 [65-84]	18	5329	RPFYRHHVIYAPSSHNKYAGE	PSMA [684-703]
17	4007	EYISEMLLRNKSRYLDLSA	NLRP4 [797-816]	18	5330	GSMKVKRQFVEFTIKEAARF	SAGE1 [854-873]
17	4008	RKQRNRCQYCRLLKCLQMGM	NR6A1 [106-125]	18	5331	QENRKII EAQRKAIQELQFG	SCP-1 [135-154]
17	4009	NLCNNKLYQLDGLSDITEKA	NXF2 [276-295]	18	5332	MFRQQQKILQQSRIVQSQR	SCP3a [153-172]
17	4010	QFIPLTFVMPNDYTKFVAEY	NYD-TSPG [176-195]	18	5333	PLKNVRKKRFRKTQKKVPDV	TAF7L [225-244]
17	4011	MTEEVWMTWRPHRPRGPIM	ODF3 [1-20]	18	5334	KLVENSLSISNPLFTSLGP	TDRD1 [144-163]
17	4012	IFSTLMLFPINIWIFELERN	ODF4 [155-174]	18	5335	GEYFYSSSTAQENLALETSSP	TEX14 [1088-1107]
17	4013	KKERPISMINEASNYNVTSD	PEPP2 [114-133]	18	5336	LKKAHRRVHTSLQLITKVG	TEX15 [1004-1023]
17	4014	PLISVKPLDNWLLIYTRNY	PIWIL1 [486-505]	18	5337	RKRRRRRLMELAEPKINWQ	THEG [120-139]
17	4015	ERINLKNTSFITSQELNWK	PIWIL2 [571-590]	18	5338	TTDKILIDVFDGLPLYDDVK	TPTE [458-477]
17	4016	PGIIRVPAPCHYAHKLAYLV	PIWIL3 [844-863]	18	5339	FWSWVGQANDIGLLKLKQEL	TSP50 [197-216]
17	4017	NDNSEAQLAHLIPELCFLTG	PIWIL4 [365-384]	18	5340	ASPLTGIADASQSSMHNALH	TYR [348-367]
17	4018	EPGEKWYQVGIISWGKSCGE	PRSS55 [259-278]	18	5341	ENSRSMKLEIFEKIESQRI	ZNF165 [188-207]
17	4019	GAKGVILYSDPADYFAPGVK	PSMA [221-240]	19	5342	GFTKRLFRELMGDHVSSTKA	ACTL8 [306-325]
17	4020	LSSVGLHMTKGLALWEAYRE	SART3 [214-233]	19	5343	QITEEQLEAVIADFSGLLEK	AFP [562-581]
17	4021	ENKLLQLKSSATYKSCQDL	se57-1 [213-232]	19	5344	AQDKAESYSLISMKGMDPK	AKAP-3 [397-416]
17	4022	LVAIFIAFYGDRKKVWFVA	SLCO6A1 [157-176]	19	5345	LSGEAAEAVHSGTSVKSSSG	CABYR [451-470]
17	4023	VAEARVYRDARGRASSEPHI	SOX-6 [602-621]	19	5346	PVQEDMALNEVLQKLKHTNR	CAGE1 [298-317]
17	4024	ADGNVKAIFYRRALAHKGLKN	SPAG1 [687-706]	19	5347	TILSPKQIKTPFQKILRDKD	CT46 [239-258]
17	4025	DSTLRLYHAHTYQHLQDVDI	SPAG9 [1109-1128]	19	5348	VAEAKMTFKRFQANEERLEI	CTAGE2 [157-176]
17	4026	TATRRKPHLLLVAVALVSS	TAG-1 [3-22]	19	5349	AAPIHDADAQESSLGLTGLQ	DKKL1 [30-49]
17	4027	NSWRPSLFYKIANVQTCPE	TEKT5 [48-67]	19	5350	ASGALVGAASGSSAGSSRG	DMRT1 [34-53]
17	4028	KTENGATCLPIPVWGLQLLL	TEX101 [219-238]	19	5351	TRNDWRVASELINILERANQ	HAGE [592-611]
17	4029	GQPSLCSFEINEIYSGCLIL	TEX14 [619-638]	19	5352	LPEIQELYQTLAKPSPAQQ	JARID1B [1360-1379]
17	4030	SCKSPKSTTAHAILRRVETE	TSGA10 [85-104]	19	5353	SDLESIFKDAKIPVSGPFLV	KOC1 [16-35]
17	4031	KVDPYRSCGFSYEQDPTLRD	TSP50 [97-116]	19	5354	SSKRDGAIANAATVLTNMAM	KU-CT-1 [408-427]
17	4032	FSDHNFAGSNKIAEILCKDL	TSPY1 [261-280]	19	5355	DLQHGSFFSTSKITSGKDY	LDHC [64-83]
17	4033	VGAVLTALLAGLVSLCRHK	TYR [484-503]	19	5356	DMNVIVVDWSRGATTFIYNR	LIPI [126-145]
18	4034	LALIGAIFLLVLYLNKRGIK	5T4 [363-382]	19	5357	WVQENYLEYRQVPGSNPARY	MAGE-A4 [251-270]
18	4035	ISLRPLLVSHVMACGGNTLY	ACTL8 [285-304]	19	5358	SVMGLYDGREHVSYYWKLRL	MAGE-A8 [229-248]
18	4036	IFCVLIAIMVKVNFQRKKWR	ADAM2 [698-717]	19	5359	NLSNDWDFPRNGLLMPLLGV	MAGE-B1 [188-207]

18	4037	FGGQKHIIHIKVKLLFSKH	ADAM29 [58-77]	19	5360	RGQTQDHQGAQITATNKKKV	MAGE-B3 [19-38]
18	4038	QHACAVMKNFGTRTFQAITV	AFP [221-240]	19	5361	RTHSTFEGFPQSLLQIPMTS	MAGE-C1 [325-344]
18	4039	EVVSDLIDSFLRNLSVTGT	AKAP-3 [328-347]	19	5362	KQEFNLVQEQYNHLLKVMGQY	MORC1 [414-433]
18	4040	KLDKYHSLNEELDFLVTSE	CAGE1 [690-709]	19	5363	VQQIQSNYDIAIAELHVQKS	MPHOSPH1 [933-952]
18	4041	CGFDIKKHVHILHFKNKYHE	CALR3 [137-156]	19	5364	TMNKRYNVSQQALDLQNLRF	NXF2 [220-239]
18	4042	PFSNLVTHLDSFLPICRVND	CDCA1 [84-103]	19	5365	YWRTSSFRMTEHNSVKPWQQ	NYD-TSPG [124-143]
18	4043	RAAVAGFFAVLFLWRSFRSV	CTAGE2 [17-36]	19	5366	NRSLGQRQNSPLPFQWRITH	ODF4 [55-74]
18	4044	CCQCSYASRDITYKLKRHMRT	CTCFL [372-391]	19	5367	RSWTYGITRGGRVFFINEEA	PEPP2 [14-33]
18	4045	WCPPPPFFYRRRVVRGPRPPN	DBPC [223-242]	19	5368	KVLRSETVLDPMFNFYHQTE	PIWIL1 [272-291]
18	4046	GTLNKVFASQWLNHRQVVC	DCAF12 [87-106]	19	5369	FKRANMDNDIALLLASPIK	PRSS55 [148-167]
18	4047	PQGRAGFGKASGALVGAAS	DMRT1 [24-43]	19	5370	RLQDFDKSNPIVLRMMNDQL	PSMA [649-668]
18	4048	ALNSCIPVSVEAFLMQASG	DPPA2 [201-220]	19	5371	KMENVQPAPDNVLLTLRPRR	SAGE1 [210-229]
18	4049	LEPHMNYTFTVEARNGVSG	EPHA2 [402-421]	19	5372	AATEAPKMSNADFALFLRK	SART3 [944-963]
18	4050	EIRFTNLTDQVITLDQVLD	FAM46D [3-22]	19	5373	GGSGAVMSERVSGLAGSIYR	SPAG9 [14-33]
18	4051	EVKFMNYPYNAVLTKKFQVTM	FBXO39 [93-112]	19	5374	NEVKRLLRSDAEAVSTRWEV	TAF7L [263-282]
18	4052	FKCFAPFRDVPKQMMQMFGL	FMR1NB [171-190]	19	5375	NESVRPYTPFEVKIRSYNRR	TAG-1 [775-794]
18	4053	SECEASKGYLTKALTGHN	FSIP1 [473-492]	19	5376	FQAENTIMLLERSIMAKEGP	TEKT5 [368-387]
18	4054	SHYLHEQVKTIKELGGYVSN	FTHL17 [136-155]	19	5377	AYDPKHFNHVRVRIMIDHNN	TPTE [289-308]
18	4055	ANASFEKDKQSILITACSAH	GASZ [103-122]	19	5378	LVERREEAQRAQAVPGPGP	TSPY1 [83-102]
18	4056	PTHGSGQVCRPPLHGSPLW	GATA-3 [77-96]	19	5379	AQYRIHTHGVFRGIQDVRRV	WT1 [284-303]
18	4057	PDATCHQVRSFFQRLQFGLK	Glypican-3 [31-50]	20	5380	GRRDARSFVEAAGTTFNPAN	AKAP-3 [543-562]
18	4058	QSQAQWPIVLQGIDLIGVAQT	HAGE [269-288]	20	5381	SKIASEMAYEAVELTAAEMR	AKAP-4 [268-287]
18	4059	HSDDYIKFLRSIRPDNMSEY	HDAC1 [68-87]	20	5382	MKGKGTDRKVLIRIMVSRSE	ANXA2 [278-297]
18	4060	YGQGHMPKPHRIRMTHNLLL	HDAC2 [25-44]	20	5383	SATEKVFKQEQEIPSVFPKTS	BRDT [166-185]
18	4061	LHHAKKFEASGFCYVNDIVI	HDAC3 [133-152]	20	5384	IKIGSEKSLHLEVEITSIVS	CABYR [409-428]
18	4062	TFTTSAALINLNVIMVTPL	IGFS11 [45-64]	20	5385	ERPEIVSTWSSAGISWRSEA	CAGE1 [260-279]
18	4063	GFILILVIFVTGLLLRKPNT	IL13RA2 [349-368]	20	5386	HKEKDKGLQTTQNGRFYAIS	CALR3 [59-78]
18	4064	VQFLLFKYQMKPITKAEIL	MAGE-A10 [142-161]	20	5387	NQKSLFKDQKFEAMLVQQNR	CCDC62 [348-367]
18	4065	FREASVCMQLFGIDVKEVD	MAGE-A11 [264-283]	20	5388	KTRSGKVFQNKMANGNQPVK	CT46 [333-352]
18	4066	LETSFQVALSRKMAELVHFL	MAGE-A12 [101-120]	20	5389	IEEKSLLLEKFSLVQKEYEG	CTAGE5 [86-105]
18	4067	VIFSKASEYLQLVFGIEVVE	MAGE-A2 [149-168]	20	5390	GSSRGGGSGSGASDLGAGSK	DMRT1 [49-68]
18	4068	MPKAGLLIIVLAIAREGDC	MAGE-A3 [196-215]	20	5391	NSYNVRRTEGFSVTLLDLAP	EPHA2 [480-499]
18	4069	GHSYILVTCLGLSYDGLLGD	MAGE-A8 [176-195]	20	5392	RPSRVHASEVESAVWYVKKF	FBXO39 [66-85]
18	4070	SMPKAALLIIVLGVILTKDN	MAGE-A9 [194-213]	20	5393	QLAEIDIKLQELSAASPTIS	FSIP1 [319-338]

18	4071	DPTRYQFLWGPRAYAEETTKM	MAGE-B1 [264-283]	20	5394	GSHTTASPNWLSPFSSKTSIH	GATA-3 [104-123]
18	4072	WEVLNAVGVYAGREHFVYGE	MAGE-C2 [250-269]	20	5395	FVNLKNITYLVLEADKMLD	HAGE [384-403]
18	4073	AMGIPFIIQCDLCLKWRVLP	MORC1 [477-496]	20	5396	GSVAGAVKLNRRQOTDAMVNW	HDAC2 [117-136]
18	4074	TLVHNGTSARATTTTPASKST	MUC-1 [971-990]	20	5397	TESVSHFSDLGQSFSFHSGN	IGFS11 [332-351]
18	4075	QEANFHIIDNVDLVVSAYCL	NLRP4 [574-593]	20	5398	TVEYELKYRNIGSETWKTII	IL13RA2 [66-85]
18	4076	LKPWLLEVNYSPALTLDCST	NYD-TSPG [380-399]	20	5399	HSVPKRQRIRKLQIRNIPPH	KOC1 [72-91]
18	4077	TPGPAAYRQTDVVRTKFKAP	ODF3 [179-198]	20	5400	FHPGGLMKLRSREADLYRFI	KU-CT-1 [853-872]
18	4078	SELSLVAFILLLVVAFSKKW	ODF4 [85-104]	20	5401	RAHAETSKMKVLEYIANANG	MAGE-A11 [389-408]
18	4079	GPQLPSWLQPERCAVFQCAQ	OIP5 [63-82]	20	5402	BEGPSTFPDLESEFQAALSR	MAGE-A6 [92-111]
18	4080	HHPNIVGYRAFTEANDGSLC	PBK [93-112]	20	5403	QIKEPVTKAEMLESVIKNYK	MAGE-A8 [128-147]
18	4081	PNVECKSMRFGMLKDHQAVT	PIWIL2 [249-268]	20	5404	KEPVTKAEMLESVIKNYKRY	MAGE-A9 [126-145]
18	4082	LQLWDLKFDTNFLSVPRVL	PIWIL3 [453-472]	20	5405	DGEHSVVFGEPAWKLTDLV	MAGE-B2 [234-253]
18	4083	MLLFSVLLLSLVGTGLGP	PRSS55 [1-20]	20	5406	STSTERSLKDSLTRTKMLV	MAGE-B4 [98-117]
18	4084	GDFGSCRSVYSKQPYTEYIS	RAGE-1 [144-163]	20	5407	QATIDTADDATVMASESLSV	MAGE-C2 [345-364]
18	4085	VYDYNCHVDLIRLLRLEGEL	SART3 [109-128]	20	5408	LDVQIQHVVEGKRALSELQ	MPHOSPH1 [1135-1154]
18	4086	MAAAPPSYCFVAFPPRAKDG	SCRN1 [1-20]	20	5409	ESLDQKLFQLQSKNMWLQQQ	NY-BR-1 [1261-1280]
18	4087	SCQDLQREISILQEQISHLQ	se57-1 [228-247]	20	5410	HKAEBEIMEQLKELKQKGD	ODF2 [377-396]
18	4088	NPVLICLALSKATEYLVIIIG	SLCO6A1 [382-401]	20	5411	TKYVFDSAPSHSISARTKAF	ODF3 [112-131]
18	4089	RRQEMRQFFTQVQQPQIPIT	SOX-6 [717-736]	20	5412	SVHLAWDLRSRLGAVVFSRV	OIP5 [90-109]
18	4090	VDYKTVLQIDCGLQLANDSV	SPAG1 [542-561]	20	5413	NDLIEERYKASQDPFPAII	PBK [124-143]
18	4091	LKDSILSIVHVKGIVLVALA	SPAG9 [999-1018]	20	5414	RGTTEIGMIGSKPFSTVKYK	PEP2 [779-798]
18	4092	HILSTSKGLIAGNLRYIEED	SPO11 [169-188]	20	5415	KRVNTRFFAQSGGRQLNPLP	PIWIL1 [742-761]
18	4093	VLWSKGTEILVNSSRVTVTP	TAG-1 [450-469]	20	5416	KTPKDSFTMSDGKEITFLEY	PIWIL2 [436-455]
18	4094	LPTRLRSALFSRYSFHDWDQS	TEKT5 [78-97]	20	5417	PSVSQLSVLSLGSVMLTDVS	PRAME [346-365]
18	4095	HCPTCVALGTCFSAPSLPCP	TEX101 [139-158]	20	5418	YSEELFPEELSVVLGTNDLT	PRSS55 [111-130]
18	4096	TEALIVCEQDVSRMRRLDE	TSGA10 [316-335]	20	5419	KFSGYPLYHSVYETVELVEK	PSMA [545-564]
18	4097	MRPEGLTYRVPERLRQGFC	TSPY1 [1-20]	20	5420	RLNPHPNILMLHEVVFDKRS	RAGE-1 [56-75]
18	4098	PPPPSQASSGQARMFPNAPY	WT1 [114-133]	20	5421	ELTKVRMARQKMEIFPLTE	SART3 [127-146]
19	4099	VPTDLPAYVRNFLTGNQLA	5T4 [85-104]	20	5422	ELEDIKVSLQRSVSTQKALE	SCP-1 [323-342]
19	4100	IYDENSYWRNQNPGSLLQLP	ACRBP [301-320]	20	5423	TGEGEFNFSEVSPVEDHLD	SCRN1 [215-234]
19	4101	IPRATIIYANISGHLCAVE	ADAM2 [557-576]	20	5424	SILQEIQISHLQFVIHSQHQN	se57-1 [237-256]
19	4102	NCSYGDFWEYTVERTKCLLE	ADAM29 [368-387]	20	5425	QQEQIARQQQLLQQQHKI	SOX-6 [232-251]
19	4103	FNQWKQATDIMEAMLKRLV	AKAP-4 [412-431]	20	5426	IIIAKMELEEVTRLLNLKDK	SPAG1 [724-743]
19	4104	HLETVILGLLKTAPQYDASE	ANXA2 [94-113]	20	5427	SSSLSIKWDPVVPFRNESAV	TAG-1 [925-944]

19	4105	EKMDNQEYKDAYKFAADVRL	BRDT [324 - 343]	20	5428	QAI IQGFSYDLLKKIDSPQR	TEX14 [152 - 171]
19	4106	YHENKKLIRCKVDGFTHTLYT	CALR3 [154 - 173]	20	5429	HVSDHNRLHLARPKAQSDK	THEG [293 - 312]
19	4107	MVAVHQQLLSWEEDRQKVL	CCDC62 [47 - 66]	20	5430	TVEKEMKSLARKAMDESEL	TSGA10 [174 - 193]
19	4108	EKMKDTVQKLKNARQEVVEK	CDCA1 [256 - 275]	20	5431	SAKEGTAFRMEAVQEGAAGV	TSPY1 [33 - 52]
19	4109	RGPLFPVDARGPFLRRGPPF	CTAGE5 [700 - 719]				

Example 19 - Process for personalized vaccination

Process for personalized vaccination consists of 3 main steps as shown in FIG. 17. First, during the visit at the oncologist the patient provides saliva sample and tumor sample (biopsy) for tumor pathology. Second step is the matching of vaccine peptides with the patient's unique genetic code: Based on the determined HLA genotype of the patient and determined tumor type of the patient, 12 tumor and patient specific peptides are selected for the patient from the Hotspot Sequences listed in Table-25. Then, the vaccine will be prepared and after fill&finish plus QC release, and vaccine vials shipped to the clinical site. At the clinic, as third step of the process, vaccine is administered to the patient by the oncologist. The manufacturing of the personalized vaccine is carried out under GMP conditions. Vaccine selection and preparation can be performed during 6-8 weeks.

Eligibility criteria for personalized vaccination are:

- ≥ 12 immunogenic peptides (12 PEPIs) from
- ≥ 12 different cancer-specific antigens (expression rate (ER) in the disease ≥ 10 %) and
- $AGP \geq 3$ (expected number of antigens expressed in the patient's tumor)
- On stock in the PEPI PANEL "Warehouse"

Example 20 - Feasibility study for a "simulated" Breast Cancer Clinical trial

We describe here a model, where the peptide set ("warehouse") consists of 100 immunogenic peptides derived from breast cancer specific TSAs (FIG. 18). These 100 peptides represent the peptide set for vaccine selection in this example. In this stock, there are available 100 mg of each peptide, that represents 25 peptide dose (for vaccination). During the feasibility study, we screened 509 HLA-genotyped breast cancer subjects and identified 82 patients (16%) who were not eligible because less, than 12 peptides were found for those patients. This means, that 82 % of patients could be treated with "patient-specific" vaccine from a panel consisting of 100 peptides. However, the amount (100 mg each) will only be enough for 32% of the patients if we intend to administer 3 doses/patient during the treatment,

therefore 267 (52%), who will have not sufficient peptides in warehouse must be also excluded from this feasibility study. Consequently, 160 patients can be enrolled and treated by the administration of 3 consecutive vaccine doses. Manufacturing (GMP) can be performed within cca. 6 months.

5

Example 21 - Vaccine selection for a breast cancer patient (Patient-C of Example 22) and for a colorectal cancer patient (Patient-D of Example 22)

The vaccine selection process from peptides listed in Table 25 is demonstrated here by two examples.

10 Patient-C's PIT vaccine described in Example 22 were designed during a completely personalized design process and manufactured individually, and demonstrated very high immunogenicity: 11 out of 12 (92%) vaccine peptides induced CD8+ T cell responses and 11/12 (92%) were resulted in CD4+ T cell specific immune responses.

By taking the HLA genotype and tumor pathology report (breast cancer) of Patient-C, patient
15 matching process according to Example 16 resulted in 116 of 3286 sequences, selected from 38 breast cancer specific TSAs (according to selection criteria of, Expression rate (ER) $\geq 10\%$). These 116 peptides are usable for vaccine selection for Patient-C and contain the PIT vaccine sequences. Three examples for random selection of 12 peptides from the 116 peptides are shown in Table 25. with expected AGP numbers.

20 PIT vaccine of Patient-C has an expected AGP value of 6.45, meaning that at least 6 vaccine-specific TSAs are likely expressed in the patient's tumor and are targeted by immune responses with at least 50% of probability. (AGP95 is 4, meaning that PIT vaccine peptides from at least 4 different TSAs TSAs are likely expressed in the patient's tumor and are targeted by immune responses in Patient-C with at least 95% probability.)

25

Table 29. Vaccine selection for Patient-C from the PEPI PANEL. Original vaccine means the PIT vaccine designed during in a completely personalized design process for Patient-C (Example 22). The peptide set matched with Patient-C breast cancer indication resulted in 116 of 3286 Sequences selected from 38 of 58 Breast cancer specific TSAs). These 116 peptides are usable
30 for vaccine selection for Patient-C. Three examples for random selection of 12 peptides from the 116 peptides are shown in this table with calculated expected AGP numbers.

Vaccines	SEQ ID NOS (AG[ER%] from Table 25)	Calculated expected AGP	CI95%
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PIT vaccine of Patient-C	5449 (SPAG9[88%]), 5432 (AKAP-4[85%]), 5433 (CTCFL[74%]), 5440 (MAGE-A11[59%]), 41 (FMR1NB[55%]), 5437 (FSIP1[42%]), 5444 (NY-BR-1[47%]), 5439 (LDHC[35%]), 5438 (GATA-3[31%]), 440 (Survivin[68%]), 5443 (MAGE-C1[16%]), 111 (PRAME[49%])	6.45	[3, 9]
Random1	2 (ACRBP[40%]), 7 (AKAP-3[40%]), 18 (CDCA1[64%]), 40 (FBXO39[38%]), 41 (FMR1NB[55%]), 42 (FSIP1[42%]), 57 (JARID1B[76%]), 60 (Lage-1[12%]), 66 (MAGE-A11[59%]), 68 (MAGE-A2[12%]), 74 (MAGE-A9[44%]), 80 (MAGE-C1[16%])	4.91	[2, 8]
Random2	107 (PIWIL2[94%]), 167 (AKAP-4[85%]), 183 (CTCFL[74%]), 192 (EpCAM[76%]), 215 (JARID1B[76%]), 405 (ODF4[63%]), 440 (Survivin[68%]), 663 (MAGE-A11[59%]), 1539 (MAGE-A9[44%]), 857 (TDRD1[38%]), 1326 (PEPP2[60%]), 1441 (ODF4[63%])	7.96	[5, 11]
Random3	18 (CDCA1[64%]), 107 (PIWIL2[94%]), 215 (JARID1B[76%]), 297 (TDRD1[38%]), 391 (MAGE-C1[16%]), 470 (AKAP-4[85%]), 490 (DKKL1[20%]), 498 (FBXO39[38%]), 1088 (PRAME[49%]), 1100 (SP17[47%]), 1800 (TSGA10[70%])	5.92	[3, 9]

For Patient-D, a similar analysis was performed. During the patient matching process according to Example 19, 136 of 3286 sequences were selected from Table 25. (derived from 37 of 53 CRC specific TSAs), based on the HLA genotype and tumor pathology report (colorectal cancer, CRC) data of Patient-D. These 136 peptides are usable for vaccine selection for Patient-D. Three examples for random selection of 13 peptides from the 136 peptides are shown in Table 30, with calculated AGP numbers. Patient-D had a PIT vaccine consisting of 13 peptides, therefore the random selection was also performed to result in 13 peptide sets.

Patient-D's PIT vaccine described in Example 22 were designed during a completely personalized design process and manufactured individually, and demonstrated very high immunogenicity: 13 out of 13 (100%) vaccine peptides induced CD8+ T cell responses and 7/13 (54%) were resulted in CD4+ T cell specific immune responses.

PIT vaccine of Patient-D has an expected AGP value of 6.60, meaning that at least 6 vaccine-specific TSAs are likely expressed in the patient's tumor and are targeted by immune responses with at least 50% of probability. (AGP95 is 4, meaning that PIT vaccine peptides from at least 4 different TSAs are likely expressed in the patient's tumor and are targeted by immune responses in Patient-D with at least 95% probability.)

Table 30. Vaccine selection for Patient-D from the PEPI PANEL. Original vaccine means the PIT vaccine designed during in a completely personalized design process for Patient-D (Example 22). The peptide set matched with Patient-D CRC indication resulted in 136 of 3286 Sequences selected from 37 of 53 CRC specific TSAs). These 136 peptides are usable for vaccine selection

for Patient-D and contain the PIT vaccine sequences. Three examples for random selection of 13 peptides from the 116 peptides are shown in this table with calculated AGP numbers.

Vaccines	SEQ ID NOS (AG[ER%] from Table 25)	Calculated expected AGP	CI95%
PIT vaccine of Patient-D	5450 (TSP50[89%]), 5436 (EpCAM[88%]), 5434 (CAGE1[74%]), 5447 (PIWIL1[48%]), 5448 (SPAG9[71%]), 2168 (AKAP-4[74%]), 5442 (MAGE-A8[44%]), 5435 (DPPA2[44%]), 40 (FBXO39[39%]), 5445 (NYD-TSPG[30%]), 5446 (PAGE4[33%]), 647 (HAGE[15%]), 1172 (Lage-1[13%])	6.60	[4, 10]
Random1	315 (5T4[85%]), 347 (DPPA2[44%]), 353 (FBXO39[39%]), 371 (Lage-1[13%]), 383 (MAGE-A6[22%]), 384 (MAGE-A8[44%]), 412 (PIWIL2[80%]), 470 (AKAP-4[74%]), 486 (CXorf48[17%]), 639 (FBXO39[39%]), 647 (HAGE[15%]), 652 (IGFS11[55%]), 657 (Lage-1[13%])	5.30	[2, 8]
Random2	1157 (FBXO39[39%]), 1160 (GASZ[22%]), 1172 (Lage-1[13%]), 1183 (MAGE-A6[22%]), 1211 (PIWIL3[96%]), 1249 (5T4[85%]), 1256 (AKAP-4[74%]), 1262 (CCDC62[13%]), 1270 (DBPC[90%]), 1274 (EpCAM[88%]), 1300 (MAGE-A3[22%]), 1365 (ZNF165[43%]), 1372 (AKAP-3[83%])	6.91	[4,10]
Random3	470 (AKAP-4[74%]), 486 (CXorf48[17%]), 639 (FBXO39[39%]), 647 (HAGE[15%]), 652 (IGFS11[55%]), 657 (Lage-1[13%]), 658 (LDHC[15%]), 686 (NYD-TSPG[30%]), 696 (PIWIL3[96%]), 713 (SPAG1[55%]), 796 (MAGE-A1[14%]), 830 (PIWIL3[96%]), 929 (MAGE-A2[18%])	5.32	[3, 8]

Example 22– Personalised Immunotherapy (PIT) design and treatment for ovarian-,

5 breast- and colorectal cancer

This Example provides proof of concept data from 4 metastatic cancer patients treated with personalized immunotherapy vaccine compositions to support the principals of binding of epitopes by multiple HLAs of a subject to induce cytotoxic T cell responses, on which the present disclosure is partly based on.

10 Composition for Treatment of Ovarian Cancer with POC01-PIT (Patient-A)

This example describes the treatment of an ovarian cancer patient with a personalised immunotherapy composition, wherein the composition was specifically designed for the patient based on her HLA genotype based on the disclosure described herein.

The HLA class I and class II genotype of a metastatic ovarian adenocarcinoma cancer patient (Patient-A) was determined from a saliva sample.

To make a personalized pharmaceutical composition for Patient-A thirteen peptides were selected, each of which met the following two criteria: (i) derived from an antigen that is

expressed in ovarian cancers, as reported in peer reviewed scientific publications; and (ii) comprises a fragment that is a T cell epitope capable of binding to at least three HLA class I of Patient-A (Table 31). In addition, each peptide is optimized to bind the maximum number of HLA class II of the patient.

5 **Table 31:. Personalized vaccine of ovarian cancer Patient-A.**

POC01 vaccine for Patient-A	Target Antigen	Antigen Expression	20mer peptides	SEQ ID NO:	MAX HLA classI	MAX HLA classII
POC01_P1	AKAP4	89%	NSLQKQLQAVLQWIAASQFN	5933	3	5
POC01_P2	BORIS	82%	SGDERSDEIVLTVSNSNVEE	5934	4	2
POC01_P3	SPAG9	76%	VQKEDGRVQAFGWSLPQKYK	5935	3	3
POC01_P4	OY-TES-1	75%	EVES TPMIMENIQELIRSAQ	5936	3	4
POC01_P5	SP17	69%	AYFESLLEKREKTNFDPAEW	5937	3	1
POC01_P6	WT1	63%	PSQASSGQARMFPNAPYLPS	5938	4	1
POC01_P7	HIWI	63%	RRSIAGFVASINEGMTRWFS	5939	3	4
POC01_P8	PRAME	60%	MQDIKMILKMVQLDSIEDLE	5940	3	4
POC01_P9	AKAP-3	58%	ANSVVS DMMVSIMKTLKIQV	5941	3	4
POC01_P10	MAGE-A4	37%	REALSNKVDELAHFLLRKYR	5942	3	2
POC01_P11	MAGE-A9	37%	ETSYEKVINYL VMLNAREPI	5943	3	4
POC01_P12a	MAGE-A10	52%	DVKEVDPTGHSFVLVTSGL	5944	3	4
POC01_P12b	BAGE	30%	SAQLLQARLMKEESPVSWR	5945	3	2

Eleven PEPI3 peptides in this immunotherapy composition can induce T cell responses in Patient-A with 84% probability and the two PEPI4 peptides (POC01-P2 and POC01-P5) with 98% probability, according to the validation of the PEPI test shown in Table 7. T cell responses target 13 antigens expressed in ovarian cancers. Expression of these cancer antigens in Patient-A was not tested. Instead the probability of successful killing of cancer cells was determined based on the probability of antigen expression in the patient's cancer cells and the positive predictive value of the ≥ 1 PEPI3+ test (AGP count). AGP count predicts the effectiveness of a vaccine in a subject: Number of vaccine antigens expressed in the patient's tumor (ovarian adenocarcinoma) with PEPI. The AGP count indicates the number of tumor antigens that the vaccine recognizes and induces a T cell response against the patient's tumor (hit the target). The AGP count depends on the vaccine-antigen expression rate in the subject's tumor and the HLA genotype of the subject. The correct value is between 0 (no PEPI presented by any expressed antigen) and maximum number of antigens (all antigens are expressed and present a PEPI).

20 The probability that Patient-A will express one or more of the 13 antigens is shown in

Fig. 19. AGP95 (AGP with 95% probability) = 5, AGP50 (the mean -expected value- of the discrete probability distribution) = 7.9, mAGP (probability that AGP is at least 2) = 100%, AP = 13.

A pharmaceutical composition for Patient-A may be comprised of at least 2 from the 13 peptides (Table 31), because the presence in a vaccine or immunotherapy composition of at least two polypeptide fragments (epitopes) that can bind to at least three HLAs of an individual (≥ 2 PEPI3+) was determined to be predictive for a clinical response. The peptides are synthesized, dissolved in a pharmaceutically acceptable solvent and mixed with an adjuvant prior to injection. It is desirable for the patient to receive personalized immunotherapy with at least two peptide vaccines, but preferable more to increase the probability of killing cancer cells and decrease the chance of relapse.

For treatment of Patient-A, the 13 peptides were formulated as 4 x 3 or 4 peptide (POC01/1, POC01/2, POC01/3, POC01/4). One treatment cycle is defined as administration of all 13 peptides within 30 days.

15 **Patient history:**

Diagnosis: Metastatic ovarian adenocarcinoma

Age: 51

Family anamnesis: colon and ovary cancer (mother) breast cancer (grandmother)

Tumor pathology:

20 2011: first diagnosis of ovarian adenocarcinoma; Wertheim operation and chemotherapy; lymph node removal

2015: metastasis in pericardial adipose tissue, excised

2016: hepatic metastases

25 2017: retroperitoneal and mesenteric lymph nodes have progressed; incipient peritoneal carcinosis with small accompanying ascites

Prior Therapy:

2012: Paclitaxel-carboplatin (6x)

2014: Caelyx-carboplatin (1x)

2016-2017 (9 months): Lymparza (Olaparib) 2x400 mg/day, oral

30 2017: Hycamtin inf. 5x2,5 mg (3x one seria/month)

PIT vaccine treatment began on 21 April 2017. FIG. 20.

2017-2018: Patient-A received 8 cycles of vaccination as add-on therapy, and lived 17 months (528 days) after start of the treatment. During this interval, after the 3rd and 4th vaccine treatment she experienced partial response as best response. She died in October 2018.

An interferon (IFN)- γ ELISPOT bioassay confirmed the predicted T cell responses of Patient-A to the 13 peptides. Positive T cell responses (defined as >5 fold above control, or >3 fold above control and >50 spots) were detected for all 13 20-mer peptides and all 13 9-mer peptides having the sequence of the PEPI of each peptide capable of binding to the maximum HLA class I alleles of Patient-A (FIG. 21).

- 10 **Patient' tumor MRI findings (Baseline April 15, 2016) (BL: baseline for tumor response evaluation on FIG. 22)**

Disease was confined primarily to liver and lymph nodes. The use of MRI limits detection of lung (pulmonary) metastasis

May 2016 – Jan 2017: Olaparib treatment (**FU1: follow up 1 on FIG. 22)**

- 15 Dec/25/2016 (before PIT vaccine treatment) There was dramatic reduction in tumor burden with confirmation of response obtained at (**FU2: follow up 2 on FIG. 22)**

Jan - Mar 2017 – TOPO protocol (topoisomerase)

April/6/2017 (**FU3 on FIG. 22)** demonstrated regrowth of existing lesions and appearance of new lesions leading to disease progression. Peritoneal carcinomatosis with increased amount of ascites. Progressive hepatic tumor and lymph node

- 20

April 21 2017 START PIT

Jul/26/17 (after the 2nd Cycle of PIT): (**FU4 on FIG. 22)** Progression / Pseudo-Progression

Rapid progression in lymph nodes, hepatic, retroperitoneal and thoracic areas, significant pleural fluid and ascites. Initiate Carboplatin, Gemcitabine, Avastin.

- 25 Sep/20/17 (after 3 Cycles of PIT): (**FU5 on FIG. 22)** Partial Response

Complete remission in the pleural region/fluid and ascites

Remission in hepatic, retroperitoneal area and lymph nodes

The findings suggest pseudo progression.

Nov/28/17 (after 4 Cycles of PIT): (**FU6 on FIG. 22)** Partial Response

- 30 Complete remission in the thoracic region. Remission in hepatic, retroperitoneal area and lymph nodes

Apr/13/18: Progression

Complete remission in the thoracic and retroperitoneal regions. Progression in hepatic centers and lymph nodes

Jun/12/2018: Stable disease

Complete remission in the thoracic and retroperitoneal regions. Minimal regression in hepatic centers and lymph nodes

July 2018: Progression

October 2018: Patient-A died

Partial MRI data for Patient-A is shown in Table 32 and FIG. 22.

10 **Table 32. Summary Table of Lesions Responses**

Lesion/ Time Point	Baseline (%Δ from BL)	FU1 (%Δ from BL)	FU2 (%Δ from BL)	FU3 (%Δ from BL)	FU4 (%Δ from BL)	FU5 (%Δ from BL)	FU6 (%Δ from BL)	Best Response Cycle	PD Time Point
TL1	NA	-56.1	-44.4	-44.8	+109.3	-47.8	-67.3	FU6	FU4
TL2	NA	-100.0	-100.0	-47.1	-13.1	-100.0	-100.0	FU1	FU3
TL3	NA	-59.4	-62.3	-62.0	-30.9	-66.7	-75.9	FU6	FU4
TL4	NA	-65.8	-100.0	-100.0	-100.0	-100.0	-100.0	FU2	NA
SUM	NA	-66.3	-76.0	-68.9	-23.5	-78.2	-85.2	FU6	FU4

Design, safety and immunogenicity of Personalised Immunotherapy Composition PBRC01 for treatment of metastatic breast cancer (Patient-B)

The HLA class I and class II genotype of metastatic breast cancer Patient-B was determined from a saliva sample. To make a personalized pharmaceutical composition for Patient-B twelve peptides were selected, each of which met the following two criteria: (i) derived from an antigen that is expressed in breast cancers, as reported in peer reviewed scientific publications; and (ii) comprises a fragment that is a T cell epitope capable of binding to at least three HLA class I of Patient-B (Table 33). In addition, each peptide is optimized to bind the maximum number of HLA class II of the patient. The twelve peptides target twelve breast cancer antigens. The probability that Patient-B will express one or more of the 12 antigens is shown in FIG. 23.

Table 33. 12 peptides for Patient-B breast cancer patient

BRC01 vaccine peptides	Target Antigen	Antigen Expression	20mer peptide	SEQ ID NO:	MAXHL A Class I	MAXHLA Class II
PBRC01_cP1	FSIP1	49%	ISDTKDYFMSKTLGIGRLKR	5946	3	6
PBRC01_cP2	SPAG9	88%	FDRNTESLFEELSSAGSGLI	5947	3	2

PBRC01_cP3	AKAP4	85%	SQKMDMSNIVLMLIQKLLNE	5948	3	6
PBRC01_cP4	BORIS	71%	SAVFHERYALIQHQTHKNE	5949	3	6
PBRC01_cP5	MAGE-A11	59%	DVKEVDPTSHSYVLVTSNL	5950	3	4
PBRC01_cP6	NY-SAR-35	49%	ENAHGQSLEEDSALEALLNF	5951	3	2
PBRC01_cP7	HOM-TES-85	47%	MASFRKLTLSKVPNHPNR	5952	3	5
PBRC01_cP8	NY-BR-1	47%	KRASQYSGQLKVLIAENTML	5953	3	6
PBRC01_cP9	MAGE-A9	44%	VDPAQLEFMFQEALKLKVAE	5954	3	8
PBRC01_cP10	SCP-1	38%	EYEREETRQVYMDLNNNIEK	5955	3	3
PBRC01_cP11	MAGE-A1	37%	PEIFGKASESLQLVFGIDVK	5956	3	3
PBRC01_cP12	MAGE-C2	21%	DSESSFTYTLDEKVAELVEF	5957	4	2

Predicted efficacy: AGP95=4; 95% likelihood that the PIT Vaccine induces CTL responses against 4 TSAs expressed in the breast cancer cells of Patient-B. Additional efficacy parameters: AGP50 = 6.45, mAGP = 100%, AP = 12.

- 5 For treatment of Patient-B the 12 peptides were formulated as 4 x 3 peptide (PBR01/1, PBR01/2, PBR01/3, PBR01/4). One treatment cycle is defined as administration of all 12 different peptide vaccines within 30 days (FIG.23C).

Patient history:

- 2013: Diagnosis: breast carcinoma diagnosis; CT scan and bone scan ruled out metastatic disease.
- 2014: bilateral mastectomy, postoperative chemotherapy
- 2016: extensive metastatic disease with nodal involvement both above and below the diaphragm. Multiple liver and pulmonary metastases.

Therapy:

- 2013-2014: Adriamycin-Cyclophosphamide and Paclitaxel
- 2017: Letrozole, Palbociclib and Gosorelin and PIT vaccine
- 2018: Worsening conditions, patient died in January

PIT vaccine treatment began on 7 April 2017. treatment schedule of Patient-B and main characteristics of disease are shown in Table 34.

20 **Table 34 – Treatment and response of Patient-B**

Date (2017)	Mar	May	Jun	Sep	Nov	Dec
Treatment regimen	PIT Vaccine					
	Palbociclib Letrozole Gosorelin		Anticancer drug treatment interruption			
Neutrophils	ND	1.1	4.5	3.4	2.4	3

(1.7-3.5/mm ³)						
CEA (<5.0 ng/ml)	99	65	23	32	128	430
CA 15-3 (<31.3 U/ml)	322	333	138	76	272	230
T1: Right axillar lymph node	15 mm & 11.6 SUV _{max}	9 mm & 2.0 SUV _{max}	nd*	nd	nd	6 mm & 0 SUV _{max}
T2: Right lung metastasis	10 mm & 4.8 SUV _{max}	7 mm & 0 SUV _{max}	nd	nd	nd	4 mm & 0 SUV _{max}
Left iliac bone metastasis	Non measurable & 4.0 SUV _{max}	Regression & 0 SUV _{max}	nd	nd	nd	Regression & 0 SUV _{max}
Multiple liver metastases	Non measurable & 11.5 SUV _{max}	Partial regression & 6.1 SUV _{max}	nd	nd	nd	Progression & 16.8 SUV _{max}

*no data

It was predicted with 95% confidence that 8-12 vaccine peptides would induce T cell responses in Patient-B. Peptide-specific T cell responses were measured in all available PBMC samples using an interferon (IFN)- γ ELISPOT bioassay (FIG. 24). The results confirmed the prediction: Nine peptides reacted positive demonstrating that T cells can recognize Patient-B's tumor cells expressing FISP1, BORIS, MAGE-A11, HOM-TES-85, NY-BR-1, MAGE-A9, SCP1, MAGE-A1 and MAGE-C2 antigens. Some tumor specific T cells were present after the 1st vaccination and boosted with additional treatments (e.g. MAGE-A1) others induced after boosting (e.g. MAGE-A9). Such broad tumor specific T cell responses are remarkable in a late stage cancer patient.

Patient-B history and results

Mar 7, 2017: Prior PIT Vaccine treatment

Hepatic multi-metastatic disease with truly extrinsic compression of the origin of the choledochal duct and massive dilatation of the entire intrahepatic biliary tract. Celiac, hepatic hilar and retroperitoneal adenopathy

Mar 2017: Treatment initiation - Letrozole, *Palbociclib*, Gosorelin & PIT Vaccine

May 2017: Drug interruption

May 26 2017: After 1 cycle of PIT

83% reduction of tumor metabolic activity (PET CT) liver, lung lymphnodes and other metastases.

June 2017: Normalized Neutrophils values indicate *Palbociclib* interruption as affirmed by the patient

4 Months Delayed Rebound of Tumor Markers

Mar to May 2017: CEA and CA remained elevated consistently with the outcome of her anti-cancer treatment (Ban, Future Oncol 2018)

June to Sept 2017: CEA and CA decreased consistently with the delayed responses to immunotherapies

Quality of life

Feb to Mar 2017: Poor, hospitalized with jaundice

April to Oct 2017: Excellent

Nov 2017: Worsening conditions (tumor escape?)

Jan 2018: Patient-B died.

Immunogenicity results are summarized in FIG. 24.

Clinical outcome measurements of the patient: One month prior to the initiation of PIT vaccine treatment PET CT documented extensive DFG avid disease with nodal involvement both above and below the diaphragm (Table 34). She had progressive multiple hepatic, multifocal osseous and pulmonary metastases and retroperitoneal adenopathy. Her intrahepatic enzymes were elevated consistent with the damage caused by her liver metastases with elevated bilirubin and jaundice. She accepted Letrozole, Palbociclib and Gosorelin as anti-cancer treatment. Two month after initiation of PIT vaccinations the patient felt very well and her quality of life normalized. In fact, her PET CT showed a significant morphometabolic regression in the liver, lung, bone and lymph node metastases. No metabolic adenopathy was identifiable at the supra-diaphragmatic stage.

The combination of Palbociclib and the personalised vaccine was likely to have been responsible for the remarkable early response observed following administration of the vaccine. Palbociclib has been shown to improve the activity of immunotherapies by increasing TSA presentation by HLAs and decreasing the proliferation of Tregs (Goel et al. Nature. 2017:471-475). The results of Patient-B treatment suggest that PIT vaccine may be used as add-on to the state-of-art therapy to obtain maximal efficacy.

Patient-B's tumor biomarkers were followed to disentangle the effects of state-of-art therapy from those of PIT vaccine. Tumor markers were unchanged during the initial 2-3 months of treatment then sharply dropped suggesting of a delayed effect, typical of immunotherapies

(Table 34). Moreover, at the time the tumor biomarkers dropped the patient had already voluntarily interrupted treatment and confirmed by the increase in neutrophil counts.

After the 5th PIT treatment the patient experienced symptoms. The levels of tumor markers and liver enzymes were increased again. 33 days after the last PIT vaccination, her PET CT showed significant metabolic progression in the liver, peritoneal, skeletal and left adrenal site confirming the laboratory findings. The discrete relapse in the distant metastases could be due to potential immune resistance; perhaps caused by downregulation of both HLA expression that impairs the recognition of the tumor by PIT induced T cells. However, the PET CT had detected complete regression of the metabolic activity of all axillary and mediastinal axillary supra-diaphragmatic targets (Table 34). These localized tumor responses may be accounted to the known delayed and durable responses to immunotherapy, as it is unlikely that after anti-cancer drug treatment interruption these tumor sites would not relapse.

Personalised Immunotherapy Composition for treatment of a patient with metastatic breast carcinoma (Patient-C)

PIT vaccine similar in design to that described for Patient-A and Patient-B was prepared for the treatment of a patient (Patient-C) with metastatic breast carcinoma. PIT vaccine contained 12 PEPIs. The PIT vaccine has a predicted efficacy of AGP = 4. The patient's treatment schedule is shown in FIG. 25.

Tumor Pathology

2011 Original tumor: HER2-, ER+, sentinel lymph node negative

2017 Multiple bone metastases: ER+, cytokeratin 7+, cytokeratin 20-, CA125-, TTF1-, CDX2-

Treatments

2011 Wide local resection, sentinel lymph nodes negative; radiotherapy

2017- Anti-cancer therapy (Tx): Letrozole (2.5 mg/day), Denosumab;

Radiation (Rx): one bone

PIT vaccine (3 cycles) as add-on to standard of care

Bioassay confirmed positive T cell responses (defined as >5 fold above control, or >3 fold above control and >50 spots) to 11 out of the 12 20-mer peptides of the PIT vaccine and 11 out of 12 9-mer peptides having the sequence of the PEPI of each peptide capable of binding to

the maximum HLA class I alleles of the patient (FIG. 26). Long-lasting memory T-cell responses were detected after 14 months of the last vaccination (FIG. 26C-D).

Treatment Outcome

Clinical results of treatment of Patient-C are shown in Table 35. Patient-C has partial response and signs of healing bone metastases.

Table 35 – Clinical results of treatment of breast cancer Patient-C

	Before PIT	+70 days* (10w)	+150 days* (21w)	+388 days* (55w)
Bone Biopsy	Met. breast cancer DCIS	Not done	RIB5 is negative	Not done
PET CT	Multiple metastases	Only RIB5 is DFG avid	Not done	Not done
CT	Multiple metastases	Not done	Not done	Healing bone mets (sclerotic foci)
CA-15-3	87	50	32	24

*After 3rd cycle of PIT vaccination

Immune responses are shown on FIG. 26. Predicted Immunogenicity, PEPI = 12 (CI95% [8,12])
 Detected Immunogenicity: 11 (20-mers) & 11 (9-mers) antigen specific T cell responses following 3 PIT vaccinations (FIG. 26A, B). After 4.5, 11 or 14 months of the last vaccination, PIT vaccine-specific immune response could still be detected (FIG. 26 C, D).

Personalised Immunotherapy Composition for treatment of patient with metastatic colorectal cancer (Patient-D)

Tumor pathology

2017 (Feb) mCRC (MSS) with liver metastases, surgery of primer tumor (in sigmoid colon). pT3 pN2b (8/16) M1. KRAS G12D, TP53-C135Y, KDR-Q472H, MET-T1010I mutations. SATB2 expression. EGFR wt, PIK3CA-I391M (non-driver).
 2017 (Jun) Partial liver resection: KRAS-G12D (35G>A) NRAS wt,
 2018 (May) 2nd resection: SATB2 expression, lung metastases 3 → 21
 Treatments
 2017 FOLFOX-4 (oxaliplatin, Ca-folate, 5-FU) → allergic reaction during 2nd treatment
 DeGramont (5-FU + Ca-folate)

2018 (Jun) → FOLFIRI plus ramucirumab, biweekly; chemoembolization

2018 (Oct) PIT vaccination (13 patient-specific peptides, 4 doses) as add-on to standard of care.

The patient's treatment schedule is shown in FIG. 27.

5 Treatment outcome

Patient in good overall condition, disease progression in lungs after 8 months confirmed by CT.

Both PIT induced and pre-existing T cell responses were measured by enriched Fluorospot from PBMC, using 9mer and 20mer peptides for stimulation (FIG. 28).

Summary of immune response rate and immunogenicity results prove the proper design for target antigen selection as well as for the induction of multi-peptide targeting immune responses, both CD4+ and CD8+ specific ones.

Table 36. Summary table of immunological analysis of Patient A-D

Patient ID	Measured immunogenicity for the different vaccine peptides*	
	CD4+ T cells	CD8+ T cells
Patient-A	13/13 (100%)	13/13 (100%)
Patient-B	9/12 (75%)	1/12 (8%)
Patient-C	11/12 (92%)	11/12 (92%)
Patient-D	7/13 (54%)	13/13 (100%)
IRR (ratio of immune responder patients)	4/4	4/4
Ratio of immunogenic peptides (median)	10/12-13	10/12-13

*Following 1-3 cycles of vaccination

CLAIMS

1. A peptide of up to 50 amino acids in length and comprising the amino acid sequence of
any of SEQ ID NOs: 1 to 2786 and/or 5432-5931.
2. A polynucleic acid or a vector that encodes a peptide according to claim 1.
3. A panel of two or more peptides according to claim 1 or two or more polynucleic acids or
vectors according to claim 2, wherein each peptide comprises, or each polynucleic acid or
vector encodes a peptide that comprises, a different amino acid sequence selected from
SEQ ID NOs: 1 to 2786 and/or 5432-5931.
4. The panel of peptides, polynucleic acids or vectors according to claim 3, wherein
each peptide or encoded peptide comprises at least one amino acid sequence selected
from one of the following groups:
 - (a) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a breast cancer-associated antigen listed in Table 24;
 - (b) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a lung cancer-associated antigen listed in Table 24;
 - (c) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a prostate cancer-associated antigen listed in Table 24;
 - (d) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a colorectal cancer-associated antigen listed in Table 24;
 - (e) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a bladder cancer-associated antigen listed in Table 24;
 - (f) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a ovarian cancer-associated antigen listed in Table 24;
 - (g) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a pancreatic cancer-associated antigen listed in Table 24;
 - (h) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a brain cancer-associated antigen listed in Table 24;
 - (i) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or
25B to be a fragment of a leukemia-associated antigen listed in Table 24;

- (j) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a lymphoma-associated antigen listed in Table 24;
 - (k) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a hepatocellular cancer-associated antigen listed in Table 24;
 - 5 (l) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a melanoma-associated antigen listed in Table 24;
 - (m) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a thyroid cancer-associated antigen listed in Table 24;
 - (n) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 10 25B to be a fragment of a pediatric cancer-associated antigen listed in Table 24;
 - (o) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a gastric cancer-associated antigen listed in Table 24;
 - (p) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a kidney cancer-associated antigen listed in Table 24
 - 15 (q) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a head and neck cancer-associated antigen listed in Table 24
 - (r) the sequences listed in Table 25A and/or Table 25B and indicated in Table 25A or 25B to be a fragment of a cervical cancer-associated antigen listed in Table 24.
- 20 5. A pharmaceutical composition or kit, comprising one or more peptides according to claim 1, one or more polynucleic acids or vectors according to claim 2, or a panel of peptides, polynucleic acids or vectors according to claim 3 or claim 4, wherein the composition or kit optionally comprise at least one pharmaceutically acceptable diluent, carrier, or preservative.
- 25
6. The pharmaceutical composition or kit of claim 5, comprising at least two peptides according to claim 1, or one or more polynucleic acids or vectors according to claim 2 that encode at least two peptides according to claim 1, wherein each peptide or encoded peptide comprises an amino acid sequence selected from SEQ ID NOs: 1 to 2786 and/or 30 5432-5931 that comprises a T cell epitope capable of binding to at least three HLA class I alleles and/or a T cell epitope capable of binding to at least three HLA class II alleles of an individual human subject.

7. A method of predicting that a specific human subject will have a CD8+ T cell response and/or a CD4+ T cell response to each peptide, or encoded peptide, of a pharmaceutical composition or kit according to claim 5, the method comprising
- 5 (i) a. determining that each peptide, or encoded peptide comprises at least one amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and
- b. predicting that the subject will have a CD8+ T cell response to each peptide of the pharmaceutical composition or each peptide, polynucleic acid or vector of the kit; and/or
- 10 (ii) a. determining that each peptide, or encoded peptide comprises at least one amino acid sequence that is a T cell epitope capable of binding to at least three HLA class II molecules of the subject; and
- b. predicting that the subject will have a CD4+ T cell response to each peptide of the pharmaceutical composition or each peptide, polynucleic acid or
- 15 vector of the kit.
8. The method of claim 7 further comprising administering the pharmaceutical composition to the subject.
- 20 9. A method of vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject, the method comprising administering to the subject a pharmaceutical composition or the peptides, polynucleic acids or vectors of a kit according to claim 5 or claim 6.
- 25 10. The method of claim 9, wherein the pharmaceutical composition or the peptides, polynucleic acids or vectors of the kit have been predicted to induce a cytotoxic T cell response and/or a helper T cell response in the subject using a method according to claim 7.
- 30 11. The method according to any one of claims 8 to 10 that is a method of treating cancer, optionally bladder cancer, brain cancer, breast cancer, colorectal cancer, gastric cancer, hepatocellular cancer, leukemia, lung cancer, lymphoma, melanoma, ovarian cancer,

pancreatic cancer, pediatric cancer, thyroid cancer, prostate cancer, kidney cancer, head and neck cancer, esophageal cancer and cervical cancer.

12. A method of preparing a pharmaceutical composition or kit for use in a method of treating cancer in a specific human subject, the method comprising
- a. selecting two or more peptides according to claim 1, or one or more polynucleic acids or vectors according to claim 2 that encode at least two peptides according to claim 1, wherein each peptide, or encoded peptide, comprises an amino acid sequence selected from SEQ ID NOs: 1 to 2786 and/or 5432-5931 that comprises a T cell epitope capable of binding to at least three HLA class I alleles and/or a T cell epitope capable of binding to at least three HLA class II alleles of the specific human subject; and
 - b. preparing a pharmaceutical composition or kit comprising the two or more peptides, or one or more polynucleic acids or vectors selected in step a.
13. A method of designing or preparing a peptide, or a polynucleic acid or vector that encodes a peptide, or a panel of peptides, or one or more polynucleic acid or vectors that encode a panel of peptides, for use in a method of inducing a T cell response against a target polypeptide, the method comprising
- (i) selecting or defining a model human population comprising a plurality of subjects each defined by HLA class I genotype and/or by HLA class II genotype;
 - (ii) identifying for each subject of the model population:
 - (a) amino acid sequences of the target polypeptide that are a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
 - (b) amino acid sequences of the target polypeptide that are a T cell epitope capable of binding to at least three HLA class II molecules of the subject;
 - (c) amino acid sequences of the target polypeptide that comprise a T cell epitope capable of binding to at least three HLA class I molecules of the subject and a T cell epitope capable of binding to at least three HLA class II molecules of the subject; or
 - (d) amino acid sequences of the target polypeptide that both
 - a. are a T cell epitope capable of binding to at least three HLA class II molecules; and

- b. comprise an amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
- (iii) selecting a polypeptide fragment window length of between 9 and 50 amino acids;
- 5 (iv) identifying a fragment of the target polypeptide that
- (a) has the length selected in step (iii); and
- (b) comprises an amino acid sequence identified in any one of step (ii) (a) to (d) in the highest proportion of subjects in the model population;
- 10 (v) optionally testing the fragment identified in step (iv) against additional pre-defined criteria, rejecting the fragment if the further pre-defined criteria are not met, and repeating step (iv) to identify an alternative fragment of the target polypeptide that
- (a) has the length selected in step (iii); and
- (b) comprises an amino acid sequence identified in step (iv) in the next highest
- 15 proportion of subjects in the model population;
- (vi) optionally repeating step (iv) and further optionally step (v) in one or more further rounds, wherein a further fragment of the target polypeptide is identified in each round, and wherein in each round subjects are excluded from the model population if any of the fragments selected in step (iv) and not rejected in step (v)
- 20 of any of the preceding rounds comprises an amino acid sequence identified in step (ii) for that subject; and
- (vii) designing or preparing a peptide, a polynucleic acid or vector that encodes a peptide, a panel of peptides, or one or more polynucleic acids or vectors that encode a panel of peptides, wherein each peptide comprises one or more of the
- 25 target polypeptide fragments identified in step (iv), (v) or (vi), optionally wherein the polypeptide fragment is flanked at the N and/or C terminus by additional amino acids that are not part of the sequence of the target polypeptide antigen.
14. The method according to claim 13, wherein the target polypeptide is expressed by a
- 30 pathogenic organism, a virus or a cancer cell, or is a cancer testes antigen, optionally wherein the target polypeptide is selected from the antigens listed in any of Tables 2 to 5.

15. The method according to claim 13 or claim 14, the method further comprising selecting one or more peptides, polynucleic acids or vectors designed or prepared according to the method of claim 13 or claim 14 for use in a method of vaccinating, providing immunotherapy to, or inducing a cytotoxic and/or helper T cell response in a subject, optionally wherein each of the one or more peptides, or encoded peptides, comprises an amino acid sequence that is
- 5 (a) a fragment of a polypeptide that is expressed by a pathogenic organism, a virus or a cancer cell; and
- (b) a T cell epitope capable of binding to at least three HLA class I molecules of the subject or a T cell epitope capable of binding to at least three HLA class II molecules of the subject.
- 10
16. The method of claim 15, further comprising administering the one or more peptides, polynucleic acids or vectors to the subject.
- 15
17. A panel of peptides, polynucleic acids or vectors designed and/or prepared according to the method of claim 13 or claim 14, or comprising or encoding two or more peptides designed and/or prepared according to the method of claim 13 or claim 14, or a panel of peptides, polynucleic acids or vectors selected according to the method of claim 15.
- 20
18. A panel of peptides, or one or more polynucleic acids or vectors encoding a panel of peptides, for use in a method of inducing a T cell response against one or more target polypeptides in a subject of a target human population, wherein each of the peptides, or encoded peptides, comprises an amino acid sequence that is
- 25 (a) 9 to 50 amino acids in length; and
- (b) comprises a fragment of the one or more target polypeptides, wherein the fragment comprises, in at least 10% of subjects of the intent-to-treat human population:
- a. an amino acid sequence of the target polypeptide that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject;
- 30 b. an amino acid sequence of the target polypeptide that is a T cell epitope capable of binding to at least three HLA class II molecules of the subject;
- c. an amino acid sequence of the target polypeptide that comprise a T cell epitope capable of binding to at least three HLA class I molecules of the subject and a T

cell epitope capable of binding to at least three HLA class II molecules of the subject; or

- d. an amino acid sequence of the target polypeptide that both
- i. is a T cell epitope capable of binding to at least three HLA class II molecules; and
 - ii. comprise an amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject

19. A pharmaceutical composition or kit comprising a panel of peptides, or one or more polynucleic acids or vectors encoding a panel of peptides according to claim 17 or claim 18, wherein the composition or kit optionally comprises at least one pharmaceutically acceptable diluent, carrier, or preservative.

20. A method of vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject, the method comprising administering to the subject a pharmaceutical composition or the panel of peptides, polynucleic acids or vectors of the kit according to claim 19.

21. The method of claim 20, wherein one or more or each of the peptides or the encoded peptides comprises an amino acid sequence that is

- (a) a fragment of a polypeptide that is expressed by a pathogenic organism, a virus or a cancer cell; and
- (b) a T cell epitope capable of binding to at least three HLA class I molecules of the subject or a T cell epitope capable of binding to at least three HLA class II molecules of the subject.