

fragments of the antigens comprising the T cell epitopes, are useful for inducing specific immune responses against tumor cells expressing these antigens and for treating or preventing cancer.

In one aspect, the present disclosure provides a polypeptide that comprises a fragment of up to 50 consecutive amino acids of a gastric cancer-associated antigen selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 1 to 30, optionally wherein the fragment is flanked at the N and/or C terminus by additional amino acids that are not part of the sequence of the gastric cancer-associated antigen.

In another aspect, the present disclosure provides a panel of two or more polypeptides as described herein, wherein each polypeptide comprises a different amino acid sequence selected from SEQ ID NOs: 1 to 30. In another aspect, the present disclosure provides a pharmaceutical composition or kit comprising one or more polypeptides as described herein, or a panel of polypeptides as described herein, or a polypeptide comprising at least two amino acid sequences selected SEQ ID NOs: 1 to 30, or one or more polynucleic acids or vectors encoding said one or more polypeptides. In yet another aspect, the present disclosure provides a pharmaceutical composition as described herein, for use in therapy for vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject, wherein the pharmaceutical composition is to be administered to the subject, optionally wherein the therapy is prophylactic and/or for treating or preventing cancer, optionally gastric cancer.

In yet another aspect, the present disclosure provides use of the pharmaceutical composition as described herein in the manufacture of a medicament for treating cancer, optionally gastric cancer. In yet another aspect, the present disclosure provides a method of identifying a human subject who is predicted to have a cytotoxic T cell response to administration of a pharmaceutical composition as described herein, the method comprising (i) determining that the active ingredient polypeptide(s) of the pharmaceutical composition comprise a sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and (ii) identifying the subject as predicted to have a cytotoxic T cell response to administration of the pharmaceutical composition.

In yet another aspect, the present disclosure provides a method of identifying a subject who is predicted to have a clinical response to the use as described herein, the method

comprising (i) determining that the active ingredient polypeptide(s) of the pharmaceutical composition comprise two or more different amino acid sequences each of which is a. a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and b. a fragment of a cancer-associated antigen expressed by cancer cells of the subject, optionally wherein the cancer-associated antigen is present in a sample obtained from the subject; and (ii) identifying the subject as predicted to have a clinical response to the use.

In yet another aspect, the present disclosure provides a method of determining the probability that a specific human subject will have a clinical response to the use as described herein, wherein one or more of the following factors corresponds to a higher probability of a clinical response: (a) presence in the active ingredient polypeptide(s) of a higher number of amino acid sequences and/or different amino acid sequences that are each a T cell epitope capable of binding to at least three HLA class I of the subject; (b) a higher number of target polypeptide antigens, comprising at least one amino acid sequence that is both A. comprised in an active ingredient polypeptide; and B. a T cell epitope capable of binding to at least three HLA class I of the subject; optionally wherein the target polypeptide antigens are expressed in the subject, further optionally wherein the target polypeptides antigens are in one or more samples obtained from the subject; (c) a higher probability that the subject expresses target polypeptide antigens, optionally a threshold number of the target polypeptide antigens and/or optionally target polypeptide antigens that have been determined to comprise at least one amino acid sequence that is both A. comprised in an active ingredient polypeptide; and B. a T cell epitope capable of binding to at least three HLA class I of the subject; and/or (d) a higher number of target polypeptide antigens that the subject is predicted to express, optionally a higher number of target polypeptide antigens that the subject expresses with a threshold probability, and/or optionally the target polypeptide antigens that have been determined to comprise at least one amino acid sequence that is both A. comprised in an active ingredient polypeptide; and B. a T cell epitope capable of binding to at least three HLA class I of the subject.

In a further aspect, the present disclosure refers to a use as described herein, wherein the subject has been identified as predicted to have a clinical response or as having above a threshold minimum probability of having a clinical response to the treatment by a method as described herein. In a further aspect, the present disclosure refers to a method of identifying a human subject who is predicted not have a clinical response to the use as described herein, the method

comprising (i) determining that the active ingredient peptide(s) of the pharmaceutical composition do not comprise two or more different amino acid sequences each of which is a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and (ii) identifying the subject as predicted not to have a clinical response to the use.

5 In a first example the disclosure provides a polypeptide that comprises a fragment of up to 50 consecutive amino acids of

(a) a gastric cancer-associated antigen selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1, wherein the fragment comprises an amino acid sequence
10 selected from any one of SEQ ID NOs: 1 to 30;

(b) a lung cancer-associated antigen selected from BRDT, PRAME, NALP4, MAGE-A12, MAGE-A2, SURVIVIN, DPPA2, NY-SAR-35, LDHC, MAGE-C2, MAGE-A3, KK-LC-1 and MAGE-A1, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 90 to 119;

15 (c) a melanoma-associated antigen selected from PRAME, MAGE-A2, MAGE-C1, SURVIVIN, MAGE-A12, Ny-ESO-1, MAGE-C2, MAGE-A6, BORIS, LAGE-1, MAGE-A11, SSX-1, MAGE-A3, MAGE-A10 and MAGE-A1, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 178 to 207; and/or

20 (d) a bladder cancer-associated antigen selected from PIWIL2, CTAGE1, MAGE-A9, EpCAM, OY-TES-1, NY-ESO-1, SURVIVIN, MAGE-C1, MAGE-A2, LAGE-1, MAGE-A3, MAGE-A8, HAGE, MAGE-A1, MAGE-C2, MAGE-A10 and MAGE-A12, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 268 to 297.

25 In some specific cases the disclosure provides a polypeptide that

(a) is a fragment of a gastric cancer-associated antigen selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 1 to 30; or

30 (b) comprises or consists of two or more fragments of one or more gastric

- cancer associated antigens selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1, wherein each fragment comprises a different amino acid sequence selected from any one of SEQ ID NOs: 1 to 30, optionally wherein the fragments overlap or are arranged end to end in the polypeptide; or
- (c) is a fragment of a lung cancer-associated antigen selected from BRDT, PRAME, NALP4, MAGE-A12, MAGE-A2, SURVIVIN, DPPA2, NY-SAR-35, LDHC, MAGE-C2, MAGE-A3, KK-LC-1 and MAGE-A1, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 90 to 119; or
- (d) comprises or consists of two or more fragments of one or more lung cancer associated antigens selected from BRDT, PRAME, NALP4, MAGE-A12, MAGE-A2, SURVIVIN, DPPA2, NY-SAR-35, LDHC, MAGE-C2, MAGE-A3, KK-LC-1 and MAGE-A1, wherein each fragment comprises a different amino acid sequence selected from any one of SEQ ID NOs: 90 to 119, optionally wherein the fragments overlap or are arranged end to end in the polypeptide; or
- (e) is a fragment of a melanoma-associated antigen selected from PRAME, MAGE-A2, MAGE-C1, SURVIVIN, MAGE-A12, Ny-ESO-1, MAGE-C2, MAGE-A6, BORIS, LAGE-1, MAGE-A11, SSX-1, MAGE-A3, MAGE-A10 and MAGE-A1, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 178 to 207; or
- (f) comprises or consists of two or more fragments of one or more melanoma associated antigens selected from PRAME, MAGE-A2, MAGE-C1, SURVIVIN, MAGE-A12, Ny-ESO-1, MAGE-C2, MAGE-A6, BORIS, LAGE-1, MAGE-A11, SSX-1, MAGE-A3, MAGE-A10 and MAGE-A1, wherein each fragment comprises a different amino acid sequence selected from any one of SEQ ID NOs: 178 to 207, optionally wherein the fragments overlap or are arranged end to end in the polypeptide; or
- (g) is a fragment of a bladder cancer-associated antigen selected from PIWIL2, CTAGE1, MAGE-A9, EpCAM, OY-TES-1, NY-ESO-1, SURVIVIN, MAGE-C1, MAGE-A2, LAGE-1, MAGE-A3, MAGE-A8, HAGE, MAGE-A1, MAGE-C2, MAGE-A10 and MAGE-A12, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 268 to 297; or

(h) comprises or consists of two or more fragments of one or more bladder cancer associated antigens selected from PIWIL2, CTAGE1, MAGE-A9, EpCAM, OY-TES-1, NY-ESO-1, SURVIVIN, MAGE-C1, MAGE-A2, LAGE-1, MAGE-A3, MAGE-A8, HAGE, MAGE-A1, MAGE-C2, MAGE-A10 and MAGE-A12, wherein each fragment comprises a different amino acid sequence selected from any one of SEQ ID NOs: 268 to 297, optionally wherein the fragments overlap or are arranged end to end in the polypeptide.

In some specific cases the polypeptide comprises or consists of fragments of at least two different cancer-associated antigens, wherein the cancer-associated antigens are selected from

(a) DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1 and wherein each fragment comprises a different amino acid sequence selected from SEQ ID NOs: 1 to 30; and/or

(b) BRDT, PRAME, NALP4, MAGE-A12, MAGE-A2, SURVIVIN, DPPA2, NY-SAR-35, LDHC, MAGE-C2, MAGE-A3, KK-LC-1 and MAGE-A1; and wherein each fragment comprises a different amino acid sequence selected from SEQ ID NOs: 90 to 119; and/or

(c) PRAME, MAGE-A2, MAGE-C1, SURVIVIN, MAGE-A12, NY-ESO-1, MAGE-C2, MAGE-A6, BORIS, LAGE-1, MAGE-A11, SSX-1, MAGE-A3, MAGE-A10 and MAGE-A1; and wherein each fragment comprises a different amino acid sequence selected from SEQ ID NOs: 178 to 207 and/or

(d) PIWIL2, CTAGE1, MAGE-A9, EpCAM, OY-TES-1, NY-ESO-1, SURVIVIN, MAGE-C1, MAGE-A2, LAGE-1, MAGE-A3, MAGE-A8, HAGE, MAGE-A1, MAGE-C2, MAGE-A10 and MAGE-A12; and wherein each fragment comprises a different amino acid sequence selected from SEQ ID NOs: 268 to 297.

In some cases the polypeptide comprises or consists of one or more amino acid sequences selected from SEQ ID NOs: 31 to 60, 90 to 119, 178 to 207 and/or 268 to 297.

In some cases the polypeptide comprises or consists of one or more amino acid sequences selected from SEQ ID NOs: 61 to 75, 120 to 149, 208 to 237, and/or 298 to 327.

In a further example the disclosure provides a panel of two or more polypeptides as described above, wherein each peptide comprises or consists of a different amino acid sequence selected from SEQ ID NOs: 1 to 30; and/or SEQ ID NOs: 31 to 60; and/or SEQ ID NOs: 61 to 75; or selected from SEQ ID NOs: 90 to 119; and/or SEQ ID NOs: 120 to 149; and/or SEQ ID NOs: 150 to 164; or selected from SEQ ID NOs: 178 to 207; and/or SEQ ID NOs: 208 to 237; and/or SEQ ID NOs: 238 to 252; or selected from SEQ ID NOs: 268 to 297; and/or SEQ ID NOs: 298 to 327; and/or SEQ ID NOs: 328 to 342.

In a further example the disclosure provides a pharmaceutical composition or kit having one or more polypeptides or panels of peptides as described above as active ingredients, or having a polypeptide comprising at least two amino acid sequences selected from SEQ ID NOs: 1 to 30; SEQ ID NOs: 31 to 60; and/or SEQ ID NOs: 61-75; and/or SEQ ID NOs: 90 to 119; SEQ ID NOs: 120 to 149; and/or SEQ ID NOs: 150 to 164; and/or SEQ ID NOs: 178 to 207; and/or SEQ ID NOs: 208 to 237; and/or SEQ ID NOs: 238 to 252; and/or SEQ ID NOs: 268 to 297; and/or SEQ ID NOs: 298 to 327; and/or SEQ ID NOs: 328 to 342 as an active ingredient.

In a further example the disclosure provides a method of inducing immune responses, (e.g. vaccination, providing immunotherapy or inducing a CD8⁺ T cell response in a subject), the method comprising administering to the subject a pharmaceutical composition, kit or the panel of polypeptides as described above. The method may be a method of treating cancer, such as gastric cancer, lung cancer, melanoma and bladder cancer.

In further examples, the disclosure provides

- the pharmaceutical composition, kit or panel of polypeptides described above for use in a method of inducing immune responses or for use in a method of treating cancer, optionally gastric cancer, lung cancer, melanoma and bladder cancer; and
- use of a peptide or a panel of peptides as described above in the manufacture of a medicament for inducing immune responses or for treating cancer, optionally gastric cancer, lung cancer, melanoma and bladder cancer.

In a further example the disclosure provides a method of identifying a human subject who will likely have a CD8⁺ T cell response to administration of a pharmaceutical composition as described above, the method comprising

- (i) determining that the active ingredient polypeptide(s) of the pharmaceutical composition comprise a sequence that is a T cell epitope capable of binding to at least three HLA class I of the subject; and
- (ii) identifying the subject as likely to have a CD8+ T cell response to administration of the pharmaceutical composition.

In a further example the disclosure provides a method of identifying a subject who will likely have a clinical response to a method of treatment as described above, the method comprising

- (i) determining that the active ingredient polypeptide(s) comprise two or more different amino acid sequences each of which is
 - a. a T cell epitope capable of binding to at least three HLA class I of the subject; and
 - b. a fragment of a cancer-associated antigen expressed by cancer cells of the subject; and
- (ii) identifying the subject as likely to have a clinical response to the method of treatment.

In a further example the disclosure provides a method of determining the likelihood that a specific human subject will have a clinical response to a method of treatment described above, wherein one or more of the following factors corresponds to a higher likelihood of a clinical response:

- (a) presence in the active ingredient polypeptide(s) of a higher number of amino acid sequences and/or different amino acid sequences that are each a T cell epitope capable of binding to at least three HLA class I of the subject;
- (b) a higher number of target polypeptide antigens, comprising at least one amino acid sequence that is both
 - A. comprised in an active ingredient polypeptide; and
 - B. a T cell epitope capable of binding to at least three HLA class I of the subject;optionally wherein the target polypeptide antigens are expressed in the subject, further optionally wherein the target polypeptides antigens are in one or more samples obtained from the subject;

(c) a higher probability that the subject expresses target polypeptide antigens, optionally a threshold number of the target polypeptide antigens and/or optionally target polypeptide antigens that have been determined to comprise at least one amino acid sequence that is both

5 A. comprised in an active ingredient polypeptide; and

 B. a T cell epitope capable of binding to at least three HLA class I of the subject; and/or

(d) a higher number of target polypeptide antigens that the subject is predicted to express, optionally a higher number of target polypeptide antigens that the subject expresses with a threshold probability, and/or optionally the target polypeptide antigens that have been

10 A. comprised in an active ingredient polypeptide; and

 B. a T cell epitope capable of binding to at least three HLA class I of the subject.

In some cases the cancer-associated antigens may be a gastric cancer antigen selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1, SSX1, a lung cancer antigen selected from BRDT, PRAME, NALP4, MAGE-A12, MAGE-A2, SURVIVIN, DPPA2NY -SAR-35, LDHC, MAGE-C2, MAGE-A3, KK-LC-1, MAGE-A1, a melanoma antigen selected from PRAME, MAGE-A2, MAGE-C1, SURVIVIN, MAGE-A12, Ny-ESO-1, MAGE-C2, MAGE-A6, BORIS, LAGE-1, MAGE-A11, SSX-1, MAGE-A3, MAGE-A10, MAGE-A1, and/or a bladder cancer antigen selected from PIWIL2, CTAGE1, MAGE-A9, EpCAM, OY-TES-1, NY-ESO-1, SURVIVIN, MAGE-C1, MAGE-A2, LAGE-1, MAGE-A3, MAGE-A8 and HAGE, MAGE-A1, MAGE-C2, MAGE-A10 and MAGE A12 . In some cases the methods above comprise the step of determining that one or more cancer-associated antigens is expressed by cancer cells of the subject. The cancer-associated antigen(s) may be present in one or more samples obtained from the subject.

In some cases administration of the pharmaceutical composition or the active ingredient polypeptides of the kit may then be selected as a method of treatment for the subject. The subject may further be treated by administration of the pharmaceutical composition or the active ingredient polypeptides.

In a further example the disclosure provides a method of treatment as described above, wherein the subject has been identified as likely to have a clinical response or as having above a threshold minimum likelihood of having a clinical response to the treatment by the method described above.

In a further example the disclosure provides a method of identifying a human subject who will likely not have a clinical response to a method of treatment as described above, the method comprising

- (i) determining that the active ingredient polypeptide(s) of the pharmaceutical composition do not comprise two or more different amino acid sequences each of which is a T cell epitope capable of binding to at least three HLA class I of the subject; and
- (ii) identifying the subject as likely not to have a clinical response to the method of treatment.

The methods described above may comprise the step of determining the HLA class I and/or class II genotype of the subject.

The present disclosure includes methods of treating a human subject likely to respond to a polypeptide(s) or pharmaceutical composition comprising the polypeptide(s) of the current disclosure comprising: (a) determining that a polypeptide(s) or pharmaceutical composition comprising the polypeptide(s) comprises an amino acid sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the human subject; and (b) administering to the human subject the polypeptide or pharmaceutical composition. In certain examples, the method further comprises using population expression data for each antigen to determine the likelihood that the human subject will have a CD8+ T cell response that targets one or more polypeptide antigens that are expressed by cancer cells of the human subject, wherein the antigen: (a) is selected from gastric cancer antigens DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 SSX1, and/or lung cancer antigens BRDT, PRAME, NALP4, MAGE-A12, MAGE-A2, SURVIVIN, DPPA2, NY-SAR-35, LDHC, MAGE-C2, MAGE-A3, KK-LC-1, MAGE-A1, and/or melanoma cancer antigens PRAME, MAGE-A2, MAGE-C1, SURVIVIN, MAGE-A12, Ny-ESO-1, MAGE-C2, MAGE-A6, BORIS, LAGE-1, MAGE-A11, SSX-1, MAGE-A3, MAGE-A10, MAGE-A1, and/or bladder cancer antigens PIWIL2, CTAGE1, MAGE-A9,

EpCAM, OY-TES-1, NY-ESO-1, SURVIVIN, MAGE-C1, MAGE-A2, LAGE-1, MAGE-A3, MAGE-A8 and HAGE, MAGE-A1, MAGE-C2, MAGE-A10 and MAGE-A12; and (b) comprises an amino acid sequence that is a fragment of an active ingredient peptide of the pharmaceutical composition, and a T cell epitope capable of binding to at least three HLA class I molecules of the human subject.

The present disclosure includes methods of treating a human subject likely to respond to a polypeptide(s) or pharmaceutical composition comprising the polypeptide(s) of the current disclosure comprising: (a) determining that a polypeptide(s) or pharmaceutical composition comprising the polypeptide(s) comprise two or more different amino acid sequences each of which is a T cell epitope capable of binding to at least three HLA class I molecules of the human subject; and a fragment of a cancer-associated antigen expressed by cancer cells of the human subject, optionally wherein the cancer-associated antigen is present in a sample obtained from the human subject; and (b) administering to the human subject the polypeptide or pharmaceutical composition.

The present disclosure includes methods of treating a human subject likely to respond to a polypeptide(s) or pharmaceutical composition comprising the polypeptide(s) of the current disclosure comprising determining any one of the following: (a) presence in a polypeptide(s) or pharmaceutical composition comprising the polypeptide(s) of a higher number of amino acid sequences and/or different amino acid sequences that are each a T cell epitope capable of binding to at least three HLA class I of the human subject; (b) a higher number of target polypeptide antigens in the human subject or a sample from the human subject, comprising at least one amino acid sequence that is both comprised in an active ingredient polypeptide, and a T cell epitope capable of binding to at least three HLA class I of the human subject; (c) a higher probability that the human subject expresses target polypeptide antigens, optionally a threshold number of the target polypeptide antigens and/or optionally target polypeptide antigens that have been determined to comprise at least one amino acid sequence that is both comprised in an active ingredient polypeptide, and a T cell epitope capable of binding to at least three HLA class I of the human subject; and/or (d) a higher number of target polypeptide antigens that the human subject is predicted to express, optionally a higher number of target polypeptide antigens that the human subject expresses with a threshold probability, and/or optionally the target polypeptide antigens that have been determined to comprise at least one amino acid sequence that is both

comprised in an active ingredient polypeptide, and a T cell epitope capable of binding to at least three HLA class I of the human subject; and (e) administering to the human subject the polypeptide or pharmaceutical composition. In certain examples, the method further comprises identifying which polypeptide antigens targeted by the polypeptide(s) or pharmaceutical composition comprising the polypeptide(s) comprise an amino acid sequence that is both comprised in an active ingredient polypeptide, and a T cell epitope capable of binding to at least three HLA class I of the human subject using population expression data for each antigen identified to determine the probability that the human subject expresses one or more of the antigens identified that together comprise at least two different amino acid sequences; and administering to the human subject the polypeptide or pharmaceutical composition. In certain examples, the at least two different amino acid sequences are comprised in the amino acid sequence of two different polypeptide antigens targeted by the active ingredient polypeptide(s).

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 examples of the disclosure set forth are considered to be illustrative and not limiting. Various changes to the described examples 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 examples 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

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CLAIMS

1. A polypeptide that comprises a fragment of up to 50 consecutive amino acids of a gastric cancer-associated antigen selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 1 to 30, optionally wherein the fragment is flanked at the N and/or C terminus by additional amino acids that are not part of the sequence of the gastric cancer-associated antigen.
2. The polypeptide of claim 1, wherein the polypeptide
 - a. is a fragment of a gastric cancer-associated antigen selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1, wherein the fragment comprises an amino acid sequence selected from any one of SEQ ID NOs: 1 to 30; or
 - b. comprises or consists of two or more fragments of one or more gastric cancer associated antigens selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1, wherein each fragment comprises a different amino acid sequence selected from any one of SEQ ID NOs: 1 to 30, optionally wherein the fragments overlap or are arranged end to end in the polypeptide.
3. The polypeptide according to claim 1 or claim 2, wherein the polypeptide comprises or consists of fragments of at least two different cancer-associated antigens, wherein the cancer-associated antigens are selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1; and wherein each fragment comprises a different amino acid sequence selected from SEQ ID NOs: 1 to 30.
4. The polypeptide according to any one of claims 1 to 3, comprising or consisting of one or more amino acid sequences selected from SEQ ID NOs: 31 to 60.

5. The polypeptide according to any one of claims 1 to 4 comprising or consisting of the amino acid sequence of any one of SEQ ID NOs: 61 to 75.
6. A panel of two or more polypeptides according to any one of claims 1 to 5, wherein each polypeptide comprises a different amino acid sequence selected from SEQ ID NOs: 1 to 30.
7. A pharmaceutical composition or kit comprising one or more polypeptides according to any one of claims 1 to 5, or a panel of polypeptides according to claim 6, or a polypeptide comprising at least two amino acid sequences selected SEQ ID NOs: 1 to 30, or one or more polynucleic acids or vectors encoding said one or more polypeptides.
8. A pharmaceutical composition according to claims 7, for use in therapy for vaccination, providing immunotherapy or inducing a cytotoxic T cell response in a subject, wherein the pharmaceutical composition is to be administered to the subject, optionally wherein the therapy is prophylactic and/or for treating or preventing cancer, optionally gastric cancer.
9. Use of the pharmaceutical composition of claim 8 in the manufacture of a medicament for treating cancer, optionally gastric cancer.
10. A method of identifying a human subject who is predicted to have a cytotoxic T cell response to administration of a pharmaceutical composition according to claim 7, the method comprising
 - (i) determining that the active ingredient polypeptide(s) of the pharmaceutical composition comprise a sequence that is a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and
 - (ii) identifying the subject as predicted to have a cytotoxic T cell response to administration of the pharmaceutical composition.
11. The method of claim 10 further comprising using population expression data for each antigen that

(a) is selected from DPPA2, CAGE-1, TSP50, HIWI, SURVIVIN, 5T4, PRAME, KK-LC-1, MAGE-A2, MAGE-A3, LAGE-1, MAGE-A10, MAGE-A1 and SSX1; and

(b) comprises an amino acid sequence that is

i. a fragment of an active ingredient peptide of the pharmaceutical composition; and

ii. a T cell epitope capable of binding to at least three HLA class I molecules of the subject;

to determine the probability that the subject will have a CD8⁺ T cell response that targets one or more polypeptide antigens that are expressed by cancer cells of the subject.

12. A method of identifying a subject who is predicted to have a clinical response to the use according to claim 9, the method comprising

(i) determining that the active ingredient polypeptide(s) of the pharmaceutical composition comprise two or more different amino acid sequences each of which is

a. a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and

b. a fragment of a cancer-associated antigen expressed by cancer cells of the subject, optionally wherein the cancer-associated antigen is present in a sample obtained from the subject; and

(ii) identifying the subject as predicted to have a clinical response to the use.

13. A method of determining the probability that a specific human subject will have a clinical response to the use according to claim 9, wherein one or more of the following factors corresponds to a higher probability of a clinical response:

(a) presence in the active ingredient polypeptide(s) of a higher number of amino acid sequences and/or different amino acid sequences that are each a T cell epitope capable of binding to at least three HLA class I of the subject;

(b) a higher number of target polypeptide antigens, comprising at least one amino acid sequence that is both

A. comprised in an active ingredient polypeptide; and

B. a T cell epitope capable of binding to at least three HLA class I of the subject;

optionally wherein the target polypeptide antigens are expressed in the subject, further optionally wherein the target polypeptides antigens are in one or more samples obtained from the subject;

(c) a higher probability that the subject expresses target polypeptide antigens, optionally a threshold number of the target polypeptide antigens and/or optionally target polypeptide antigens that have been determined to comprise at least one amino acid sequence that is both

A. comprised in an active ingredient polypeptide; and

B. a T cell epitope capable of binding to at least three HLA class I of the subject;

and/or

(d) a higher number of target polypeptide antigens that the subject is predicted to express, optionally a higher number of target polypeptide antigens that the subject expresses with a threshold probability, and/or optionally the target polypeptide antigens that have been determined to comprise at least one amino acid sequence that is both

A. comprised in an active ingredient polypeptide; and

B. a T cell epitope capable of binding to at least three HLA class I of the subject.

14. The method of claim 13, wherein the method comprises

(i) identifying which polypeptide antigens targeted by the active ingredient polypeptide(s) comprise an amino acid sequence that is both

A. comprised in an active ingredient polypeptide; and

B. a T cell epitope capable of binding to at least three HLA class I of the subject;

(ii) using population expression data for each antigen identified in step (i) to determine the probability that the subject expresses one or more of the antigens identified in step (i) that together comprise at least two different amino acid sequences of step (i); and

- (iii) determining the probability that the subject will have a clinical response to administration of the pharmaceutical composition, kit or panel of polypeptides, wherein a higher probability determined in step (ii) corresponds to a higher probability of clinical response.

15. The method of claim 14, wherein the at least two different amino acid sequences are comprised in the amino acid sequence of two different polypeptide antigens targeted by the active ingredient polypeptide(s).

16. The method of any one of claims 12 to 15 further comprising selecting or recommending administration of the pharmaceutical composition or the peptides, polynucleic acids or vectors of the kit for the subject,.

17. A use according to claim 9, wherein the subject has been identified as predicted to have a clinical response or as having above a threshold minimum probability of having a clinical response to the treatment by a method according to any one of claims 12 to 15.

18. The pharmaceutical composition of claim 8 or the use of claim 9 or 17 wherein the treatment is to be administered in combination with chemotherapy, targeted therapy or a checkpoint inhibitor.

19. A method of identifying a human subject who is predicted not have a clinical response to the use according to claim 9, the method comprising

- (i) determining that the active ingredient peptide(s) of the pharmaceutical composition do not comprise two or more different amino acid sequences each of which is a T cell epitope capable of binding to at least three HLA class I molecules of the subject; and
- (ii) identifying the subject as predicted not to have a clinical response to the use.