CLAIMS

1. A composition for use in the treatment of a patient who has cancer, the composition comprising a population of activated T cells that selectively recognize cells in the patient that aberrantly express a peptide, wherein said peptide consists of the amino acid sequence of ILQDGQFLV (SEQ ID NO: 157).
2. Use of a composition in the manufacture of a medicament for the treatment of a patient who has cancer, the composition comprising a population of activated T cells that selectively recognize cells in the patient that aberrantly express a peptide, wherein said peptide consists of the amino acid sequence of ILQDGQFLV (SEQ ID NO: 157), wherein said cancer is selected from the group consisting of hepatocellular carcinoma (HCC), colorectal carcinoma (CRC), glioblastoma (GB), gastric cancer (GC), esophageal cancer, non-small cell lung cancer (NSCLC), pancreatic cancer (PC), renal cell carcinoma (RCC), benign prostate hyperplasia (BPH), prostate cancer (PCA), ovarian cancer (OC), melanoma, breast cancer (BRCA), chronic lymphocytic leukemia (CLL), Merkel cell carcinoma (MCC), small cell lung cancer (SCLC), Non-Hodgkin lymphoma (NHL), acute myeloid leukemia (AML), gallbladder cancer and cholangiocarcinoma (GBC, CCC), urinary bladder cancer (UBC), and uterine cancer (UEC).
3. The composition of claim 1 or use of claim 2, wherein the T cells are autologous to the patient.
4. The composition of claim 1 or use of claim 2, wherein the T cells are obtained from a healthy donor.
5. The composition of claim 1 or use of claim 2, wherein the T cells are obtained from tumor infiltrating lymphocytes or peripheral blood mononuclear cells.
6. The composition of claim 1 or use of claim 2, further comprising expanding T cells in vitro.
7. The composition of claim 1 or use of claim 2, wherein the peptide is in a complex with an MHC molecule.
8. The composition of claim 1 or use of claim 2, wherein the composition further comprises an adjuvant.
9. The composition or use of claim 8, wherein the adjuvant is selected from the group consisting of imiquimod, resiguimod, GM-CSF, cyclophosphamide, Sunitinib, bevacizumab, interferon-alpha, CpG, oligonucleotides and derivatives, poly-(I:C) and derivatives, RNA, sildenafil, and particulate formations with PLG and virosomes.
10. The composition of claim 1 or use of claim 2, wherein the activated T cells are cytotoxic T cells produced by contacting T cells, in vitro, with an antigen presenting cell that expresses the peptide in a complex with an MHC class I molecule on the surface of the antigen presenting cell, for a period of time sufficient to activate said T cell specifically against the peptide.
11. The composition of claim 1 or use of claim 2, wherein the antigen presenting cell is infected with a recombinant virus expressing the peptide.
12. The composition or use of claim 11, wherein the antigen presenting cell is a dendritic cell or a macrophage.
13. The composition or use of claim 10, further comprising stimulating the activated T cells in the presence of an anti-CD28 antibody and IL-12 to clonally expand the T cells.
14. The composition of claim 1 or use of claim 2, wherein the population of activated T cells comprises CD8-positive cells.
15. A composition for use in the treatment of a patient who has HCC, CRC, GB, GC, esophageal cancer, NSCLC, PC, RCC, BPH, PCA, OC, melanoma, BRCA, CLL,

~~MCC, SCLC, NHL, AML, GBC, CCC, UBC, and/or UEC, the composition comprising a peptide in the form of a pharmaceutically acceptable salt and an adjuvant, wherein said peptide consists of the amino acid sequence of ILQDGQFLV (SEQ ID NO: 157), thereby inducing a T-cell response to the HCC, CRC, GB, GC, esophageal cancer, NSCLC, PC, RCC, BPH, PCA, OC, melanoma, BRCA, CLL, MCC, SCLC, NHL, AML, GBC, CCC, UBC, and/or UEC.~~

16. ~~Use of a composition in the manufacture of a medicament for the treatment of a patient who has HCC, CRC, GB, GC, esophageal cancer, NSCLC, PC, RCC, BPH, PCA, OC, melanoma, BRCA, CLL, MCC, SCLC, NHL, AML, GBC, CCC, UBC, and/or UEC, the composition comprising a peptide in the form of a pharmaceutically acceptable salt and an adjuvant, wherein said peptide consists of the amino acid sequence of ILQDGQFLV (SEQ ID NO: 157), thereby inducing a T-cell response to the HCC, CRC, GB, GC, esophageal cancer, NSCLC, PC, RCC, BPH, PCA, OC, melanoma, BRCA, CLL, MCC, SCLC, NHL, AML, GBC, CCC, UBC, and/or UEC.~~
17. ~~The composition of claim 15 or use of claim 16, wherein the T cell response is a cytotoxic T cell response.~~

1. A peptide comprising an amino acid sequence of SEQ ID No. 155 or an amino acid sequence selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 13, SEQ ID No. 15 to SEQ ID No. 154 and SEQ ID No. 156 to SEQ ID No. 288, and variant sequences thereof which are at least 88% homologous to SEQ ID No. 155, SEQ ID No. 1 to SEQ ID No. 13, SEQ ID No. 15 to SEQ ID No. 154 and SEQ ID No. 156 to SEQ ID No. 288, and wherein said variant binds to molecule(s) of the major histocompatibility complex (MHC) and/or induces T cells cross-reacting with said variant peptide; and a pharmaceutical acceptable salt thereof, wherein said peptide is not a full-length polypeptide.

2. The peptide according to claim 1, wherein said peptide has the ability to bind to an MHC class-I or –II molecule, and wherein said peptide, when bound to said MHC, is capable of being recognized by CD4 and/or CD8 T cells.

3. The peptide or variant thereof according to claim 1 or 2, wherein the amino acid sequence thereof comprises a continuous stretch of amino acids according to any one of SEQ ID No. 155, SEQ ID No. 1 to SEQ ID No. 13, SEQ ID No. 15 to SEQ ID No. 154 and SEQ ID No. 156 to SEQ ID No. 288.

4. The peptide or variant thereof according to any of claims 1 to 3, wherein said peptide or variant thereof has an overall length of from 8 to 100, preferably from 8 to 30, and more preferred from 8 to 16 amino acids, and most preferred wherein the peptide consists or

consists essentially of an amino acid sequence according to any of SEQ ID No. 155, SEQ ID No. 1 to SEQ ID No. 13, SEQ ID No. 15 to SEQ ID No. 154 and SEQ ID No. 156 to SEQ ID No. 288.

5. The peptide or variant thereof according to any of Claims 1 to 4, wherein said peptide is modified and/or includes non-peptide bonds.

6. The peptide or variant thereof according to any of Claims 1 to 5, wherein said peptide is part of a fusion protein, in particular comprising N-terminal amino acids of the HLA-DR antigen-associated invariant chain (Ii).

7. A nucleic acid, encoding a peptide or variant thereof according to any one of claims 1 to 6, optionally linked to a heterologous promoter sequence.

8. An expression vector expressing the nucleic acid according to claim 7.

9. A recombinant host cell comprising the peptide according to claim 1 to 6, the nucleic acid according to claim 7 or the expression vector according to claim 8, wherein said host cell preferably is an antigen presenting cell such as a dendritic cell.

10. The peptide or variant thereof according to any one of claims 1 to 6, the nucleic acid according to claim 7, the expression vector according to claim 8, or the host cell according to claim 9 for use in medicine.

11. A method for producing the peptide or variant thereof according to any one of claims 1 to 6, the method comprising culturing the host cell according to claim 9 that presents the peptide according to claim 1 to 6, or expresses the nucleic acid according to claim 7 or comprises the expression vector according to claim 8, and isolating the peptide or variant thereof from the host cell or its culture medium.

12. An *in vitro* method for producing activated T lymphocytes, the method comprising contacting *in vitro* T cells with antigen loaded human class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell or an artificial construct mimicking an antigen-presenting cell for a period of time sufficient to activate said T cells in an antigen specific manner, wherein said antigen is a peptide according to any one of claims 1 to 4

13. An activated T lymphocyte, produced by the method according to claim 12, that selectively recognizes a cell which presents a polypeptide comprising an amino acid sequence given in any one of claims 1 to 4.

14. A method for killing target cells in a patient which target cells present a polypeptide comprising an amino acid sequence given in any one of claims 1 to 4, the method comprising administering to the patient an effective number of activated T cells as defined in claim 13.

15. An antibody, in particular a soluble or membrane-bound antibody, that specifically recognizes the peptide or variant thereof according to any of claims 1 to 5, preferably the peptide or variant thereof according to any of claims 1 to 5 when bound to an MHC molecule.

16. The peptide according to any one of claims 1 to 6, the nucleic acid according to claim 7, the expression vector according to claim 8, the cell according to claim 9, the activated T lymphocyte according to claim 13 or the antibody according to claim 15 for use in the diagnosis and/or treatment of cancer, or for use in the manufacture of a medicament against cancer.

17. The peptide according to any one of claims 1 to 6, the nucleic acid according to claim 7, the expression vector according to claim 8, the cell according to claim 9, the activated T lymphocyte according to claim 13 or the antibody according to claim 15 for use according to claim 16, wherein said cancer is selected from the group of hepatocellular carcinoma (HCC), colorectal carcinoma (CRC), glioblastoma (GB), gastric cancer (GC), esophageal cancer, non-small cell lung cancer (NSCLC), pancreatic cancer (PC), renal cell carcinoma (RCC),

benign prostate hyperplasia (BPH), prostate cancer (PCA), ovarian cancer (OC), melanoma, breast cancer, chronic lymphocytic leukemia (CLL), Merkel cell carcinoma (MCC), small cell lung cancer (SCLC), Non-Hodgkin lymphoma (NHL), acute myeloid leukemia (AML), gallbladder cancer and cholangiocarcinoma (GBC, CCC), urinary bladder cancer (UBC), uterine cancer (UEC), and other tumors that show an overexpression of a protein from which a peptide SEQ ID No. 155, SEQ ID No. 1 to SEQ ID No. 13, SEQ ID No. 15 to SEQ ID No. 154 and SEQ ID No. 156 to SEQ ID No. 288 is derived from.

18. A kit comprising:

a) a container comprising a pharmaceutical composition containing the peptide(s) or the variant according to any one of claims 1 to 6, the nucleic acid(s) according to claim 7, the expression vector(s) according to claim 8, the cell(s) according to claim 10, the activated T lymphocyte(s) according to claim 13 or the antibody according to claim 15, in solution or in lyophilized form;

b) optionally, a second container containing a diluent or reconstituting solution for the lyophilized formulation;

c) optionally, at least one more peptide selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 288, and

d) optionally, instructions for (i) use of the solution or (ii) reconstitution and/or use of the lyophilized formulation.

19. The kit according to claim 18, further comprising one or more of (iii) a buffer, (iv) a diluent, (v) a filter, (vi) a needle, (vii) a syringe, or (viii) an adjuvant.

20. The kit according to claim 18 or 19, wherein said peptide is selected from the group consisting of SEQ ID No. 155, SEQ ID No. 1 to SEQ ID No. 13, SEQ ID No. 15 to SEQ ID No. 154 and SEQ ID No. 156 to SEQ ID No. 288.

21. A method for producing a personalized anti-cancer vaccine, said method comprising:

a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from said individual patient;

b) comparing the peptides as identified in a) with a warehouse of peptides that have been pre-screened for immunogenicity and/or over-presentation in tumors as compared to normal tissues;

c) selecting at least one peptide from the warehouse that matches a TUMAP identified in the patient; and

d) formulating the personalized vaccine based on step c).

22. The method according to claim 21, wherein said TUMAPs are identified by:

a1) comparing expression data from the tumor sample to expression data from a sample of normal tissue corresponding to **the** tissue type of the tumor sample to identify proteins that are over-expressed or aberrantly expressed in the tumor sample; and

a2) correlating the expression data with sequences of MHC ligands bound to MHC class I and/or class II molecules in the tumor sample to identify MHC ligands derived from proteins over-expressed or aberrantly expressed by the tumor.

23. The method according to claim 21 or 22, wherein the sequences of MHC ligands are identified by eluting bound peptides from MHC molecules isolated from the tumor sample, and sequencing the eluted ligands.

24. The method according to any of claims 21 to 23, wherein the normal tissue corresponding to the tissue type of the tumor sample is obtained from the same patient.

25. The method according to any of claims 21 to 24, wherein the peptides included in the warehouse are identified based on the following steps:

aa. Performing genome-wide messenger ribonucleic acid (mRNA) expression analysis by highly parallel methods, such as microarrays or sequencing-based expression profiling, comprising identify genes that over-expressed in a malignant tissue, compared with a normal tissue or tissues;

ab. Selecting peptides encoded by selectively expressed or over-expressed genes as detected in step aa, and

ac. Determining an induction of in vivo T-cell responses by the peptides as selected comprising *in vitro* immunogenicity assays using human T cells from healthy donors or said patient; or

ba. Identifying HLA ligands from said tumor sample using mass spectrometry;

bb. Performing genome-wide messenger ribonucleic acid (mRNA) expression analysis by highly parallel methods, such as microarrays or sequencing-based expression profiling, comprising identify genes that over-expressed in a malignant tissue, compared with a normal tissue or tissues;

bc. Comparing the identified HLA ligands to said gene expression data;

bd. Selecting peptides encoded by selectively expressed or over-expressed genes as detected in step bc;

be. Re-detecting of selected TUMAPs from step bd on tumor tissue and lack of or infrequent detection on healthy tissues and confirming the relevance of over-expression at the mRNA level; and

bf. Determining an induction of in vivo T-cell responses by the peptides as selected comprising *in vitro* immunogenicity assays using human T cells from healthy donors or said patient.

26. The method according to any of claims 21 to 25, wherein the immunogenicity of the peptides included in the warehouse is determined by a method comprising in vitro immunogenicity assays, patient immunomonitoring for individual HLA binding, MHC multimer staining, ELISPOT assays and/or intracellular cytokine staining.

27. The method according to any of claims 21 to 26, wherein said warehouse comprises a plurality of peptides selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 288.

28. The method according to any of claims 21 to 27, further comprising identifying at least one mutation that is unique to the tumor sample relative to normal corresponding tissue from the individual patient, and selecting a peptide that correlates with the mutation for inclusion in the vaccine or for the generation of cellular therapies.

29. The method according to claim 28, wherein said at least one mutation is identified by whole genome sequencing.

30. A T-cell receptor, preferably a recombinant, soluble or membrane-bound T-cell receptor, that is reactive with an HLA ligand, wherein said ligand has at least 75% identity to an amino acid sequence selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 288.

31. The T-cell receptor according to claim 30, wherein said amino acid sequence is at least 88% identical to SEQ ID No. 155, SEQ ID No. 1 to SEQ ID No. 13, SEQ ID No. 15 to SEQ ID No. 154 and SEQ ID No. 156 to SEQ ID No. 288.

32. The T-cell receptor according to claim 30 or 31, wherein said amino acid sequence consists any of SEQ ID No. 155, SEQ ID No. 1 to SEQ ID No. 13, SEQ ID No. 15 to SEQ ID No. 154 and SEQ ID No. 156 to SEQ ID No. 288.

33. The T-cell receptor according to any of claims 30 to 32, wherein said T-cell receptor is provided as a soluble molecule and optionally carries a further effector function such as an immune stimulating domain or toxin.

34. A nucleic acid, encoding for a TCR according to any one of claims 30 to 33, optionally linked to a heterologous promoter sequence.

35. An expression vector expressing the nucleic acid according to claim 34.

36. A recombinant host cell comprising the nucleic acid according to claim 34 or the nucleic acid encoding an antibody according to claim 15 or the expression vector according to claim 35, wherein said host cell preferably is a T cell or NK cell.

37. A method for producing the T cell receptor according to any claims 30 to 33, said method comprising culturing a host cell according to Claim 36, and isolating said T cell receptor from said host cell and/or its culture medium.

38. An aptamer that specifically recognizes the peptide or variant thereof according to any of claims 1 to 5, preferably the peptide or variant thereof according to any of claims 1 to 5 that is bound to an MHC molecule.

39. A pharmaceutical composition comprising at least one active ingredient selected from the group consisting of the peptide according to any one of claims 1 to 6, the nucleic acid according to claim 7, the expression vector according to claim 8, the cell according to claim 9, the activated T lymphocyte according to claim 13 or the antibody according to claim 15 or T-cell receptor according to any one of claims 30 to 32 or the aptamer according to claim 38, and a pharmaceutically acceptable carrier, and optionally additional pharmaceutically acceptable excipients and/or stabilizers.

40. The pharmaceutical composition according to claim 39, wherein (i) the pharmaceutical composition further comprises an adjuvant, and/or (ii) wherein the pharmaceutical composition is a vaccine or a cellular therapeutic agent.

41. The pharmaceutical composition according to claim 40, wherein the adjuvant is an interleukin, including IL-2, IL-15 or a combination thereof.