

NOVEL TUMOR ANTIGENS FOR MELANOMA AND USES THEREOF**CROSS REFERENCE TO RELATED APPLICATIONS**

The present application claims the benefit of U.S. provisional patent application serial No. 63/496,084, filed on April 14, 2023, and U.S. provisional patent application serial No. 63/515,147
5 filed on July 24, 2023, which are incorporated herein by reference in their entirety.

SEQUENCE LISTING

A sequence listing is submitted herewith as an XML file named G17971-00091_Seq Listing.xml, created on April 11, 2024, and having a size of ~ 995 793 bytes. The content of the
aforementioned file is hereby incorporated by reference in its entirety.

10 TECHNICAL FIELD

The present disclosure generally relates to the field of cancer, and more particularly to the treatment of cancers such as melanoma.

BACKGROUND ART

Cutaneous melanoma is an aggressive form of skin cancer with over 100,000 US cases in
15 2021 (Siegel *et al.*, *CA Cancer J Clin.* 2021;71(1):7-33); annually, melanoma causes over 7000 deaths. Tumor stage is determined by histopathologic and clinical factors, which include the Breslow depth of the tumor, ulceration status, spread of disease from the primary tumor to lymph nodes, and the presence of metastasis. These factors are summarized into an overall stage denoted by a Roman numeral from 0 to IV, with Stage 0 disease being the earliest and Stage IV
20 being the most advanced. Patients within a stage should theoretically have similar outcomes, but there is still significant heterogeneity within each stage. For example, most patients with Stage I disease will be cured by surgery, but a significant minority (5-10%) may go on to develop metastasis at a later time.

While immune checkpoint blockade (ICB) therapy has significantly improved the outcome
25 of metastatic melanoma, most patients do not derive long-term benefits. Previous studies suggest that treatment failure is partly due to insufficient immune recognition of tumor antigens (TAs). Notably, immune targeting of TAs in melanoma has focused on TAs derived from non-synonymous genomic mutations.

In view of this, there is a need to identify the tumor antigens that can elicit therapeutic
30 immune responses against melanoma. Such antigens could be used as vaccines ($\pm$ immune checkpoint inhibitors) or as targets for T-cell receptor-based approaches (cell therapy, bispecific biologics).

The present description refers to a number of documents, the content of which is herein incorporated by reference in their entirety.

SUMMARY

In various aspects and embodiments, the present disclosure provides the following items 1 to 79:

1. A tumor antigen peptide (TAP) comprising or consisting of one of the amino acid sequences set forth in any one of SEQ ID NOs:1-505.
2. The TAP of item 1, wherein the TAP binds to an HLA-A*01:01 molecule and comprises or consists of the sequence of SEQ ID NO: 11, 14, 20, 27, 29, 37, 86, 87, 121, 150, 165, 173, 279, 288, 299, 308, 312, 316, 319, 331, 340, 352, 362, 363, 384, 395, 398, 411, 419, 429, 458, 474, 476, 487, 492, 500, or 501.
3. The TAP of item 1, wherein the TAP binds to an HLA-A*02:01 molecule and comprises or consists of the sequence of SEQ ID NO: 1, 2, 4, 19, 22, 25, 40, 50, 52, 54, 60, 65, 67, 76, 81, 89, 91, 103, 107, 120, 124, 128, 135, 157, 175, 179, 186, 188, 201, 208, 218, 219, 228, 232, 233, 240, 250, 257, 261, 263, 265, 266, 282, 286, 298, 311, 315, 317, 325, 333, 337, 349, 367, 373, 387, 388, 393, 399, 404, 412, 414, 415, 422, 434, 437, 455, 480, 489, or 494.
4. The TAP of item 1, wherein the TAP binds to an HLA-A*02:09 molecule and comprises or consists of the sequence of SEQ ID NO: 22, 40, 50, 62, 83, 89, 232, 265, 282, 311, 315, 317, 337, 349, 367, 399, 407, 412, or 494.
5. The TAP of item 1, wherein the TAP binds to an HLA-A*03:01 molecule and comprises or consists of the sequence of SEQ ID NO: 209, 247, 272, 347, or 505.
6. The TAP of item 1, wherein the TAP binds to an HLA-A*23:01 molecule and comprises or consists of the sequence of SEQ ID NO: 48, 84, 129, 151, 152, 171, 174, 182, 223, 237, 245, 290, 358, 397, 426, 446, 481, 482, or 486.
7. The TAP of item 1, wherein the TAP binds to an HLA-A*24:02 molecule and comprises or consists of the sequence of SEQ ID NO: 31, 244 or 481.
8. The TAP of item 1, wherein the TAP binds to an HLA-A*25:01 molecule and comprises or consists of the sequence of SEQ ID NO: 11, 31, 249, 289, 403, 425, 464, or 490.
9. The TAP of item 1, wherein the TAP binds to an HLA-A*26:01 molecule and comprises or consists of the sequence of SEQ ID NO: 11, 20, 27, 39, 41, 42, 45, 114, 116, 122, 168, 181, 268, 284, 329, 364, 398, 417, 430, 440, 447, 452, 457, 460, 462, 475, 490, or 497.
10. The TAP of item 1, wherein the TAP binds to an HLA-A*30:01 molecule and comprises or consists of the sequence of SEQ ID NO: 26, 304 or 376.
11. The TAP of item 1, wherein the TAP binds to an HLA-A*30:02 molecule and comprises or consists of the sequence of SEQ ID NO: 117, 185, 190, 193, 197, 256, 294, 323, 471, or 485.
12. The TAP of item 1, wherein the TAP binds to an HLA-A*33:01 molecule and comprises or consists of the sequence of SEQ ID NO: 248.
13. The TAP of item 1, wherein the TAP binds to an HLA-A*68:01 molecule and comprises or consists of the sequence of SEQ ID NO: 6-8, 12, 15, 23, 28, 41, 42, 47, 51, 53, 56, 59, 64, 66,

68, 70, 73-75, 77, 79, 80, 82, 85, 88, 92, 93, 96-99, 101, 102, 108-112, 118, 119, 123, 130, 131, 134, 137, 138, 141, 142, 144-147, 149, 153, 154, 156, 158, 160, 161, 166, 169, 172, 176, 184, 198, 202, 203, 212, 214, 216, 217, 220, 224, 226, 229, 234, 236, 239, 248, 254, 269, 270, 275, 280, 283, 287, 293, 300, 301, 303, 306, 310, 314, 320, 328, 332, 348, 354, 355, 359, 360, 366, 5 369, 370, 372, 381, 382, 386, 389, 390, 392, 394, 402, 405, 406, 409, 413, 418, 424, 428, 436, 441-445, 449, 456, 459, 465-468, 473, 479, 483, 488, 493, 499, or 502.

14. The TAP of item 1, wherein the TAP binds to an HLA-B*07:02 molecule and comprises or consists of the sequence of SEQ ID NO: 35, 36, 43, 104, 125, 127, 139, 140, 187, 191, 196, 206, 231, 243, 246, 251, 252, 260, 281, 291, 292, 321, 330, 361, 408, 432, 435, 439, 451, 461, 491, 10 or 503.

15. The TAP of item 1, wherein the TAP binds to an HLA-B*08:01 molecule and comprises or consists of the sequence of SEQ ID NO: 21, 162, 189, 286, 307, 309, 317, 339, 343, 349, or 414.

16. The TAP of item 1, wherein the TAP binds to an HLA-B*13:02 molecule and comprises or consists of the sequence of SEQ ID NO: 207, 311, 393, 400, or 455.

15 17. The TAP of item 1, wherein the TAP binds to an HLA-B*14:01 molecule and comprises or consists of the sequence of SEQ ID NO: 396.

18. The TAP of item 1, wherein the TAP binds to an HLA-B*15:01 molecule and comprises or consists of the sequence of SEQ ID NO: 11, 26, 30, 63, 113, 132, 148, 192, 195, 200, 207, 210, 222, 235, 238, 258, 262, 267, 276, 295, 297, 305, 309, 318, 326, 336, 342, 374, 377, 383, 401, 20 421, 427, 433, 438, 450, 463, 470, or 477.

19. The TAP of item 1, wherein the TAP binds to an HLA-B*18:01 molecule and comprises or consists of the sequence of SEQ ID NO: 3, 10, 33, 225 or 396.

20. The TAP of item 1, wherein the TAP binds to an HLA-B*37:01 molecule and comprises or consists of the sequence of SEQ ID NO: 302.

25 21. The TAP of item 1, wherein the TAP binds to an HLA-B*38:01 molecule and comprises or consists of the sequence of SEQ ID NO: 26, 180, 338, 341, 378, 380, 416, 448, 454, 496, or 498.

22. The TAP of item 1, wherein the TAP binds to an HLA-B*40:01 molecule and comprises or consists of the sequence of SEQ ID NO: 215 or 322.

23. The TAP of item 1, wherein the TAP binds to an HLA-B*40:02 molecule and comprises or 30 consists of the sequence of SEQ ID NO: 213, 215, 339, or 351.

24. The TAP of item 1, wherein the TAP binds to an HLA-B*44:02 molecule and comprises or consists of the sequence of SEQ ID NO: 346, 353, 356, or 453.

25. The TAP of item 1, wherein the TAP binds to an HLA-B*49:01 molecule and comprises or consists of the sequence of SEQ ID NO: 9, 57, 78, 115, 136, 167, 255, 273, 274, 278, 313, 339, 35 480, 484, or 495.

26. The TAP of item 1, wherein the TAP binds to an HLA-B*51:01 molecule and comprises or consists of the sequence of SEQ ID NO: 227 or 259.

27. The TAP of item 1, wherein the TAP binds to an HLA-C*03:03 molecule and comprises or consists of the sequence of SEQ ID NO: 24, 69, 204 or 388.
28. The TAP of item 1, wherein the TAP binds to an HLA-C*03:04 molecule and comprises or consists of the sequence of SEQ ID NO: 24, 49, 69, 159, 241, 242 or 334.
- 5 29. The TAP of item 1, wherein the TAP binds to an HLA-C*06:02 molecule and comprises or consists of the sequence of SEQ ID NO: 13, 34 or 72.
30. The TAP of item 1, wherein the TAP binds to an HLA-C*07:01 molecule and comprises or consists of the sequence of SEQ ID NO: 13, 75, 133, 163, 183, 199, 205, 285, 334, 391 or 472.
31. The TAP of item 1, wherein the TAP binds to an HLA-C*07:02 molecule and comprises or
10 consists of the sequence of SEQ ID NO: 13, 32, 36, 105, 177, 339, 371 or 478.
32. The TAP of item 1, wherein the TAP binds to an HLA-C*08:02 molecule and comprises or consists of the sequence of SEQ ID NO: 18, 54 or 379.
33. The TAP of item 1, wherein the TAP binds to an HLA-C*12:03 molecule and comprises or consists of the sequence of SEQ ID NO: 24, 49, 58, 71, 94, 162, 178, 242, 289, 344, 345, 357,
15 367, 368, 375, 423 or 431.
34. The TAP of item 1, wherein the TAP binds to an HLA-C*14:02 molecule and comprises or consists of the sequence of SEQ ID NO: 105, 271, 350, 365, 385, 410, 423, or 504.
35. The TAP of any one of items 1-34, which is encoded by a sequence located a non-protein coding region of the genome or by a long non-coding RNA.
- 20 36. The TAP of item 35, wherein said non-protein coding region of the genome is an intergenic region.
37. The TAP of item 35, wherein said non-protein coding region of the genome is an intron.
38. The TAP of any one of items 1 to 37, wherein said TAP is conjugated to a molecule that increases protease resistance, plasma protein binding, plasma half-life and/or intracellular
25 penetration of the TAP, for example a fatty acid, a protein (e.g., albumin), a sugar or polysaccharide, or a polymer (e.g., polyethylene glycol).
39. A combination comprising at least two of the TAPs defined in any one of items 1-38.
40. A synthetic long peptide (SLP) comprising at least one of the amino acid sequences defined in item 1.
- 30 41. A nucleic acid encoding one or more of the TAPs of items 1 to 38, the combination of item 39, or the SLP of item 40.
42. The nucleic acid of item 41, wherein the nucleic acid is an mRNA, and wherein the mRNA optionally comprises one or more 5'-end modifications, 3'-end modifications, and/or modified nucleosides to increase stability, improve translation and/or reduce immunogenicity of the mRNA.
- 35 43. The nucleic acid of item 41, wherein the nucleic acid is a DNA.
44. The nucleic acid of any one of items 41-43, wherein the nucleic acid is a component of a viral vector.

45. A vesicle or particle comprising the TAP of any one of items 1-38, the combination of item 39, the SLP of item 40, or the nucleic acid of any one of items 41-44.
46. The vesicle or particle of item 45, wherein the vesicle is a lipid nanoparticle (LNP).
47. The vesicle or particle of item 45 or 46, which comprises a cationic lipid.
- 5 48. A composition comprising the TAP of any one of items 1-38, the combination of item 39, the SLP of item 40, the nucleic acid of any one of items 41-44, or the vesicle or particle of any one of items 45-47, and a pharmaceutically acceptable carrier.
49. A vaccine comprising the TAP of any one of items 1-38, the combination of item 39, the SLP of item 40, the nucleic acid of any one of items 41-44, the vesicle or particle of any one of items 45-47, or the composition of item 47, and an adjuvant.
- 10 50. An isolated major histocompatibility complex (MHC) class I molecule comprising the TAP of any one of items 1-38 in its peptide binding groove.
51. The isolated MHC class I molecule of item 50, which is in the form of a multimer.
52. The isolated MHC class I molecule of item 51, wherein said multimer is a tetramer.
- 15 53. An isolated cell comprising (i) the TAP of any one of items 1-38; (ii) the combination of item 39; (iii) the SLP of item 40; (iv) the nucleic acid of any one of items 41-44; or (v) a vector comprising a nucleotide sequence encoding the TAP of any one of items 1-38, the combination of item 39 or the SLP of item 40.
54. An isolated cell expressing at its surface major histocompatibility complex (MHC) class I molecules comprising the TAP of any one of items 1-38 or combination of item 39 in their peptide binding groove.
- 20 55. The cell of item 53 or 54, which is an antigen-presenting cell (APC).
56. The cell of item 55, wherein said APC is a dendritic cell.
57. A T-cell receptor (TCR) that specifically recognizes the isolated MHC class I molecule of any one of items 50-52 and/or MHC class I molecules expressed at the surface of the cell of any one of items 54-56, or a nucleic acid encoding said TCR.
- 25 58. The TCR of item 57, which is a soluble TCR.
59. An antibody or an antigen-binding fragment thereof that specifically binds to the isolated MHC class I molecule of any one of items 50-52 and/or MHC class I molecules expressed at the surface of the cell of any one of items 54-56, or a nucleic acid encoding said antibody or antigen-binding fragment thereof.
- 30 60. The TCR of item 57 or 58, or the antibody or antigen-binding fragment thereof according to item 59, which is a bispecific TCR or a bispecific antibody or antigen-binding fragment thereof.
61. The TCR, antibody or antigen-binding fragment thereof according to item 60, wherein the bispecific antibody or antigen-binding fragment thereof is a single-chain diabody (scDb).
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62. The TCR, antibody or antigen-binding fragment thereof according to item 60 or 61, wherein the bispecific TCR, antibody or antigen-binding fragment thereof also specifically binds to a T cell signaling molecule.
63. The TCR, antibody or antigen-binding fragment thereof according to item 62, wherein the T
5 cell signaling molecule is a CD3 chain.
64. A chimeric antigen receptor (CAR) comprising the antibody or an antigen-binding fragment thereof of item 59, or a nucleic acid encoding said CAR.
65. An isolated cell expressing at its cell surface the TCR of item 57 or the CAR of item 64.
66. The isolated cell of item 65, which is a CD8⁺ T lymphocyte.
- 10 67. A cell population comprising at least 0.5% of the isolated cell as defined in item 65 or 66.
68. A method of treating cancer in a subject comprising administering to the subject an effective amount of:
- (a) a TAP comprising or consisting of any one of the sequences set forth in SEQ ID NOs: 1-505 or any combination thereof, or a synthetic long peptide (SLP) comprising at least one
15 of the sequences set forth in SEQ ID NOs: 1-505;
 - (b) at least one nucleic acid encoding the TAP, combination thereof or SLP defined in (a);
 - (c) a vesicle or particle comprising the TAP, combination thereof or SLP defined in (a) or the at least one nucleic acid defined in (b);
 - (d) a composition comprising the TAP, combination thereof or SLP defined in (a), the at
20 least one nucleic acid defined in (b), or the vesicle or particle defined in (c), and a pharmaceutically acceptable carrier;
 - (e) a vaccine comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), the vesicle or particle defined in (c), or the composition defined in (d), and an adjuvant;
 - 25 (f) a cell expressing at its surface major histocompatibility complex (MHC) class I molecules comprising the TAP or combination thereof defined in (a) in their peptide binding groove;
 - (g) a cell expressing at its cell surface a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) that specifically recognizes MHC class I molecules expressed at the surface of the cell defined in (f); or
 - 30 (h) a soluble TCR, an antibody or an antigen-binding fragment thereof, or a CAR, that specifically binds to the MHC class I molecules expressed at the surface of the cell defined in (f), or a nucleic acid encoding said soluble TCR, antibody, antigen-binding fragment thereof, or CAR.
69. The method of item 68, wherein the cancer is melanoma.
- 35 70. The method of item 68 or 69, further comprising administering at least one additional antitumor agent or therapy to the subject.

71. The method of item 70, wherein said at least one additional antitumor agent or therapy is a chemotherapeutic agent, immunotherapy, an immune checkpoint inhibitor, radiotherapy or surgery.

72. Use of:

- 5 (a) a TAP comprising or consisting of any one of the sequences set forth in SEQ ID NOs: 1-505 or any combination thereof, or a synthetic long peptide (SLP) comprising at least one of the sequences set forth in SEQ ID NOs: 1-505;
- (b) at least one nucleic acid encoding the TAP, combination thereof or SLP defined in (a);
- 10 (c) a vesicle or particle comprising the TAP, combination thereof or SLP defined in (a) or the at least one nucleic acid defined in (b);
- (d) a composition comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), or the vesicle or particle defined in (c), and a pharmaceutically acceptable carrier;
- 15 (e) a vaccine comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), the vesicle or particle defined in (c), or the composition defined in (d), and an adjuvant;
- (f) a cell expressing at its surface major histocompatibility complex (MHC) class I molecules comprising the TAP or combination thereof defined in (a) in their peptide binding groove;
- 20 (g) a cell expressing at its cell surface a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) that specifically recognizes MHC class I molecules expressed at the surface of the cell defined in (f); or
- (h) a soluble TCR, an antibody or an antigen-binding fragment thereof, or a CAR, that specifically binds to the MHC class I molecules expressed at the surface of the cell defined in (f), or a nucleic acid encoding said soluble TCR, antibody, antigen-binding fragment thereof, or CAR;
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for treating cancer in a subject, or for the manufacture of a medicament for treating cancer in a subject.

73. The use of item 72, wherein said cancer is melanoma.

74. The use of item 72 or 73, further comprising the use at least one additional antitumor agent or therapy.

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75. The use of item 74, wherein said at least one additional antitumor agent or therapy is a chemotherapeutic agent, immunotherapy, an immune checkpoint inhibitor, radiotherapy or surgery.

76. An agent for use in treating cancer in a subject, wherein the agent is:

- 35 (a) a TAP comprising or consisting of any one of the sequences set forth in SEQ ID NOs: 1-505 or any combination thereof, or a synthetic long peptide (SLP) comprising at least one of the sequences set forth in SEQ ID NOs: 1-505;

- (b) at least one nucleic acid encoding the TAP, combination thereof or SLP defined in (a);
 - (c) a vesicle or particle comprising the TAP, combination thereof or SLP defined in (a) or the at least one nucleic acid defined in (b);
 - (d) a composition comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), or the vesicle or particle defined in (c), and a pharmaceutically acceptable carrier;
 - (e) a vaccine comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), the vesicle or particle defined in (c), or the composition defined in (d), and an adjuvant;
 - (f) a cell expressing at its surface major histocompatibility complex (MHC) class I molecules comprising the TAP or combination thereof defined in (a) in their peptide binding groove;
 - (g) a cell expressing at its cell surface a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) that specifically recognizes MHC class I molecules expressed at the surface of the cell defined in (f); or
 - (h) a soluble TCR, an antibody or an antigen-binding fragment thereof, or a CAR, that specifically binds to the MHC class I molecules expressed at the surface of the cell defined in (f), or a nucleic acid encoding said soluble TCR, antibody, antigen-binding fragment thereof, or CAR.
77. The agent for use according to item 76, wherein said cancer is melanoma.
78. The agent for use according to item 76 or 77, further comprising the use at least one additional antitumor agent or therapy to the subject.
79. The agent for use according to item 78, wherein said at least one additional antitumor agent or therapy is a chemotherapeutic agent, immunotherapy, an immune checkpoint inhibitor, radiotherapy or surgery.

Other objects, advantages and features of the present disclosure will become more apparent upon reading of the following non-restrictive description of specific embodiments thereof, given by way of example only with reference to the accompanying drawings.

BRIEF DESCRIPTION OF DRAWINGS

In the appended drawings:

FIGs. 1A-E show that aeTSAs are immunogenic and can contribute to the response to ICB in melanoma. **FIG. 1A:** Box plots showing the number of TA-HLA pairs (i.e., the sum of the HLA alleles per sample capable of presenting each expressed TA) per pre-treatment sample (grey dots) from Riaz et al.⁸, according to the response groups from the original study. P-values from unpaired two-tailed T-test. **FIG. 1B:** Box plots showing the number of TA-HLA pairs in pre- and on-treatment samples from Riaz et al.⁸, according to the response groups from the original study.

Grey lines connect pre- and on-treatment samples per patient; p-values from paired two-tailed T-test. **FIG. 1C:** Pearson's correlation between the number of expanded T-cell clones and the number of TA-HLA pairs lost on-therapy per patient (colored dots) from Riaz et al.⁸, according to the response groups from the original study. Patients with stable disease (SD) were excluded due to the low number of samples with both RNA-seq and TCR-seq data (n = 2). **FIG. 1D:** CD8 T cell clonotypes expanded in the on-treatment sample from responder Pt44 in the Riaz et al. cohort⁸, expressed as a percentage of total clonotypes, where the IGF2BP1-derived aeTSA IMKKIRESY-specific TCRB clonotype is highlighted. The grey lines connect each expanded TCRB clonotype in pre- and on-treatment samples (left) and the RNA expression of the cognate aeTSA in the pre- and on-treatment samples from Pt44 (right).

FIGs. 2A-D show the predicted presentation of unmutated TAs in melanoma and NSCLC samples from patients receiving ICB. **FIG. 2A:** Box plots showing the number of TA-HLA pairs (i.e., the sum of the HLA alleles per sample capable of presenting each expressed TA) per pre-treatment sample (grey dots) from various published studies in melanoma^{11,12,19-21} according to the response groups from the original studies. P-values from unpaired two-tailed T-test; no adjustments were made for multiple testing. **FIGs. 2B-C:** Box plots showing the number of TA-HLA pairs in pre- and on-treatment samples from Gide et al.¹¹ (**FIG. 2B**) and Du et al.¹² (**FIG. 2C**) according to the response groups from the original studies. Grey lines connect pre- and on-treatment samples per patient, p-values from paired two-tailed T-test; no adjustments were made for multiple testing. **FIG. 2D:** Box plots showing the difference in purity scores from ESTIMATE between on- and pre-therapy samples, where negative values indicate a decrease in tumor purity on-therapy in samples from Riaz et al.⁸ (upper). The lower heatmap shows Pearson's correlation coefficient between the purity change (from the upper panel) and the change in the number of TA-HLA pairs in on- vs. pre-ICB samples from corresponding patients. Box plots show the median and interquartile range (IQR), and whiskers extend to the largest value no further than 1.5 * IQR from the box hinges.

FIG. 3A depicts the results of a FEST assay showing the expansion of specific T cell clonotypes following *in vitro* stimulation with the indicated aeTSAs selected based on their complete loss of RNA expression in at least one responder on-therapy from Riaz et al.⁸

FIG. 3B shows that the immunogenicity predictor PRIME 2.0 identifies melanoma aeTSAs described herein as immunogenic targets. PRIME scores of each peptide-HLA allele pairs were calculated by PRIME 2.0 for aeTSAs (n=200 binding 27 HLA alleles) and mTSAs (n=5 binding 5 HLA alleles) identified and reported herein as well as for immunogenic (n=590 binding 53 HLA alleles) and non-immunogenic (n=5887 binding 62 HLA alleles) peptide sequences used to train PRIME2.0. For each unique peptide sequence, the score of the highest scoring HLA allele was kept and used for plotting. Groups were compared using non-parametric Mann-Whitney U tests, where ns stands for not significant; *** P value <1E-10.

FIGs. 4A-D show TA sharing and expression regulation across cancer samples. **FIG. 4A:** Stacked bar chart showing the proportion of TA types (and absolute TA numbers) shared between different numbers of melanoma samples analyzed. **FIG. 4B:** Box plots showing the proportion of TCGA samples expressing each TA (grey dots) at least two times higher than the 95th percentile value for the respective TA in GTEx samples except testis for melanoma TAs. Box plots show the median and interquartile range (IQR), and whiskers extend to the largest value no further than 1.5 * IQR from the box hinges. **FIGs. 4C-D:** Spearman's correlation between the RPHM expression of each melanoma TA and the corresponding omics values [FPKM expression, copy-number variation, methylation β -value, and tumor mutational burden (TMB)] across the analyzed SKCM samples from TCGA (**FIG. 4C**), and the proportion of TAs with a significant correlation (p -adj < 0.05, heatmap cells with * in **FIG. 4C** among TAs with omics data available (non-empty cells in **FIG. 4C**) (**FIG. 4D**).

FIG. 5 shows box plots showing the stemness scores obtained using ssGSEA in the TCGA samples studied herein across the LUAD, LUSC, and SKCM cohorts. P-values from two-sided Wilcoxon test.

FIGs. 6A-B show annotation of scRNA-seq data from previous studies of melanoma. **FIG. 6A:** balloon plot showing the average expression and proportion of cells expressing the indicated genes used for cluster annotation in each cluster identified across cutaneous melanoma samples from Zhang et al.¹⁴. The genes used for cluster annotation were obtained from the original article. **FIG. 6B:** UMAPs showing the clusters identified (upper) and their cell type annotation according to the genes in (**FIG. 6A**) (lower) across cutaneous melanoma samples from Zhang et al.¹⁴.

FIGs. 7A-B show the expression of unmutated TAs in scRNA-seq data from melanoma. **FIG. 7A:** Box plots showing the read count of cancer-specific melanoma TAs from **FIG. 8A** across cell types from cutaneous melanoma samples from Zhang et al.¹⁴. Each grey dot represents one TA per cell. **FIG. 7B:** Box plots showing the read count of melanoma TAs expressed in non-cancer cell types from cutaneous melanoma samples from Zhang et al.¹⁴. Each grey dot represents one TA per cell.

FIGs. 8A-C show TA expression in scRNA-seq data from melanoma. **FIG. 8A:** Bar plots showing the proportion (and absolute numbers) of melanoma TAs expressed (read count above 1) in cancer cells only in cutaneous melanoma scRNA-seq data from Zhang et al.¹⁴. **FIG. 8B:** Proportion of cell doublets among cells expressing a TA (cells expressing TA > 1 read count) vs. the TA-negative cell fraction per annotated cell type from cutaneous melanomas from Zhang et al.¹⁴. Each grey dot represents a TA expressed in at least one cell of the respective cell type. **FIG. 8C:** Box plots show the normalized expression of *MLANA* (upper panel) and *PMEL* (lower panel) in cell types from cutaneous melanoma samples, comparing cells expressing at least one TA (TApos) vs. cells negative for all TAs (TAneg), per TA type identified in melanoma. All box plots show the median and interquartile range (IQR), and whiskers extend to the largest value no further

than 1.5 * IQR from the box hinges. P-values from two-sided Wilcoxon's nonparametric test; no adjustments were made for multiple testing.

DETAILED DISCLOSURE

5 The use of the terms "a" and "an" and "the" and similar referents in the context of describing the technology (especially in the context of the following claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context.

The terms "comprising", "having", "including", and "containing" are to be construed as open-ended terms (i.e., meaning "including, but not limited to") unless otherwise noted.

10 All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context.

The use of any and all examples, or exemplary language ("e.g.", "such as") provided herein, is intended merely to better illustrate embodiments of the claimed technology and does not pose a limitation on the scope unless otherwise claimed.

15 No language in the specification should be construed as indicating any non-claimed element as essential to the practice of embodiments of the claimed technology.

Herein, the term "about" has its ordinary meaning. The term "about" is used to indicate that a value includes an inherent variation of error for the device or the method being employed to determine the value, or encompass values close to the recited values, for example within 10% of the recited values (or range of values).

20 Recitation of ranges of values herein are merely intended to serve as a shorthand method of referring individually to each separate value falling within the range, unless otherwise indicated herein, and each separate value is incorporated into the specification as if it were individually recited herein. All subsets of values within the ranges are also incorporated into the specification as if they were individually recited herein.

25 Where features or aspects of the disclosure are described in terms of Markush groups or list of alternatives, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member, or subgroup of members, of the Markush group or list of alternatives.

30 Unless specifically defined otherwise, all technical and scientific terms used herein shall be taken to have the same meaning as commonly understood by one of ordinary skill in the art (e.g., in stem cell biology, cell culture, molecular genetics, immunology, immunohistochemistry, protein chemistry, and biochemistry).

35 Unless otherwise indicated, the recombinant protein, cell culture, and immunological techniques utilized in the present disclosure are standard procedures, well known to those skilled in the art. Such techniques are described and explained throughout the literature in sources such as, J. Perbal, A Practical Guide to Molecular Cloning, John Wiley and Sons (1984), J. Sambrook

et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbour Laboratory Press (1989), T. A. Brown (editor), Essential Molecular Biology: A Practical Approach, Volumes 1 and 2, IRL Press (1991), D. M. Glover and B. D. Hames (editors), DNA Cloning: A Practical Approach, Volumes 1-4, IRL Press (1995 and 1996), and F. M. Ausubel *et al.* (editors), Current Protocols in Molecular Biology, Greene Pub. Associates and Wiley-Interscience (1988, including all updates until present), Ed Harlow and David Lane (editors) Antibodies: A Laboratory Manual, Cold Spring Harbour Laboratory, (1988), and J. E. Coligan *et al.* (editors) Current Protocols in Immunology, John Wiley & Sons (including all updates until present).

In the studies described herein, the present inventors have identified 505 tumor antigens (TAs) discovered using comprehensive proteogenomic analyses of cutaneous melanomas. Of these 505 TAs, five (1%) derive from mutated sequences and 500 (99%) from unmutated genomic sequences. While mutated TAs were rare and patient-specific, unmutated TAs were shared among tumor samples. Unmutated TAs belong to three classes: i) 200 aberrantly-expressed tumor-specific antigens (aeTSAs) absent from normal tissues, ii) 129 tumor-associated antigens (TAAs) overexpressed in tumors relative to normal tissues, and iii) 171 lineage-specific antigens (LSAs) expressed specifically in melanoma samples, normal skin, and melanocytes. While a majority of TAAs (88%) derive from exons of annotated protein-coding genes, around half of the aeTSAs (53%) and LSAs (45%) derive from allegedly non-coding genomic regions such as ncRNAs, introns, and intergenic regions. The novel tumor antigen candidates identified herein, which includes melanocyte lineage-specific antigens (LSAs), tumor-associated antigens (TAAs) and tumor-specific antigens (TSAs), may be useful, *e.g.*, for immunotherapies and vaccines against cancers expressing the tumor antigen candidates, such as melanoma.

The present disclosure relates to a tumor antigen peptide (TAP) (or tumor-specific peptide), such as a melanoma TAP, comprising, or consisting of, one of the amino acid sequences set forth in any one of SEQ ID NOs:1-505:

Peptide sequence	SEQ ID NO:	Peptide sequence	SEQ ID NO:	Peptide sequence	SEQ ID NO:
TLDDAVHGV	1	KLGINNVSF	170	MEKEDYHSL	339
YQIGQVQGV	2	KYISQFQVF	171	MEKEDYHSLY	340
NEYSNITRLY	3	QTAAVSGVK	172	YHSLYQSHL	341
RLLADLTGA	4	LTPLNHPPFSY	173	YMVPIPLY	342
TPLSPDPTL	5	VFINKKYVF	174	LMEKEDYHSL	343
STYYWPRPR	6	NLITEEHPV	175	FAHEAPAF	344
DSFSATETR	7	ELVKVIDGSSR	176	FASPLTGIA	345
ETSYVKVLH	8	FHSLPIHLF	177	HEAPFLPW	346
AEMLGSVV	9	YSHDYSYY	178	VLFKKFIQK	347
EELSVLEVF	10	FQIEKLTP	179	APAFPLPWH	348
FVQENYLEY	11	EHSVENGSI	180	LLMEKEDYHSL	349
IVQQPTEEK	12	ETIQNTHSF	181	HYVVSMDAL	350

SVFAHPRKL	13	YYSIWKTQI	182	WEQEIQKL	351
ASSLPTTMNY	14	SYFFHGLSF	183	LMEKEDYHSLY	352
IVQQPTTEKR	15	ESFQQPYIPR	184	LEQASRIWSW	353
LPTTMNYPL	16	KQVPSRVLY	185	NIFDLSAPEK	354
GSNPARYEF	17	MLFNKDLDAA	186	EAPAFLPWHR	355
TADDATVM	18	APRSAEPRAT	187	SEIWRDIDF	356
VLEHVVRV	19	YLDPGAVHAVF	188	AAMVGAVL	357
EVDPIGHLY	20	TLKKHKIV	189	TFLGVGQESF	358
QIMPKAGL	21	VGVPISLY	190	ESWPSVFYNR	359
KVLEHVVRV	22	SPRPQPEL	191	ISQDTTVGR	360
QVPGSNPAR	23	KLSFPDSKF	192	RPWSGPYIL	361
FVYGEPREL	24	KNKDEYIHFY	193	SSDYVIPIGTY	362
TLPTFDPTKV	25	RAFEGRRRGW	194	DSDPDSFQDY	363
NQIMPKTGF	26	RLKARPSTY	195	DTRPWSGPY	364
EVDPIGHVY	27	APSLHATL	196	HYYSVKKTF	365
ELVRRILSR	28	AQKEPTGNY	197	NVCGSQQGR	366
MEVDPIGHLY	29	LSLGTACR	198	YMNGTMSQV	367
SVMSSNVSF	30	SRNPTSXY	199	MAKRTTHPL	368
TVPSSFPSW	31	SLNDDHQIY	200	RPWSGPYILR	369
KYKDYFPVI	32	YVDPMITEI	201	MTVDSLUNK	370
MEVDPIGHVY	33	PSFSPYAKR	202	TRPWSGPYIL	371
TVYGEPRKL	34	HVNGSRPHAR	203	TTHPLFVIATR	372
GPDVREGTL	35	ITVRLAPPL	204	FVWTHYYSV	373
VYDGREHTV	36	SANPLSHRY	205	LSKEEKNHF	374
LMEVDPIGHLY	37	VPLAHSSSA	206	RAANQVFVL	375
KYKDYFPVILK	38	GQVPTTEVV	207	MVRSATLIK	376
EVFEGREDSIF	39	KTWGQYWQV	208	NQVFLHSY	377
GVYDGREHTV	40	ALNFPGSQK	209	HNSTEFLL	378
EVVPISHLY	41	YVWKTWGQY	210	SQDVAGTTF	379
NAVGVYAGR	42	MPTAESTGM	211	AHNSTEFLL	380
RPDSRLLEL	43	HTMEVTVYHRR	212	STEFLLIER	381
SVFAHPRKLLM	44	EAAAGIGIL	213	EGFFTRQER	382
EVFEGREDSVF	45	EGFDHRDSK	214	FQKVLVSY	383
RVSHSHASF	46	AEEAAGIGIL	215	FTDFMGQIVY	384
ATFLQRKVLRL	47	LTSSMVTPL	216	YFQKVLVSY	385
SYVKVLHHL	48	TSSMVTPLR	217	ALVNMPPHYR	386
FAFGEPREL	49	GLSNLTHVL	218	GVMSSLYTV	387
KMAELVHFL	50	QLLALLPSL	219	LLSNTVSTL	388
FAHGHPLYTR	51	EAAQPMTKK	220	RVFHETGAQR	389
GVYAGREHFV	52	RVLGKPSW	221	SASDHCRSR	390
NTAIATFLQRK	53	VLYPVLESY	222	RRDGGIIY	391
TLDEKVAEL	54	PYLGQMINL	223	VAALIANPR	392
RLLELHITM	55	ELFSYLIEK	224	RLLGTEFQV	393
EVPNSSPPR	56	EEQYIAQF	225	FSIIGVSRR	394
VEVTLREV	57	EAAQPMTKKR	226	LSSDGMIEY	395
ISGGPRISY	58	MPMQDIKMI	227	DEYFLPSL	396

GVPGPLLILPR	59	RLSEGDVMHL	228	SYIGLKGLYF	397
GVYDGEHHSV	60	HASSYSISPEK	229	FTGFGGALGY	398
KISGGPRISY	61	MPMQDIKMIL	230	KTWDQVPFSV	399
FLYNQTNIRM	62	SPSVSQLSVL	231	RVADIPIKP	400
GQYQLVVS	63	RLDQLLRHV	232	SVAKHTQSY	401
GVDDLVRFR	64	ALLERASATL	233	QTKGGQTTWAR	402
KVLEYVIKV	65	TVAPTPATAR	234	ETGSSFMSF	403
HTLPALSRR	66	SQSPSVSQL	235	SLYSYFQKV	404
ALREEEEGV	67	STVAPTPATAR	236	QTKGGQTTWARR	405
TTINFTRQR	68	QYIAQFTSQF	237	TVVAALIANPR	406
SAYGEPRKL	69	GQHLHLETF	238	HLMVKDWQL	407
STANVTRAH	70	TIASVLVAR	239	NPLSKLSVL	408
SAFPTTINF	71	SLLQHLIGL	240	FVIPSTKDSNR	409
FRAVITKKV	72	TASPRSPVM	241	HYQVQTHL	410
AAAGVSSTK	73	AAFDGRHSQTL	242	ASDILSFAHKY	411
FPTTINFTR	74	SPRRLVEL	243	RLGQGVPLV	412
TTSEKIHVR	75	LYVDSLFFL	244	SVPDHVQPSK	413
GLYDGMEHL	76	VFLREFPNF	245	RLLEKHISL	414
STANVTRAHGR	77	RPRFSTATEIA	246	SLFGVSERL	415
IEDPKAGLHV	78	ALIANPRRK	247	NHYQVQTHL	416
GVVGPQGLR	79	DFMGQIVYR	248	DLVGKDVTRVY	417
NVFAHATGESR	80	EIPDTVMGL	249	SLSPPTLPR	418
FLFGEPKRL	81	VMSSTLYTV	250	LADNGTLGKY	419
SAFPTTINFTR	82	SPQHKPRL	251	KAMYIRVSY	420
RLFSEDIHV	83	EPKPPTTGL	252	MQPKLKQVF	421
VYMPANTTF	84	IPDTIASVL	253	AIQDQDILL	422
EAVGFQPPR	85	TDFMGQIVYR	254	AFDRAVHF	423
EVDPTSHSY	86	GEDDEHRKI	255	NTPNIVSLR	424
LLDPAQRNLY	87	RLRGSIQSRY	256	RVADIPIKPW	425
SGISQVFQR	88	HLDESPAYL	257	HYIPLQTI	426
RLFSEDIHVA	89	KMEETTVTY	258	VMKGINQGY	427
VFDVGKGNM	90	LPTDLFNSV	259	ATSPPASVR	428
KASEKIFYV	91	RPQGLAVL	260	ALEKDTPRY	429
EAAAARFRPR	92	SLSEKSPEV	261	QVMKGINQGY	430
MSISMSLLK	93	GAFREGPPY	262	AAFDRAVHF	431
KASPSSLPH	94	YLNGATVVA	263	RPLRIKGVF	432
RTLQQGVLDQW	95	SMYLHTEGF	264	RQVMKGINQGY	433
TTATTFRAR	96	HILSHLHEV	265	KLDTTVKNI	434
NPSHLITPR	97	SISEAPLTV	266	LPRTPRPDL	435
ETMETLRTSR	98	HQINSEATF	267	ITYTESNSR	436
MVWEGHPRERR	99	DIQEGVGAF	268	RLQGSVTLV	437
LPDGSRVEL	100	SALGVITIK	269	SQFPSKNLPAF	438
DVVTGNVPLK	101	TVNDFTQNPR	270	LPRTPRPDLIL	439
ENPSHLITPR	102	SFIQAGSSY	271	DTAPQSHQV	440
SLARTILHL	103	GVTITKTLK	272	MAILGTAGR	441
KPHYGLRAI	104	AERPQGLAV	273	SVSSHILHR	442

AFLDIHTAL	105	REKGPVKEV	274	STSPGTGVRK	443
KMSEFVYRF	106	TSVPPFNLR	275	EVAEVLGSVK	444
FLVTKVTM	107	LSRLPSIAF	276	EIPRTPSEGR	445
HTTSVMENK	108	FPVHAAEF	277	VFLKFSRRF	446
LVSIIAVR	109	GEISASHV	278	SVSSHLIHR	447
ITSGVKVKK	110	AADGGQHWY	279	THLEDPHLM	448
VSIPIAVRR	111	EISASHVSR	280	SVFPRTSSR	449
DIIELEGLR	112	SPRIPFSTF	281	GQYQSKPWTF	450
HLKPPELGF	113	KLMDPGSLPPL	282	VPRPTSTVGL	451
QVIVKIIHG	114	ETKPEFERR	283	NSVSSHLIHR	452
AEQEIMKKV	115	ETIMKFLKM	284	QEEDNLLRYF	453
EVPLKILAH	116	RRAHLWSTF	285	THLEDPHML	454
IVKIIGHFY	117	HLQEKQLSL	286	ATTNILEHV	455
SLVSIPIAVR	118	ELSVVTSER	287	MTLRPTQPR	456
MVSPGVSLFK	119	YLDQQVPYTF	288	ETRPNNNSKF	457
VLMMKLEDL	120	EAIPRIPLR	289	HSITEPLLY	458
YSDLHTPGRY	121	GYLDQQVPYTF	290	HLFLQPPSKR	459
EVARFLTY	122	SPKLGGIGF	291	ETVRFTSSF	460
SVGDLMAPR	123	YPEKSRGCL	292	SPMPIPLYL	461
VLWRGDSPL	124	TTIPFSTLRQR	293	ESYGRYTFY	462
QPRQGSPVAA	125	SLGAHSPALY	294	KSQGSFISF	463
KQTGIRHSY	126	SQNGQLIHY	295	GTILHIGVF	464
RPRQDAISV	127	KAKEHTANISW	296	KVFSGSSKR	465
KLITQIRTA	128	RVSKSDSTF	297	SSFSTLASLDK	466
SYLSEHSAAIF	129	SLNSQVTGL	298	TTQGAAPQR	467
TSVGDLMAPR	130	NSDLSEKLEY	299	HTTQGAAPQR	468
EIPTGVAKR	131	DSSTVGLQR	300	KIFQERAAF	469
SQINLSQIY	132	RASAIIR	301	GQITHNTSF	470
RRPSGGFRL	133	SQETLPLKI	302	ISLKPLIARY	471
EVFNVKNTFPK	134	STFDGLDRR	303	KHSDLILFW	472
KVLGGGWT	135	RVKEIVINK	304	MVWEGHPRER	473
HEAPGQHSEV	136	AQPHHGVY	305	STDLPILLK	474
EVSHPNMSGR	137	EVIQLKERDRK	306	EVISINTGHF	475
DTAPATFLR	138	EVKEKTEL	307	ETERVLEKSSY	476
KPQKDLHFI	139	TDPETLHY	308	KIKTINLRY	477
RVRGAGTHL	140	KMKEKTQEL	309	YVSQKVSDF	478
TAPIIVAQR	141	STFDGLDRRR	310	DAGIPVYHR	479
TSWDTKFYEK	142	KMSELQTYV	311	TILEAEILHQA	480
KVFAEHKISY	143	GTDPETLHY	312	EYAQKTPLF	481
DAFQGIANR	144	TEEKGSILI	313	TWTPHGIRI	482
IVADPRVPR	145	DTAMPAHSR	314	EVHEGGVARF	483
TGFSTSLGR	146	KLQEALKTI	315	REIEIEGRL	484
ATAPIIVAQR	147	GTDPETLHYF	316	SWLPIPAKY	485
GQFLVKSGY	148	SLKNRIESV	317	RYSERVYTI	486
WTSRTVQNK	149	NLKDPVGVY	318	FTDSQGNDIK	487
ATYGGSDHYI	150	FTETNPQVY	319	SVPSDFLSLR	488

VYIAELEKI	151	ETQEAEVAVSR	320	RQMSLEFRA	489
VFLDRAVSI	152	SPRPESGTV	321	ETISPRPSI	490
MPSPIDHPR	153	SEFAKDPSL	322	GPAGGRGVI	491
EAVRHILHGSR	154	KVIKKIGHY	323	LTDHHIKEY	492
YPAGNVKEL	155	RTWQTRKQF	324	EAVPYNGSLFK	493
SVPRSLASR	156	AMAHKVIKA	325	NLLAEIHGV	494
ALIKHVANA	157	KLKQFQKEY	326	KEGPVTRGA	495
YTANLVPVR	158	SPLEDEESL	327	VHVDLNLGF	496
LSSSLVTKL	159	NSTDFTTDR	328	HTVQGLAGF	497
QNSNVLA VR	160	ETKDTKGRYF	329	MRIEDSHTKL	498
TTTKNTLNK	161	RPRVSSTEM	330	SALSSAQPR	499
HNYINLHSL	162	LMDKSSTIY	331	SPSIKSLLVY	500
HLKDYFEEY	163	GTLRPLKVRR	332	PTDATLNRLLY	501
SPEYFTSYL	164	ILSEGSVPL	333	WTSQPPNYEK	502
ATDVLDHLY	165	TVYNFRTTEL	334	PAPRPVAPTL	503
QTFEESLGR	166	LPSSADVEF	335	VYLHSNSTL	504
HEQPELQKV	167	RLPSSADVEF	336	SLYAWTQSH	505
MATDVLDHLY	168	ALMDKSLHV	337		
TSGSLLFPR	169	MHNALHIYM	338		

In general, peptides such as tumor antigen peptides (TAPs) presented in the context of HLA class I vary in length from about 7 or 8 to about 15, or preferably 8 to 14 amino acid residues. In some embodiments of the methods of the disclosure, longer peptides comprising the TAP sequences defined herein are artificially loaded into cells such as antigen presenting cells (APCs), processed by the cells and the TAP is presented by MHC class I molecules at the surface of the APC. In this method, peptides/polypeptides longer than 15 amino acid residues can be loaded into APCs, are processed by proteases in the APC cytosol providing the corresponding TAP as defined herein for presentation. In some embodiments, the precursor peptide/polypeptide that is used to generate the TAP defined herein is for example 1000, 500, 400, 300, 200, 150, 100, 75, 50, 45, 40, 35, 30, 25, 20 or 15 amino acids or less. Thus, all the methods and processes using the TAPs described herein include the use of longer peptides or polypeptides (including the native protein), i.e., tumor antigen precursor peptides/polypeptides, to induce the presentation of the "final" 8-14 TAP following processing by the cell (APCs). In some embodiments, the herein-mentioned TAP is about 8 to 14, 8 to 13, or 8 to 12 amino acids long (e.g., 8, 9, 10, 11, 12 or 13 amino acids long), small enough for a direct fit in an HLA class I molecule. In an embodiment, the TAP comprises 20 amino acids or less, preferably 15 amino acids or less, more preferably 14 amino acids or less. In an embodiment, the TAP comprises at least 7 amino acids, preferably at least 8 amino acids or less, more preferably at least 9 amino acids.

The term "amino acid" as used herein includes both L- and D-isomers of the naturally occurring amino acids as well as other amino acids (e.g., naturally-occurring amino acids, non-naturally-occurring amino acids, amino acids which are not encoded by nucleic acid sequences,

etc.) used in peptide chemistry to prepare synthetic analogs of TAPs. Examples of naturally occurring amino acids are glycine, alanine, valine, leucine, isoleucine, serine, threonine, etc. Other amino acids include for example non-genetically encoded forms of amino acids, amino acid analogs as well as a conservative substitution of an L-amino acid. Naturally-occurring non-genetically encoded amino acids and amino acid analogs include, for example, beta-alanine, 3-amino-propionic acid, 2,3-diaminopropionic acid, alpha-aminoisobutyric acid (Aib), 4-amino-butylalanine, *N*-methylglycine (sarcosine), hydroxyproline, ornithine (e.g., L-ornithine), citrulline, *t*-butylalanine, *t*-butylglycine, *N*-methylisoleucine, phenylglycine, cyclohexylalanine, norleucine (Nle), norvaline, 2-naphthylalanine, pyridylalanine, 3-benzothienyl alanine, 4-chlorophenylalanine, 2-fluorophenylalanine, 3-fluorophenylalanine, 4-fluorophenylalanine, penicillamine, 1,2,3,4-tetrahydro-isoquinoline-3-carboxylic acid, beta-2-thienylalanine, methionine sulfoxide, L-homoarginine (Hoarg), *N*-acetyl lysine, 2-amino butyric acid, 2-amino butyric acid, 2,4-diaminobutyric acid (D- or L-), *p*-aminophenylalanine, *N*-methylvaline, homocysteine, homoserine (HoSer), cysteic acid, epsilon-amino hexanoic acid, delta-amino valeric acid, benzyloxy-tyrosine, β -phenylalanine or 2,3-diaminobutyric acid (D- or L-), etc. These amino acids are well known in the art of biochemistry/peptide chemistry. Thus, one or more of the amino acids in the TAPs described herein (SEQ ID NOs:1-505) may be replaced by a non-genetically encoded amino acid and/or an amino acid analog. The TAPs may also be modified to improve the proteolytic stability of the peptides, for example by the incorporation of methyl-amino acids, β -amino acids or peptoids. In an embodiment, the TAP comprises only naturally-occurring amino acids.

In embodiments, the TAPs described herein include peptides with altered sequences containing substitutions of functionally equivalent amino acid residues, relative to the herein-mentioned sequences. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of a similar polarity (having similar physico-chemical properties) which acts as a functional equivalent, resulting in a silent alteration. Substitution for an amino acid within the sequence may be selected from other members of the class to which the amino acid belongs. For example, positively charged (basic) amino acids include arginine, lysine and histidine (as well as homoarginine and ornithine). Nonpolar (hydrophobic) amino acids include leucine, isoleucine, alanine, phenylalanine, valine, proline, tryptophan and methionine. Uncharged polar amino acids include serine, threonine, cysteine, tyrosine, asparagine and glutamine. Negatively charged (acidic) amino acids include glutamic acid and aspartic acid. The amino acid glycine may be included in either the nonpolar amino acid family or the uncharged (neutral) polar amino acid family. Substitutions made within a family of amino acids are generally understood to be conservative substitutions. The herein-mentioned TAP may comprise all L-amino acids, all D-amino acids or a mixture of L- and D-amino acids. In an embodiment, the herein-mentioned TAP comprises all L-amino acids.

In an embodiment, in the sequences of the TAPs comprising or consisting of one of sequences of SEQ ID NOs: 1-505, the amino acid residues that do not substantially contribute to interactions with the T-cell receptor may be modified by replacement with other amino acid whose incorporation does not substantially affect T-cell reactivity and does not eliminate binding to the relevant MHC.

The TAP may also be modified by replacing one or more of the amide bonds of the peptide that may improve chemical stability and/or enhanced biological/pharmacological properties (e.g., half-life, absorption, potency, efficiency, etc.). Typical peptide bond replacements include esters, polyamines and derivatives thereof as well as substituted alkanes and alkenes, such as aminomethyl and ketomethylene. For example, the above-mentioned TAP may have one or more amide bonds replaced by linkages such as $-\text{CH}_2\text{NH}-$, $-\text{CH}_2\text{S}-$, $-\text{CH}_2-\text{CH}_2-$, $-\text{CH}=\text{CH}-$ (*cis* or *trans*), $-\text{CH}_2\text{SO}-$, $-\text{CH}(\text{OH})\text{CH}_2-$, or $-\text{COCH}_2-$.

The TAP may also be N- and/or C-terminally capped or modified to prevent degradation, increase stability, affinity and/or uptake. Thus, in another aspect, the present disclosure provides a modified TAP of the formula $\text{Z}^1\text{-X-Z}^2$, wherein X is a TAP comprising, or consisting of, one of the amino acid sequences of SEQ ID NOs: 1-505.

In an embodiment, the amino terminal residue (*i.e.*, the free amino group at the N-terminal end) of the TAP is modified (e.g., for protection against degradation), for example by covalent attachment of a moiety/chemical group (Z^1). Z^1 may be a straight chained or branched alkyl group of one to eight carbons, or an acyl group ($\text{R-CO}-$), wherein R is a hydrophobic moiety (e.g., acetyl, propionyl, butanyl, iso-propionyl, or iso-butanyl), or an aroyl group ($\text{Ar-CO}-$), wherein Ar is an aryl group. In an embodiment, the acyl group is a $\text{C}_1\text{-C}_{16}$ or $\text{C}_3\text{-C}_{16}$ acyl group (linear or branched, saturated or unsaturated), in a further embodiment, a saturated $\text{C}_1\text{-C}_6$ acyl group (linear or branched) or an unsaturated $\text{C}_3\text{-C}_6$ acyl group (linear or branched), for example an acetyl group ($\text{CH}_3\text{-CO}-$, Ac). In an embodiment, Z^1 is absent. The carboxy terminal residue (*i.e.*, the free carboxy group at the C-terminal end of the TAP) of the TAP may be modified (e.g., for protection against degradation), for example by amidation (replacement of the OH group by a NH_2 group), thus in such a case Z^2 is a NH_2 group. In an embodiment, Z^2 may be an hydroxamate group, a nitrile group, an amide (primary, secondary or tertiary) group, an aliphatic amine of one to ten carbons such as methyl amine, iso-butylamine, iso-valerylamine or cyclohexylamine, an aromatic or arylalkyl amine such as aniline, naphthylamine, benzylamine, cinnamylamine, or phenylethylamine, an alcohol or CH_2OH . In an embodiment, Z^2 is absent. In an embodiment, the TAP comprises one of the amino acid sequences of SEQ ID NOs: 1-505. In an embodiment, the TAP consists of one of the amino acid sequences of SEQ ID NOs: 1-505, *i.e.*, wherein Z^1 and Z^2 are absent.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*01:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 11, 14, 20, 27, 29, 37, 86, 87,

121, 150, 165, 173, 279, 288, 299, 308, 312, 316, 319, 331, 340, 352, 362, 363, 384, 395, 398, 411, 419, 429, 458, 474, 476, 487, 492, 500, or 501.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*02:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 1, 2, 4, 19, 22, 25, 40, 50, 52, 54, 60, 65, 67, 76, 81, 89, 91, 103, 107, 120, 124, 128, 135, 157, 175, 179, 186, 188, 201, 208, 218, 219, 228, 232, 233, 240, 250, 257, 261, 263, 265, 266, 282, 286, 298, 311, 315, 317, 325, 333, 337, 349, 367, 373, 387, 388, 393, 399, 404, 412, 414, 415, 422, 434, 437, 455, 480, 489, or 494.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*02:09 molecule, comprising or consisting of the sequence of SEQ ID NO: 22, 40, 50, 62, 83, 89, 232, 265, 282, 311, 315, 317, 337, 349, 367, 399, 407, 412, or 494.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*03:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 209, 247, 272, 347, or 505.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*23:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 48, 84, 129, 151, 152, 171, 174, 182, 223, 237, 245, 290, 358, 397, 426, 446, 481, 482, or 486.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*24:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 31, 244 or 481.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*25:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 11, 31, 249, 289, 403, 425, 464, or 490.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*26:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 11, 20, 27, 39, 41, 42, 45, 114, 116, 122, 168, 181, 268, 284, 329, 364, 398, 417, 430, 440, 447, 452, 457, 460, 462, 475, 490, or 497.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*30:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 26, 304 or 376.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*30:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 117, 185, 190, 193, 197, 256, 294, 323, 471, or 485.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*32:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 17, 44, 46, 61, 95, 106, 126, 143, 170, 194, 208, 221, 264, 296, 324, 326, 401, 414, 420, 425 or 469.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*33:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 248.

In another aspect, the present disclosure provides a TAP binding to an HLA-A*68:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 6-8, 12, 15, 23, 28, 41, 42,

47, 51, 53, 56, 59, 64, 66, 68, 70, 73-75, 77, 79, 80, 82, 85, 88, 92, 93, 96-99, 101, 102, 108-112, 118, 119, 123, 130, 131, 134, 137, 138, 141, 142, 144-147, 149, 153, 154, 156, 158, 160, 161, 166, 169, 172, 176, 184, 198, 202, 203, 212, 214, 216, 217, 220, 224, 226, 229, 234, 236, 239, 248, 254, 269, 270, 275, 280, 283, 287, 293, 300, 301, 303, 306, 310, 314, 320, 328, 332, 348, 354, 355, 359, 360, 366, 369, 370, 372, 381, 382, 386, 389, 390, 392, 394, 402, 405, 406, 409, 413, 418, 424, 428, 436, 441-445, 449, 456, 459, 465-468, 473, 479, 483, 488, 493, 499, or 502.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*07:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 35, 36, 43, 104, 125, 127, 139, 140, 187, 191, 196, 206, 231, 243, 246, 251, 252, 260, 281, 291, 292, 321, 330, 361, 408, 432, 435, 439, 451, 461, 491, or 503.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*08:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 21, 162, 189, 286, 307, 309, 317, 339, 343, 349, or 414.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*13:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 207, 311, 393, 400, or 455.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*14:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 396.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*15:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 11, 26, 30, 63, 113, 132, 148, 192, 195, 200, 207, 210, 222, 235, 238, 258, 262, 267, 276, 295, 297, 305, 309, 318, 326, 336, 342, 374, 377, 383, 401, 421, 427, 433, 438, 450, 463, 470, or 477.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*18:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 3, 10, 33, 225 or 396.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*35:03 molecule, comprising or consisting of the sequence of SEQ ID NO: 5, 16, 100, 155, 164, 211, 230, 253, 259, 277, 327, or 335.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*37:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 302.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*38:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 26, 180, 338, 341, 378, 380, 416, 448, 454, 496, or 498.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*40:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 215 or 322.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*40:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 213, 215, 339, or 351.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*44:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 346, 353, 356, or 453.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*49:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 9, 57, 78, 115, 136, 167, 255, 273, 274, 278, 313, 339, 480, 484, or 495.

In another aspect, the present disclosure provides a TAP binding to an HLA-B*51:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 227 or 259.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*03:03 molecule, comprising or consisting of the sequence of SEQ ID NO: 24, 69, 204 or 388.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*03:04 molecule, comprising or consisting of the sequence of SEQ ID NO: 24, 49, 69, 159, 241, 242 or 334.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*04:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 90, 257, or 423.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*06:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 13, 34 or 72.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*07:01 molecule, comprising or consisting of the sequence of SEQ ID NO: 13, 75, 133, 163, 183, 199, 205, 285, 334, 391 or 472.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*07:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 13, 32, 36, 105, 177, 339, 371 or 478.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*08:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 18, 54 or 379.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*12:03 molecule, comprising or consisting of the sequence of SEQ ID NO: 24, 49, 58, 71, 94, 162, 178, 242, 289, 344, 345, 357, 367, 368, 375, 423 or 431.

In another aspect, the present disclosure provides a TAP binding to an HLA-C*14:02 molecule, comprising or consisting of the sequence of SEQ ID NO: 105, 271, 350, 365, 385, 410, 423, or 504.

The TAPs of the disclosure may be produced by expression in a host cell comprising a nucleic acid encoding the TAPs (recombinant expression) or by chemical synthesis (e.g., solid-phase peptide synthesis). Peptides can be readily synthesized by manual and/or automated solid phase procedures well known in the art. Suitable syntheses can be performed for example by utilizing "T-boc" or "Fmoc" procedures. Techniques and procedures for solid phase synthesis are described in for example Solid Phase Peptide Synthesis: A Practical Approach, by E. Atherton and R. C. Sheppard, published by IRL, Oxford University Press, 1989. Alternatively, the TAPs may be prepared by way of segment condensation, as described, for example, in Liu *et al.*, *Tetrahedron Lett.* 37: 933-936, 1996; Baca *et al.*, *J. Am. Chem. Soc.* 117: 1881-1887, 1995; Tam

et al., *Int. J. Peptide Protein Res.* 45: 209-216, 1995; Schnolzer and Kent, *Science* 256: 221-225, 1992; Liu and Tam, *J. Am. Chem. Soc.* 116: 4149-4153, 1994; Liu and Tam, *Proc. Natl. Acad. Sci. USA* 91: 6584-6588, 1994; and Yamashiro and Li, *Int. J. Peptide Protein Res.* 31: 322-334, 1988). Other methods useful for synthesizing the TAPs are described in Nakagawa *et al.*, *J. Am. Chem. Soc.* 107: 7087-7092, 1985. In an embodiment, the TAP is chemically synthesized (synthetic peptide). Another embodiment of the present disclosure relates to a non-naturally occurring peptide wherein said peptide consists or consists essentially of an amino acid sequences defined herein and has been synthetically produced (e.g., synthesized) as a pharmaceutically acceptable salt. The salts of the TAPs according to the present disclosure differ substantially from the peptides in their state(s) *in vivo*, as the peptides as generated *in vivo* are no salts. The non-natural salt form of the peptide may modulate the solubility of the peptide, in particular in the context of pharmaceutical compositions comprising the peptides, e.g., the peptide vaccines as disclosed herein. Preferably, the salts are pharmaceutically acceptable salts of the peptides.

In an embodiment, the herein-mentioned TAP is substantially pure. A compound is "substantially pure" when it is separated from the components that naturally accompany it. Typically, a compound is substantially pure when it is at least 60%, more generally 75%, 80% or 85%, preferably over 90% and more preferably over 95%, by weight, of the total material in a sample. Thus, for example, a polypeptide that is chemically synthesized or produced by recombinant technology will generally be substantially free from its naturally associated components, e.g., components of its source macromolecule. A nucleic acid molecule is substantially pure when it is not immediately contiguous with (i.e., covalently linked to) the coding sequences with which it is normally contiguous in the naturally occurring genome of the organism from which the nucleic acid is derived. A substantially pure compound can be obtained, for example, by extraction from a natural source; by expression of a recombinant nucleic acid molecule encoding a peptide compound; or by chemical synthesis. Purity can be measured using any appropriate method such as column chromatography, gel electrophoresis, HPLC, etc. In an embodiment, the TAP is in solution. In another embodiment, the TAP is in solid form, e.g., lyophilized.

In an embodiment, the TAP is encoded by a sequence located a non-protein coding region of the genome. In an embodiment, the TAP is encoded by a sequence located in an intergenic region. In another embodiment, the TAP is encoded by a non-coding RNA (ncRNA). In another embodiment, the TAP is encoded by a sequence located in an intron. In another embodiment, the TAP is encoded by a sequence located in an untranslated region (UTR), for example a 5'UTR. In another embodiment, the TAP is encoded by a sequence located in a non-coding exon.

In another aspect, the disclosure further provides a synthetic long peptide (SLP) comprising at least one of the TAP described herein. In an embodiment, the SLP comprises at least two

TAPs, wherein at least one of the TAP is a TAP as described herein. In an embodiment, the SLP comprises at least two, three, four or five of the TAPs described herein. In an embodiment, the SLP comprises at least 10, 15, 20, 25, 30, 35 or 40 of the TAPs described herein. In an embodiment, the SLP comprises at least one of the TAPs described herein linked to one or more amino acid sequences or domains that confer desired properties to the SLP, such as sequences or domains that stabilize the SLP and/or that improve processing and presentation by MHC molecules, for example a sequence comprising a motif cleavable by cellular proteases such as cathepsins. In another embodiment, the SLP comprises at least one of the TAPs described herein, and a TAP that binds to MHC class II molecules. The TAPs may be directly attached to each other, or may be indirectly attached via a linker such as a short amino acid linker. In embodiments, the linker comprises about 4 to about 20 amino acids, or about 4 to about 15 amino acids, *e.g.*, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 or 15 amino acids. In an embodiment, the linker comprises glycine residues, serine residues, proline residues, threonine residues, or a mixture thereof. The linker may include sequences promoting the processing of the SLP to release the TAPs, such as a cathepsin-sensitive linker (*e.g.*, a linker of 4-6 amino acids comprising the sequence LVGS (SEQ ID NO:1138), ASLG (SEQ ID NO:1139), PIVG (SEQ ID NO:1140), LLSV (SEQ ID NO:1141), VLSVG (SEQ ID NO:1142) or LLSVGG (SEQ ID NO:1143), see Rabu *et al.*, *Oncoimmunology*. 2019; 8(4): e1560919). In an embodiment, the SLP has a length of 200, 150, 100, 90, 80, 70, 60 or 50 amino acids or less. In a further embodiment, the SLP has a length of 20 to 50, 45 or 40 amino acids, for example from 20 or 25 amino acids to 30, 35 or 40 amino acids.

The TAPs or SLPs described herein may further comprise one or more modifications that confer additional biological properties to the TAPs or SLPs such as protease resistance, plasma protein binding, increased plasma half-life, intracellular penetration, etc. Such modifications include, for example, covalent attachment of molecules/moiety to the TAPs or SLPs such as fatty acids (*e.g.*, C₆-C₁₈), attachment of proteins such as albumin (see, *e.g.*, U.S. Patent No. 7,268,113); sugars/polysaccharides (glycosylation), biotinylation or PEGylation (see, *e.g.*, U.S. Patent Nos. 7,256,258 and 6,528,485). The above description of modification of the TAPs or SLPs does not limit the scope of the approaches nor the possible modifications that can be engineered. Thus, in another aspect, the present disclosure provides a conjugate comprising the TAPs or SLPs described herein and one or more additional molecules or agents (hereinafter secondary molecules or agents). The TAPs or SLPs may be conjugated to any type of synthetic or natural secondary molecules or agents, such as peptides, proteins, saccharides/polysaccharides, lipids, naturally-occurring or synthetic polymers/co-polymers, etc. to modify one or more properties of the TAPs or SLPs.

In another aspect, the disclosure further provides a nucleic acid (isolated) encoding the herein-mentioned TAPs or a tumor antigen precursor-peptide or SLP. In an embodiment, the

nucleic acid comprises from about 21 nucleotides to about 45 nucleotides, from about 24 to about 45 nucleotides, for example 24, 27, 30, 33, 36, 39, 42 or 45 nucleotides. "Isolated" as used herein refers to a peptide or nucleic acid molecule separated from other components that are present in the natural environment of the molecule or a naturally occurring source macromolecule (e.g., including other nucleic acids, proteins, lipids, sugars, etc.). "Synthetic", as used herein, refers to a peptide or nucleic molecule that is not isolated from its natural sources, e.g., which is produced through recombinant technology or using chemical synthesis. In an embodiment, the nucleic acid (DNA, RNA) encoding the TAP of the disclosure comprises or consists of any one of the sequences set forth in **Table 1** below or a corresponding RNA sequence. In an embodiment, the nucleic acid encoding the TAP is an mRNA molecule. In other embodiments, the nucleic acid encoding the TAP or SLP is a self-amplifying mRNA (saRNA), a trans-amplifying mRNA (taRNA) or a circular mRNA (circRNA) (see, e.g., Liu *et al.*, *Nature Reviews Cancer*, Volume 23, August 2023, pages 526–543).

Table 1: Nucleotide sequence of the nucleic acids encoding the TSAs, TAAs and LSAs identified herein

Peptide Sequence (SEQ ID NO:)	Encoding nucleotide sequence
TLDDAVHGV (1)	ACTCTCGATGACGCCGTCCACGGCGTT (506)
YQIGQVQGV (2)	TACCAAATTGGCCAAGTTCAAGGTGTA (507)
NEYSNITRLY (3)	AATGAATATTCTAACATTACCCGGCTTTAT (508)
RLLADLTGA (4)	CGGCTCCTGGCTGATCTCACTGGGGCC (509)
TPLSPDPTL (5)	ACTCCATTGTCTCCTGACCCACCCCTC (510)
STYYWPRPR (6)	TCGACCTATTATTGGCCTAGACCAAGG (511)
DSFSATETR (7)	GATTCTTTCTCCGCTACTGAGACACGG (512)
ETSYVKVLH (8)	GAAACCAGCTATGTGAAAGTCCTGCAC (513)
AEMLSVV (9)	GCAGAAATGCTGGGGAGTGTCGTC (514)
EELSVLEVF (10)	GAGGAGCTGAGTGTGTTAGAGGTGTTT (515)
FVQENYLEY (11)	TTCGTGCAGGAAACTACCTGGAGTAC (516)
IVQQPTEEK (12)	ATTGTCCAGCAGCCCACTGAGGAAAAA (517)
SVFAHPRKL (13)	AGTGTCTTTGCGCATCCCAGGAAGCTG (518); AGTGTCTTCGCACATCCCAGGAAGCTG (519)
ASSLPTTMNY (14)	GCCTCCAGCCTCCCCACTACCATGAACTAC (520)
IVQQPTEEKR (15)	ATTGTCCAGCAGCCCACTGAGGAAAAACGT (521)
LPTTMNYPL (16)	CTCCCCACTACCATGAACTACCCTCTC (522)
GSNPARYEF (17)	GGCAGTAATCCTGCGCGCTATGAGTTC (523)
TADDATVM (18)	ACCGCAGATGATGCCACTGTCATG (524)
VLEHVVRV (19)	GTCCTGGAGCATGTGGTCAGGGTC (525)
EVDPIGHLV (20)	GAAGTGGACCCCATCGGCCACTTGTAC (526)
QIMPKAGL (21)	CAGATCATGCCCAAGGCAGGCCTC (527)
KVLEHVVRV (22)	AAAGTCCTGGAGCATGTGGTCAGGGTC (528)
QVPGSNPAR (23)	CAGGTACCCGGCAGTAATCCTGCGCGC (529)
FVYGEPREL (24)	TTCGTCTATGGGGAGCCTAGGGAGCTC (530)
TLPTFDPTKV (25)	ACTCTGCCCACTTTTGATCCCACTAAAGTG (531)
NQIMPKTGF (26)	AATCAGATCATGCCCAAGACAGGCTTC (532)
EVDPIGHVY (27)	GAAGTGGACCCCATCGGCCACGTGTAC (533)
ELVRRILSR (28)	GAGCTGTTCCGCAGGATCCTGTCCCGG (534)

MEVDPIGHLY (29)	ATGGAAGTGGACCCCATCGGCCACTTGTAC (535)
SVMSSNVSF (30)	AGTGTCTATGTCCAGCAACGTCTCCTTT (536)
TVPSSFPSW (31)	ACTGTTCCCTAGTTCCTTTCCATCCTGG (537)
KYKDYPVI (32)	AAGTACAAAGATTACTTTCTGTGATA (538)
MEVDPIGHVY (33)	ATGGAAGTGGACCCCATCGGCCACGTGTAC (539)
TVYGEPRKL (34)	ACTGTCTATGGGGAGCCCAGGAACTG (540)
GPDVREGTL (35)	GGTCCTGATGTCAGGGAGGGGACTCTG (541)
VYDGREHTV (36)	GTGTATGATGGGAGGGAGCACACTGTC (542)
LMEVDPIGHLY (37)	CTGATGGAAGTGGACCCCATCGGCCACTTGTAC (543)
KYKDYPVILK (38)	AAGTACAAAGATTACTTTCTGTGATACTCAAG (544)
EVFEGREDSIF (39)	GAGGTGTTTGAGGGGAGGGAAGACAGTATCTTC (545)
GVYDGREHTV (40)	GGGGTGTATGATGGGAGGGAGCACACTGTC (546)
EVVPISHLY (41)	GAAGTGGTCCCCATCAGCCACTTGTAC (547)
NAVGVYAGR (42)	AATGCAGTAGGGTATATGCTGGGAGG (548)
RPDSRLLEL (43)	AGGCCGACAGCCGCTGCTTGAGTTG (549)
SVFAHPRKLLM (44)	AGTGTCTTCGCACATCCCAGGAAGCTGCTCATG (550)
EVFEGREDSVF (45)	GAGGTGTTTGAGGGGAGGGAGGACAGTGTCTTC (551)
RVSHSHASF (46)	CGAGTATCTCACTCACATGCTTCTTTT (552)
ATFLQRKVLRL (47)	GCCACCTTTTTGCAGAGGAAGGTACTGAGG (553)
SYVKVLHHL (48)	AGCTATGTGAAAGTCTGCACCATTTG (554)
FAFGEPREL (49)	TTTGCCTTTGGGGAGCCCAGGGAGCTC (555)
KMAELVHFL (50)	AAGATGGCTGAGTTGGTTTCAATTTCTG (556)
FAHGHPLYTR (51)	TTTGGCCACGGGCACCCACTGTACACACGC (557)
GVYAGREHFV (52)	GGGGTATATGCTGGGAGGGAGCACTTCGTC (558)
NTAIATFLQRK (53)	AACACTGCTATTGCCACCTTTTTGCAGAGGAAG (559)
TLDEKVAEL (54)	ACACTAGATGAAAAGGTGGCCGAGTTA (560)
RLELHITM (55)	CGCCTGCTTGAGTTGCACATCACGATG (561)
EVPNSSPPR (56)	GAGGTGCCCAACTCTTCTCCTCCTCGT (562)
VEVTLREV (57)	GTGGAAGTCACCTGCGGGAGGTG (563)
ISGGPRISY (58)	ATCAGTGGAGGACCTCGCATTTCTAC (564)
GVPGLLILPR (59)	GGAGTCCCCGGACCCCTCCTCATCCTTCCCAGG (565)
GVYDGEHVS (60)	GGAGTCTATGATGGAGAGGAGCACTCAGTC (566)
KISGGPRISY (61)	AAGATCAGTGGAGGACCTCGCATTTCTAC (567)
FLYNQTNIRM (62)	TTTCTATATAATCAGACAAATATTAGGATG (568)
GQYQLVVSL (63)	GGCCAGTACCAGCTGGTGGTGGAGCCTG (569)
GVDDLVR (64)	GGAGTTGATGACCTTGTTCAGAAAGG (570)
KVLEYVIKV (65)	AAAGTCCTTGAGTATGTGATCAAGGTC (571)
HTLPALSRR (66)	CACACTTTACCAGCCCTTTCTAGAAGG (572)
ALREEEEGV (67)	GCTTTGAGAGAGGAGGAAGAGGGAGTC (573)
TTINFTRQR (68)	ACTACCATCACTTCACTCGACAGAGG (574)
SAYGEPRKL (69)	AGTGCCTATGGGGAGCCCAGGAAGCTG (575)
STANVTRAH (70)	AGCACTGCCAATGTGACGCGGGCCAC (576)
SAFPTTINF (71)	TCCGCCTTTCCCACTACCATCAACTTC (577)
FRAVITKKV (72)	TTCCGAGCAGTAATCACTAAGAAGGTG (578)
AAAGVSSTK (73)	GCGGCTGCGGGTGTTCATCCACAAAA (579)
FPTTINFTR (74)	TTCCCACTACCATCACTTCACTCGA (580)
TTSEKIHERR (75)	ACTACCTCTGAGAAGATTACGAGAGA (581)
GLYDGMELH (76)	GGGCTGTATGATGGGATGGAGCACCTC (582)
STANVTRAHGR (77)	AGCACTGCCAATGTGACGCGGGCCACGGCCGC (583)
IEDPKAGLHV (78)	ATAGAGGACCCAAAGGCAGGGCTGCATGTG (584)
GVVGPQGLR (79)	GGTGTGGTGGGCCCCAGGGCCTGAGG (585)
NVFAHATGESR (80)	AATGTATTTGCTCATGCAACTGGGGAATCAAGG (586)
FLFGEPKRL (81)	TTCCTCTTTGGGGAGCCCAAGAGGCTC (587)

SAFPTTINFTR (82)	TCCGCCTTTCCCACTACCATCAACTTCACTCGA (588)
RLFSEDIHV (83)	AGGCTCTTCTCAGAAGACATACATGTC (589)
VYMPANTTF (84)	GTTTACATGCCTGCTAATACAACATTT (590)
EAVGFQPPR (85)	GAGGCTGTGGGCTTTCAACCACCACGA (591)
EVDPTSHSY (86)	GAAGTGGACCCCACTAGCCACTCCTAT (592)
LLDPAQRNLY (87)	TTACTGGACCCAGCTCAGAGAAACCTGTAC (593)
SGISQVFQR (88)	TCTGGAATCTCGCAAGTCTTCCAGAGG (594)
RLFSEDIHVA (89)	AGGCTCTTCTCAGAAGACATACATGTCGCC (595)
VFDVGKGNM (90)	GTGTTTGATGTTGGCAAAGGAAACATG (596)
KASEKIFYV (91)	AAAGCCTCGGAGAAAACTTCTATGTG (597)
EAFAFRFPR (92)	GAGGCCGCCGCTGCCTTCAGGTTTCCGAGA (598)
MSISMSLLK (93)	ATGAGTATCTCCATGTCTTTATTGAAA (599)
KASPSSLPH (94)	AAGGCATCCCCCAGCTCTCTGCCTCAT (600)
RTLQQGVLDW (95)	AGAACCTTGACAGCAAGGAGTTCTCCAAGACTGG (601)
TTATTFRAT (96)	ACTACTGCCACGACTTTTAGAGCGCGT (602)
NPSHLITPR (97)	AATCCTAGCCATCTCATCACACCCAGA (603)
ETMETLRTSR (98)	GAGACAATGGAGACTCTGAGAACATCCAGA (604)
MVWEGHPRERR (99)	ATGGTATGGGAGGGGCATCCCAGAGAAAGAAGA (605)
LPDGSRVEL (100)	CTCCCAGACGGCTCCCGCGTGGAGCTG (606)
DVVTGNVPLK (101)	GATGTTGTGACTGGCAACGTGCCTCTAAAA (607)
ENPSHLITPR (102)	GAGAATCCTAGCCATCTCATCACACCCAGA (608)
SLARTILHL (103)	TCACTGGCCAGGACTATACTCCATCTC (609)
KPHYGLRAI (104)	AAACCACATTATGGATTGAGAGCAATC (610)
AFLDIHTAL (105)	GCCTTCTGGACATCCACACAGCCCTG (611)
KMSEFVYRF (106)	AAGATGTCAGAGTTTGTCTACAGATTT (612)
FLVTKVTM (107)	TTTTTAGTGACAAAGACTGTGACTATG (613)
HTTSVMENK (108)	CACACCACCTCTGTGATGGAGAACAAG (614)
LVSIAVAVR (109)	CTTGTGAGCATTCCCATTCAGTAAGA (615)
ITSGVKVKK (110)	ATTACATCAGGAGTAAAGTGAAGAAA (616)
VSIPIAVRR (111)	GTGAGCATTCCCATTCAGTAAGAAGA (617)
DIELQEGLR (112)	GACATCATTGAGCTCCAGGAGGGGCTGAGA (618)
HLKPPELGF (113)	CATCTCAAGCCTCCAGAGCTGGGCTTC (619)
QVIVKIIGH (114)	CAGGTCATCGTGAATATCATCGGACAT (620)
AEQEIMKKV (115)	GCCGAGCAGGAAATAATGAAGAAAGTT (621)
EVPLKILAH (116)	GAGGTTCCCCTGAAGATCCTGGCCCAT (622)
IVKIIGHFY (117)	ATCGTGAAATCATCGGACATTTCTAT (623)
SLVSIPIAVR (118)	TCTCTTGTGAGCATTCCCATTCAGTAAGA (624)
MVSPGVSLFK (119)	ATGGTTTCTCCTGGAGTTTCTCTATTCAA (625)
VLMMKLEDL (120)	GTGTTGATGATGAAGTTGGAAGATTTG (626)
YSDLHTPGRY (121)	TATTCGGACTTACACACCCCTGGGAGGTAT (627)
EVARFLTY (122)	GAAGTGGCCCGGTTCTGACCTACTAC (628)
SVGDLMAPR (123)	AGTGTGCGGAGACCTCATGGCTCCCCGG (629)
VLWRGDSPL (124)	GTGCTCTGGAGAGGTGACTCTCCTCTA (630)
QPRQGSPVAA (125)	CAGCCCCGCCAGGGCTCACCTGTGGCAGCG (631)
KQTGIRHSY (126)	AAACAAACAGGTATTAGGCACAGTTAT (632)
RPRQDAISV (127)	AGACCCAGACAAGATGCCATTTTCAGTA (633)
KLITQIRTA (128)	AAACTGATAACACAGATACGTACAGCA (634)
SYLSEHSAAIF (129)	TCTTATTTGTCTGAGCACTCTGCAGCTATTTTC (635)
TSVGDLMAPR (130)	ACCAGTGTGCGGAGACCTCATGGCTCCCCGG (636)
EIPTGVAKR (131)	GAGATACCAACTGGGGTGGCCAAGCGG (637)
SQINLSQIY (132)	AGTCAAATCAACCTTAGCCAAATTTAT (638)
RRPSGGFRL (133)	CGAAGACCCTCAGGCGGGTTCCGGCTC (639)
EVFNVKNTFPK (134)	GAAGTATTTAATGTAAAAAATACATTTCCAAAG (640)

KVLGGGWTV (135)	AAGGTCTTAGGAGGTGGATGGACTGTC (641)
HEAPGQHSEV (136)	CATGAGGCTCCTGGCCAGCACAGTGAAGTT (642)
EVSHPNMSGR (137)	GAAGTAAGCCACCCTAACATGAGTGGCAGA (643)
DTAPATFLR (138)	GACACAGCCCCAGCCACCTTCCTACGG (644)
KPQKDLHFI (139)	AAACCCCAAAAAGACCTGCACCTTCATA (645)
RVRGAGTHL (140)	CGAGTGCCTGGGGCAGGAACACACCTG (646)
TAPIIVAQR (141)	ACGGCTCCCATTATTGTGGCTCAGAGA (647)
TSWDTKFYEK (142)	ACGAGCTGGGATACCAAGTTCTATGAAAAG (648)
KVFAEHKISY (143)	AAAGTGTTCGCGGAGCACAAGATCTCCTAC (649)
DAFQGIANR (144)	GACGCCTTCCAGGGCATCGCCAACAGG (650)
IVADPRVPR (145)	ATTGTGGCCGACCCGCGGGTGCCCCGT (651)
TGFSTSLGR (146)	ACAGGCTTCTCCACGAGCCTGGGCAGA (652)
ATAPIIVAQR (147)	GCCACGGCTCCCATTATTGTGGCTCAGAGA (653)
GQFLVKSGY (148)	GGCCAGTTCTTGGTCAAATCCGGCTAC (654)
WTSRVLQNK (149)	TGCACTTCCAGAACGGTGCAAAATAAA (655)
ATYGGSDHYI (150)	GCCACATATGGGGTTTCAGATCATTACATT (656)
VYIAELEKI (151)	GTTTACATTGCAGAGTTGGAAGATA (657)
VFLDRAVSI (152)	GTGTTCTTGACCGCGCCGTGTCCATC (658)
MPSPIDHPR (153)	ATGCCAGTCCCATCGACCACCCAAGG (659)
EAVRHILHGSR (154)	GAAGCAGTAAGGCACATCTTACATGGCAGCAGG (660)
YPAGNVKEL (155)	TACCCAGCAGGCAACGTCAAAGAGCTA (661)
SVPRSLASR (156)	AGCGTACCCAGAAGCCTGGCATCCCGG (662)
ALIKHVANA (157)	GCGCTAATTAAGCACGTTGCGAACGCA (663)
YTANLVPVR (158)	TACACGGCAAATCTGGTCCAGTTAGA (664)
LSSSLVTKL (159)	TTGTCCTCTTCCCTTGTACCAAACCTT (665)
QNSNVLA VR (160)	CAGAACAGTAATGTTTTAGCAGTGAGG (666)
TTTKNTLNK (161)	ACGACAACAAAAACACCTTGAACAAA (667)
HNYINLHSL (162)	CACAATTATATTAATTTGCATTCTCTG (668)
HLKDYFEEY (163)	CACCTTAAAGATTACTTTGAGGAATAT (669)
SPEYFTSYL (164)	TCTCCAGAATATTTTACCAGCTATCTG (670)
ATDVL D HLY (165)	GCCACAGATGTTTTGGACCACTTATAT (671)
QTFEESLGR (166)	CAGACCTTTGAGGAATCACTGGGAAGA (672)
HEQPELQKV (167)	CATGAACAGCCAGAACTGCAGAAGGTA (673)
MATDVL D HLY (168)	ATGGCCACAGATGTTTTGGACCACTTATAT (674)
TSGLLFPR (169)	ACTTCTGGCAGTCTCCTGTTTCCCAGA (675)
KLGINNVSF (170)	AAGCTTGAATAAATAACGTTTCCTTT (676)
KYISQFQVF (171)	AAATATATTTACAATTTCAAGTATTC (677)
QTA AVSGVK (172)	CAGACTGCGGCTGTGTCGGGAGTAAAG (678)
LTPLNHPFSY (173)	TTGACACCATTAAACCATCCTTTTCTAC (679)
VFINKKYVF (174)	GTTTTATAAATAAAAAGTACGTTTTT (680)
NLITEEHPV (175)	AACCTCATCACTGAGGAGCATCCTGTC (681)
ELVKVIDGSSR (176)	GAGTTAGTGAAGGTCATTGATGGAAGCTCCAGG (682)
FHSLPIHLF (177)	TTTCACTCACTTCCAATTCATTTGTTT (683)
YSHDYSYY (178)	TATTCTCATGATTACTCTTACTAT (684)
FQIEKLTPL (179)	TTCCAGATAGAAAAATTGACACCCCTG (685)
EHSVENGSI (180)	GAGCACTCTGTTGAAAATGGCAGTATT (686)
ETIQNTHSF (181)	GAGACAATTCAAAACACACATTCATTT (687)
YYSIWKTQI (182)	TACTACAGTATTTGGAAGACACAAATT (688)
SYFFHGLSF (183)	TCTTATTATTTTACGGCCTGTCATTT (689)
ESFQQPYIPR (184)	GAGTCTTTTCAACAACCTTATATCCCAGG (690)
KQVPSRVLY (185)	AAACAGGTACCCTCTAGGGTCCTCTAC (691)
MLFNKDL DAA (186)	ATGTTATTTAATAAAGATTTGGATGCAGCA (692)
APRSAEPRAT (187)	GCCCCACGGTCAGCAGAGCCACGGGCCACC (693)

YLDPGAVHAVF (188)	TATCTGGATCCTGGGGCAGTGCATGCAGTGTTC (694)
TLKKHKIV (189)	ACCCTTAAGAAACATAAGATAGTT (695)
VGVPISLY (190)	GTGGGTGTGCAATCAGCACTCTGTAT (696)
SPRPQPEL (191)	AGCCCCGCCCCCAGCCAGAGCTC (697)
KLSFPDSKF (192)	AAGCTTTCCTTCCCTGATTCAAAATTT (698)
KNKDEYIHFY (193)	AAAAACAAAGATGAATATATCCATTTTTTAC (699)
RAFEGRRRGW (194)	AGGGCATTGAGGGGAGAAGAAGAGGATGG (700)
RLKARPSTY (195)	CGTCTCAAGGCCAGGCCTTCCACCTAC (701)
APSLHATL (196)	GCCCCCTCTCTTCACGCCACACTC (702)
AQKEPTGNY (197)	GCGCAGAAAGAACCCACTGGCAATTAC (703)
LSLGTACR (198)	CTCTCACTGGGTACCACAGCTTGCAGG (704)
SRNPTSXY (199)	AGCAGAAACCCTACAAGCTACAAGTAT (705)
SLNNDHDIY (200)	AGCCTAAATAATGACGATCACCAGATATAC (706)
YVDPMITEI (201)	TATGTTGATCCCATGATTACAGAGATA (707)
PSFSPYAKR (202)	CCCAGCTTTTCTCCATATGCAAAAAGG (708)
HVNGSRPHAR (203)	CACGTCAACGGCTCCCGCCCCCATGCACGG (709)
ITVRLAPPL (204)	ATAACAGTGAGATTGGCTCCTCCACTC (710)
SANPLSHRY (205)	TCAGCCAATCCCCTAAGTCATAGATAC (711)
VPLAHSSSA (206)	GTGCTCTTGCTCATTCCAGCTCAGCC (712)
GQVPTTEVV (207)	GGCCAAGTGCTACTACAGAAGTTGTG (713)
KTWGQYWQV (208)	AAGACCTGGGGCCAATACTGGCAAGTT (714)
ALNFPQSQK (209)	GCCTTGAACCTCCCTGGAAGCCAAAAG (715)
YVWKTWQY (210)	TATGTCTGGAAGACCTGGGGCCAATAC (716)
MPTAESTGM (211)	ATGCCAACTGCAGAGAGCACAGGTATG (717)
HTMEVTYHRR (212)	CACACCATGGAAGTGACTGTCTACCATCGCCGG (718)
EEAAGIGIL (213)	GAAGAGCCGCTGGGATCGGCATCCTG (719)
EGFDHRDSK (214)	GAAGGGTTTGATCATCGGGACAGCAAA (720)
AEEAAGIGIL (215)	GCTGAAGAGGCCGCTGGGATCGGCATCCTG (721)
LTSSMVTTPR (216)	CTCACTTCATCTATGGTTACCCCAAGA (722)
TSSMVTTPRR (217)	ACTTCATCTATGGTTACCCCAAGAAGG (723)
GLSNLTHVL (218)	GGGCTGAGCAATCTGACCCACGTGCTG (724)
QLLALLPSL (219)	CAGCTCCTTGCCCTCCTGCCTTCCCTG (725)
EAAQPMTKK (220)	GAAGCAGCTCAGCCCATGACAAAGAAG (726)
RVLGKTPSW (221)	AGGGTTTTAGGAACAAAGCCTTCTGG (727)
VLYPVPLESY (222)	GTGCTGTATCCTGTCCCCCTGGAGAGTTAT (728)
PYLQMINL (223)	CCTTACCTGGGCCAGATGATTAATCTG (729)
ELFSYLIEK (224)	GAATTGTTCTCCTACCTCATTGAGAAA (730)
EEQYIAQF (225)	GAAGAGCAGTATATCGCCAGTTC (731)
EAAQPMTKKR (226)	GAAGCAGCTCAGCCCATGACAAAGAAGCGA (732)
MPMQDIKMI (227)	ATGCCCATGCAGGATATCAAGATGATC (733)
RLSEGDMVHL (228)	CGGCTTTCGGAAGGGGATGTGATGCATCTG (734)
HASSYISPEK (229)	CATGCATCTTCTACATTTCCCCGGAGAAG (735)
MPMQDIKMIL (230)	ATGCCCATGCAGGATATCAAGATGATCCTG (736)
SPSVSQLSVL (231)	AGTCCCAGCGTCAGTCAGCTAAGTGTCTG (737)
RLDQLLRHV (232)	CGCCTGGATCAGTTGCTCAGGCACGTG (738)
ALLERASATL (233)	GCTCTGCTGGAGAGAGCCTCTGCCACCCTC (739)
TVAPTPATAR (234)	ACCGTCGCTCCTACCCCGGCCACCGCTCGG (740)
SQSPSVSQL (235)	TCCAGAGTCCCAGCGTCAGTCAGCTA (741)
STVAPTPATAR (236)	TCGACCGTCGCTCCTACCCCGGCCACCGCTCGG (742)
QYIAQFTSQF (237)	CAGTATATCGCCAGTTCACCTCTCAGTTC (743)
GQHLHLETF (238)	GGACAACATCTTCACCTGGAGACCTTC (744)
TIASVLVAR (239)	ACAATTGCAAGTGTGTTGGTTGCAAGA (745)
SLLQHLIGL (240)	AGTCTCCTGCAGCACCTCATCGGGCTG (746)

TASPRSPVM (241)	ACAGCCAGTCCCAGGAGCCCAGTAATG (747)
AAFDGRHSQTL (242)	GCAGCCTTTGACGGGAGACACAGCCAGACCCTG (748)
SPRRLVEL (243)	AGCCCACGGAGACTTGTGGAGCTG (749)
LYVDSLFFL (244)	CTCTATGTGGACTCTTTATTTTTCCTT (750)
VFLREFPNF (245)	GTCTTCCTGAGAGAATTTCTTAATTTT (751)
RPRFSTATEIA (246)	AGGCCCAGATTCTCCACTGCTACCGAGATCGCC (752)
ALIANPRRK (247)	GCTTTGATTGCTAACCCAAGGAGGAAG (753)
DFMGQIVYR (248)	GATTTTCATGGGCCAGATTGTGTACCGC (754)
EIPDVTMGL (249)	GAAATTCCTGATACAGTAATGGGCCTT (755)
VMSSTLYTV (250)	GTAATGTCCAGCACCCCTGTACACTGTG (756)
SPQHKPRL (251)	TCACCTCAGCACAAAGCCACGACTG (757)
EPKPPTTGL (252)	GAGCCTAAGCCACCCACCACAGGGCTT (758)
IPDTIASVL (253)	ATACCAGACACAATTGCAAGTGTGTTG (759)
TDFMGQIVYR (254)	ACAGATTTTCATGGGCCAGATTGTGTACCGC (760)
GEDDEHRKI (255)	GGAGAAGATGATGAACACAGAAAAATT (761)
RLRGSIQSRY (256)	CGTTTGCGGGGTTCCATTACAGAGCCGATAC (762)
HLDESPAYL (257)	CACTTGATGAGAGCCCCGCCTACCTC (763)
KMEETTVTY (258)	AAGATGGAAGAACTACGGTCACATAT (764)
LPTDLFNSV (259)	CTCCCAACAGATCTGTTTAATAGTGTG (765)
RPQGLAVL (260)	AGGCCTCAGGGCCTGGCTGTCTCTG (766)
SLSEKSPEV (261)	AGTCTATCTGAAAAGTCTCCAGAAAGTC (767)
GAFREGPPY (262)	GGTGCATTTTCGAGAGGGGCGCCCTAC (768)
YLNGATVVA (263)	TACCTCAATGGGGCTACTGTTGTAGCA (769)
SMYHLTEGF (264)	TCAATGTACCTCCACACAGAGGGCTTC (770)
HILSHLHEV (265)	CACATTCTGAGTCACTTGCATGAAGTC (771)
SISEAPLTEV (266)	AGTATCTCTGAAGCCCCACTTACAGAGTT (772)
HQINSEATF (267)	CACCAGATCAACAGTGAAGCCACATTT (773)
DIKQEGVGAF (268)	GACATCAAGCAGGAAGGGGTGCGTGCATTT (774)
SALGVTITK (269)	AGCGCTCTGGGAGTTACTATTACCAAA (775)
TVNDFTQNP (270)	ACAGTGAATGACTTTACCCAAAACCCAGG (776)
SFIQAGSSY (271)	TCTTTTCATCCAAGCAGGATCCTCGTAT (777)
GVTITKTLK (272)	GGAGTTACTATTACCAAACTCTCAAG (778)
AERPQGLAV (273)	GCTGAGAGGCCTCAGGGCCTGGCTGTC (779)
REKGPVKEV (274)	AGGGAAAAGGGACCCGTCAAGGAAGTT (780)
TSVPPFNLR (275)	ACCTCAGTGCCTCCCTTCAACCTAAGA (781)
LSRLPSIAF (276)	TTATCACGCCTTCCAAGCATTGCCTTT (782)
FPVHAAEFK (277)	TTCCCAGTTTCATGCTGCTGAGAAGTTC (783)
GEISASHV (278)	GGGGAGATCTCTGCATCACATGTC (784)
AADGGQHWY (279)	GCTGCAGATGGGGGTCAACACTGGACGTAT (785)
EISASHVSR (280)	GAGATCTCTGCATCACATGTCAGCAGG (786)
SPRIPFSTF (281)	TCGCCCCGGATCCCGTTCAGCACCTTC (787)
KLMDPGSLPPL (282)	AAGCTCATGGACCCGGGCTCCCTGCCGCCCTC (788)
ETKPEFERR (283)	GAAACAAAGCCAGAGTTTGAAAGGAGG (789)
ETIMKFLKM (284)	GAGACGATCATGAAATTTTGAATG (790)
RRHLWSTF (285)	AGGCGCGCCACCTTTGGAGCACTTTT (791)
HLQEKQLSL (286)	CATCTCCAGGAAAAGCTGCAGAGTTTG (792)
ELSVVTSER (287)	GAACCTCAGTGGTCACAAGTGAGAGA (793)
YLDQQVPYTF (288)	TACTTGACCAGCAAGTGCCCTACACCTTC (794)
EAIPRIPL (289)	GAAGCAATTCCTCGAATCCCTCGCTTG (795)
GYLDQQVPYTF (290)	GGATACTTGACCAGCAAGTGCCCTACACCTTC (796)
SPKLGIGF (291)	AGCCCTAACTGGGCGGGATTGGATTT (797)
YPEKSRGCL (292)	TATCCTGAGAAATCACGTGGATGCCTC (798)
TTIPFSTLRQR (293)	ACCACCATTCCCTTACGCACTCTACGTCAGAGG (799)

SLGAHSPALY (294)	AGCCTGGGTGCCCACAGTCCTGCCCTGTAC (800)
SQNGQLIHY (295)	TCTCAAAATGGACAATAATCCATTAC (801)
KAKEHTANISW (296)	AAAGCCAAGGAGCACACCGCCAATATTTTCATGG (802)
RVSKSDSTF (297)	AGGGTATCAAAGTCAGATTCTACTTTC (803)
SLNSQVTGL (298)	TCCCTCAATTCTCAAGTCACAGGTCTT (804)
NSDLSEKLEY (299)	AACTCAGATTTAAGTGAAAAATTGGAATAT (805)
DSSTVGLQR (300)	GACAGTTCCTACTGTTGGGCTTCAGCGA (806)
RASAIHQ (301)	AGAGCTTCAGCTATTATAATTTCAGAGA (807)
SQETLPLKI (302)	TCCAGGAAACACTTCCACTCAAGATT (808)
STFDGLDRR (303)	AGCACCTTTGATGGTTTAGACAGAAGA (809)
RVKEIVINK (304)	CGAGTGAAGGAGATTGTAATCAACAAG (810)
AQPHHGVY (305)	GCTCAGCCCCACCATGGTGTGCCATAT (811)
EVIQLKERDRK (306)	GAAGTAATACAGTTAAAAAGACGAGACCGTAAG (812)
EVKEKTEL (307)	GAGGTGAAGGAAAAGACGGAATC (813)
TDPTLHY (308)	ACTGACCCTGAGACCCTGCACTAC (814)
KMKEKTQEL (309)	AAAATGAAGGAGAAAAACACAAGAGCTT (815)
STFDGLDRRR (310)	AGCACCTTTGATGGTTTAGACAGAAGAAGA (816)
KMSELQTYV (311)	AAAATGTCAGAGCTGCAGACCTATGTT (817)
GTDPTLHY (312)	GGCACTGACCCTGAGACCCTGCACTAC (818)
TEEKGSILI (313)	ACAGAGGAAAAGGGGAGCATTTTAATT (819)
DTAMPAHSR (314)	GACACTGCTATGCCTGCCCATTCAGA (820)
KLQEALKTI (315)	AAGCTCCAGGAAGCACTGAAGACCATC (821)
GTDPTLHYF (316)	GGCACTGACCCTGAGACCCTGCACTACTTC (822)
SLKNRIESV (317)	AGTTTAAAAAATCGAATTGAATCTGTA (823)
NLKDPVGVY (318)	AACCTTAAAGACCCAGTTGGGGTATAC (824)
FTETNPQVY (319)	TTCACAGAGACCAACCCACAAGTGATAC (825)
ETQEAEEVAVSR (320)	GAAACCCAGGAGGCAGAGGTTGCAGTGAGCCGA (826)
SPRPESGTV (321)	TCTCCCAGACCAGAGTCGGGTACTGTT (827)
SEFAKDPSL (322)	TCTGAGTTTGCGAAGGATCCGTCCTC (828)
KVIKKIGHY (323)	AAGGTTATCAAGAAAATTGGACATTAT (829)
RTWQTRKQF (324)	AGGACGTGGCAAACCAGAAAACAGTTT (830)
AMAHKVIKA (325)	GCCATGGCCCCACAAAGTAATTAAGCT (831)
KLKQFQKEY (326)	AAACTAAACAGTTTCAGAAGGAATAT (832)
SPLDEESL (327)	TCTCCATTGGAAGATGAAGAGTCATTA (833)
NSTDFTTDR (328)	AACTCTACAGACTTTACCACTGACAGA (834)
ETKDTKGRYF (329)	GAAACGAAGGATACCAAAGGTCGTTATTTT (835)
RPRVSSTEM (330)	CGGCCTCGAGTATCCTCCACAGAAATG (836)
LMDKSSTIY (331)	TTAATGGACAAATCAAGCACTATTTAC (837)
GTLRPLKVR (332)	GGGACCCTCCGGCCGCTCAAAGTTCGCAGG (838)
ILSEGSVPL (333)	ATCCTGAGTGAAGGATCCGTCCTCTC (839)
TVYNFRTEL (334)	ACAGTCTATAATTTTAGGACTGAACTT (840)
LPSSADVEF (335)	CTCCCCTCTTCAGCTGATGTAGAATTT (841)
RLPSSADVEF (336)	AGGCTCCCCTCTTCAGCTGATGTAGAATTT (842)
ALMDKSLHV (337)	GCCTTGATGGATAAAAGTCTTCATGTT (843)
MHNALHIY (338)	ATGCACAATGCCTTGACATCTATATG (844)
MEKEDYHSL (339)	ATGGAGAAAGAGGATTACCACAGCTTG (845)
MEKEDYHSLY (340)	ATGGAGAAAGAGGATTACCACAGCTTGAT (846)
YHSLYQSHL (341)	TACCACAGCTTGATCAGAGCCATTTA (847)
YMPFIPLY (342)	TACATGGTTCCTTTTATACCACTGTAC (848)
LMEKEDYHSL (343)	CTCATGGAGAAAGAGGATTACCACAGCTTG (849)
FAHEAPFL (344)	TTTGCCCATGAAGCACCAGCTTTTCTG (850)
FASPLTGIA (345)	TTTGCTAGTCCACTTACTGGGATAGCG (851)
HEAPFLPW (346)	CATGAAGCACCAGCTTTTCTGCCTTGG (852)

VLFFKFIQK (347)	GTCCTCTTCAAGAAGTTTATCCAGAAG (853)
APAFLPWHR (348)	GCACCAGCTTTTCTGCCTTGGCATAGA (854)
LLMEKEDYHSL (349)	CTCCTCATGGAGAAAGAGGATTACCACAGCTTG (855)
HYVVSMDAL (350)	CATTATTATGTGTCAATGGATGCACTG (856)
WEQEIQKL (351)	TGGGAACAAGAAATCCAGAAGCTG (857)
LMEKEDYHSLY (352)	CTCATGGAGAAAGAGGATTACCACAGCTTGTAT (858)
LEQASRIWSW (353)	TTGGAACAAGCGAGTCGGATCTGGTCATGG (859)
NIFDLSAPEK (354)	AACATCTTCGATTTGAGTGCCCCAGAGAAG (860)
EAPAFLPWHR (355)	GAAGCACCAGCTTTTCTGCCTTGGCATAGA (861)
SEIWRDIDF (356)	TCTGAAATCTGGAGAGACATTGATTTT (862)
AAMVGAVL (357)	GCGGCGATGGTAGGGGCCGTCCTC (863)
TFLGVGQESF (358)	ACTTTCCTTGGGGTAGGACAGGAAAGCTTT (864)
ESWPSVFYNR (359)	GAGTCGTGGCCTTCCGTCTTTTATAATAGG (865)
ISQDTTVGR (360)	ATTTCTCAGGACACAACGTGGGACGT (866)
RPWSGPYIL (361)	AGGCCCTGGAGTGGTCCCTACATCCTA (867)
SSDYVIPIGTY (362)	AGCTCAGACTATGTCATCCCCATAGGGACCTAT (868)
DSDPDSFQDY (363)	GATTCAGACCCAGACTCTTTTCAAGACTAC (869)
DTRPWSGPY (364)	GACACAAGGCCCTGGAGTGGTCCCTAC (870)
HYYSVKKTF (365)	CACTATTACTCAGTCAAAAAGACTTTC (871)
NVCGSQQGR (366)	AATGTCTGTGGCTCTCAGCAAGGCCGG (872)
YMNGTMSQV (367)	TATATGAATGGAACAATGTCCCAGGTA (873)
MAKRTHPL (368)	ATGGCAAAGCGCACAACTCACCCTTTA (874)
RPWSGPYILR (369)	AGGCCCTGGAGTGGTCCCTACATCCTACGA (875)
MTVDLSLVNK (370)	ATGACGGTGGACAGCCTAGTGAACAAG (876)
TRPWSGPYIL (371)	ACAAGGCCCTGGAGTGGTCCCTACATCCTA (877)
TTHPLFVIATR (372)	ACAACCTCACCCTTTATTTGTCATTGCCACCAGG (878)
FVWTHYYSV (373)	TTTGTGTTGGACACACTATTACTCAGTC (879)
LSKEEKNHF (374)	TTAAGTAAAGAAGAAAAGAACCCTTT (880)
RAANQVFVL (375)	AGAGCTGCAAACCAGGTCTTTGTTTTG (881)
MVRSATLIK (376)	ATGGTGAGAAGCGCTACCCTCATTA (882)
NQVFLVHSY (377)	AACCAGGTCTTTGTTTTGCACTCTTAT (883)
HNSTEFLLI (378)	CACAACCTCCACAGAGTTTCTCATC (884)
SQDVAGTTF (379)	TCTCAGGATGTTGCAGGCACAACCTTTC (885)
AHNSTEFLLI (380)	GCACACAACCTCCACAGAGTTTCTCATC (886)
STEFLLIYER (381)	TCCACAGAGTTTCTCATCTACGAAAGA (887)
EGFFTRQER (382)	GAAGGGTTTTTCACGAGACAGGAGCGC (888)
FQKVLVSY (383)	TTTCAGAAAGTTTTGGTATCCTAC (889)
FTDFMGQIVY (384)	TTACACAGATTTTCATGGGCCAGATTGTGTAC (890)
YFQKVLVSY (385)	TACTTTCAGAAAGTTTTGGTATCCTAC (891)
ALVNMPPHYR (386)	GCACTGGTGAACATGCCTCCTCACTACCGC (892)
GVMSSSTLYTV (387)	GGTGTAATGTCCAGCACCTGTACACTGTG (893)
LLSNTVSTL (388)	TTGCTATCTAATACGGTCTCAACACTA (894)
RVFHETGAQR (389)	AGGGTTTTTTCACGAGACAGGAGCGCAGAGA (895)
SASDHCRSR (390)	TCGGCCAGCGACCACTGCCGGTCCAGG (896)
RRDGGIIY (391)	CGCAGAGATGGAGGCATCATAATCTAT (897)
VAALIANPR (392)	GTAGCAGCTTTGATTGCTAACCCAAGG (898)
RLLGTEFQV (393)	AGACTGTTGGGTACAGAATTCCAGGTC (899)
FSIIGVSRR (394)	TTCTCCATCATCGGAGTTTCCCGAAGG (900)
LSSDGMIEY (395)	TTGTCATCAGATGGAATGTACGAGTAT (901)
DEYFLPSL (396)	GATGAATACTTCTACCCTCCCTG (902)
SYIGLKGLYF (397)	TCCTACATTGGATTAAAGGGTCTTTACTTC (903)
FTGFGGALGY (398)	TTACAGGTTTTGGAGGTGCCCTGGGTAC (904)
KTWDQVPFSV (399)	AAGACCTGGGACCAGGTGCCTTTCTCCGTG (905)

RVADIPIKP (400)	AGGGTGGCGGATATTCCAATAAAGCCA (906)
SVAKHTQSY (401)	TCTGTTGCCAAGCACACCCAGAGCTAC (907)
QTKGGQTTWAR (402)	CAGACAAAAGGGGGCCAAACATGGGCGAGA (908)
ETGSSFMSF (403)	GAAACAGGAAGTTCATTCATGAGTTTT (909)
SLYSYFQKV (404)	TCACTTTATTCTTACTTTTCAGAAAGTT (910)
QTKGGQTTWARR (405)	CAGACAAAAGGGGGCCAAACATGGGCGAGAAGG (911)
TVVAALIANPR (406)	ACTGTTGTAGCAGCTTTGATTGCTAACCCAAGG (912)
HLMVKDWQL (407)	CATCTCATGGTGAAAGATTGGCAGCTG (913)
NPLSKLSVL (408)	AACCCTCTAAGTAAGCTCTCTGTGCTC (914)
FVIPSTKDSNR (409)	TTTGTAATTCCTAGCACGAAAGACTCTAACAGG (915)
HYQVQTHL (410)	CACTATCAGGTGCAGACCCACCTC (916)
ASDILSFAHKY (411)	GCCTCGGACATCCTGTCTTTGCGCACAAGTAC (917)
RLGQGVPLV (412)	AGACTGGGGCAGGGCGTGCCCTCGTG (918)
SVPDHVQPSK (413)	AGTGACCAGACCATGTCCAACCTCTAAG (919)
RLLEKHISL (414)	AGGCTGCTGGAAAAGCACATCTCCCTG (920)
SLFGVSERL (415)	TCCCTCTTTGGGGTCTCAGAGAGATTG (921)
NHYQVQTHL (416)	AATCACTATCAGGTGCAGACCCACCTC (922)
DLVGKDVTRVY (417)	GACCTGGTTGGAAAGGATGTAACAAGAGTGTAC (923)
SLSPPTLPR (418)	TCTCTCAGTCCTCCAACACTACCAAGA (924)
LADNGTLGKY (419)	CTGGCTGACAATGGCACCCCTGGGCAAGTAT (925)
KAMYIRVSY (420)	AAAGCCATGTATATCCGTGTATCCTAT (926)
MQPKLKQVF (421)	ATGCAGCCCAAGCTGAAACAAGTCTTT (927)
AIQDGILL (422)	GCAATTATTCAGGATGGCATCTTGCTG (928)
AFDRAVHF (423)	GCGTTTGACAGAGCTGTTCACTTC (929)
NTPNIVSLR (424)	AATACTCCTAACATTGTCTCTTTAAGA (930)
RVADIPIKPW (425)	AGGGTGGCGGATATTCCAATAAAGCCATGG (931)
HYIPLQTI (426)	CACTATATAATCCCACTGCAAAACAATA (932)
VMKGINQGY (427)	GTCATGAAGGGCATTAAATCAAGGTTAT (933)
ATSPPASVR (428)	GCGACGTCCCCGCCGCTCGGTCCGC (934)
ALEKDTPRY (429)	GCACTGGAGAAGGATACCCCCAGGTAT (935)
QVMKGINQGY (430)	CAAGTCATGAAGGGCATTAAATCAAGGTTAT (936)
AAFDRVHF (431)	GCAGCGTTTGACAGAGCTGTTCACTTC (937)
RPLRIKGVF (432)	AGACCGCTGAGGATCAAAGGGGTTTTTC (938)
RQVMKGINQGY (433)	AGGCAAGTCATGAAGGGCATTAAATCAAGGTTAT (939)
KLDTTVKNI (434)	AAACTGGACCACTGTAAAGAACATC (940)
LPRTPRPDL (435)	CTTCCGCGAACTCCTCGCCCCGACCTC (941)
ITYTESNSR (436)	ATAACTTACACCGAAAGCAACTCAAGG (942)
RLQGSVTLV (437)	CGACTTCAGGGATCTGTACCCCTCGTC (943)
SQFPSKNLPAF (438)	TCTCAATTCCCAAGTAAAAATCTTCCTGCTTTT (944)
LPRTPRPDLIL (439)	CTTCCGCGAACTCCTCGCCCCGACCTCATCCTT (945)
DTAPQSHQV (440)	GACACTGCCCCACAATCCCATCAAGTC (946)
MAILGTAGR (441)	ATGGCTATCCTGGGCACAGCGGGGCGG (947)
SVSSHLIHR (442)	TCTGTGTCCTCTCACCTCATTATAGATA (948)
STSPGTGVRK (443)	TCCACGTCACCAGGGACAGGAGTCAGGAAA (949)
EVAEVLGSKV (444)	GAAGTGGCTGAAGTCCTTGGGAGTGTGAAG (950)
EIPRTPSEGR (445)	GAGATACCACGAACCCCTCAGAAGGAAGA (951)
VFLKFSRRF (446)	GTGTTTTTAAATTCTCCAGAAGATTT (952)
SVSSHLIHRY (447)	TCTGTGTCCTCTCACCTCATTATAGATAC (953)
THLEDPLHM (448)	ACACATCTAGAAGACCCTCACCTTATG (954)
SVFPRTSSR (449)	AGTGTCTTTCCCAGGACCTCCTCCAGA (955)
GQYGQSKPWTF (450)	GGGCAGTATGGACAAAGTAAGCCTTGGACTTTT (956)
VPRPTSTVGL (451)	GTTCCAAGACCTACCAGCACAGTAGGATTA (957)
NSVSSHLIHRY (452)	AATTCTGTGTCCTCTCACCTCATTATAGATAC (958)

QEEDNLLRYF (453)	CAAGAAGAAGACAACCTTCTAAGATACTTT (959)
THLEDPHML (454)	ACACATCTAGAAGACCCTCACCTTATGCTT (960)
ATTNILEHV (455)	GCTACAACAAACATCCTTGAACATGTA (961)
MTLRPTQPR (456)	ATGACTCTGAGGCCTACACAGCCACGT (962)
ETRPNNSKF (457)	GAAACAAGACCGAACAACCTCCAAGTTC (963)
HSITEPLLY (458)	CACTCAATCACGGAGCCTCTGCTCTAT (964)
HLFLQPPSKR (459)	CATTTATTCTTACAACCTCCAAGCAAAAGA (965)
ETVRFTSSF (460)	GAGACAGTTAGATTTACTTCCTCTTTT (966)
SPMPIPLYL (461)	TCCCCAATGCCTATACCCCCATTGTATCTT (967)
ESYGRYTFY (462)	GAATCTTATGGTAGGTATACTTTTTAC (968)
KSQGSFISF (463)	AAATCACAAGGTTCAATTTATTTCTTT (969)
GTILHIGVF (464)	GGTACTATCTTGACATAGGTGTATTT (970)
KVFSGSSKR (465)	AAAGTATTTTCTGGAAGCAGCAAGAGG (971)
SSFSTLASLDK (466)	TCAAGCTTCAGCACCTTGCATCTCTGGATAAA (972)
TTQGAAPQR (467)	ACCACCCAGGGAGCTGCTCCTCAGAGG (973)
HTTQGAAPQR (468)	CATACCACCCAGGGAGCTGCTCCTCAGAGG (974)
KIFQERAAF (469)	AAGATCTTCCAAGAGAGGGCAGCCTTT (975)
GQITHNTSF (470)	GGGCAAATCACACATAACACTTCATTC (976)
ISLKPLIARY (471)	ATTAGTCTCAAGCCTTTGATAGCACGGTAT (977)
KHSDLILFW (472)	AAGCATTCTGATTTGATTTTATTCTGG (978)
MVWEGHPRER (473)	ATGGTATGGGAGGGGCATCCCAGAGAAAGA (979)
STDLPILLK (474)	TCAACTGATTTGCCCATCTTCTTAAA (980)
EVISINTGHF (475)	GAGGTAATTTCTATCAACACTGGACATTTT (981)
ETERVLEKSSY (476)	GAGACAGAGCGGGTCTGGAGAAGTCTTCTTAC (982)
KIKTINLRY (477)	AAGATAAAAACTATAAATCTGAGATAT (983)
YVSQKVSD (478)	TATGTGAGTCAGAAAAGTTTCAGACTTT (984)
DAGIPVYHR (479)	GATGCAGGCATCCCTGTGTACCACCGA (985)
TILEAEILHQA (480)	ACCATCTTGGAAGCAGAGATCCTTCACCAGGCA (986)
EYAQKTPLF (481)	GAATATGCTCAGAAAACACCTCTCTTT (987)
TWTPHGIRI (482)	ACATGGACACCACATGGTATCAGAATC (988)
EVHEGGVARF (483)	GAGGTCCACGAAGGTGGAGTTGCTCGATTT (989)
REIEIEGRL (484)	AGAGAAATAGAAATAGAGGGAAGATTA (990)
SWLPIPAKY (485)	TCCTGGCTGCCAATCCCAGCCAAATAT (991)
RYSERVYTI (486)	CGCTACTCCGAAAGGGTCTACACTATC (992)
FTDSQGNL (487)	TTACAGACTCGCAGGGCAATGACATTAAA (993)
SVPDFLSLR (488)	TCAGTGCCAAGCGACTTCTGAGTCTCAGG (994)
RQMSLEFRA (489)	CGGCAGATGAGTCTGGAGTTCAGGGCA (995)
ETISPRPSI (490)	GAAACCATCTCCCCAGGCCTTCAATA (996)
GPAGGRGVI (491)	GGGCCAGCAGGAGGAAGGGGAGTCATC (997)
LTDHHIKEY (492)	CTGACTGACCATCACATAAAAGAATAC (998)
EAVPYNGSLFK (493)	GAAGCAGTACCTTATAATGGTTCCTTGTTCAA (999)
NLLAEIHGV (494)	AATCTGCTGGCGGAGATCCACGGTGTG (1000)
KEGPVTRGA (495)	AAAGAGGGGCCAGTGACGCGAGGAGCA (1001)
VHVDLNLGF (496)	GTACACGTGGATTTGAATCTTGGCTTC (1002)
HTVQGLAGF (497)	CACACTGTACAGGGACTAGCTGGATTT (1003)
MRIEDSHKL (498)	ATGCGTATAGAGGACGCCACACTAAGCTT (1004)
SALSSAQPR (499)	AGTGCCCTGTCTTCAGCCCAGCCCAGG (1005)
SPSIKSLVY (500)	TCCCCTTCCATCAAAAAGTCTACTAGTTTAT (1006)
PTDATLNRLY (501)	CCAAGTATGCCACTTTAAACCGTTTGCTCTAC (1007)
WTSQPPNYEK (502)	TGGACTTCCCAGCCCCCAAATATGAGAAA (1008)
PAPRPVAPTL (503)	CCCGCCCCCGCCCCGTGGCACCCACCCTG (1009)
VYLHSNSTL (504)	GTATATCTCCATTCTAACAGCACATTA (1010)
SLYAWTQSH (505)	TCTTTGTATGCCTGGACTCAGAGCCAC (1011)

Of course, because of the degeneracy of the genetic code, the TAPs described herein may be encoded by variants of the above-noted sequences.

A nucleic acid of the disclosure may be used for recombinant expression of the TAP or SLP
5 of the disclosure, and may be included in a vector or plasmid, such as a cloning vector or an expression vector, which may be transfected into a host cell. In an embodiment, the disclosure provides a cloning, expression or viral vector or plasmid comprising a nucleic acid sequence encoding the TAP of the disclosure. Alternatively, a nucleic acid encoding a TAP of the disclosure may be incorporated into the genome of the host cell. In either case, the host cell expresses the
10 TAP or protein encoded by the nucleic acid. The term "host cell" as used herein refers not only to the particular subject cell, but to the progeny or potential progeny of such a cell. A host cell can be any prokaryotic (e.g., *E. coli*) or eukaryotic cell (e.g., insect cells, yeast cells, plant cells, or mammalian cells) capable of expressing the TAPs described herein. The vector or plasmid contains the necessary elements for the transcription and translation of the inserted coding
15 sequence, and may contain other components such as resistance genes, cloning sites, etc. Methods that are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding peptides or polypeptides and appropriate transcriptional and translational control/regulatory elements operably linked thereto. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such
20 techniques are described in Sambrook, *et al.* (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. *et al.* (1989) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, N.Y. "Operably linked" refers to a juxtaposition of components, particularly nucleotide sequences, such that the normal function of the components can be performed. Thus, a coding sequence that is operably linked to regulatory
25 sequences refers to a configuration of nucleotide sequences wherein the coding sequences can be expressed under the regulatory control, that is, transcriptional and/or translational control, of the regulatory sequences. "Regulatory/control region" or "regulatory/control sequence", as used herein, refers to the non-coding nucleotide sequences that are involved in the regulation of the expression of a coding nucleic acid. Thus, the term regulatory region includes promoter
30 sequences, regulatory protein binding sites, upstream activator sequences, and the like. The vector (e.g., expression vector) may have the necessary 5' upstream and 3' downstream regulatory elements such as promoter sequences such as CMV, PGK and EF-1 α promoters, ribosome recognition and binding TATA box, and 3' UTR AAUAAA transcription termination sequence for the efficient gene transcription and translation in its respective host cell. Other
35 suitable promoters include the constitutive promoter of simian vims 40 (SV40) early promoter, mouse mammary tumor virus (MMTV), HIV LTR promoter, MoMuLV promoter, avian leukemia virus promoter, EBV immediate early promoter, and Rous sarcoma vims promoter. Human gene

promoters may also be used, including, but not limited to the actin promoter, the myosin promoter, the hemoglobin promoter, and the creatine kinase promoter. In certain embodiments inducible promoters are also contemplated as part of the vectors expressing the TAP. This provides a molecular switch capable of turning on expression of the polynucleotide sequence of interest or turning off expression. Examples of inducible promoters include, but are not limited to a metallothionine promoter, a glucocorticoid promoter, a progesterone promoter, or a tetracycline promoter. Examples of vectors are plasmid, autonomously replicating sequences, and transposable elements. Additional exemplary vectors include, without limitation, plasmids, phagemids, cosmids, artificial chromosomes such as yeast artificial chromosome (YAC), bacterial artificial chromosome (BAC), or PI-derived artificial chromosome (PAC), bacteriophages such as lambda phage or M13 phage, and animal viruses. Examples of categories of animal viruses useful as vectors include, without limitation, retrovirus (including lentivirus), adenovirus, adeno-associated virus, herpesvirus (e.g., herpes simplex virus), poxvirus, baculovirus, papillomavirus, and papovavirus (e.g., SV40). Examples of expression vectors are Lenti-X™ Bicistronic Expression System (Neo) vectors (Contech), pCneo vectors (Promega) for expression in mammalian cells; pLenti4/V5-DEST™, pLenti6/V5-DEST™, and pLenti6.2N5-GW/lacZ (Invitrogen) for lentivirus-mediated gene transfer and expression in mammalian cells. The coding sequences of the TAPs disclosed herein can be ligated into such expression vectors for the expression of the TAP in mammalian cells.

In certain embodiments, the nucleic acids encoding the TAP of the present disclosure are provided in a viral vector. A viral vector can be those derived from adenovirus, vaccinia virus, retrovirus, lentivirus, or foamy virus. As used herein, the term "viral vector" refers to a nucleic acid vector construct that includes at least one element of viral origin and has the capacity to be packaged into a viral vector particle. The viral vector can contain the coding sequence for the various proteins described herein in place of nonessential viral genes. In another embodiment, the nucleic acids encoding the TAP of the present disclosure are provided in a self-amplifying or self-replicating RNA (srRNA) vectors. srRNAs are derived from positive-strand RNA viruses where the structural proteins have been removed and replaced with heterologous genes of interest. srRNAs have been successfully derived from flaviviruses, nodamura viruses, nidoviruses, and alphaviruses with therapeutic versions of the technology providing the structural proteins in *trans* to create single cycle viral replicon particles (VRPs) (see, e.g., Aliahmad et al. Next generation self-replicating RNA vectors for vaccines and immunotherapies. Cancer Gene Ther (2022). <https://doi.org/10.1038/s41417-022-00435-8>). The vector and/or particle can be utilized for the purpose of transferring DNA, RNA or other nucleic acids into cells either *in vitro* or *in vivo*. Numerous forms of viral vectors are known in the art.

In embodiment, the nucleic acid (DNA, RNA) encoding the TAP of the disclosure is comprised within a vesicle or nanoparticle such as a lipid vesicle (e.g., liposome) or lipid

nanoparticle (LNP), or any other suitable vehicle. Thus, in another aspect, the present disclosure provides a vesicle or nanoparticle, such as a lipid vesicle or nanoparticle, comprising a nucleic acid, such as an mRNA, encoding one or more of the TAP described herein.

The term liposome as used herein in accordance with its usual meaning, referring to
5 microscopic lipid vesicles composed of a bilayer of phospholipids or any similar amphipathic lipids (e.g., sphingolipids) encapsulating an internal aqueous medium.

The term "lipid nanoparticle" refers to liposome-like structure that may include one or more lipid bilayer rings surrounding an internal aqueous medium similar to liposomes, or micellar-like structures that encapsulates molecules (e.g., nucleic acids) in a non-aqueous core. Lipid
10 nanoparticles typically contain cationic lipids, such as ionizable cationic lipids. Examples of cationic lipids that may be used for LNPs include DOTMA, DOSPA, DOTAP, ePC, DLin-MC3-DMA, C12-200, ALC-0315, cKK-E12, Lipid H (SM-102), OF-Deg-Lin, A2-Iso5-2DC18, 306O₁₀, BAME-O16B, TT3, 9A1P9, FTT5, COATSOME[®] SS-E, COATSOME[®] SS-EC, COATSOME[®] SS-OC and COATSOME[®] SS-OP (see, e.g., Hou *et al.*, *Nature Reviews Materials*, volume 6, pages
15 1078-1094 (2021); Tenchov *et al.*, *ACS Nano*, 15, 16982-17015 (2021)).

Liposomes and lipid nanoparticles typically include other lipid components such as lipids, lipid-like materials, and polymers that can improve liposome or nanoparticle properties, such as stability, delivery efficacy, tolerability and biodistribution. These include phospholipids (e.g., phosphatidylcholines, phosphatidylethanolamines, phosphatidylserines, and
20 phosphatidylglycerol) such as 1,2-distearoyl-*sn*-glycero-3-phosphocholine (DSPC) and DOPE, sterols (such as cholesterol and cholesterol derivatives), PEGylated lipids (PEG-lipids) such as 1,2-dimyristoyl-*rac*-glycero-3-methoxypolyethylene glycol-2000 (PEG₂₀₀₀-DMG) and 1,2-distearoyl-*rac*-glycero-3-methoxypolyethylene glycol-2000 (PEG₂₀₀₀-DSG).

In an embodiment, the lipid nanoparticle according to the present disclosure comprises one
25 or more cationic lipids, such as ionizable cationic lipids. Examples of ionizable cationic lipids include those listed in PCT publications Nos. WO 2017/061150 and WO 2019/188867, which encompassed ionizable cationic lipids commercialized under the tradenames COATSOME[®] SS-E, COATSOME[®] SS-EC, COATSOME[®] SS-OC and COATSOME[®] SS-OP.

The nucleic acid (e.g., mRNA) encoding one or more of the TAP, may be modified, for
30 example to increase stability and/or reduce immunogenicity. For example, the 5' end may be capped to stabilize the molecule and decrease immunogenicity (for example, as described in US10519189 and US10494399). One or more nucleosides of the mRNA may be modified or substituted with 1-methyl pseudo-uridine to either increase stability of the molecule or reduce recognition of the molecule by the innate immune system. A form of modified nucleosides are
35 described in US9371511. Other types of modifications that may be made to the mRNA include incorporation of anti-reverse cap analog (ARCA), 5'-methyl-cytidine triphosphate (m5CTP), N6-methyl-adenosine-5'-triphosphate (m6ATP), 2-thio-uridine triphosphate (s2UTP), pseudouridine

triphosphate, N¹Methylpseudouridine triphosphate or 5-Methoxyuridine triphosphate (5moUTP). The mRNA may also include additional modifications to the 5'- and/or 3'-untranslated regions (UTRs) and polyadenylation (polyA) tail (see, for example, Kim et al., *Molecular & cellular toxicology* vol. 18,1 (2022): 1-8). All these modifications and other modifications to the nucleic acid (e.g., mRNA) encoding the TAP are encompassed by the present disclosure.

In another aspect, the present disclosure provides an MHC class I molecule comprising (i.e., presenting or bound to) one or more of the TAPs comprising or consisting of the sequence of SEQ ID NOs: 1-505 defined herein.

In an embodiment, the MHC class I molecule is an HLA-A*01:01 molecule. In an embodiment, the MHC class I molecule is an HLA-A*02:01 molecule. In an embodiment, the MHC class I molecule is an HLA-A*02:09 molecule. In an embodiment, the MHC class I molecule is an HLA-A*03:01 molecule. In an embodiment, the MHC class I molecule is an HLA-A*03:01. In an embodiment, the MHC class I molecule is an HLA-A*23:01 molecule. In an embodiment, the MHC class I molecule is an HLA-A*24:02 molecule. In an embodiment, the MHC class I molecule is an HLA-A*25:01 molecule. In an embodiment, the MHC class I molecule is an HLA-A*26:01 molecule. In an embodiment, the MHC class I molecule is an HLA-A*30:01 molecule. In an embodiment, the MHC class I molecule is an HLA-A*30:02 molecule. In an embodiment, the MHC class I molecule is an HLA-A*33:01 molecule. In an embodiment, the MHC class I molecule is an HLA-A*68:01 molecule. In an embodiment, the MHC class I molecule is an HLA-B*07:02 molecule. In an embodiment, the MHC class I molecule is an HLA-B*08:01 molecule. In an embodiment, the MHC class I molecule is an HLA-B*13:02 molecule. In an embodiment, the MHC class I molecule is an HLA-B*14:01 molecule. In an embodiment, the MHC class I molecule is an HLA-B*15:01 molecule. In an embodiment, the MHC class I molecule is an HLA-B*18:01 molecule. In an embodiment, the MHC class I molecule is an HLA-B*35:03 molecule. In an embodiment, the MHC class I molecule is an HLA-B*37:01 molecule. In an embodiment, the MHC class I molecule is an HLA-B*38:01 molecule. In an embodiment, the MHC class I molecule is an HLA-B*40:01. In an embodiment, the MHC class I molecule is an HLA-B*40:02. In an embodiment, the MHC class I molecule is an HLA-B*44:02. In an embodiment, the MHC class I molecule is an HLA-B*49:01. In an embodiment, the MHC class I molecule is an HLA-B*51:01. In an embodiment, the MHC class I molecule is an HLA-C*03:03. In an embodiment, the MHC class I molecule is an HLA-C*03:04. In an embodiment, the MHC class I molecule is an HLA-C*04:01. In an embodiment, the MHC class I molecule is an HLA-C*06:02. In an embodiment, the MHC class I molecule is an HLA-C*07:01 molecule. In an embodiment, the MHC class I molecule is an HLA-C*07:02 molecule. In an embodiment, the MHC class I molecule is an HLA-C*08:02 molecule. In an embodiment, the MHC class I molecule is an HLA-C*12:03 molecule. In an embodiment, the MHC class I molecule is an HLA-C*14:02 molecule.

In an embodiment, the TAP (e.g., comprising or consisting of the sequence of SEQ ID NOs: 1-505 defined herein) is non-covalently bound to the MHC class I molecule (i.e., the TAP is loaded into, or non-covalently bound to the peptide binding groove/pocket of the MHC class I molecule). In another embodiment, the TAP is covalently attached/bound to the MHC class I molecule (alpha chain). In such a construct, the TAP and the MHC class I molecule (alpha chain) are produced as a synthetic fusion protein, typically with a short (e.g., 5 to 20 residues, preferably about 8-12, e.g., 10) flexible linker or spacer (e.g., a polyglycine linker). In another aspect, the disclosure provides a nucleic acid encoding a fusion protein comprising a TAP defined herein fused to an MHC class I molecule (alpha chain). In an embodiment, the MHC class I molecule (alpha chain) – peptide complex is multimerized. Accordingly, in another aspect, the present disclosure provides a multimer of MHC class I molecule loaded (covalently or not) with the herein-mentioned TAP. Such multimers may be attached to a tag, for example a fluorescent tag, which allows the detection of the multimers. A great number of strategies have been developed for the production of MHC multimers, including MHC dimers, tetramers, pentamers, octamers, etc. (reviewed in Bakker and Schumacher, *Current Opinion in Immunology* 2005, 17:428-433). MHC multimers are useful, for example, for the detection and purification of antigen-specific T cells. Thus, in another aspect, the present disclosure provides a method for detecting or purifying (isolating, enriching) CD8⁺ T lymphocytes specific for a TAP defined herein, the method comprising contacting a cell population with a multimer of MHC class I molecule loaded (covalently or not) with the TAP; and detecting or isolating the CD8⁺ T lymphocytes bound by the MHC class I multimers. CD8⁺ T lymphocytes bound by the MHC class I multimers may be isolated using known methods, for example fluorescence activated cell sorting (FACS) or magnetic activated cell sorting (MACS).

In yet another aspect, the present disclosure provides a cell (e.g., a host cell), in an embodiment an isolated cell, comprising the herein-mentioned nucleic acid, vector or plasmid of the disclosure, i.e., a nucleic acid or vector encoding one or more TAPs. In another aspect, the present disclosure provides a cell expressing at its surface an MHC class I molecule (e.g., an MHC class I molecule of one of the alleles disclosed above) bound to or presenting a TAP according to the disclosure. In one embodiment, the host cell is a eukaryotic cell, such as a mammalian cell, preferably a human cell, a cell line or an immortalized cell. In another embodiment, the cell is an antigen-presenting cell (APC). In one embodiment, the host cell is a primary cell, a cell line or an immortalized cell. In another embodiment, the cell is an antigen-presenting cell (APC). Nucleic acids and vectors can be introduced into cells via conventional transformation or transfection techniques. The terms "transformation" and "transfection" refer to techniques for introducing foreign nucleic acid into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, electroporation, microinjection and viral-mediated transfection. Suitable methods for transforming or transfecting host cells can for example be found in Sambrook *et al.* (*supra*), and other

laboratory manuals. Methods for introducing nucleic acids into mammalian cells *in vivo* are also known, and may be used to deliver the vector or plasmid of the disclosure to a subject for gene therapy.

Cells such as APCs can be loaded with one or more TAPs using a variety of methods known in the art. As used herein "loading a cell" with a TAP means that RNA or DNA encoding the TAP, or the TAP, is transfected into the cells or alternatively that the APC is transformed with a nucleic acid encoding the TAP. The cell can also be loaded by contacting the cell with exogenous TAPs that can bind directly to MHC class I molecule present at the cell surface (e.g., peptide-pulsed cells). The TAPs may also be fused to a domain or motif that facilitates its presentation by MHC class I molecules, for example to an endoplasmic reticulum (ER) retrieval signal, a C-terminal Lys-Asp-Glu-Leu sequence (see Wang *et al.*, *Eur J Immunol.* 2004 Dec;34(12):3582-94).

In another aspect, the present disclosure provides a composition or peptide combination/pool comprising any one of, or any combination of, the TAPs defined herein (or a nucleic acid encoding said peptide(s)). In an embodiment, the composition comprises any combination of the TAPs defined herein (any combination of 2, 3, 4, 5, 6, 7, 8, 9, 10 or more TAPs), or a combination of nucleic acids encoding said TAPs). Compositions comprising any combination/sub-combination of the TAPs defined herein are encompassed by the present disclosure. In another embodiment, the combination or pool may comprise one or more known tumor antigens.

Thus, in another aspect, the present disclosure provides a composition comprising any one of, or any combination of, the TAPs defined herein (e.g., comprising or consisting of the sequence of SEQ ID NOs: 1-505 defined herein) and a cell expressing an MHC class I molecule (e.g., a MHC class I molecule of one of the alleles disclosed above). APC for use in the present disclosure are not limited to a particular type of cell and include professional APCs such as dendritic cells (DCs), Langerhans cells, macrophages and B cells, which are known to present proteinaceous antigens on their cell surface so as to be recognized by CD8⁺ T lymphocytes. For example, an APC can be obtained by inducing DCs from peripheral blood monocytes and then contacting (stimulating) the TAPs, either *in vitro*, *ex vivo* or *in vivo*. APC can also be activated to present a TAP *in vivo* where one or more of the TAPs of the disclosure are administered to a subject and APCs that present a TAP are induced in the body of the subject. The phrase "inducing an APC" or "stimulating an APC" includes contacting or loading a cell with one or more TAPs, or nucleic acids encoding the TAPs such that the TAPs are presented at its surface by MHC class I molecules. As noted herein, according to the present disclosure, the TAPs may be loaded indirectly for example using longer peptides/polypeptides comprising the sequence of the TAPs (including the native protein), which is then processed (e.g., by proteases) inside the APCs to generate the TAP/MHC class I complexes at the surface of the cells. After loading APCs with TAPs and allowing the APCs to present the TAPs, the APCs can be administered to a subject as

a vaccine. For example, the *ex vivo* administration can include the steps of: (a) collecting APCs from a first subject, (b) contacting/loading the APCs of step (a) with a TAP to form MHC class I/TAP complexes at the surface of the APCs; and (c) administering the peptide-loaded APCs to a second subject in need for treatment.

5 The first subject and the second subject may be the same subject (*e.g.*, autologous vaccine), or may be different subjects (*e.g.*, allogeneic vaccine). Alternatively, according to the present disclosure, use of a TAP described herein (or a combination thereof) for manufacturing a composition (*e.g.*, a pharmaceutical composition) for inducing antigen-presenting cells is provided. In addition, the present disclosure provides a method or process for manufacturing a
10 pharmaceutical composition for inducing antigen-presenting cells, wherein the method or the process includes the step of admixing or formulating the TAP, or a combination thereof, with a pharmaceutically acceptable carrier. Cells such as APCs expressing a MHC class I molecule (*e.g.*, any of the above-noted HLA molecules) loaded with any one of, or any combination of, the TAPs defined herein, may be used for stimulating/amplifying CD8⁺ T lymphocytes, for example
15 autologous CD8⁺ T lymphocytes. Accordingly, in another aspect, the present disclosure provides a composition comprising any one of, or any combination of, the TAPs defined herein (or a nucleic acid or vector encoding same); a cell expressing an MHC class I molecule and a T lymphocyte, more specifically a CD8⁺ T lymphocyte (*e.g.*, a population of cells comprising CD8⁺ T lymphocytes).

20 In an embodiment, the composition further comprises a buffer, an excipient, a carrier, a diluent and/or a medium (*e.g.*, a culture medium). In a further embodiment, the buffer, excipient, carrier, diluent and/or medium is/are pharmaceutically acceptable buffer(s), excipient(s), carrier(s), diluent(s) and/or medium (media). As used herein "pharmaceutically acceptable buffer, excipient, carrier, diluent and/or medium" includes any and all solvents, buffers, binders,
25 lubricants, fillers, thickening agents, disintegrants, plasticizers, coatings, barrier layer formulations, lubricants, stabilizing agent, release-delaying agents, dispersion media, coatings, antibacterial and antifungal agents, isotonic agents, and the like that are physiologically compatible, do not interfere with effectiveness of the biological activity of the active ingredient(s) and that are not toxic to the subject. The use of such media and agents for pharmaceutically
30 active substances is well known in the art (Rowe et al., Handbook of pharmaceutical excipients, 2003, 4th edition, Pharmaceutical Press, London UK). Except insofar as any conventional media or agent is incompatible with the active compound (peptides, cells), use thereof in the compositions of the disclosure is contemplated. In an embodiment, the buffer, excipient, carrier and/or medium is a non-naturally occurring buffer, excipient, carrier and/or medium. In an
35 embodiment, one or more of the TAPs defined herein, or the nucleic acids (*e.g.*, mRNAs) encoding said one or more TAPs, are comprised within or complexed to a lipid vesicle or liposome,

e.g., a cationic liposome (see, e.g., Vitor MT *et al.*, *Recent Pat Drug Deliv Formul.* 2013 Aug;7(2):99-110) or suitable other carriers.

In another aspect, the present disclosure provides a composition comprising one of more of the any one of, or any combination of, the TAPs defined herein (e.g., comprising or consisting of the sequence of SEQ ID NOs: 1-505 defined herein) (or a nucleic acid such as a mRNA encoding said peptide(s)), and a buffer, an excipient, a carrier, a diluent and/or a medium. For compositions comprising cells (e.g., APCs, T lymphocytes), the composition comprises a suitable medium that allows the maintenance of viable cells. Representative examples of such media include saline solution, Earl's Balanced Salt Solution (Life Technologies®) or PlasmaLyte® (Baxter International®). In an embodiment, the composition (e.g., pharmaceutical composition) is an "immunogenic composition", "vaccine composition" or "vaccine". The term "Immunogenic composition", "vaccine composition" or "vaccine" as used herein refers to a composition or formulation comprising one or more TAPs, nucleic acids or vaccine vector and which is capable of inducing an immune response against the one or more TAPs present therein when administered to a subject. Vaccination methods for inducing an immune response in a mammal (e.g., human) comprise use of a vaccine or vaccine vector to be administered by any conventional route known in the vaccine field, e.g., via a mucosal (e.g., ocular, intranasal, pulmonary, oral, gastric, intestinal, rectal, vaginal, or urinary tract) surface, via a parenteral (e.g., subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route, or topical administration (e.g., via a transdermal delivery system such as a patch). In an embodiment, the TAP (or a combination thereof) is conjugated to a carrier protein (conjugate vaccine) to increase the immunogenicity of the TAP(s). The present disclosure thus provides a composition (conjugate) comprising a TAP (or a combination thereof), or a nucleic acid encoding the TAP or combination thereof, and a carrier protein. For example, the TAP(s) or nucleic acid(s) may be conjugated or complexed to a Toll-like receptor (TLR) ligand (see, e.g., Zom *et al.*, *Adv Immunol.* 2012, 114: 177-201) or polymers/dendrimers (see, e.g., Liu *et al.*, *Biomacromolecules.* 2013 Aug 12;14(8):2798-806) such as polymer-linked TLR agonists (see, e.g., Lynn *et al.*, *Nature Biotechnology* 33: 1201-1210 (2015); Lynn *et al.*, *Nature Biotechnology* 38: 320-332 (2020)). In an embodiment, the immunogenic composition or vaccine further comprises an adjuvant. "Adjuvant" refers to a substance which, when added to an immunogenic agent such as an antigen (TAPs, nucleic acids and/or cells according to the present disclosure), nonspecifically enhances or potentiates an immune response to the agent in the host upon exposure to the mixture. Examples of adjuvants currently used in the field of vaccines include (1) mineral salts (aluminum salts such as aluminum phosphate and aluminum hydroxide, calcium phosphate gels), squalene, (2) oil-based adjuvants such as oil emulsions and surfactant based formulations, e.g., MF59 (microfluidised detergent stabilised oil-in-water emulsion), QS21 (purified saponin), AS02 [SBAS2] (oil-in-water emulsion + MPL + QS-21), (3) particulate adjuvants, e.g., virosomes (unilamellar liposomal vehicles

incorporating influenza haemagglutinin), AS04 ([SBAS4] aluminum salt with MPL), ISCOMS (structured complex of saponins and lipids), polylactide co-glycolide (PLG), (4) microbial derivatives (natural and synthetic), e.g., monophosphoryl lipid A (MPL), Detox (MPL + *M. Phlei* cell wall skeleton), AGP [RC-529] (synthetic acylated monosaccharide), DC_Chol (lipoidal immunostimulators able to self-organize into liposomes), OM-174 (lipid A derivative), CpG motifs (synthetic oligonucleotides containing immunostimulatory CpG motifs), modified Cholera toxin (CT) and *Escherichia coli* enterotoxin (LT) (genetically modified bacterial toxins to provide non-toxic adjuvant effects), (5) endogenous human immunomodulators, e.g., hGM-CSF or hIL-12 (cytokines that can be administered either as protein or plasmid encoded), Immudaptin (C3d tandem array) and/or (6) inert vehicles, such as gold particles, and the like.

In an embodiment, the TAP(s) (e.g., comprising or consisting of the sequence of SEQ ID NOs: 1-505 defined herein) (or a nucleic acid such as a mRNA encoding said peptide(s)) or composition comprising same is/are in lyophilized form. In another embodiment, the TAP(s), nucleic acid(s) or composition comprising same is/are in a liquid composition. In a further embodiment, the TAP(s) or nucleic acid(s) is/are at a concentration of about 0.01 µg/mL to about 100 µg/mL in the composition. In further embodiments, the TAP(s) or nucleic acid(s) is/are at a concentration of about 0.2 µg/mL to about 50 µg/mL, about 0.5 µg/mL to about 10, 20, 30, 40 or 50 µg/mL, about 1 µg/mL to about 10 µg/mL, or about 2 µg/mL, in the composition.

As noted herein, cells such as APCs that express an MHC class I molecule loaded with or bound to any one of, or any combination of, the TAPs defined herein, may be used for stimulating/amplifying CD8⁺ T lymphocytes *in vivo* or *ex vivo*. Accordingly, in another aspect, the present disclosure provides T cell receptor (TCR) molecules capable of interacting with or binding the herein-mentioned MHC class I molecule/TAP complex, and nucleic acid molecules encoding such TCR molecules, and vectors comprising such nucleic acid molecules. A TCR according to the present disclosure is capable of specifically interacting with or binding a TAP loaded on, or presented by, an MHC class I molecule, preferably at the surface of a living cell *in vitro* or *in vivo*.

The term TCR as used herein refers to an immunoglobulin superfamily member having a variable binding domain, a constant domain, a transmembrane region, and a short cytoplasmic tail; see, e.g., Janeway et al, Immunobiology: The Immune System in Health and Disease, 3rd Ed., Current Biology Publications, p. 4:33, 1997) capable of specifically binding to an antigen peptide bound to a MHC receptor. A TCR can be found on the surface of a cell and generally is comprised of a heterodimer having α and β chains (also known as TCRα and TCRβ, respectively). Like immunoglobulins, the extracellular portion of TCR chains (e.g., α-chain, β-chain) contain two immunoglobulin regions, a variable region (e.g., TCR variable α region or Vα and TCR variable β region or Vβ; typically amino acids 1 to 116 based on Rabat numbering at the N-terminus), and one constant region (e.g., TCR constant domain α or Cα and typically amino acids 117 to 259 based on Rabat, TCR constant domain β or Cβ, typically amino acids 117 to 295 based on Rabat)

adjacent to the cell membrane. Also, like immunoglobulins, the variable domains contain complementary determining regions (CDRs, 3 in each chain) separated by framework regions (FRs). In certain embodiments, a TCR is found on the surface of T cells (or T lymphocytes) and associates with the CD3 complex.

5 A TCR and in particular nucleic acids encoding a TCR of the disclosure may for instance be applied to genetically transform/modify T lymphocytes (e.g., CD8⁺ T lymphocytes) or other types of lymphocytes generating new T lymphocyte clones that specifically recognize an MHC class I/TAP complex. In a particular embodiment, T lymphocytes (e.g., CD8⁺ T lymphocytes) obtained from a patient are transformed to express one or more TCRs that recognize a TAP and
10 the transformed cells are administered to the patient (autologous cell transfusion). In a particular embodiment, T lymphocytes (e.g., CD8⁺ T lymphocytes) obtained from a donor are transformed to express one or more TCRs that recognize a TAP and the transformed cells are administered to a recipient (allogenic cell transfusion). In another embodiment, the disclosure provides a T lymphocyte e.g., a CD8⁺ T lymphocyte transformed/transfected by a vector or plasmid encoding
15 a TAP-specific TCR. In a further embodiment the disclosure provides a method of treating a patient with autologous or allogenic cells transformed with a TAP-specific TCR. In certain embodiments, TCRs are expressed in primary T cells (e.g., cytotoxic T cells) by replacing an endogenous locus, e.g., an endogenous TRAC and/or TRBC locus, using, e.g., CRISPR, TALEN, zinc finger nuclease, or other targeted disruption systems.

20 In another embodiment, the present disclosure provides a nucleic acid encoding the above-noted TCR. In a further embodiment, the nucleic acid is present in a vector, such as the vectors described above.

In yet a further embodiment the use of a tumor antigen-specific TCR in the manufacture of autologous or allogenic cells for the treatment of cancer, such as melanoma, is provided.

25 In some embodiments, patients treated with the compositions (e.g., pharmaceutical compositions) of the disclosure are treated prior to or following treatment with an anti-tumor agent and/or immunotherapy (e.g., CAR therapy, immune checkpoint inhibitor therapy). Compositions of the disclosure include: allogenic T lymphocytes (e.g., CD8⁺ T lymphocyte) activated *ex vivo* against a TAP; allogenic or autologous APC vaccines loaded with a TAP; vaccines including TAPs
30 of nucleic acids (e.g. mRNA) encoding TAPs and allogenic or autologous T lymphocytes (e.g., CD8⁺ T lymphocyte) or lymphocytes transformed with a tumor antigen-specific TCR. The method to provide T lymphocyte clones capable of recognizing a TAP according to the disclosure may be generated for and can be specifically targeted to tumor cells expressing the TAP in a subject (e.g., graft recipient), for example an allogenic T lymphocyte and/or donor lymphocyte infusion (DLI)
35 recipient. Hence the disclosure provides a CD8⁺ T lymphocyte encoding and expressing a T cell receptor capable of specifically recognizing or binding a TAP/MHC class I molecule complex. Said T lymphocyte (e.g., CD8⁺ T lymphocyte) may be a recombinant (engineered) or a naturally

selected T lymphocyte. This specification thus provides at least two methods for producing CD8⁺ T lymphocytes of the disclosure, comprising the step of bringing undifferentiated lymphocytes into contact with a TAP/MHC class I molecule complex (typically expressed at the surface of cells, such as APCs) under conditions conducive of triggering T cell activation and expansion, which
5 may be done *in vitro* or *in vivo* (i.e., in a patient administered with a APC vaccine wherein the APC is loaded with a TAP or in a patient treated with a TAP vaccine). Using a combination or pool of TAPs bound to MHC class I molecules, it is possible to generate a population CD8⁺ T lymphocytes capable of recognizing a plurality of TAPs. Alternatively, tumor antigen-specific or targeted T lymphocytes may be produced/generated *in vitro* or *ex vivo* by cloning one or more
10 nucleic acids (genes) encoding a TCR (more specifically the alpha and beta chains) that specifically binds to a MHC class I molecule/TAP complex (i.e. engineered or recombinant CD8⁺ T lymphocytes). Nucleic acids encoding a TAP-specific TCR of the disclosure, may be obtained using methods known in the art from a T lymphocyte activated against a TAP *ex vivo* (e.g., with an APC loaded with a TAP); or from an individual exhibiting an immune response against
15 peptide/MHC molecule complex. TAP-specific TCRs of the disclosure may be recombinantly expressed in a host cell and/or a host lymphocyte obtained from a graft recipient or graft donor, and optionally differentiated *in vitro* to provide cytotoxic T lymphocytes (CTLs). The nucleic acid(s) (transgene(s)) encoding the TCR alpha and beta chains may be introduced into a T cells (e.g., from a subject to be treated or another individual) using any suitable methods such as transfection
20 (e.g., electroporation) or transduction (e.g., using viral vector). The engineered CD8⁺ T lymphocytes expressing a TCR specific for a TAP may be expanded *in vitro* using well known culturing methods.

The present disclosure provides methods for making the immune effector cells which express the TCRs as described herein. In one embodiment, the method comprises transfecting
25 or transducing immune effector cells, e.g., immune effector cells isolated from a subject, such as a subject having melanoma, such that the immune effector cells express one or more TCR as described herein. In certain embodiments, the immune effector cells are isolated from an individual and genetically modified without further manipulation *in vitro*. Such cells can then be directly re-administered into the individual. In further embodiments, the immune effector cells are
30 first activated and stimulated to proliferate *in vitro* prior to being genetically modified to express a TCR. In this regard, the immune effector cells may be cultured before or after being genetically modified (i.e., transduced or transfected to express a TCR as described herein).

Prior to *in vitro* manipulation or genetic modification of the immune effector cells described herein, the source of cells may be obtained from a subject. In particular, the immune effector cells
35 for use with the TCRs as described herein comprise T cells. T cells can be obtained from a number of sources, including peripheral blood mononuclear cells (PBMCs), bone marrow, lymph nodes tissue, cord blood, thymus tissue, tissue from a site of infection, ascites, pleural effusion, spleen

tissue, and tumors. In certain embodiments, T cell can be obtained from a unit of blood collected from the subject using any number of techniques known to the skilled person, such as FICOLL™ separation. In one embodiment, cells from the circulating blood of an individual are obtained by apheresis. The apheresis product typically contains lymphocytes, including T cells, monocytes, granulocyte, B cells, other nucleated white blood cells, red blood cells, and platelets. In one embodiment, the cells collected by apheresis may be washed to remove the plasma fraction and to place the cells in an appropriate buffer or media for subsequent processing. In one embodiment of the invention, the cells are washed with PBS. In an alternative embodiment, the washed solution lacks calcium and may lack magnesium or may lack many if not all divalent cations. As would be appreciated by those of ordinary skill in the art, a washing step may be accomplished by methods known to those in the art, such as by using a semi-automated flow-through centrifuge. After washing, the cells may be resuspended in a variety of biocompatible buffers or other saline solution with or without buffer. In certain embodiments, the undesirable components of the apheresis sample may be removed in the cell directly resuspended culture media. In certain embodiments, T cells are isolated from peripheral blood mononuclear cells (PBMCs) by lysing the red blood cells and depleting the monocytes, for example, by centrifugation through a PERCOLL™ gradient. A specific subpopulation of T cells, such as CD28⁺, CD4⁺, CD8⁺, CD45RA⁺, and CD45RO⁺ T cells, can be further isolated by positive or negative selection techniques. For example, enrichment of a T cell population by negative selection can be accomplished with a combination of antibodies directed to surface markers unique to the negatively selected cells. One method for use herein is cell sorting and/or selection via negative magnetic immunoadherence or flow cytometry that uses a cocktail of monoclonal antibodies directed to cell surface markers present on the cells negatively selected. For example, to enrich for CD8⁺ cells by negative selection, a monoclonal antibody cocktail typically includes antibodies to CD14, CD20, CD11b, CD16, HLA-DR, and CD4. Flow cytometry and cell sorting may also be used to isolate cell populations of interest for use in the present disclosure. PBMC may be used directly for genetic modification with the TCRs using methods as described herein. In certain embodiments, after isolation of PBMC, T lymphocytes are further isolated and in certain embodiments, both cytotoxic and helper T lymphocytes can be sorted into naive, memory, and effector T cell subpopulations either before or after genetic modification and/or expansion.

The present disclosure provides isolated immune cells such as T lymphocytes (e.g., CD8⁺ T lymphocytes) that are specifically induced, activated and/or amplified (expanded) by a TAP (i.e., a TAP bound to MHC class I molecules expressed at the surface of cell), or a combination of TAPs. The present disclosure also provides a composition comprising CD8⁺ T lymphocytes capable of recognizing a TAP, or a combination thereof, according to the disclosure (i.e., one or more TAPs bound to MHC class I molecules) and said TAP(s).

In another aspect, the present disclosure provides a cell population or cell culture (e.g., a CD8⁺ T lymphocyte population) enriched in T lymphocytes (e.g., CD8⁺ T lymphocytes) that specifically recognize one or more MHC class I molecule/TAP complex(es) as described herein. Such enriched population may be obtained by performing an *ex vivo* expansion of specific T lymphocytes (e.g., TILs) using cells such as APCs that express MHC class I molecules loaded with (e.g., presenting) one or more of the TAPs disclosed herein. "Enriched" as used herein means that the proportion of tumor antigen-specific T lymphocytes (e.g., CD8⁺ T lymphocytes) in the population is significantly higher relative to a native population of cells, i.e., which has not been subjected to a step of *ex vivo*-expansion of specific T lymphocytes. In an embodiment, the cell population is a TIL population or is derived from TILs, e.g., TILs isolated from a patient and expanded *ex vivo*. In a further embodiment, the proportion of TAP-specific T lymphocytes (e.g., CD8⁺ T lymphocytes) in the cell population is at least about 0.5%, for example at least about 1%, 1.5%, 2% or 3%. In some embodiments, the proportion of TAP-specific T lymphocytes (e.g., CD8⁺ T lymphocytes) in the cell population is about 0.5 to about 10%, about 0.5 to about 8%, about 0.5 to about 5%, about 0.5 to about 4%, about 0.5 to about 3%, about 1% to about 5%, about 1% to about 4%, about 1% to about 3%, about 2% to about 5%, about 2% to about 4%, about 2% to about 3%, about 3% to about 5% or about 3% to about 4%. Such cell population or culture (e.g., a CD8⁺ T lymphocyte population) enriched in T lymphocytes (e.g., CD8⁺ T lymphocytes) that specifically recognizes one or more MHC class I molecule/peptide (TAP) complex(es) of interest may be used in tumor antigen-based cancer immunotherapy, as detailed below. In some embodiments, the population of TAP-specific T lymphocytes (e.g., CD8⁺ T lymphocytes) is further enriched, for example using affinity-based systems such as multimers of MHC class I molecule loaded (covalently or not) with the TAP(s) defined herein. Thus, the present disclosure provides a purified or isolated population of TAP-specific T lymphocytes (e.g., CD8⁺ T lymphocytes), e.g., in which the proportion of TAP-specific T lymphocytes (e.g., CD8⁺ T lymphocytes) is at least about 50%, 60%, 70%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%.

In another aspect, the present disclosure provides an antibody or an antigen-binding fragment thereof (e.g., a TCR mimic or TCR-like antibody), or a soluble TCR, that specifically binds to a complex comprising a TAP as described herein bound to an HLA molecule, such as the HLA molecules defined herein. The term "antibody or antigen-binding fragment thereof" as used herein refers to any type of antibody/antibody fragment including monoclonal antibodies (including full-length monoclonal antibodies), polyclonal antibodies, multispecific antibodies, humanized antibodies, CDR-grafted antibodies, chimeric antibodies and antibody fragments so long as they exhibit the desired antigenic specificity/binding activity. Antibody fragments comprise a portion of a full-length antibody, generally an antigen binding or variable region thereof. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments, diabodies, linear antibodies, single-chain antibody molecules (e.g., single-chain Fv, scFv), single domain

antibodies (e.g., from camelids), shark NAR single domain antibodies, and multispecific antibodies formed from antibody fragments, single-chain diabodies (scDBs), bispecific T cell engagers (BiTEs), dual affinity retargeting molecules (DARTs), bivalent scFv-Fcs, and trivalent scFv-Fcs. Antibody fragments can also refer to binding moieties comprising CDRs or antigen binding domains including, but not limited to, V_H regions (V_H, V_H-V_H), anticalins, PepBodies, antibody-T-cell epitope fusions (Troybodies) or Peptibodies. In an embodiment, the antibody or antigen-binding fragment thereof is a single-chain antibody, preferably a single-chain Fv (scFv). In an embodiment, the antibody or antigen-binding fragment thereof comprises at least one constant domain, e.g., a constant domain of a light and/or heavy chain, or a fragment thereof. In a further embodiment, the antibody or antigen-binding fragment thereof comprises a Fragment crystallizable (Fc) fragment of the constant heavy chain of an antibody. In an embodiment, the antibody or antigen-binding fragment is a scFv comprising a Fc fragment (scFv-Fc). In an embodiment, the scFv component is connected to the Fc fragment by a linker, for example a hinge. The presence of an Fc region is useful to induce a complement-dependent cytotoxicity (CDC), antibody-dependent cellular phagocytosis (ADCP), or antibody-dependent cellular cytotoxicity (ADCC) response against a tumor cell.

In an embodiment, the antibody or antigen-binding fragment thereof is a multispecific antibody or an antigen-binding fragment thereof, such as a bispecific antibody or an antigen-binding fragment thereof, wherein at least one of the antigen-binding domains of the multispecific antibody or antibody fragment recognize(s) a complex comprising a TAP as described herein bound to an HLA molecule. In an embodiment, at least one of the antigen-binding domains of the multispecific antibody or antibody fragment recognize(s) an immune cell effector molecule. The term "immune cell effector molecule" refers to a molecule (e.g., protein) expressed by an immune cell and whose engagement by the multispecific antibody or antibody fragment leads to activation of the immune cells. Examples of immune cell effector molecules include the CD3 signaling complex in T cells such as CD8 T cells and the various activating receptors on NK cells (NKG2D, KIR2DS, Nkp44, etc.). In a further embodiment, at least one of the antigen-binding domains of the multispecific antibody or antibody fragment recognize(s) and engage(s) the CD3 signaling complex in T cells (e.g., anti-CD3). In a further embodiment, the multispecific antibody or antibody fragment is a single-chain diabody (scDb). In a further embodiment, the scDb comprises a first antibody fragment (e.g., scFv) that binds to a complex comprising a TAP as described herein bound to an HLA molecule and a second antibody fragment (e.g., scFv) that binds to and engages an immune cell effector molecule, such as the CD3 signaling complex in T cells (e.g., anti-CD3 scFv). Such constructs may be used for example to induce the cytotoxic T cell-mediated killing of tumor cells expressing the tumor antigen/MHC complex recognized by the multispecific antibody or antibody fragment. Antibodies or antigen-binding fragments thereof may also be used as a chimeric antigen receptor (CAR) to produce CAR T cells, CAR NK cells, etc. CAR combines a

ligand-binding domain (e.g., antibody or antibody fragment) that provides specificity for a desired antigen (e.g., MHC/TAP complex) with an activating intracellular domain (or signal transducing domain) portion, such as a T cell or NK cell activating domain, providing a primary activation signal. Antigen-binding fragments of antibodies, and more particularly scFv, capable of binding to
5 molecules expressed by tumor cells are commonly used as ligand-binding domains in CAR.

In an embodiment, the soluble TCR is a soluble therapeutic bispecific TCR (see, e.g., Robinson *et al.*, *FEBS J.* 2021 Nov;288(21):6159-6173; Dilchert *et al.*, *Antibodies* (Basel). 2022 May 10;11(2):34).

In an embodiment, the TCR or soluble TCR comprises a TCR beta (β) chain comprising a
10 complementary determining region 3 (CDR3) comprising one of the amino acid sequences set forth in Table 3 (right column).

In an embodiment, the soluble TCR, antibody or antibody fragment (e.g., TCR-mimic) is attached to an antitumor agent to form an antibody-drug conjugate (ADC). Such ADC permits to target the antitumor agent to tumor cells expressing one or more of the TAPs described herein
15 (see, e.g., Shen *et al.*, *Asian J Pharm Sci.* 2020 Nov;15(6):777-785).

The present disclosure also provides a nucleic acid such as an mRNA encoding the soluble TCR, antibody, antibody fragment or CAR described herein. Such nucleic acids may be formulated into suitable vehicles such as lipid nanoparticles are described above, and may be used in the treatment of cancers such as melanoma, as described below.

20 Thus, in another aspect, the present disclosure provides a host cell, preferably an immune cell such as a T cell or NK cell, expressing the antibody or antibody fragment (e.g., scFv) described herein, i.e., a CAR T cell or NK cell.

The present disclosure further relates to a pharmaceutical composition or vaccine comprising the above-noted immune cell (CD8⁺ T lymphocytes, CAR T cell, CAR NK cell) or
25 population of TAP-specific CD8⁺ T lymphocytes. Such pharmaceutical composition or vaccine may comprise one or more pharmaceutically acceptable excipients and/or adjuvants, as described above.

In another aspect, the present disclosure further relates to the use of any of the TAP comprising or consisting of any of the sequences of SEQ ID NOs:1-505 defined herein, nucleic
30 acid, expression vector, T cell receptor, antibody/antibody fragment, cell (e.g., T lymphocyte, APC, CAR T cell, CAR NK cell), and/or composition according to the present disclosure, or any combination thereof, as a medicament or in the manufacture of a medicament for the treatment of cancer (e.g., melanoma). The present disclosure relates to any TAP, nucleic acid, expression vector, T cell receptor, antibody/antibody fragment, cell (e.g., T lymphocyte, APC), and/or
35 composition (e.g., vaccine composition) according to the present disclosure, or any combination thereof, for use in the treatment of cancer (e.g., melanoma), e.g., as a melanoma cancer vaccine. The TAP sequences identified herein may be used for the production of synthetic peptides to be

used i) for *in vitro* priming and expansion of tumor antigen-specific T cells to be injected into tumor patients and/or ii) as vaccines to induce or boost the anti-tumor T cell response in cancer (e.g., melanoma) patients.

In another aspect, the present disclosure provides the use of a TAP described herein (e.g.,
5 comprising or consisting of any of the sequences of SEQ ID NOs:1-505 defined herein), or a combination thereof (e.g., a peptide pool), or of one or more nucleic acid(s) encoding the TAP(s), as a vaccine for treating cancer (e.g., melanoma) in a subject. The present disclosure also provides the TAP described herein, or a combination thereof (e.g., a peptide pool), or of one or more nucleic acid(s) encoding the TAP(s), for use as a vaccine for treating cancer (e.g.,
10 melanoma) in a subject. In an embodiment, the subject is a recipient of TAP-specific T lymphocytes (e.g., CD8⁺ T lymphocytes). Accordingly, in another aspect, the present disclosure provides a method of treating cancer, and more particularly melanoma (e.g., of reducing the number of tumor cells, killing tumor cells), said method comprising administering (infusing) to a subject in need thereof an effective amount of T lymphocytes (e.g., CD8⁺ T lymphocytes)
15 recognizing (i.e., expressing a TCR that binds) one or more MHC class I molecule/TAP complexes (expressed at the surface of a cell such as an APC). In an embodiment, the method further comprises administering an effective amount of the TAP, or a combination thereof, or of one or more nucleic acid(s) encoding the TAP(s), and/or a cell (e.g., an APC such as a dendritic cell) expressing MHC class I molecule(s) loaded with the TAP(s), to said subject after
20 administration/infusion of said CD8⁺ T lymphocytes. In yet a further embodiment, the method comprises administering to a subject in need thereof a therapeutically effective amount of a dendritic cell loaded with one or more TAPs. In yet a further embodiment the method comprises administering to a patient in need thereof a therapeutically effective amount of an allogenic or autologous cell that expresses a recombinant TCR that binds to a TAP presented by an MHC
25 class I molecule.

In another aspect, the present disclosure provides the use of T lymphocytes (e.g., CD8⁺ T lymphocytes) that recognize one or more MHC class I molecules loaded with (presenting) a TAP, or a combination thereof, for treating cancer, and more particularly melanoma (e.g., of reducing the number of tumor cells, killing tumor cells) in a subject. In another aspect, the present
30 disclosure provides the use of T lymphocytes (e.g., CD8⁺ T lymphocytes) that recognize one or more MHC class I molecules loaded with (presenting) a TAP, or a combination thereof, for the preparation/manufacture of a medicament for treating cancer, and more particularly melanoma (e.g., for reducing the number of tumor cells, killing tumor cells) in a subject. In another aspect, the present disclosure provides T lymphocytes (e.g., CD8⁺ T lymphocytes) that recognize one or
35 more MHC class I molecule(s) loaded with (presenting) a TAP, or a combination thereof, for use in the treatment of cancer, and more particularly melanoma (e.g., for reducing the number of tumor cells, killing tumor cells), in a subject. In a further embodiment, the use further comprises

the use of an effective amount of a TAP (or a combination thereof), or of one or more nucleic acid(s) encoding the TAP(s), and/or of a cell (e.g., an APC) that expresses one or more MHC class I molecule(s) loaded with (presenting) a TAP, after the use of said TAP-specific T lymphocytes.

5 The present disclosure also provides a method of generating an immune response against tumor cells (e.g., melanoma cells) expressing human class I MHC molecules loaded with any of the TAP disclosed herein (e.g., comprising or consisting of any of the sequences of SEQ ID NO:1-505 defined herein) or combination thereof in a subject, the method comprising administering cytotoxic T lymphocytes that specifically recognizes the class I MHC molecules loaded with the
10 TAP or combination of TAPs. The present disclosure also provides the use of cytotoxic T lymphocytes that specifically recognizes class I MHC molecules loaded with any of the TAP or combination of TAPs disclosed herein for generating an immune response against tumor cells expressing the human class I MHC molecules loaded with the TAP or combination thereof.

 The TAP, combination thereof (e.g., a peptide pool), nucleic acid(s) encoding the TAP(s),
15 as well as antibodies, TCR, cells (e.g., CD8 T cells, APC), vaccines and compositions disclosed herein may be used of the prevention or treatment of any cancer that expresses the TAP, such as melanoma.

 TAP, combination thereof (e.g., a peptide pool), nucleic acid(s) encoding the TAP(s), as well as antibodies/antibody fragments, TCR, cell (e.g., T lymphocyte, CAR T or NK cell, APC),
20 vaccines and compositions disclosed herein may be used for inducing or stimulating an immune response against cancer cells expressing the TAP. In an embodiment, the cancer is melanoma. In an embodiment, the melanoma is cutaneous melanoma. In an embodiment, the melanoma is of the superficial spreading subtype. In an embodiment, the melanoma is of the nodular subtype. In an embodiment, the melanoma is of the lentigo maligna subtype. In an embodiment, the
25 melanoma is of the nodular subtype. In an embodiment, the melanoma is of the acral lentiginous subtype. In an embodiment, the melanoma is ocular melanoma (e.g., choroidal melanoma, iris melanoma or uveal melanoma). In an embodiment, the melanoma is mucosal melanoma. In an embodiment, the melanoma is a stage 0 melanoma. In an embodiment, the melanoma is a stage 1 melanoma. In an embodiment, the melanoma is a stage 2 melanoma. In an embodiment, the
30 melanoma is a stage 3 melanoma. In an embodiment, the melanoma is a stage 4 melanoma. In an embodiment, the melanoma is a relapsing melanoma. In an embodiment, the melanoma is a chemotherapy-resistant melanoma.

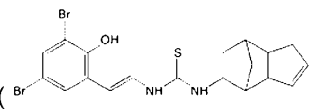
 In an embodiment, the methods or uses described herein further comprise determining the HLA class I alleles expressed by the patient prior to the treatment/use, and administering or using
35 TAPs that bind to one or more of the HLA class I alleles expressed by the patient. For example, if it is determined that the patient expresses HLA-01*01 and HLA-B40*01, any combinations of (i) the TAPs of SEQ ID NO: 11, 14, 20, 27, 29, 37, 86, 87, 121, 150, 165, 173, 279, 288, 299, 308,

312, 316, 319, 331, 340, 352, 362, 363, 384, 395, 398, 411, 419, 429, 458, 474, 476, 487, 492, 500, and/or 501 (that bind to HLA-A01*01) and (ii) the TAPs of SEQ ID NO:215 and/or 322 (that bind to HLA-B40*01) may be administered or used in the patient.

In some embodiments, patients treated with the compositions (e.g., pharmaceutical compositions) of the disclosure are treated prior to or following treatment with allogenic stem cell transplant (ASCL), allogenic lymphocyte infusion or autologous lymphocyte infusion.

In an embodiment, the TAP, nucleic acid, expression vector, T cell receptor, antibody/antibody fragment, cell (e.g., T lymphocyte, CAR T or NK cell, APC), and/or composition according to the present disclosure, or any combination thereof, may be used in combination with one or more additional active agents or therapies to treat melanoma, such as chemotherapy (e.g., vinca alkaloids, agents that disrupt microtubule formation (such as colchicines and its derivatives, monomethyl auristatin E (MMAE)), anti-angiogenic agents, therapeutic antibodies, EGFR targeting agents, tyrosine kinase targeting agent (such as tyrosine kinase inhibitors), transitional metal complexes, proteasome inhibitors, antimetabolites (such as nucleoside analogs), alkylating agents, platinum-based agents, anthracycline antibiotics, topoisomerase inhibitors, macrolides, retinoids (such as all-trans retinoic acids or a derivatives thereof), geldanamycin or a derivative thereof (such as 17-AAG), inhibitors of CDK4/6, TGF- β , WNT- β -catenin, MYC or PI3K, surgery, immune checkpoint inhibitors or immunotherapeutic agents (e.g., PD-1/PD-L1 inhibitors such as anti-PD-1/PD-L1 antibodies, CTLA-4 inhibitors such as anti-CTLA-4 antibodies, B7-1/B7-2 inhibitors such as anti-B7-1/B7-2 antibodies, TIM3 inhibitors such as anti-TIM3 antibodies, BTLA inhibitors such as anti-BTLA antibodies, CD47 inhibitors such as anti-CD47 antibodies, GITR inhibitors such as anti-GITR antibodies), antibodies against tumor antigens (e.g., anti-CD19, anti-CD22 antibodies), cell-based therapies (e.g., CAR T cells, CAR NK cells), and cytokines such as IL-2, IL-7, IL-21, and IL-15. In an embodiment, the TAP, nucleic acid, expression vector, T cell receptor, cell (e.g., T lymphocyte, APC), and/or composition according to the present disclosure is administered/used in combination with an immune checkpoint inhibitor. In an embodiment, the TAP, nucleic acid, expression vector, T cell receptor, cell (e.g., T lymphocyte, APC), and/or composition according to the present disclosure is administered/used in combination with radiotherapy. In an embodiment, the TAP, nucleic acid, expression vector, T cell receptor, antibody/antibody fragment, cell (e.g., T lymphocyte, CAR T or NK cell, APC), and/or composition according to the present disclosure is administered/used in combination with surgery. In an embodiment, the TAP, nucleic acid, expression vector, T cell receptor, antibody/antibody fragment, cell (e.g., T lymphocyte, CAR T or NK cell, APC), and/or composition according to the present disclosure is administered/used in combination with inhibitors of CDK4/6, TGF- β and/or WNT- β -catenin. Several CDK4/6 inhibitors are in clinical trials including Palbociclib (PD-0332991, Ibrance), Ribociclib (LEE-011, Kisqali), Abemaciclib (LY2835219, Verzenios), SHR6390 and Trilaciclib (G1T28). Inhibitors of TGF- β include antisense inhibitors such as AP12009

(Trabedersen) and ISTH0036, antibodies and ligand traps such as GC1008 (Fresolimumab), LY2382770, and P144, vaccines targeting the TGF- β pathway such as Belagenpumatucel-L (Lucanix™), and FANG™ or vigil (Gemogenovatumel-T), as well as small molecule inhibitors such as LY2157299 (Galunisertib) and TEW-7197. Inhibitors of the WNT- β -catenin pathway include

- 5 amino acid starvators (asparaginase), GSK3 inhibitors, C2 (, WNT974, ETC-1922159, RXC004, CGX1321, OTSA101-DTPA-90Y, Vantictumab (OMP-18R5), Ipafricept (OMP-54F28), PRI-724, SM08502, secreted frizzled-related proteins/peptides and Tankyrase inhibitors (XAV939, JW-55, RK-287107, and G007-LK).

- The additional therapy may be administered prior to, concurrent with, or after the
 10 administration of the TAP, nucleic acid, expression vector, T cell receptor, antibody/antibody fragment, cell (e.g., T lymphocyte, CAR T or NK cell, APC), and/or composition according to the present disclosure.

EXAMPLES

- The present disclosure is illustrated in further details by the following non-limiting example.
 15

Example 1: Identification of melanoma tumor antigen candidates

- Acquisition of samples.* The 12 flash-frozen cutaneous melanoma specimens used in this study were purchased from Tissue Solutions. The project was approved by the Research Ethics Boards of the Université de Montréal. Between 700 mg and 1.4 g per tumor were used for mass
 20 spectrometry analyses and between 30 mg and 70 mg were used for RNA-Sequencing. The immunopeptidomic and RNA-Sequencing data for the 7 patient-derived melanoma cell lines from Chong *et al.*¹ were downloaded from the European Genome-phenome Archive (EGA), accession number EGAS00001003724.

- Immunoprecipitation of MHC I.* The W6/32 antibodies (BioXcell) were incubated in PBS for
 25 60 min at room temperature with PureProteome™ protein A magnetic beads (Millipore) at a ratio of 1 mg of antibody per mL of slurry. Antibodies were covalently cross-linked to magnetic beads using dimethylpimelidate, as described previously². The beads were stored at 4°C in PBS pH 7.2 and 0.02% NaN₃. Primary tumor tissue samples were cut into small pieces (cubes, approx. 3 mm in size) and 6 ml of ice-cold PBS containing protein inhibitor cocktail (Sigma, cat#P8340-5ml) was
 30 added. Tissues were homogenized twice for 20 seconds using an Ultra Turrax T25 homogenizer (IKA-Labortechnik) set at a speed of 20,000rpm. Then, 700 μ l of ice-cold 10X lysis buffer (5% w/v CHAPS) was added to each sample. After 60-minute incubation with tumbling at 4°C, tissue samples were spun at 16,000g for 20 minutes at 4°C. Supernatants were transferred into new tubes containing 1 mg of W6/32 antibody covalently-cross-linked protein A magnetic beads.

Samples were incubated with tumbling for 20hrs at 4°C and placed on a magnet to recover bound MHC I complexes to magnetic beads. Magnetic beads were first washed with 8 × 1 mL PBS, then with 1 × 1 mL of 0.1X PBS and finally with 1 × 1 mL of water. MHC I complexes were eluted from the magnetic beads by acidic treatment using 1% trifluoroacetic acid (TFA). To remove any residual magnetic beads, eluates were transferred into 2 mL Costar mL Spin-X centrifuge tube filters (0.45 µm, Corning) and spun 5 min at 1500g. Filtrates containing peptides were separated from MHC I subunits (HLA molecules and β-2 macroglobulin) using home-made stage tips packed with two 1 mm diameter octadecyl (C-18) solid-phase extraction disks (EMPORE). Stage tips were pre-washed first with methanol then with 80% acetonitrile (ACN) in 0.1% TFA, followed by 0.1% TFA and finally with 1% TFA. Samples were loaded onto the stage tips and the peptides were retained on the stage tips while the HLA molecules and β-2 macroglobulin were found in the flow through. Stage tips were washed with 1% TFA and then with 0.1% TFA, and peptides were eluted with 30% ACN in 0.1% TFA. The peptides were dried using vacuum centrifugation and then stored at -20°C until MS analysis.

TMT labeling. TMT labeling was performed for the 12 primary melanoma samples used in the study. The samples were reconstituted in 20 µL of 200 mM HEPES buffer, pH 8.2. The TMT reagents (Thermo Fisher Scientific) were dissolved in 40 µL of anhydrous ACN (Sigma-Aldrich) and 50 or 100 µg of reagent was added to the peptides. The solution was gently mixed and incubated for 90 min without agitation at RT before the reaction was quenched by hydroxylamine (Thermo Fisher Scientific). Samples were desalted on Silica C18 UltraMicroSpin™ Column (The Nest Group), dried down and reconstituted in 4% FA (EMD Millipore).

Liquid Chromatography-tandem MS analyses. Dried peptide extracts were resuspended in 4% FA and loaded on a homemade C18 analytical column (20 cm x 150 µm i.d. packed with C18 Jupiter Phenomenex) with a 106-minute gradient from 0% to 30% ACN (0.2% FA) and a 600 nL/min flow rate on an EASY-nLC II system. 2 samples were analyzed with a Q-Exactive HF and 10 samples with an Orbitrap Fusion mass spectrometer (Thermo Fisher Scientific). For Q-Exactive HF, analyses were done in positive ion mode with Nanospray 2 source at 1.6 kV. Each full MS spectrum, acquired with a 60,000 resolution was followed by 20 MS/MS spectra, where the most abundant multiply charged ions were selected for MS/MS sequencing with a resolution of 60,000, an automatic gain control target of 2×10^4 , an injection time of 800 ms and collisional energy of 28%. Analyses with Orbitrap Fusion mass spectrometer were done in positive ion mode with Nanoflex source at 2.8kV. Each full MS spectrum, acquired with a 120,000 resolution was followed by 20 MS/MS spectra, where the most abundant multiply charged ions were selected for MS/MS sequencing with a resolution of 50,000, an automatic gain control target of 2×10^4 , an injection time of 1000ms, and collisional energy of 35%.

Construction of MS databases. Cancer-specific proteomes were assembled using k-mer profiling as described^{3,4}. k-mers (33-nucleotide-long) present more than once in the mTECs k-

mer database were removed from each cancer sample database, and the remaining k-mers were assembled into contigs. Finally, the contigs were 3-frame translated, and the different polypeptides were linked with "JJ" linkers. Each of these databases was concatenated with the corresponding sample's canonical proteome and used for TA identification.

- 5 *MAP identification.* LC-MS/MS data were searched against the relevant database using Peaks X Pro (Bioinformatics Solution Inc.). For peptide identification, tolerance was set at 10 ppm and 0.01Da for precursor and fragment ions, respectively. Oxidation (M) and deamidation were set as variable modifications. In addition, for the TMT labeling, the occurrences of K and N-term were set as fixed modifications, and the occurrence of STY was set as a variable modification.
- 10 Following peptide identification, the modified target-decoy approach built-in PEAKS was used to apply a sample-specific threshold on the PEAKS scores to ensure a false discovery rate (FDR) of 5%, calculated as the ratio between the number of decoy hits and the number of target hits above the score threshold. PEAKS scores corresponding to a 5% FDR for each sample were determined, and peptides that passed the threshold were further filtered to match the following
- 15 criteria: peptide length between 8 and 11 amino acids, eluted ligand likelihood prediction rank to any of the sample's HLA alleles < 2% based on NetMHCpan-4.1b⁵. These filtering steps were performed with the use of MAPDP⁶.

- Selection of TSAs, TAAs and LSAs.* TA candidates were selected as previously described^{3,4} based on their source RNA expression in the cancer sample of origin and mTECs (FC ≥ 10). The expression of the TA candidates' coding sequences was then evaluated in normal tissues from GTEx (n = up to 50 samples per tissue, 50 tissues), mTECs (n = 11), purified blood and bone marrow samples (n = 115), purified melanocytes (n = 11), melanoma samples from TCGA (n = 150, TCGA_SKCM), and melanoma cell lines from Chong et al.¹ (n = 7) using BamQuery^{4,7}. TAs listed herein are the peptides meeting the following criteria:

- 25 1. mTSAs are derived from mutated genomic sequences supported by at least 5 reads and 5% reads at locus; the mutation is not reported in dbSNP version 155 (except if annotated as 'pathogenic');
2. For unmutated TAs, the 95th percentile RNA expression value in TCGA_SKCM is at least 2 times higher than the 95th percentile RNA expression value in GTEx (except testis and skin) and mTEC samples;
- 30 A) for aeTSAs: The aeTSA's source RNA is expressed below 8.55 reads per hundred million (rphm) in more than 90% normal samples from mTECs, melanocytes, blood and bone marrow cells, and each GTEx tissue except the testis; the mean expression is at least 2 times higher in TCGA_SKCM compared to normal GTEx skin; and the mean expression is at least 2 times higher in
- 35 melanoma cell lines compared to purified melanocytes;

B) for TAAs: The TAA's source RNA can be expressed above 8.55 reads per hundred million (rphm) in >10% of samples from any normal tissues (GTEx, melanocytes, mTECs and/or blood and bone marrow cells), but the mean expression is at least 2 times higher in TCGA_SKCM compared to mTECs and each GTEx tissue except testis, and the mean expression in melanoma cell lines is at least 2 times higher compared to purified melanocytes.

C) For LSAs: The LSA's source RNA is expressed above 8.55 rphm in at least 10% of GTEx skin samples or purified melanocytes, and the mean expression in GTEx skin is higher compared to all other GTEx tissues; and is expressed below 8.55 rphm in more than 90% normal samples from mTECs, blood and bone marrow cells, and each GTEx tissue except the testis and skin.

TCGA analyses. TCGA RNA-seq gene expression data for hg38 were retrieved as upper quartile-normalized fragments per kilobase of transcript per million mapped reads (FPKM-UQ) using the R package TCGAbiolinks. For genes with duplicate entries, we calculated the average expression across entries. FPKM-UQ values were then used for correlations with each TA's RPHM expression from BamQuery, or to perform single-sample gene set enrichment analyses (ssGSEA) for the stemness gene set reported by Miranda et al.¹⁸ using the R package GSVA. Processed level 3 methylation data (HM450) from the Liftover Pipeline for TCGA samples were previously retrieved using the TCGAbiolinks package. Only probes within 2 kb of the transcription start site of a given TA-source gene were kept. The mean beta value was used for genes associated with multiple probes. For focal CNV correlations, processed hg38 gene-level copy number scores were previously retrieved using the TCGAbiolinks package. Mean DNA copy-number values were used for multiple segments associated with a TA-coding region. Mutation rate data for TCGA samples were retrieved from Firebrowse (<http://firebrowse.org/>) as the number of non-synonymous mutations per base (*rate_non* column). All correlations with TA RPHM expression were performed with the *rcorr* function in R. P-values were adjusted using the Benjamini-Hochberg method.

The characteristics of the TSAs, TAAs and LSAs identified herein are described in **Tables 2A-2C**.

Table 2A: characteristics of the TSAs, TAAs and LSAs identified herein

Peptide Sequence (SEQ ID NO:)	Categ.	HLA Allele	Sample	Biotype
TLDDAVHGV (1)	aeTSA	HLA-A02:01	T1185B_Melanoma_ctrl	Intergenic
YQIGQVQGV (2)	aeTSA	HLA-A02:01	Me290_Melanoma	ncRNA
NEYSNITRLY ³ (3)	mTSA	HLA-B18:01	0MM745_Melanoma_ctrl	annotated_ORF
RLLADLTGA ⁴ (4)	mTSA	HLA-A02:01	Me275_Melanoma	annotated_ORF
TPLSPDPTL ⁵ (5)	mTSA	HLA-B35:03	T1015A_Melanoma	5UTR
STYYWPRPR (6)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
DSFSATETR (7)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA

ETSYVKVLH (8)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
AEMLGSVV (9)	aeTSA	HLA-B49:01	T1015A_Melanoma	annotated_ORF
EELSVLEVF (10)	aeTSA	HLA-B18:01	258_20T	annotated_ORF
FVQENYLEY (11)	aeTSA	HLA-A25:01, HLA-A26:01, HLA-A01:01, HLA-B15:01	258_20T, ONVC_Melanoma_ctrl, Me290_Melanoma, 1496_16T_Melanoma	annotated_ORF
IVQQPTEEK (12)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SVFAHPRKL (13)	aeTSA	HLA-C06:02, HLA-C07:01, HLA-C07:02	T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma	annotated_ORF
ASSLPTTMNY (14)	aeTSA	HLA-A01:01	Me290_Melanoma	annotated_ORF
IVQQPTEEKR (15)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
LPTTMNYPL (16)	aeTSA	HLA-B35:03	T1015A_Melanoma	annotated_ORF
GSNPARYEF (17)	aeTSA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
TADDATVM (18)	aeTSA	HLA-C08:02	738_20T	annotated_ORF
VLEHVVRV (19)	aeTSA	HLA-A02:01	Me275_Melanoma	annotated_ORF
EVDPIGHLY (20)	aeTSA	HLA-A01:01, HLA-A26:01	1836_18T, ONVC_Melanoma_ctrl, OMM745_Melanoma_ctrl, Me290_Melanoma	annotated_ORF
QIMPKAGL (21)	aeTSA	HLA-B08:01	OMM745_Melanoma_ctrl	annotated_ORF
KVLEHVVRV (22)	aeTSA	HLA-A02:09, HLA-A02:01	T1015A_Melanoma, T1185B_Melanoma_ctrl, Me275_Melanoma	annotated_ORF
QVPGSNPAR (23)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
FVYGEPREL (24)	aeTSA	HLA-C12:03, HLA-C03:03, HLA-C03:04	258_20T, 1367_16T, 542_20T, 738_20T, T1185B_Melanoma_ctrl	annotated_ORF
TLPTFDPTKV (25)	aeTSA	HLA-A02:01	542_20T, Me275_Melanoma	annotated_ORF
NQIMPKTGF (26)	aeTSA	HLA-B38:01, HLA-B15:01	ONVC_Melanoma_ctrl	annotated_ORF
EVDPIGHVY (27)	aeTSA	HLA-A26:01, HLA-A01:01	Me290_Melanoma, OD5P_Melanoma_ctrl	annotated_ORF
ELVRRILSR (28)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
MEVDPIGHLY (29)	aeTSA	HLA-A01:01	OMM745_Melanoma_ctrl	annotated_ORF
SVMSSNVSF (30)	aeTSA	HLA-B15:01	1367_16T	annotated_ORF
TVPSSFPSW (31)	aeTSA	HLA-A25:01, HLA-A24:02	258_20T, 1496_16T_Melanoma	annotated_ORF
KYKDYFPVI (32)	aeTSA	HLA-C07:02	542_20T	annotated_ORF
MEVDPIGHVY (33)	aeTSA	HLA-B18:01	OMM745_Melanoma_ctrl	annotated_ORF
TVYGEPRKL (34)	aeTSA	HLA-C06:02	T1185B_Melanoma_ctrl	annotated_ORF
GPDVREGTL (35)	aeTSA	HLA-B07:02	Me275_Melanoma	annotated_ORF
VYDGREHTV (36)	aeTSA	HLA-C07:02	Me275_Melanoma	annotated_ORF
LMEVDPIGHLY (37)	aeTSA	HLA-A01:01	Me290_Melanoma	annotated_ORF
KYKDYFPVILK (38)	aeTSA	HLA-A30:01	542_20T	annotated_ORF
EVFEGREDSIF (39)	aeTSA	HLA-A26:01	ONVC_Melanoma_ctrl	annotated_ORF
GVYDGREHTV (40)	aeTSA	HLA-A02:09, HLA-A02:01	T1015A_Melanoma, T1185B_Melanoma_ctrl, Me275_Melanoma, 1496_16T_Melanoma	annotated_ORF
EVVPISHLY (41)	aeTSA	HLA-A26:01, HLA-A68:01	2883_18T, ONVC_Melanoma_ctrl, T1185B_Melanoma_ctrl	annotated_ORF
NAVGVYAGR (42)	aeTSA	HLA-A26:01, HLA-A68:01	ONVC_Melanoma_ctrl, T1185B_Melanoma_ctrl	annotated_ORF
RPDSRLLEL (43)	aeTSA	HLA-B07:02	Me275_Melanoma	annotated_ORF
SVFAHPRKLLM (44)	aeTSA	HLA-A32:01	T1015A_Melanoma	annotated_ORF

EVFEGREDSVF (45)	aeTSA	HLA-A26:01	2883_18T,0NVC_Melanoma_ctrl	annotated_ORF
RVSHSHASF (46)	aeTSA	HLA-A32:01	T1015A_Melanoma	ncRNA
ATFLQRKVLRL (47)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
SYVKVLHHL (48)	aeTSA	HLA-A23:01	Me275_Melanoma	annotated_ORF
FAFGEPREL (49)	aeTSA	HLA-C12:03, HLA-C03:04	258_20T,738_20T,0NVC_Melanoma_ctrl,T1185B_Melanoma_ctrl	annotated_ORF
KMAELVHFL (50)	aeTSA	HLA-A02:09, HLA-A02:01	T1015A_Melanoma, T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma	annotated_ORF
FAHGHPLYTR (51)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
GVYAGREHFV (52)	aeTSA	HLA-A02:01	542_20T	annotated_ORF
NTAIATFLQRK (53)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
TLDEKVAEL (54)	aeTSA	HLA-C08:02, HLA-A02:01	1367_16T,542_20T, 738_20T	annotated_ORF
RLELHITM (55)	aeTSA	HLA-A02:01	Me275_Melanoma	annotated_ORF
EVPNSSPPR (56)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
VEVTLREV (57)	aeTSA	HLA-B49:01	T1015A_Melanoma	annotated_ORF
ISGGPRISY (58)	aeTSA	HLA-C12:03	0NVC_Melanoma_ctrl	annotated_ORF
GVPGLLLPR (59)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
GVYDGEHVS (60)	aeTSA	HLA-A02:01	T1185B_Melanoma_ctrl, Me275_Melanoma	annotated_ORF
KISGGPRISY (61)	aeTSA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
FLYNQTNIRM (62)	aeTSA	HLA-A02:09	T1015A_Melanoma	ncRNA
GQYQLVVSL (63)	aeTSA	HLA-B15:01	1367_16T	annotated_ORF
GVDDLVRFR (64)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	5UTR
KVLEYVIKV (65)	aeTSA	HLA-A02:01	T1185B_Melanoma_ctrl, Me275_Melanoma, 1496_16T_Melanoma	annotated_ORF
HTLPALSRR (66)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
ALREEEEGV (67)	aeTSA	HLA-A02:01	T1185B_Melanoma_ctrl, Me275_Melanoma	annotated_ORF
TTINFTRQR (68)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SAYGEPRKL (69)	aeTSA	HLA-C03:04, HLA-C03:03	T1185B_Melanoma_ctrl, 1496_16T_Melanoma	annotated_ORF
STANVTRAH (70)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SAFPTTINF (71)	aeTSA	HLA-C12:03	542_20T	annotated_ORF
FRAVITKKV (72)	aeTSA	HLA-C06:02	T1185B_Melanoma_ctrl	annotated_ORF
AAAGVSSTK (73)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
FPTTINFTR (74)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
TTSEKIH (75)	aeTSA	HLA-C07:01, HLA-A68:01	T1015A_Melanoma, T1185B_Melanoma_ctrl	annotated_ORF
GLYDGMEHL (76)	aeTSA	HLA-A02:01	Me275_Melanoma	annotated_ORF
STANVTRAHGR (77)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
IEDPKAGLHV (78)	aeTSA	HLA-B49:01	T1015A_Melanoma	annotated_ORF
GVVGPQGLR (79)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
NVFAHATGESR (80)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
FLFGEPKRL (81)	aeTSA	HLA-A02:01	T1185B_Melanoma_ctrl	annotated_ORF
SAFPTTINFTR (82)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
RLFSEDIHV (83)	aeTSA	HLA-A02:09	T1015A_Melanoma	Intergenic
VYMPANTTF (84)	aeTSA	HLA-A23:01	Me275_Melanoma	Introns
EAVGFQPPR (85)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
EVDPTSHSY (86)	aeTSA	HLA-A01:01	0MM745_Melanoma_ctrl	annotated_ORF
LLDPAQRNLY (87)	aeTSA	HLA-A01:01	0D5P_Melanoma_ctrl	annotated_ORF
SGISQVFQR (88)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF

RLFSEDIHVA (89)	aeTSA	HLA-A02:09, HLA-A02:01	T1015A_Melanoma, Me290_Melanoma, Me275_Melanoma	Intergenic
VFDVGKGNM (90)	aeTSA	HLA-C04:01	T1015A_Melanoma	ncRNA
KASEKIFYV (91)	aeTSA	HLA-A02:01	Me275_Melanoma	annotated_ORF
EAAAAFRFPR (92)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
MSISMSLLK (93)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
KASPSSLPH (94)	aeTSA	HLA-C12:03	0D5P_Melanoma_ctrl	Introns
RTLQQGVLDW (95)	aeTSA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
TTATTFRAR (96)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
NPSHLITPR (97)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
ETMETLRTSR (98)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
MWVEGHPRERR (99)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
LPDGSRVEL (100)	aeTSA	HLA-B35:03	T1015A_Melanoma	annotated_ORF
DVVTGNVPLK (101)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
ENPSHLITPR (102)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
SLARTILHL (103)	aeTSA	HLA-A02:01	542_20T	Introns
KPHYGLRAI (104)	aeTSA	HLA-B07:02	Me275_Melanoma	annotated_ORF
AFLDIHTAL (105)	aeTSA	HLA-C07:02, HLA-C14:02	0D5P_Melanoma_ctrl	Intergenic
KMSEFVYRF (106)	aeTSA	HLA-A32:01	T1015A_Melanoma	5UTR
FLVTKTVTM (107)	aeTSA	HLA-A02:01	Me275_Melanoma	ncRNA
HTTSVMENK (108)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
LVSIIPIAVR (109)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
ITSGVKVKK (110)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
VSIPIAVRR (111)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
DIELQEGLR (112)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
HLKPPELGF (113)	aeTSA	HLA-B15:01	0D5P_Melanoma_ctrl	Intergenic
QVIVKIIGH (114)	aeTSA	HLA-A26:01	0NVC_Melanoma_ctrl	annotated_ORF
AEQEIMKKV (115)	aeTSA	HLA-B49:01	T1015A_Melanoma	annotated_ORF
EVPLKILAH (116)	aeTSA	HLA-A26:01	0NVC_Melanoma_ctrl	annotated_ORF
IVKIIGHFY (117)	aeTSA	HLA-A30:02	0MM745_Melanoma_ctrl	annotated_ORF
SLVSIPIAVR (118)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
MVSPGVSLFK (119)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
VLMMKLEDL (120)	aeTSA	HLA-A02:01	Me275_Melanoma	Introns
YSDLHTPGRY (121)	aeTSA	HLA-A01:01	0MM745_Melanoma_ctrl, Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
EVARFLTY (122)	aeTSA	HLA-A26:01	0NVC_Melanoma_ctrl	annotated_ORF
SVGDLMAPR (123)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
VLWRGDSPL (124)	aeTSA	HLA-A02:01	Me275_Melanoma	ncRNA
QPRQGSPVAA (125)	aeTSA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
KQTGIRHSY (126)	aeTSA	HLA-A32:01	T1015A_Melanoma	Introns
RPRQDAISV (127)	aeTSA	HLA-B07:02	0D5P_Melanoma_ctrl	Intergenic
KLITQIRTA (128)	aeTSA	HLA-A02:01	Me275_Melanoma	ncRNA
SYLSEHSAIF (129)	aeTSA	HLA-A23:01	Me275_Melanoma	Introns
TSVGDLMAPR (130)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
EIPTGVAKR (131)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
SQINLSQIY (132)	aeTSA	HLA-B15:01	0D5P_Melanoma_ctrl	3UTR
RRPSGGFRL (133)	aeTSA	HLA-C07:01	Me290_Melanoma	Intergenic
EVFNVKNTFPK (134)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
KVLGGGWTV (135)	aeTSA	HLA-A02:01	Me290_Melanoma	ncRNA

HEAPGQHSEV (136)	aeTSA	HLA-B49:01	T1015A_Melanoma	ncRNA
EVSHPNMSGGR (137)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
DTAPATFLR (138)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
KPQKDLHFI (139)	aeTSA	HLA-B07:02	0D5P_Melanoma_ctrl	ncRNA
RVRGAGTHL (140)	aeTSA	HLA-B07:02	0D5P_Melanoma_ctrl	ncRNA
TAPIIVAQR (141)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
TSWDTKFYEK (142)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
KVFAEHKISY (143)	aeTSA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
DAFQGIANR (144)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
IVADPRVPR (145)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
TGFSTSLGR (146)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Introns
ATAPIIVAQR (147)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
GQFLVKSGY (148)	aeTSA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
WTSRTVQNK (149)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
ATYGGSDHYI ¹ (150)	mTSA	HLA-A01:01	Me290_Melanoma	annotated_ORF
VYIAELEKI (151)	aeTSA	HLA-A23:01	Me275_Melanoma	annotated_ORF
VFLDRAVSI ⁶ (152)	aeTSA	HLA-A23:01	Me275_Melanoma	annotated_ORF
MPSPIDHPR (153)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
EAVRHILHGSR (154)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
YPAGNVKEL (155)	aeTSA	HLA-B35:03	T1015A_Melanoma	annotated_ORF
SVPRSLASR (156)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
ALIKHVANA (157)	aeTSA	HLA-A02:01	Me275_Melanoma	Introns
YTANLVPVR (158)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
LSSSLVTKL (159)	aeTSA	HLA-C03:04	T1185B_Melanoma_ctrl	Intergenic
QNSNVLA VR (160)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Introns
TTTKNTLNK (161)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
HNYINLHSL (162)	aeTSA	HLA-B08:01, HLA-C12:03	1713_19T, 0NVC_Melanoma_ctrl	Intergenic
HLKDYFEEY ² (163)	mTSA	HLA-C07:01	1772_19T	annotated_ORF
SPEYFTSYL (164)	aeTSA	HLA-B35:03	T1015A_Melanoma	Intergenic
ATDVL DHLY (165)	aeTSA	HLA-A01:01	1713_19T,534_20T, Me290_Melanoma, 0D5P_Melanoma_ctrl	ncRNA
QTFEESLGR (166)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
HEQPELQKV (167)	aeTSA	HLA-B49:01	T1015A_Melanoma	retained_intron
MATDVL DHLY (168)	aeTSA	HLA-A26:01	0NVC_Melanoma_ctrl	ncRNA
TSGSLFPR (169)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
KLGINNVSR (170)	aeTSA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
KYISQFQVF (171)	aeTSA	HLA-A23:01	Me275_Melanoma	Intergenic
QTA AVSGVK (172)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
LTPLNH PFSY (173)	aeTSA	HLA-A01:01	0D5P_Melanoma_ctrl	Intergenic
VFINKKYVF (174)	aeTSA	HLA-A23:01	Me275_Melanoma	Intergenic
NLITEEHPV (175)	aeTSA	HLA-A02:01	Me275_Melanoma	Intergenic
ELVKVIDGSSR (176)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Introns
FHSLPIHLF (177)	aeTSA	HLA-C07:02	Me275_Melanoma	Intergenic
YSHDYSYY (178)	aeTSA	HLA-C12:03	0D5P_Melanoma_ctrl	Intergenic
FQIEKL TPL (179)	aeTSA	HLA-A02:01	T1185B_Melanoma_ctrl	ncRNA
EHSVENGSI (180)	aeTSA	HLA-B38:01	0NVC_Melanoma_ctrl	ncRNA
ETIQNTHSF (181)	aeTSA	HLA-A26:01	0NVC_Melanoma_ctrl	Introns
YYSIWKTQI (182)	aeTSA	HLA-A23:01	Me275_Melanoma	ncRNA
SYF FHGLSF (183)	aeTSA	HLA-C07:01	0MM745_Melanoma_ctrl	Introns
ESFQQPYIPR (184)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Introns
KQVPSRVLY (185)	aeTSA	HLA-A30:02	0MM745_Melanoma_ctrl	retained_intron

MLFNKDLDA (186)	aeTSA	HLA-A02:01	Me275_Melanoma	Introns
APRSAEPRAT (187)	aeTSA	HLA-B07:02	Me275_Melanoma	Intergenic
YLDPGAVHAVF (188)	aeTSA	HLA-A02:01	Me275_Melanoma	Intergenic
TLKKHKIV (189)	aeTSA	HLA-B08:01	0MM745_Melanoma_ctrl	annotated_ORF
VGVPISLTLY (190)	aeTSA	HLA-A30:02	0MM745_Melanoma_ctrl	Intergenic
SPRPQPEL (191)	aeTSA	HLA-B07:02	0D5P_Melanoma_ctrl	Intergenic
KLSFPDSKF (192)	aeTSA	HLA-B15:01	0D5P_Melanoma_ctrl	Intergenic
KNKDEYIHFY (193)	aeTSA	HLA-A30:02	0MM745_Melanoma_ctrl	Introns
RAFEGRRRGW (194)	aeTSA	HLA-A32:01	T1015A_Melanoma	ncRNA
RLKAR P STY ⁷ (195)	aeTSA	HLA-B15:01	0D5P_Melanoma_ctrl	ncRNA
APSLHATL (196)	aeTSA	HLA-B07:02	0D5P_Melanoma_ctrl	Introns
AQKEPTGNY (197)	aeTSA	HLA-A30:02	0MM745_Melanoma_ctrl	Intergenic
LSLGTACR (198)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
SRNPTSYKY (199)	aeTSA	HLA-C07:01	0MM745_Melanoma_ctrl	Intergenic
SLNNDHDIY (200)	aeTSA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
YVDPMITEI (201)	aeTSA	HLA-A02:01	Me290_Melanoma	annotated_ORF
PSFSPYAKR (202)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
HVNGSRPHAR (203)	aeTSA	HLA-A68:01	T1185B_Melanoma_ctrl	Frameshift
ITVRLAPPL (204)	aeTSA	HLA-C03:03	1496_16T_Melanoma	ncRNA
SANPLSHRY (205)	aeTSA	HLA-C07:01	T1015A_Melanoma	Introns
VPLAHSSA (206)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
GQVPTTEVV (207)	TAA	HLA-B13:02, HLA-B15:01	1496_16T_Melanoma	annotated_ORF
KTWGQYWQV (208)	TAA	HLA-A02:01, HLA-A32:01	1758_19T, 542_20T, 534_20T, T1015A_Melanoma, Me290_Melanoma	annotated_ORF
ALNFPGSQK (209)	TAA	HLA-A03:01	1836_18T	annotated_ORF
YVWKTWGQY (210)	TAA	HLA-B15:01	1682_16T_Melanoma	annotated_ORF
MPTAESTGM (211)	TAA	HLA-B35:03	1836_18T, T1015A_Melanoma	annotated_ORF
HTMEVTVYHRR (212)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
EEAAGIGIL (213)	TAA	HLA-B40:02	1758_19T	annotated_ORF
EGFDHRDSK (214)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
AEAAAGIGIL (215)	TAA	HLA-B40:02, HLA-B40:01	1758_19T	annotated_ORF
LTSSMVTPT (216)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	Frameshift
TSSMVTPT (217)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	Frameshift
GLSNLTHVL (218)	TAA	HLA-A02:01	Me290_Melanoma, Me275_Melanoma	annotated_ORF
QLLALLPSL (219)	TAA	HLA-A02:01	542_20T, 738_20T, 534_20T	annotated_ORF
EAAQPMTKK (220)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
RVLGTPKPSW (221)	TAA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
VLYPVPLESY (222)	TAA	HLA-B15:01	1367_16T, 0D5P_Melanoma_ctrl	annotated_ORF
PYLGQMINL (223)	TAA	HLA-A23:01	Me275_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
ELFSYLIEK (224)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
EEQYIAQF (225)	TAA	HLA-B18:01	258_20T	annotated_ORF
EAAQPMTKKR (226)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
MPMQDIKMI (227)	TAA	HLA-B51:01	1758_19T	annotated_ORF
RLSEGDVMHL (228)	TAA	HLA-A02:01	Me290_Melanoma, Me275_Melanoma	annotated_ORF
HASSYISPEK (229)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
MPMQDIKMIL (230)	TAA	HLA-B35:03	1836_18T	annotated_ORF

SPSVSQLSVL (231)	TAA	HLA-B07:02	542_20T, Me275_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
RLDQLLRHV (232)	TAA	HLA-A02:09, HLA-A02:01	T1015A_Melanoma, Me290_Melanoma	annotated_ORF
ALLERASATL (233)	TAA	HLA-A02:01	Me290_Melanoma	annotated_ORF
TVAPTPATAR (234)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	5UTR
SQSPSVSQL (235)	TAA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
STVAPTPATAR (236)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	5UTR
QYIAQFTSQF (237)	TAA	HLA-A23:01	Me275_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
GQHLHLETF (238)	TAA	HLA-B15:01	1367_16T, 0D5P_Melanoma_ctrl	annotated_ORF
TIASVLVAR (239)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SLLQHILGL (240)	TAA	HLA-A02:01	1758_19T, 542_20T, 738_20T, 534_20T	annotated_ORF
TASPRSPVM (241)	TAA	HLA-C03:04	T1185B_Melanoma_ctrl	annotated_ORF
AAFDGRHSQTL (242)	TAA	HLA-C12:03, HLA-C03:04	542_20T, 0NVC_Melanoma_ctrl, 0D5P_Melanoma_ctrl	annotated_ORF
SPRRLVEL (243)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
LYVDSLFFL (244)	TAA	HLA-A24:02	1772_19T, 1758_19T	annotated_ORF
VFLREFPNF (245)	TAA	HLA-A23:01	Me275_Melanoma	3UTR
RPRFSTATEIA (246)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
ALIANPRRK (247)	TAA	HLA-A03:01	1836_18T	annotated_ORF
DFMGQIVYR (248)	TAA	HLA-A68:01, HLA-A33:01	T1185B_Melanoma_ctrl, 1682_16T_Melanoma	annotated_ORF
EIPDVMGL (249)	TAA	HLA-A25:01	1713_19T	annotated_ORF
VMSSTLYTV (250)	TAA	HLA-A02:01	534_20T, T1185B_Melanoma_ctrl, Me275_Melanoma	annotated_ORF
SPQHKPRL (251)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
EPKPPTTGL (252)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	Introns
IPDTIASVL (253)	TAA	HLA-B35:03	1836_18T	annotated_ORF
TDFMGQIVYR (254)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
GEDDEHRKI (255)	TAA	HLA-B49:01	T1015A_Melanoma	ncRNA
RLRGSISQRY ⁸ (256)	TAA	HLA-A30:02	0MM745_Melanoma_ctrl	annotated_ORF
HLDESPAYL (257)	TAA	HLA-C04:01, HLA-A02:01	T1015A_Melanoma	annotated_ORF
KMEETTVTY (258)	TAA	HLA-B15:01	0D5P_Melanoma_ctrl	ncRNA
LPTDLFNSV (259)	TAA	HLA-B51:01, HLA-B35:03	1758_19T, T1015A_Melanoma	annotated_ORF
RPQGLAVL (260)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
SLSEKSPEV (261)	TAA	HLA-A02:01	T1185B_Melanoma_ctrl	3UTR
GAFREGPPY (262)	TAA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
YLANGTVVA (263)	TAA	HLA-A02:01	Me290_Melanoma, Me275_Melanoma	annotated_ORF
SMYLHTEGF (264)	TAA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
HILSHLHEV (265)	TAA	HLA-A02:01, HLA-A02:09	1758_19T, T1015A_Melanoma, T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma, 1496_16T_Melanoma	annotated_ORF
SISEAPLTEV (266)	TAA	HLA-A02:01	Me290_Melanoma	annotated_ORF
HQINSEATF (267)	TAA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
DIKQEGVGAF (268)	TAA	HLA-A26:01	0NVC_Melanoma_ctrl	annotated_ORF
SALGVITIK (269)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
TVNDFTQNPR (270)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SFIQAGSSY (271)	TAA	HLA-C14:02	0D5P_Melanoma_ctrl	annotated_ORF

GVTITKTLK (272)	TAA	HLA-A03:01	1836_18T	annotated_ORF
AERPQGLAV (273)	TAA	HLA-B49:01	T1015A_Melanoma	annotated_ORF
REKGPVKEV (274)	TAA	HLA-B49:01	T1015A_Melanoma	annotated_ORF
TSVPPFNLR (275)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
LSRLPSIAF (276)	TAA	HLA-B15:01	0D5P_Melanoma_ctrl	ncRNA
FPVHAAEFK (277)	TAA	HLA-B35:03	T1015A_Melanoma	ncRNA
GEISASHV (278)	TAA	HLA-B49:01	T1015A_Melanoma	annotated_ORF
AADGGQHWY (279)	TAA	HLA-A01:01	Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
EISASHVSR (280)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SPRIPFSTF (281)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
KLMDPGSLPPL (282)	TAA	HLA-A02:09, HLA-A02:01	T1015A_Melanoma, Me290_Melanoma, Me275_Melanoma	annotated_ORF
ETKPEFERR (283)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
ETIMKFLKM (284)	TAA	HLA-A26:01	0NVC_Melanoma_ctrl	annotated_ORF
RRAHLWSTF (285)	TAA	HLA-C07:01	T1015A_Melanoma	Intergenic
HLQEKLQSL (286)	TAA	HLA-A02:01, HLA-B08:01	1758_19T, Me290_Melanoma, Me275_Melanoma	annotated_ORF
ELSVVTSER (287)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
YLDQQVPYTF (288)	TAA	HLA-A01:01	Me290_Melanoma	annotated_ORF
EAIPRIPL (289)	TAA	HLA-A25:01, HLA-C12:03	1713_19T, 0NVC_Melanoma_ctrl	annotated_ORF
GYLDQQVPYTF (290)	TAA	HLA-A23:01	0D5P_Melanoma_ctrl	annotated_ORF
SPKLGIGF (291)	TAA	HLA-B07:02	Me275_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
YPEKSRGCL (292)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
TTIPFSTLRQR (293)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	3UTR
SLGAHSPALY (294)	TAA	HLA-A30:02	0MM745_Melanoma_ctrl	annotated_ORF
SQNGQLIH (295)	TAA	HLA-B15:01	1367_16T, 0D5P_Melanoma_ctrl	annotated_ORF
KAKEHTANISW (296)	TAA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
RVSKSDSTF (297)	TAA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
SLNSQVTGL (298)	TAA	HLA-A02:01	Me275_Melanoma	annotated_ORF
NSDLSEKLEY (299)	TAA	HLA-A01:01	1836_18T, 0MM745_Melanoma_ctrl, Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
DSSTVGLQR (300)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
RASAIHQ (301)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SQETLPLKI (302)	TAA	HLA-B37:01	1496_16T_Melanoma	annotated_ORF
STFDGLDRR (303)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
RVKEIVINK (304)	TAA	HLA-A30:01	542_20T	annotated_ORF
AQPHHGVPY (305)	TAA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
EVIQLKERDRK (306)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
EVKEKTEL (307)	TAA	HLA-B08:01	0MM745_Melanoma_ctrl	annotated_ORF
TDPETLHY (308)	TAA	HLA-A01:01	0D5P_Melanoma_ctrl	annotated_ORF
KMKEKTQEL (309)	TAA	HLA-B08:01, HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
STFDGLDRRR (310)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
KMSELQTYV (311)	TAA	HLA-A02:01, HLA-A02:09, HLA-B13:02	1758_19T, 542_20T, T1015A_Melanoma, T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma, 1496_16T_Melanoma	annotated_ORF
GTDPETLHY (312)	TAA	HLA-A01:01	0D5P_Melanoma_ctrl	annotated_ORF

TEEKGSILI (313)	TAA	HLA-B49:01	T1015A_Melanoma	annotated_ORF
DTAMPAHSR (314)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
KLQEALKTI (315)	TAA	HLA-A02:09, HLA-A02:01	T1015A_Melanoma, Me290_Melanoma, Me275_Melanoma	annotated_ORF
GTDPETLHYF (316)	TAA	HLA-A01:01	0D5P_Melanoma_ctrl	annotated_ORF
SLKNRIESV (317)	TAA	HLA-B08:01, HLA-A02:09, HLA-A02:01	0MM745_Melanoma_ctrl, T1015A_Melanoma, Me290_Melanoma, Me275_Melanoma	annotated_ORF
NLKDPVGVY (318)	TAA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
FTETNPQVY (319)	TAA	HLA-A01:01	1836_18T, 0D5P_Melanoma_ctrl	annotated_ORF
ETQEA EVA VSR (320)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
SPRPESGTV (321)	TAA	HLA-B07:02	Me275_Melanoma	annotated_ORF
SEFAKDPSL (322)	TAA	HLA-B40:01	T1185B_Melanoma_ctrl	annotated_ORF
KVIKKIGHY (323)	TAA	HLA-A30:02	0MM745_Melanoma_ctrl	annotated_ORF
RTWQTRKQF (324)	TAA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
AMAHKVIKA (325)	TAA	HLA-A02:01	Me290_Melanoma, Me275_Melanoma	annotated_ORF
KLKQFQKEY (326)	TAA	HLA-A32:01, HLA-B15:01	T1015A_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
SPLDEESL (327)	TAA	HLA-B35:03	1836_18T	annotated_ORF
NSTDFTTDR (328)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
ETKDTKGRYF (329)	TAA	HLA-A26:01	0NVC_Melanoma_ctrl	annotated_ORF
RPRVSSTEM (330)	TAA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
LMDKSSTIY (331)	TAA	HLA-A01:01	0D5P_Melanoma_ctrl	annotated_ORF
GTLRPLKVR (332)	TAA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
ILSEGSVPL (333)	TAA	HLA-A02:01	1758_19T	annotated_ORF
TVYNFRTEL (334)	TAA	HLA-C03:04, HLA-C07:01	Me290_Melanoma	Intergenic
LPSSADVEF (335)	LSA	HLA-B35:03	1836_18T	annotated_ORF
RLPSSADVEF (336)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
ALMDKSLHV (337)	LSA	HLA-A02:01, HLA-A02:09	1758_19T, 542_20T, T1015A_Melanoma, T1185B_Melanoma_ctrl	annotated_ORF
MHNALHIYM (338)	LSA	HLA-B38:01	542_20T	annotated_ORF
MEKEDYHSL (339)	LSA	HLA-B40:02, HLA-B49:01, HLA-B08:01, HLA-C07:02	1758_19T, T1015A_Melanoma, Me290_Melanoma	annotated_ORF
MEKEDYHSLY (340)	LSA	HLA-A01:01	Me290_Melanoma	annotated_ORF
YHSLYQSHL (341)	LSA	HLA-B38:01	542_20T, 0NVC_Melanoma_ctrl	annotated_ORF
YMVPIPLY (342)	LSA	HLA-B15:01	1367_16T	annotated_ORF
LMEKEDYHSL (343)	LSA	HLA-B08:01	Me290_Melanoma	annotated_ORF
FAHEAPFL (344)	LSA	HLA-C12:03	0D5P_Melanoma_ctrl	annotated_ORF
FASPLTGIA (345)	LSA	HLA-C12:03	542_20T	annotated_ORF
HEAPFLPW (346)	LSA	HLA-B44:02	1836_18T	annotated_ORF
VLFKKFIQK (347)	LSA	HLA-A03:01	1836_18T	Frameshift
APAFLPWHR (348)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
LLMEKEDYHSL (349)	LSA	HLA-A02:01, HLA-B08:01, HLA-A02:09	1758_19T, 542_20T, 738_20T, 534_20T, T1015A_Melanoma, T1185B_Melanoma_ctrl, Me290_Melanoma	annotated_ORF
HYYVSMDAL (350)	LSA	HLA-C14:02	0D5P_Melanoma_ctrl	annotated_ORF
WEQEIQKL (351)	LSA	HLA-B40:02	1758_19T	annotated_ORF
LMEKEDYHSLY (352)	LSA	HLA-A01:01	1713_19T, 1836_18T, 534_20T, Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF

LEQASRIWSW (353)	LSA	HLA-B44:02	1836_18T	annotated_ORF
NIFDLSAPEK (354)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
EAPAFLPWHR (355)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SEIWRDIDF (356)	LSA	HLA-B44:02	1836_18T	annotated_ORF
AAMVGAVL (357)	LSA	HLA-C12:03	258_20T, 542_20T	annotated_ORF
TFLGVGQESF (358)	LSA	HLA-A23:01	0D5P_Melanoma_ctrl	annotated_ORF
ESWPSVFYNR (359)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
ISQDTTVGR (360)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Frameshift
RPWSGPYIL (361)	LSA	HLA-B07:02	542_20T, Me275_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
SSDYVIPIGTY (362)	LSA	HLA-A01:01	0D5P_Melanoma_ctrl	annotated_ORF
DSDPDSFQDY (363)	LSA	HLA-A01:01	1713_19T, 1367_16T, Me290_Melanoma	annotated_ORF
DTRPWSGPY (364)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	annotated_ORF
HYYSVKKTF (365)	LSA	HLA-C14:02	0D5P_Melanoma_ctrl	annotated_ORF
NVCGSQQGR (366)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
YMNGTMSQV (367)	LSA	HLA-C01:02, HLA-A02:01, HLA-C12:03, HLA-A02:09	2883_18T, 1758_19T, 1713_19T, 542_20T, 738_20T, 534_20T, T1015A_Melanoma, T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma, 0D5P_Melanoma_ctrl, 1496_16T_Melanoma, 1682_16T_Melanoma	annotated_ORF
MAKRTHPL (368)	LSA	HLA-C12:03	0D5P_Melanoma_ctrl	annotated_ORF
RPWSGPYILR (369)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
MTVDSLUNK (370)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
TRPWSGPYIL (371)	LSA	HLA-C07:02	Me275_Melanoma	annotated_ORF
TTHPLFVIATR (372)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
FWWTHYYSV (373)	LSA	HLA-A02:01	Me290_Melanoma	annotated_ORF
LSKEEKNHF (374)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
RAANQVFVL (375)	LSA	HLA-C12:03	0D5P_Melanoma_ctrl	5UTR
MVRSATLIK (376)	LSA	HLA-A30:01	542_20T	5UTR
NQVFVLHSY (377)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	5UTR
HNSTFLI (378)	LSA	HLA-B38:01	542_20T	annotated_ORF
SQDVAGTTF (379)	LSA	HLA-C08:02	1367_16T	annotated_ORF
AHNSTFLI (380)	LSA	HLA-B38:01	542_20T	annotated_ORF
STFLIYER (381)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
EGFFTRQER (382)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
FQKVLVSYS (383)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
FTDFMGQIVY (384)	LSA	HLA-A01:01	1713_19T, 1836_18T, 534_20T, Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
YFQKVLVSYS (385)	LSA	HLA-C14:02	0D5P_Melanoma_ctrl	annotated_ORF
ALVNMPPHYR (386)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
GVMSTLYTV (387)	LSA	HLA-A02:01	T1185B_Melanoma_ctrl	annotated_ORF
LLSNTVSTL (388)	LSA	HLA-C03:03, HLA-A02:01	1367_16T, T1185B_Melanoma_ctrl	annotated_ORF
RVFHETGAQR (389)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Frameshift
SASDHCRSR (390)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
RRDGGIIY (391)	LSA	HLA-C07:01	T1015A_Melanoma	annotated_ORF
VAALIANPR (392)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF

RLLGTEFQV (393)	LSA	HLA-A02:01, HLA-B13:02	1758_19T, 542_20T, 534_20T, T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma	annotated_ORF
FSIIGVSRR (394)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Frameshift
LSSDGMYYEY (395)	LSA	HLA-A01:01	Me290_Melanoma	annotated_ORF
DEYFLPSL (396)	LSA	HLA-B18:01, HLA-B14:01	1713_19T, 258_20T, 738_20T	annotated_ORF
SYIGLKGLYF (397)	LSA	HLA-A23:01	Me275_Melanoma	annotated_ORF
FTGFGGALGY (398)	LSA	HLA-A26:01, HLA-A01:01	Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
KTWDQVPFSV (399)	LSA	HLA-A02:01, HLA-A02:09	542_20T, 534_20T, T1015A_Melanoma, T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma	annotated_ORF
RVADIPIKP (400)	LSA	HLA-B13:02	T1185B_Melanoma_ctrl	Frameshift
SVAKHTQSY (401)	LSA	HLA-A32:01, HLA-B15:01	T1015A_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
QTKGGQTWAR (402)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
ETGSSFMSF (403)	LSA	HLA-A25:01	1713_19T	ncRNA
SLYSYFQKV (404)	LSA	HLA-A02:01	534_20T, T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma	annotated_ORF
QTKGGQTWARR (405)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
TVVAALIANPR (406)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
HLMVKDWQL (407)	LSA	HLA-A02:09	T1015A_Melanoma	annotated_ORF
NPLSKLSVL (408)	LSA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
FVIPSTKDSNR ⁹ (409)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
HYQVQTHL (410)	LSA	HLA-C14:02	0D5P_Melanoma_ctrl	annotated_ORF
ASDILSFAHKY (411)	LSA	HLA-A01:01	Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
RLGQGVPLV (412)	LSA	HLA-A02:09, HLA-A02:01	T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma	annotated_ORF
SVPDHVQPSK (413)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Frameshift
RLLEKHISL (414)	LSA	HLA-A32:01, HLA-A02:01, HLA-B08:01	T1015A_Melanoma, T1185B_Melanoma_ctrl, Me290_Melanoma, Me275_Melanoma	annotated_ORF
SLFGVSERL (415)	LSA	HLA-A02:01	Me275_Melanoma	ncRNA
NHYQVQTHL (416)	LSA	HLA-B38:01	542_20T, 0NVC_Melanoma_ctrl	annotated_ORF
DLVGKDVTRVY (417)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	annotated_ORF
SLSPPTLPR (418)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	5UTR
LADNGTLGKY (419)	LSA	HLA-A01:01	Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
KAMYIRVSY (420)	LSA	HLA-A32:01	T1015A_Melanoma	annotated_ORF
MQPKLKQVF (421)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
AIQDGILL (422)	LSA	HLA-A02:01	534_20T	5UTR
AFDRAVHF (423)	LSA	HLA-C12:03, HLA-C04:01, HLA-C14:02	0NVC_Melanoma_ctrl, T1015A_Melanoma, 0D5P_Melanoma_ctrl	ncRNA

NTPNIVSLR (424)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
RVADIPIKPW (425)	LSA	HLA-A25:01, HLA-A32:01	258_20T, T1015A_Melanoma	Frameshift
HYIPLQTI (426)	LSA	HLA-A23:01	0D5P_Melanoma_ctrl	5UTR
VMKGINQGY (427)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	ncRNA
ATSPPASVR (428)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
ALEKDTPRY (429)	LSA	HLA-A01:01	Me290_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
QVMKGINQGY (430)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	ncRNA
AAFDRAVHF (431)	LSA	HLA-C12:03	1713_19T, 542_20T, 0NVC_Melanoma_ctrl, 0D5P_Melanoma_ctrl	ncRNA
RPLRIKGVF (432)	LSA	HLA-B07:02	542_20T, Me275_Melanoma, 0D5P_Melanoma_ctrl	ncRNA
RQVMKGINQGY (433)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	ncRNA
KLDTTVKNI (434)	LSA	HLA-A02:01	Me290_Melanoma, Me275_Melanoma	annotated_ORF _frameshift- 3UTR
LPRTPRPDL (435)	LSA	HLA-B07:02	0D5P_Melanoma_ctrl	ncRNA
ITYTESNSR (436)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
RLQGSVTLV (437)	LSA	HLA-A02:01	Me290_Melanoma	ncRNA
SQFPSKNLPAF (438)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	ncRNA
LPRTPRPDLIL (439)	LSA	HLA-B07:02	0D5P_Melanoma_ctrl	ncRNA
DTAPQSHQV (440)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	ncRNA
MAILGTAGR (441)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Introns
SVSSHLIHR (442)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
STSPGTGVRK (443)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
EVAEVLGSVK (444)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
EIPRTPSEGR (445)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
VFLKFSRRF (446)	LSA	HLA-A23:01	Me275_Melanoma, 0D5P_Melanoma_ctrl	ncRNA
SVSSHLIHR (447)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	ncRNA
THLEDPLHM (448)	LSA	HLA-B38:01	0NVC_Melanoma_ctrl	ncRNA
SVFPRTSSR (449)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
GQYGQSKPWTF (450)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
VPRPTSTVGL (451)	LSA	HLA-B07:02	Me275_Melanoma, 0D5P_Melanoma_ctrl	annotated_ORF
NSVSSHLIHR (452)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	ncRNA
QEEDNLLRYF (453)	LSA	HLA-B44:02	1836_18T	ncRNA
THLEDPLHML (454)	LSA	HLA-B38:01	0NVC_Melanoma_ctrl	ncRNA
ATTNILEHV (455)	LSA	HLA-B13:02, HLA-A02:01	Me290_Melanoma	annotated_ORF
MTLRPTQPR (456)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
ETRPNN SKF (457)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	ncRNA
HSITEPLLY ¹⁰ (458)	LSA	HLA-A01:01	0D5P_Melanoma_ctrl	Introns
HLFLQPPSKR (459)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
ETVRFTSSF ¹¹ (460)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	5UTR
SPMPIPLYL (461)	LSA	HLA-B07:02	0D5P_Melanoma_ctrl	ncRNA
ESYGRYTFY (462)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	Introns
KSQGSFISF (463)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	Introns
GTILHIGVF (464)	LSA	HLA-A25:01	1713_19T	retained_intron
KVFSGSSKR (465)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF

SSFSTLASLDK (466)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
TTQGAAPQR (467)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Introns
HTTQGAAPQR (468)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Introns
KIFQERAAF (469)	LSA	HLA-A32:01	T1015A_Melanoma	5UTR
GQITHNTSF (470)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	annotated_ORF
ISLKPLIARY (471)	LSA	HLA-A30:02	0MM745_Melanoma_ctrl	Introns
KHSDLILFW (472)	LSA	HLA-C07:01	T1015A_Melanoma	3UTR
MVWEGHPRER (473)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
STDLPILLK (474)	LSA	HLA-A01:01	Me290_Melanoma	ncRNA
EVISINTGHF (475)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	Intergenic
ETERVLEKSSY (476)	LSA	HLA-A01:01	0D5P_Melanoma_ctrl	annotated_ORF
KIKTINLRY (477)	LSA	HLA-B15:01	0D5P_Melanoma_ctrl	Introns
YVSQKVSD (478)	LSA	HLA-C07:02	Me275_Melanoma	Introns
DAGIPVYHR (479)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
TILEAEILHQA (480)	LSA	HLA-B49:01, HLA-A02:01	T1015A_Melanoma, Me275_Melanoma	Introns
EYAQKTPLF ¹² (481)	LSA	HLA-A24:02, HLA-A23:01	1758_19T, Me275_Melanoma, 0D5P_Melanoma_ctrl	Introns
TWTPHGIRI (482)	LSA	HLA-A23:01	0D5P_Melanoma_ctrl	Introns
EVHEGGVARF (483)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
REIEIEGRL (484)	LSA	HLA-B49:01	T1015A_Melanoma	ncRNA
SWLPIPAKY (485)	LSA	HLA-A30:02	0MM745_Melanoma_ctrl	annotated_ORF
RYSERVYTI (486)	LSA	HLA-A23:01	0D5P_Melanoma_ctrl	annotated_ORF
FTDSQGNDIK (487)	LSA	HLA-A01:01	Me290_Melanoma	annotated_ORF
SVPSDFLSLR (488)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Intergenic
RQMSLEFRA (489)	LSA	HLA-A02:01	Me275_Melanoma	Introns
ETISPRPSI (490)	LSA	HLA-A25:01, HLA-A26:01	1713_19T, 0NVC_Melanoma_ctrl	ncRNA
GPAGGRGVI (491)	LSA	HLA-B07:02	0D5P_Melanoma_ctrl	annotated_ORF
LTDHHIKEY (492)	LSA	HLA-A01:01	Me290_Melanoma	Introns
EAVPYNGSLFK (493)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	ncRNA
NLLAEIHGV (494)	LSA	HLA-A02:09, HLA-A02:01	T1015A_Melanoma, Me290_Melanoma, Me275_Melanoma	annotated_ORF
KEGPVTRGA (495)	LSA	HLA-B49:01	T1015A_Melanoma	5UTR
VHVDLNLGF (496)	LSA	HLA-B38:01	0NVC_Melanoma_ctrl	Introns
HTVQGLAGF (497)	LSA	HLA-A26:01	0NVC_Melanoma_ctrl	Introns
MR ¹ IEDSHTKL ¹³ (498)	LSA	HLA-B38:01	0NVC_Melanoma_ctrl	ncRNA
SALSSAQPR (499)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	annotated_ORF
SPSIKSLLVY (500)	LSA	HLA-A01:01	Me290_Melanoma	Introns
PTDATLNRLLY (501)	LSA	HLA-A01:01	0D5P_Melanoma_ctrl	annotated_ORF
WTSQPPNYEK (502)	LSA	HLA-A68:01	T1185B_Melanoma_ctrl	Introns
PAPRPVAPTL (503)	LSA	HLA-B07:02	0D5P_Melanoma_ctrl	Introns
VYLHSNSTL (504)	LSA	HLA-C14:02	0D5P_Melanoma_ctrl	Intergenic
SLYAWTQSH (505)	LSA	HLA-A03:01	0NVC_Melanoma_ctrl	Intergenic

¹ Reference peptide: ATYGGSDDYI² Reference peptide: HL²RDYFEEY³ Reference peptide: NEY³PNITRLY⁴ Reference peptide: RLLAD⁴PTGA5 ⁵ Reference peptide: TPLSP⁵GPTL

- 6 Reference peptide: VCLDRAVSI
- 7 Reference peptide: RLKATPSTY
- 8 Reference peptide: RLWGSIQSRV
- 9 Reference peptide: FVIPSMKDSNR
- 5 10 Reference peptide: HSIMEPLLY
- 11 Reference peptide: ETVKFTSSF
- 12 Reference peptide: EYAQKTLLF
- 13 Reference peptide: MHIEDSHTKL

10 **Table 2B: characteristics of the TSAs, TAAs and LSAs identified herein (continued)**

Peptide (SEQ ID NO:)	Gene	Gene ID	Nucleotide (SEQ ID NO:)
1	NA	NA	ACTCTCGATGACGCCGTCACGGCGTT (506)
2	ZYG11AP1	ENSG00000232242	TACCAAATTGGCCAAGTTCAAGGTGTA (507)
3	CPD	ENSG00000108582	AATGAATATTCTAACATTACCCGGCTTTAT (508)
4	PRDX5	ENSG00000126432	CGGCTCCTGGCTGATCTCACTGGGGCC (509)
5	KIAA0895L	ENSG00000196123	ACTCCATTGTCTCCTGACCCACCCCTC (510)
6	GAGE12C; GAGE12G	ENSG00000237671; ENSG00000215269	TCGACCTATTATTGGCCTAGACCAAGG (511)
7	XAGE1B	ENSG00000204382	GATTCTTTCTCCGCTACTGAGACACGG (512)
8	MAGEA6	ENSG00000197172	GAAACCAGCTATGTGAAAGTCCTGCAC (513)
9	MAGEA6	ENSG00000197172	GCAGAAATGCTGGGGAGTGTCGTC (514)
10	MAGEA3	ENSG00000221867	GAGGAGCTGAGTGTGTTAGAGGTGTTT (515)
11	MAGEA6; MAGEA3	ENSG00000197172; ENSG00000221867	TTCGTGCAGGAAAACCTACCTGGAGTAC (516)
12	PAGE5	ENSG00000158639	ATTGTCCAGCAGCCCACTGAGGAAAAA (517)
13	MAGEA12; MAGEA2	ENSG00000213401; ENSG00000268606	AGTGTCTTTGCGCATCCCAGGAAGCTG (518); AGTGTCTTCGCACATCCCAGGAAGCTG (519)
14	MAGEA3	ENSG00000221867	GCCTCCAGCCTCCCCACTACCATGAACCTAC (520)
15	PAGE5	ENSG00000158639	ATTGTCCAGCAGCCCACTGAGGAAAAACGT (521)
16	MAGEA3	ENSG00000221867	CTCCCCACTACCATGAACCTACCTCTC (522)
17	MAGEA4	ENSG00000147381	GGCAGTAATCCTGCGCGCTATGAGTTC (523)
18	MAGEC2	ENSG00000046774	ACCGCAGATGATGCCACTGTCATG (524)
19	MAGEA4	ENSG00000147381	GTCTTGAGCATGTGGTCAGGGTC (525)
20	MAGEA3	ENSG00000221867	GAAGTGGACCCCATCGGCCACTTGTAC (526)
21	MAGEA3	ENSG00000221867	CAGATCATGCCCAAGGCAGGCCTC (527)
22	MAGEA4	ENSG00000147381	AAAGTCCTGGAGCATGTGGTCAGGGTC (528)
23	MAGEA4	ENSG00000147381	CAGGTACCCGGCAGTAATCCTGCGCGC (529)
24	MAGEC2	ENSG00000046774	TTCGTCTATGGGGAGCCTAGGGAGCTC (530)
25	PAGE5	ENSG00000158639	ACTCTGCCCACTTTTGATCCCACTAAAGTG (531)
26	MAGEA6	ENSG00000197172	AATCAGATCATGCCCAAGACAGGCTTC (532)
27	MAGEA6	ENSG00000197172	GAAGTGGACCCCATCGGCCACGTGTAC (533)
28	CTAG2	ENSG00000126890	GAGCTGGTCCGCAGGATCCTGTCCCGG (534)
29	MAGEA3	ENSG00000221867	ATGGAAGTGGACCCCATCGGCCACTTGTAC (535)
30	MAGEC2	ENSG00000046774	AGTGTCTATGTCAGCAACGTCTCCTTT (536)
31	MAGEC2	ENSG00000046774	ACTGTTCTAGTTCCTTTCCATCCTGG (537)
32	MAGEC2	ENSG00000046774	AAGTACAAAGATTACTTTCTGTGATA (538)
33	MAGEA6	ENSG00000197172	ATGGAAGTGGACCCCATCGGCCACGTGTAC (539)
34	MAGEA4	ENSG00000147381	ACTGTCTATGGGGAGCCCAGGAAACTG (540)
35	PAGE5	ENSG00000158639	GGTCTGATGTCAGGGAGGGGACTCTG (541)
36	MAGEA4	ENSG00000147381	GTGTATGATGGGAGGGAGCACACTGTC (542)
37	MAGEA3	ENSG00000221867	CTGATGGAAGTGGACCCCATCGGCCACTTGTAC (543)
38	MAGEC2	ENSG00000046774	AAGTACAAAGATTACTTTCTGTGATACTCAAG (544)
39	MAGEA6	ENSG00000197172	GAGGTGTTTGAGGGGAGGGAAGACAGTATCTTC (545)

40	MAGEA4	ENSG00000147381	GGGGTGTATGATGGGAGGGAGCACACTGTC (546)
41	MAGEA2; MAGEA2B	ENSG00000268606; ENSG00000183305	GAAGTGGTCCCCATCAGCCACTTGTAC (547)
42	MAGEC2	ENSG00000046774	AATGCAGTAGGGGTATATGCTGGGAGG (548)
43	CTAG2	ENSG00000126890	AGGCCGGACAGCCGCTGCTTGAGTTG (549)
44	MAGEA2	ENSG00000268606	AGTGTCTTCGCACATCCCAGGAAGCTGCTCATG (550)
45	MAGEA2; MAGEA2B	ENSG00000268606; ENSG00000183305	GAGGTGTTTGAGGGGAGGGAGGACAGTGTCTTC (551)
46	FRG2DP	ENSG00000261711	CGAGTATCTCACTCACATGCTTCTTTT (552)
47	LINC00578	ENSG00000236385	GCCACCTTTTTGCAGAGGAAGGTACTGAGG (553)
48	MAGEA12	ENSG00000213401	AGCTATGTGAAAGTCCTGCACCATTTG (554)
49	MAGEC1	ENSG00000155495	TTTGCCTTTGGGGAGCCCAGGGAGCTC (555)
50	MAGEA12	ENSG00000213401	AAGATGGCTGAGTTGGTTCAATTTCTG (556)
51	PRSS56	ENSG00000237412	TTTGCCACGGGCACCCACTGTACACACGC (557)
52	MAGEC2	ENSG00000046774	GGGGTATATGCTGGGAGGGAGCACTTCGTC (558)
53	AC026355.3	ENSG00000236385	AACACTGCTATTGCCACCTTTTTGCAGAGGAAG (559)
54	MAGEC2	ENSG00000046774	ACACTAGATGAAAAGGTGGCCGAGTTA (560)
55	CTAG2	ENSG00000126890	CGCCTGCTTGAGTTGCACATCACGATG (561)
56	MAGEC1	ENSG00000155495	GAGGTGCCCAACTCTTCTCCTCCTCGT (562)
57	MAGEA12	ENSG00000213401	GTGGAAGTCACCCTGCGGGAGGTG (563)
58	MAGEA6	ENSG00000197172	ATCAGTGGAGGACCTCGCATTTCTCTAC (564)
59	NA	NA	GGAGTCCCCGGACCCCTCCTCATCCTTCCCAGG (565)
60	MAGEB2	ENSG00000099399	GGAGTCTATGATGGAGAGGAGCACTCAGTC (566)
61	MAGEA6	ENSG00000197172	AAGATCAGTGGAGGACCTCGCATTTCTCTAC (567)
62	FRG2DP	ENSG00000261711	TTTCTATATAATCAGACAAAATTAGGATG (568)
63	ITIH6	ENSG00000102313	GGCCAGTACCAGCTGGTGGTGAGCCTG (569)
64	MAGEA2	ENSG00000268606	GGAGTTGATGACCTTGTTTCAGAAGG (570)
65	MAGEA1	ENSG00000198681	AAAGTCCTTGAGTATGTGATCAAGGTC (571)
66	NA	NA	CACACTTTACCAGCCCTTTCTAGAAGG (572)
67	MAGEA1	ENSG00000198681	GCTTTGAGAGAGGAGGAAGAGGGAGTC (573)
68	MAGEA1	ENSG00000198681	ACTACCATCAACTTCACTCGACAGAGG (574)
69	MAGEA1	ENSG00000198681	AGTGCCTATGGGGAGCCCAGGAAGCTG (575)
70	PRSS56	ENSG00000237412	AGCACTGCCAATGTGACGCGGGCCAC (576)
71	MAGEA1	ENSG00000198681	TCCGCCTTTCCCACTACCATCAACTTC (577)
72	MAGEA1	ENSG00000198681	TTCCGAGCAGTAATCACTAAGAAGGTG (578)
73	MAGEB2	ENSG00000099399	GCGGCTGCGGGTGTTCATCCACAAAA (579)
74	MAGEA1	ENSG00000198681	TTTCCCACTACCATCAACTTCACTCGA (580)
75	SSX2	ENSG00000241476	ACTACCTCTGAGAAGATTCACGAGAGA (581)
76	MAGEA10	ENSG00000124260	GGGCTGTATGATGGGATGGAGCACCTC (582)
77	PRSS56	ENSG00000237412	AGCACTGCCAATGTGACGCGGGCCACGGCCGC (583)
78	ITIH6	ENSG00000102313	ATAGAGGACCCAAAGGCAGGGCTGCATGTG (584)
79	FAM178B	ENSG00000168754	GGTGTGGTGGGCCCCCAGGGCCTGAGG (585)
80	AL035541.1	ENSG00000227297	AATGTATTTGCTCATGCAACTGGGGAATCAAGG (586)
81	MAGEA11	ENSG00000185247	TTCCTCTTTGGGGAGCCCAAGAGGCTC (587)
82	MAGEA1	ENSG00000198681	TCCGCCTTTCCCACTACCATCAACTTCACTCGA (588)
83	NA	NA	AGGCTCTTCTCAGAAGACATACATGTC (589)
84	AL390957.1	ENSG00000285280	GTTTACATGCCTGCTAATACAACATTT (590)
85	LINC00221	ENSG00000270816	GAGGCTGTGGGCTTTCAACCACCACGA (591)
86	MAGEA11	ENSG00000185247	GAAGTGGACCCCACTAGCCACTCCTAT (592)

87	ZNF560	ENSG00000198028	TTACTGGACCCAGCTCAGAGAAACCTGTAC (593)
88	TRIM48	ENSG00000150244	TCTGGAATCTCGCAAGTCTTCCAGAGG (594)
89	NA	NA	AGGCTCTTCTCAGAAGACATACATGTCGCC (595)
90	LINC00326	ENSG00000231023	GTGTTTGATGTTGGCAAAGGAAACATG (596)
91	SSX2	ENSG00000241476	AAAGCCTCGGAGAAAATCTTCTATGTG (597)
92	LINC00221	ENSG00000270816	GAGGCCGCCGCTGCCTTCAGGTTTCCGAGA (598)
93	NA	NA	ATGAGTATCTCCATGTCTTTATTGAAA (599)
94	AL162457.2	ENSG00000225106	AAGGCATCCCCCAGCTCTCTGCCTCAT (600)
95	ZNF560	ENSG00000198028	AGAACCCTTGCAAGGAGTTCTCCAAGACTGG (601)
96	MAGEB1	ENSG00000214107	ACTACTGCCACGACTTTTAGAGCGCGT (602)
97	NA	NA	AATCCTAGCCATCTCATCACACCCAGA (603)
98	LINC00221	ENSG00000270816	GAGACAATGGAGACTCTGAGAACATCCAGA (604)
99	AC011294.1	ENSG00000233539	ATGGTATGGGAGGGGCATCCCAGAGAAAGA (605)
100	ACTL8	ENSG00000117148	CTCCCAGACGGCTCCCGCGTGGAGCTG (606)
101	CT55	ENSG00000169551	GATGTTGTGACTGGCAACGTGCCTCTAAAA (607)
102	NA	NA	GAGAATCCTAGCCATCTCATCACACCCAGA (608)
103	LHFPL3	ENSG00000187416	TCACTGGCCAGGACTATACTCCATCTC (609)
104	CT55	ENSG00000169551	AAACCACATTATGGATTGAGAGCAATC (610)
105	NA	NA	GCCTTTCTGGACATCCACACAGCCCTG (611)
106	PACIN2	ENSG00000100266	AAGATGTCAGAGTTTGTCTACAGATTT (612)
107	CNIH3	ENSG00000143786	TTTTTAGTGACAAAGACTGTGACTATG (613)
108	AC023824.3	ENSG00000260958	CACACCACCTCTGTGATGGAGAACAAG (614)
109	NA	NA	CTTGTGAGCATTCCCATTGCAGTAAGA (615)
110	NA	NA	ATTACATCAGGAGTAAAAGTGAAGAAA (616)
111	NA	NA	GTGAGCATTCCCATTGCAGTAAGAAGA (617)
112	SLC25A24P1	ENSG00000241361	GACATCATTGAGCTCCAGGAGGGGCTGAGA (618)
113	NA	NA	CATCTCAAGCCTCCAGAGCTGGGCTTC (619)
114	IGF2BP1	ENSG00000159217	CAGGTCATCGTGAAAATCATCGGACAT (620)
115	IGF2BP1	ENSG00000159217	GCCGAGCAGGAAATAATGAAGAAAGTT (621)
116	IGF2BP1	ENSG00000159217	GAGGTTCCCCTGAAGATCCTGGCCCAT (622)
117	IGF2BP1	ENSG00000159217	ATCGTGAAAATCATCGGACATTTCTAT (623)
118	NA	NA	TCTCTGTGAGCATTCCCATTGCAGTAAGA (624)
119	NA	NA	ATGTTTCTCCTGGAGTTTCTCTATTCAA (625)
120	AKAP6	ENSG00000151320	GTGTTGATGATGAAGTTGGAAGTTTG (626)
121	PTCHD4	ENSG00000244694	TATTCGGAATTACACACCCCTGGGAGGTAT (627)
122	ACCSL	ENSG00000205126	GAAGTGGCCCGGTTCTGACCTACTAC (628)
123	FAM230C	ENSG00000279516	AGTGTGCGGAGACCTCATGGCTCCCCGG (629)
124	LINC02434	ENSG00000248370	GTGCTCTGGAGAGGTGACTCTCCTCTA (630)
125	IGF2BP1	ENSG00000159217	CAGCCCCGCCAGGGCTCACCTGTGGCAGCG (631)
126	LINC01320	ENSG00000228262	AAACAAACAGGTATTAGGCACAGTTAT (632)
127	NA	NA	AGACCCAGACAAGATGCCATTTCACTA (633)
128	AC093791.1	ENSG00000250038	AAACTGATAACACAGATACGTACAGCA (634)
129	SUGCT-AS1	ENSG00000203446	TCTATTTGTCTGAGCACTCTGCAGCTATTTT (635)
130	FAM230C	ENSG00000279516	ACCAGTGTGCGGAGACCTCATGGCTCCCCGG (636)
131	MAGEA6-DT	ENSG00000286051	GAGATACCAACTGGGGTGGCCAAGCGG (637)
132	PTCHD4	ENSG00000244694	AGTCAAATCAACCTTAGCCAAATTTAT (638)
133	NA	NA	CGAAGACCCTCAGGCGGTTCCGGCTC (639)
134	NA	NA	GAAGTATTTAATGTAAAAAATACATTTCCAAAG (640)
135	L3MBTL4-AS1	ENSG00000264707	AAGGTCTTAGGAGGTGGATGGACTGTC (641)
136	LAD1_pseudogene	ENSG00000267389	CATGAGGCTCCTGGCCAGCACAGTGAAGTT (642)

137	AC116424.1	ENSG00000250129	GAAGTAAGCCACCCTAACATGAGTGGCAGA (643)
138	LINC02109	ENSG00000259786	GACACAGCCCCAGCCACCTTCCTACGG (644)
139	LINC02199	ENSG00000250198	AAACCCCAAAAAGACCTGCACTTCATA (645)
140	novel_gene	ENSG00000289352	CGAGTGCGTGGGGCAGGAACACACCTG (646)
141	NA	NA	ACGGCTCCCATTTATTGTGGCTCAGAGA (647)
142	METTL9	ENSG00000197006	ACGAGCTGGGATACCAAGTTCTATGAAAAG (648)
143	IGF2BP1	ENSG00000159217	AAAGTGTTCGCGAGCACAAGATCTCCTAC (649)
144	NA	NA	GACGCCTTCAGGGCATCGCCAACAGG (650)
145	TEX13C	ENSG00000282815	ATTGTGGCCGACCCGCGGGTGCCCCGT (651)
146	CCL17	ENSG00000102970	ACAGGCTTCTCCACGAGCCTGGGCAGA (652)
147	NA	NA	GCCACGGCTCCCATTTATTGTGGCTCAGAGA (653)
148	IGF2BP1	ENSG00000159217	GGCCAGTTCCTTGGTCAAATCCGGCTAC (654)
149	NA	NA	TGGACTTCCAGAACGGTGCAAAATAAA (655)
150	RICTOR	ENSG00000164327	GCCACATATGGGGTTTCAGATCATTACATT (656)
151	SMC1B	ENSG00000077935	GTTTACATTGCAGAGTTGGAAAAGATA (657)
152	BIRC7	ENSG00000101197	GTGTTCTGGACCGCGCCGTGTCCATC (658)
153	AC106771.1	ENSG00000248783	ATGCCAGTCCCATCGACCACCAAGG (659)
154	NA	NA	GAAGCAGTAAGGCACATCTTACATGGCAGCAGG (660)
155	NLRP4	ENSG00000160505	TACCCAGCAGGCAACGTCAAAGAGCTA (661)
156	LINC02260	ENSG00000250456	AGCGTACCCAGAAGCCTGGCATCCCCGG (662)
157	GBX2-AS1	ENSG00000233611	GCGCTAATTAAGCACGTTGCGAACGCA (663)
158	MAGEA4-AS1	ENSG00000229967	TACACGGCAAATCTGGTTCCAGTTAGA (664)
159	NA	NA	TTGTCCTCTTCCCTTGTCAACCAAACTT (665)
160	WIPF1	ENSG00000115935	CAGAACAGTAATGTTTTCAGTGAGG (666)
161	AP003900.1	ENSG00000277693	ACGACAACAAAAACACCTTGAAACAAA (667)
162	NA	NA	CACAATTATATTAATTTGCATTCTCTG (668)
163	HNRNPA2B1	ENSG00000122566	CACCTTAAAGATTACTTTGAGGAATAT (669)
164	NA	NA	TCTCCAGAATATTTTACCAGCTATCTG (670)
165	novel_gene	ENSG00000287550	GCCACAGATGTTTTGGACCACTTATAT (671)
166	NA	NA	CAGACCTTTGAGGAATCACTGGGAAGA (672)
167	CST1	ENSG00000170373	CATGAACAGCCAGAAGTGCAGAAAGGTA (673)
168	novel_gene	ENSG00000287550	ATGGCCACAGATGTTTTGGACCACTTATAT (674)
169	NA	NA	ACTTCTGGCAGTCTCCTGTTTCCAGAG (675)
170	NLRP4	ENSG00000160505	AAGCTTGGAATAAATAACGTTTCCTTT (676)
171	NA	NA	AAATATATTTTCAATTTCAAGTATTC (677)
172	NA	NA	CAGACTGCGGCTGTGTGCGGAGTAAAG (678)
173	NA	NA	TTGACACCATTAAACCATCCTTTTTCTAC (679)
174	NA	NA	GTATTTATAAATAAAAAGTACGTTTTT (680)
175	NA	NA	AACCTCATCACTGAGGAGCATCCTGTC (681)
176	AL807740.1	ENSG00000283400	GAGTTAGTGAAGGTCATTGATGGAAGCTCCAGG (682)
177	NA	NA	TTTCACTCACTTCCAATTCATTTGTTT (683)
178	NA	NA	TATTCTCATGATTACTCTTACTAT (684)
179	novel_gene	ENSG00000286099	TTCCAGATAGAAAAATTGACACCCCTG (685)
180	AL137220.1	ENSG00000225775	GAGCACTCTGTTGAAAATGGCAGTATT (686)
181	LINC00466	ENSG00000224209	GAGACAATTCAAAACACACATTCATTT (687)
182	AC018558.1	ENSG00000260857	TACTACAGTATTTGGAAGACACAAATT (688)
183	AC003092.1	ENSG00000236453	TCTTATTATTTTACGGCCTGTCAATTT (689)
184	novel_gene	ENSG00000287308	GAGTCTTTTCAACAACCTTATATCCCAGG (690)
185	RUVBL1	ENSG00000175792	AAACAGGTACCCTCTAGGGTCTCTAC (691)
186	GPR158	ENSG00000151025	ATGTTATTTAATAAAGATTTGGATGCAGCA (692)
187	NA	NA	GCCCCACGGTCAGCAGAGCCACGGGCCACC (693)
188	NA	NA	TATCTGGATCCTGGGGCAGTGCATGCAGTGTTC (694)
189	ZNF716	ENSG00000182111	ACCCCTTAAGAAACATAAGATAGTT (695)
190	NA	NA	GTGGGTGTGCCAATCAGCACTCTGTAT (696)

191	NA	NA	AGCCCCCGCCCCCAGCCAGAGCTC (697)
192	NA	NA	AAGCTTTCCTTCCCTGATTCAAAATTT (698)
193	SEMA3A	ENSG00000075213	AAAAACAAAGATGAATATATCCATTTTAC (699)
194	LINC00511	ENSG00000227036	AGGGCATTGAGGGGAGAAGAAGAGGATGG (700)
195	PRRC2A	ENSG00000204469	CGTCTCAAGGCCAGGCCTTCCACCTAC (701)
196	novel_gene	ENSG00000287308	GCCCCCTCTCTTCACGCCACACTC (702)
197	NA	NA	GCGCAGAAAGAACCCACTGGCAATTAC (703)
198	NA	NA	CTCTCACTGGGTACCACAGCTTGCAGG (704)
199	NA	NA	AGCAGAAACCCTACAAGCTACAAGTAT (705)
200	TEX15	ENSG00000133863	AGCCTAAATAATGACGATCACCAGATATAC (706)
201	IL23R	ENSG00000162594	TATGTTGATCCCATGATTACAGAGATA (707)
202	NA	NA	CCCAGCTTTTCTCCATATGCAAAAAGG (708)
203	CTSB	ENSG00000164733	CACGTCAACGGCTCCCGCCCCATGCACGG (709)
204	MIR4307HG	ENSG00000257612	ATAACAGTGAGATTGGCTCCTCCACTC (710)
205	LINC02941	ENSG00000236013	TCAGCCAATCCCCTAAGTCATAGATAC (711)
206	PMEL	ENSG00000185664	GTGCCTCTTGCTCATTCCAGCTCAGCC (712)
207	PMEL	ENSG00000185664	GGCCAAGTGCCTACTACAGAAGTTGTG (713)
208	PMEL	ENSG00000185664	AAGACCTGGGGCCAATACTGGCAAGTT (714)
209	PMEL	ENSG00000185664	GCCTTGAACCTCCCTGGAAGCCAAAAG (715)
210	PMEL	ENSG00000185664	TATGTCTGGAAGACCTGGGGCCAATAC (716)
211	PMEL	ENSG00000185664	ATGCCAACTGCAGAGAGCACAGGTATG (717)
212	PMEL	ENSG00000185664	CACACCATGGAAGTGACTGTCTACCATCGCCGG (718)
213	MLANA	ENSG00000120215	GAAGAGGCCGCTGGGATCGGCATCCTG (719)
214	MLANA	ENSG00000120215	GAAGGGTTTGATCATCGGGACAGCAAA (720)
215	MLANA	ENSG00000120215	GCTGAAGAGGCCGCTGGGATCGGCATCCTG (721)
216	MLANA	ENSG00000120215	CTCACTTCATCTATGGTTACCCCAAGA (722)
217	MLANA	ENSG00000120215	ACTTCATCTATGGTTACCCCAAGAAGG (723)
218	PRAME	ENSG00000185686	GGGCTGAGCAATCTGACCCACGTGCTG (724)
219	PRAME	ENSG00000185686	CAGCTCCTTGCCCTCCTGCCTTCCCTG (725)
220	PRAME	ENSG00000185686	GAAGCAGCTCAGCCCATGACAAAGAAG (726)
221	PLA1A	ENSG00000144837	AGGGTTTTAGGAACAAAGCCTTCCTGG (727)
222	PRAME	ENSG00000185686	GTGCTGTATCCTGTCCCCCTGGAGAGTTAT (728)
223	PRAME	ENSG00000185686	CCTTACCTGGGCCAGATGATTAATCTG (729)
224	PRAME	ENSG00000185686	GAATTGTTCTCCTACCTCATTGAGAAA (730)
225	PRAME	ENSG00000185686	GAAGAGCAGTATATCGCCAGTTC (731)
226	PRAME	ENSG00000185686	GAAGCAGCTCAGCCCATGACAAAGAAGCGA (732)
227	PRAME	ENSG00000185686	ATGCCCATGCAGGATATCAAGATGATC (733)
228	PRAME	ENSG00000185686	CGGCTTTCGGAAGGGGATGTGATGCATCTG (734)
229	PRAME	ENSG00000185686	CATGCATCTTCTACATTTCCCCGGAGAAG (735)
230	PRAME	ENSG00000185686	ATGCCCATGCAGGATATCAAGATGATCCTG (736)
231	PRAME	ENSG00000185686	AGTCCCAGCGTCAGTCAGCTAAGTGTCCTG (737)
232	PRAME	ENSG00000185686	CGCCTGGATCAGTTGCTCAGGCACGTG (738)
233	PRAME	ENSG00000185686	GCTCTGCTGGAGAGAGCCCTGCCACCCTC (739)
234	VGf	ENSG00000128564	ACCGTCGCTCCTACCCCGCCACCGCTCGG (740)
235	PRAME	ENSG00000185686	TCCCAGAGTCCCAGCGTCAGTCAGCTA (741)
236	VGf	ENSG00000128564	TCGACCGTCGCTCCTACCCCGGCCACCGCTCGG (742)
237	PRAME	ENSG00000185686	CAGTATATCGCCAGTTACCTCTCAGTTC (743)
238	PRAME	ENSG00000185686	GGACAACATCTTCACCTGGAGACCTTC (744)
239	SLC24A5	ENSG00000188467	ACAATTGCAAGTGTGTTGTTGCAAGA (745)
240	PRAME	ENSG00000185686	AGTCTCCTGCAGCACCTCATCGGGCTG (746)
241	XAGE1B	ENSG00000204382	ACAGCCAGTCCCAGGAGCCCAGTAATG (747)

242	PRAME	ENSG00000185686	GCAGCCTTTGACGGGAGACACAGCCAGACCCTG (748)
243	PRAME	ENSG00000185686	AGCCACGAGACTTGTGGAGCTG (749)
244	PRAME	ENSG00000185686	CTCTATGTGGACTCTTTATTTTCCTT (750)
245	DCT	ENSG00000080166	GTCTTCCTGAGAGAATTTCTAATTTT (751)
246	CHCHD6	ENSG00000159685	AGGCCAGATTCTCCACTGCTACCGAGATCGCC (752)
247	SLC45A2	ENSG00000164175	GCTTTGATTGCTAACCCAAGGAGGAAG (753)
248	SLC45A2	ENSG00000164175	GATTTTCATGGGCCAGATTGTGTACCGC (754)
249	SLC24A5	ENSG00000188467	GAAATTCCTGATACAGTAATGGGCCTT (755)
250	SLC45A2	ENSG00000164175	GTAATGTCCAGCACCTGTACACTGTG (756)
251	CA14	ENSG00000118298	TCACCTCAGCACAAGCCACGACTG (757)
252	CHCHD6	ENSG00000159685	GAGCCTAAGCCACCCACCACAGGGCTT (758)
253	SLC24A5	ENSG00000188467	ATACCAGACACAATTGCAAGTGTGTTG (759)
254	SLC45A2	ENSG00000164175	ACAGATTTTCATGGGCCAGATTGTGTACCGC (760)
255	LHFPL3-AS1	ENSG00000226869	GGAGAAGATGATGAACACAGAAAAATT (761)
256	PRAME	ENSG00000185686	CGTTTGCGGGGTTCCATTGAGAGCCGATAC (762)
257	ETV4	ENSG00000175832	CACTTGATGAGAGCCCCGCCTACCTC (763)
258	LHFPL3-AS1	ENSG00000226869	AAGATGGAAGAACTACGGTCACATAT (764)
259	ROPN1B	ENSG00000114547	CTCCCAACAGATCTGTTTAATAGTGTG (765)
260	CA14	ENSG00000118298	AGGCCTCAGGGCCTGGCTGTCTCTG (766)
261	CSAG1	ENSG00000198930	AGTCTATCTGAAAAGTCTCCAGAAGTC (767)
262	ETV4	ENSG00000175832	GGTGCAATTCGAGAGGGGCCGCCCTAC (768)
263	SLC45A2	ENSG00000164175	TACCTCAATGGGGCTACTGTTGTAGCA (769)
264	ETV4	ENSG00000175832	TCAATGTACCTCCACACAGAGGGCTTC (770)
265	CA14	ENSG00000118298	CACATTCTGAGTCACTTGATGAAGTC (771)
266	SLC45A2	ENSG00000164175	AGTATCTCTGAAGCCCCACTTACAGAGGTT (772)
267	CA14	ENSG00000118298	CACCAGATCAACAGTGAAGCCACATTT (773)
268	ETV4	ENSG00000175832	GACATCAAGCAGGAAGGGGTCGGTGCATTT (774)
269	ROPN1B	ENSG00000114547	AGCGCTCTGGGAGTTACTATTACCAAA (775)
270	ROPN1	ENSG00000065371	ACAGTGAATGACTTTACCCAAAACCCAGG (776)
271	CA14	ENSG00000118298	TCTTTCATCCAAGCAGGATCCTCGTAT (777)
272	ROPN1B	ENSG00000114547	GGAGTTACTATTACCAAACTCTCAAG (778)
273	CA14	ENSG00000118298	GCTGAGAGGCCTCAGGGCCTGGCTGTC (779)
274	CSAG1	ENSG00000198930	AGGGAAAAGGGACCCGTCAGGAAGTT (780)
275	CA14	ENSG00000118298	ACCTCAGTGCCTCCCTTCAACCTAAGA (781)
276	LINC00520	ENSG00000258791	TTATCACGCCTTCCAAGCATTGCCTTT (782)
277	BANCR	ENSG00000278910	TTCCCAGTTTCATGCTGCTGAGAAGTTC (783)
278	ROPN1	ENSG00000065371	GGGGAGATCTCTGCATCACATGTC (784)
279	CA14	ENSG00000118298	GCTGCAGATGGGGGTCAACACTGGACGTAT (785)
280	ROPN1	ENSG00000065371	GAGATCTCTGCATCACATGTCAGCAGG (786)
281	ROPN1	ENSG00000065371	TCGCCCCGGATCCCGTTTCAGCACCTTC (787)
282	ETV4	ENSG00000175832	AAGCTCATGGACCCGGGCTCCCTGCCGCCCTC (788)
283	ALX1	ENSG00000180318	GAAACAAAGCCAGAGTTTGAAAGGAGG (789)
284	SLC6A15	ENSG00000072041	GAGACGATCATGAAATTTTGAAATG (790)
285	NA	NA	AGGCGCGCCCACTTTGGAGACTTTT (791)
286	CENPF	ENSG00000117724	CATCTCCAGGAAAAGCTGCAGAGTTTG (792)
287	CENPF	ENSG00000117724	GAACTCTCAGTGGTCACAAGTGAGAGA (793)
288	ETV4	ENSG00000175832	TACTTGGACCAGCAAGTGCCCTACACCTTC (794)
289	TRPM1	ENSG00000134160	GAAGCAATTCCTCGAATCCCTCGCTTG (795)
290	ETV4	ENSG00000175832	GGATACTTGACCAGCAAGTGCCCTACACCTTC (796)
291	SLC6A15	ENSG00000072041	AGCCCTAAACTGGGCGGATTGGATTT (797)
292	SLC5A4	ENSG00000100191	TATCCTGAGAAATCACGTGGATGCCCTC (798)
293	ZNF595	ENSG00000272602	ACCACCATTCCCTTCAGCACTCTACGTGAGAGG (799)
294	FAM178B	ENSG00000168754	AGCCTGGGTGCCACAGTCTGCCCTGTAC (800)

295	SLC5A4	ENSG00000100191	TCTCAAAATGGACAATAATCCATTAC (801)
296	ALX1	ENSG00000180318	AAAGCCAAGGAGCACACCGCCAATATTTTCATGG (802)
297	ENTHD1	ENSG00000176177	AGGGTATCAAAGTCAGATTCTACTTTT (803)
298	IL12RB2	ENSG00000081985	TCCCTCAATTCTCAAGTCACAGGTCTT (804)
299	CENPF	ENSG00000117724	AACTCAGATTTAAGTGAAAAATTGGAATAT (805)
300	PRC1	ENSG00000198901	GACAGTTCCACTGTTGGGCTTCAGCGA (806)
301	ASPM	ENSG00000066279	AGAGCTTCAGCTATTATAATTCAGAGA (807)
302	ENTHD1	ENSG00000176177	TCCCAGGAAACACTTCCACTCAAGATT (808)
303	LRP2	ENSG00000081479	AGCACCTTTGATGGTTTAGACAGAAGA (809)
304	ENTHD1	ENSG00000176177	CGAGTGAAGGAGATTGTAATCAACAAG (810)
305	DLGAP5	ENSG00000126787	GCTCAGCCCCACCATGGTGTGCCATAT (811)
306	KIF4A	ENSG00000090889	GAAGTAATACAGTTAAAAGAACGAGACCGTAAG (812)
307	CENPF	ENSG00000117724	GAGGTGAAGGAAAAGACGGAAGCTC (813)
308	RDH8	ENSG00000080511	ACTGACCCTGAGACCCTGCACTAC (814)
309	CENPF	ENSG00000117724	AAAATGAAGGAGAAAACACAAGAGCTT (815)
310	LRP2	ENSG00000081479	AGCACCTTTGATGGTTTAGACAGAAGAAGA (816)
311	CENPF	ENSG00000117724	AAAATGTCAGAGCTGCAGACCTATGTT (817)
312	RDH8	ENSG00000080511	GGCACTGACCCTGAGACCCTGCACTAC (818)
313	IL12RB2	ENSG00000081985	ACAGAGGAAAAGGGGAGCATTTTAATT (819)
314	EXO1	ENSG00000174371	GACACTGCTATGCCTGCCCATTCAAGA (820)
315	PRR11	ENSG00000068489	AAGCTCCAGGAAGCACTGAAGACCATC (821)
316	RDH8	ENSG00000080511	GGCACTGACCCTGAGACCCTGCACTACTTC (822)
317	ARHGAP11A	ENSG00000198826	AGTTTAAAAAATCGAATTGAATCTGTA (823)
318	KIF23	ENSG00000137807	AACCTTAAAGACCCAGTTGGGGTATAC (824)
319	LRP2	ENSG00000081479	TTCACAGAGACCAACCCACAAGTGATAC (825)
320	NA	NA	GAAACCCAGGAGGCAGAGGTTGCAGTGAGCCGA (826)
321	EXO1	ENSG00000174371	TCTCCCAGACCAGAGTCGGGTACTGTT (827)
322	PRC1	ENSG00000198901	TCTGAGTTTGCGAAGGATCCGTCCTC (828)
323	EXO1	ENSG00000174371	AAGGTTATCAAGAAAATTGGACATTAT (829)
324	ASPM	ENSG00000066279	AGGACGTGGCAAACCAGAAAACAGTTT (830)
325	EXO1	ENSG00000174371	GCCATGGCCCACAAAGTAATTAAGCT (831)
326	DEPDC1	ENSG00000024526	AAACTAAAACAGTTTCAGAAGGAATAT (832)
327	CLSPN	ENSG00000092853	TCTCCATTGGAAGATGAAGAGTCATTA (833)
328	CLSPN	ENSG00000092853	AACTCTACAGACTTTACCAGTGACAGA (834)
329	SKA1	ENSG00000154839	GAAACGAAGGATACCAAAGGTCGTTATTTT (835)
330	MCM10	ENSG00000065328	CGGCCTCGAGTATCCTCCACAGAAATG (836)
331	KIF14	ENSG00000118193	TTAATGGACAAATCAAGCACTATTTAC (837)
332	SLC24A4	ENSG00000140090	GGGACCCTCCGGCCGCTCAAAGTTCGCAGG (838)
333	PRC1	ENSG00000198901	ATCCTGAGTGAAGGATCCGTCCTCTC (839)
334	NA	NA	ACAGTCTATAATTTTAGGACTGAAGTT (840)
335	TYR	ENSG00000077498	CTCCCCCTCTTCAGCTGATGTAGAATTT (841)
336	TYR	ENSG00000077498	AGGCTCCCCTCTTCAGCTGATGTAGAATTT (842)
337	MLANA	ENSG00000120215	GCCTTGATGGATAAAAGTCTTCATGTT (843)
338	TYR	ENSG00000077498	ATGCACAATGCCTTGACACTCTATATG (844)
339	TYR	ENSG00000077498	ATGGAGAAAGAGGATTACCACAGCTTG (845)
340	TYR	ENSG00000077498	ATGGAGAAAGAGGATTACCACAGCTTGAT (846)
341	TYR	ENSG00000077498	TACCACAGCTTGATCAGAGCCATTTA (847)
342	TYR	ENSG00000077498	TACATGGTTCCTTTTATACCACTGTAC (848)
343	TYR	ENSG00000077498	CTCATGGAGAAAGAGGATTACCACAGCTTG (849)
344	TYR	ENSG00000077498	TTTGCCCATGAAGCACCAGCTTTTCTG (850)
345	TYR	ENSG00000077498	TTTGCTAGTCCACTTACTGGGATAGCG (851)
346	TYR	ENSG00000077498	CATGAAGCACCAGCTTTTCTGCCTTGG (852)
347	TYR	ENSG00000077498	GTCCCTCTTCAAGAAGTTTATCCAGAAG (853)
348	TYR	ENSG00000077498	GCACCAGCTTTTCTGCCTTGGCATAGA (854)

349	TYR	ENSG00000077498	CTCCTCATGGAGAAAGAGGATTACCACAGCTTG (855)
350	TYR	ENSG00000077498	CATTATTATGTGTCAATGGATGCACTG (856)
351	TYR	ENSG00000077498	TGGGAACAAGAAATCCAGAAGCTG (857)
352	TYR	ENSG00000077498	CTCATGGAGAAAGAGGATTACCACAGCTTGAT (858)
353	TYR	ENSG00000077498	TTGGAACAAGCGAGTCGGATCTGGTCATGG (859)
354	TYR	ENSG00000077498	AACATCTTCGATTTGAGTGCCCCAGAGAAG (860)
355	TYR	ENSG00000077498	GAAGCACCAGCTTTTCTGCCTTGGCATAGA (861)
356	TYR	ENSG00000077498	TCTGAAATCTGGAGAGACATTGATTTT (862)
357	TYR	ENSG00000077498	GCGGCGATGGTAGGGGCCGTCCTC (863)
358	TYRP1	ENSG00000107165	ACTTTCCTTGGGGTAGGACAGGAAAGCTTT (864)
359	TYR	ENSG00000077498	GAGTCGTGGCCTTCCGTCTTTTATAATAGG (865)
360	TYRP1	ENSG00000107165	ATTTCTCAGGACACAACGTGGGACGT (866)
361	DCT	ENSG00000080166	AGGCCCTGGAGTGGTCCCTACATCCTA (867)
362	TYR	ENSG00000077498	AGCTCAGACTATGTCATCCCCATAGGGACCTAT (868)
363	TYR	ENSG00000077498	GATTCAGACCCAGACTCTTTTCAAGACTAC (869)
364	DCT	ENSG00000080166	GACACAAGGCCCTGGAGTGGTCCCTAC (870)
365	TYRP1	ENSG00000107165	CACTATTACTCAGTCAAAAAGACTTTC (871)
366	DCT	ENSG00000080166	AATGTCTGTGGCTCTCAGCAAGGCCCGG (872)
367	TYR	ENSG00000077498	TATATGAATGGAACAATGTCCCAGGTA (873)
368	TYRP1	ENSG00000107165	ATGGCAAAGCGCACAACTCACCTTTA (874)
369	DCT	ENSG00000080166	AGGCCCTGGAGTGGTCCCTACATCCTACGA (875)
370	DCT	ENSG00000080166	ATGACGGTGGACAGCCTAGTGAACAAG (876)
371	DCT	ENSG00000080166	ACAAGGCCCTGGAGTGGTCCCTACATCCTA (877)
372	TYRP1	ENSG00000107165	ACAACCTACCCCTTTATTTGTCAATTGCCACCAGG (878)
373	TYRP1	ENSG00000107165	TTTGTGGACACACTATTACTCAGTC (879)
374	TYRP1	ENSG00000107165	TTAAGTAAAGAAGAAAAGAACCACTTT (880)
375	TYRP1	ENSG00000107165	AGAGCTGCAAACCAAGGTCTTTGTTTTG (881)
376	DCT	ENSG00000080166	ATGGTGAGAAGCGCTACCCTCATTTAA (882)
377	TYRP1	ENSG00000107165	AACCAGGTCTTTGTTTTGCACTCTTAT (883)
378	SLC45A2	ENSG00000164175	CACAACCTCCACAGAGTTTCTCATC (884)
379	SLC24A5	ENSG00000188467	TCTCAGGATGTTGCAGGCACAACCTTC (885)
380	SLC45A2	ENSG00000164175	GCACACAACCTCCACAGAGTTTCTCATC (886)
381	SLC45A2	ENSG00000164175	TCCACAGAGTTTCTCATCTACGAAAGA (887)
382	SLC24A5	ENSG00000188467	GAAGGGTTTTTCACGAGACAGGAGCGC (888)
383	SLC45A2	ENSG00000164175	TTTCAGAAAGTTTGGTATCCTAC (889)
384	SLC45A2	ENSG00000164175	TTACACAGATTTTCATGGGCCAGATTGTGTAC (890)
385	SLC45A2	ENSG00000164175	TACTTTCAGAAAGTTTGGTATCCTAC (891)
386	SLC45A2	ENSG00000164175	GCACTGGTGAACATGCCTCCTCACTACCGC (892)
387	SLC45A2	ENSG00000164175	GGTGTAAATGTCCAGCACCTGTACACTGTG (893)
388	SLC24A5	ENSG00000188467	TTGCTATCTAATACGGTCTCAACACTA (894)
389	SLC24A5	ENSG00000188467	AGGGTTTTTCACGAGACAGGAGCGCAGAGA (895)
390	SLC45A2	ENSG00000164175	TCGGCCAGCGACCACTGCCGGTCCAGG (896)
391	SLC24A5	ENSG00000188467	CGCAGAGATGGAGGCATCATAATCAT (897)
392	SLC45A2	ENSG00000164175	GTAGCAGCTTTGATTGCTAACCCAAGG (898)
393	SLC45A2	ENSG00000164175	AGACTGTTGGGTACAGAATTCCAGGTC (899)
394	SLC24A5	ENSG00000188467	TTCTCCATCATCGGAGTTTCCCGAAGG (900)
395	SLC45A2	ENSG00000164175	TTGTCATCAGATGGAATGTACGAGTAT (901)
396	SLC24A5	ENSG00000188467	GATGAATACTTCTACCTCCCTG (902)
397	SLC45A2	ENSG00000164175	TCCTACATTGGATTAAAGGGTCTTTACTTC (903)
398	SLC45A2	ENSG00000164175	TTACAGGTTTTGGAGGTGCCCTGGGTTAC (904)
399	PMEL	ENSG00000185664	AAGACCTGGGACCAGGTGCCTTTCTCCGTG (905)
400	TRPM1	ENSG00000134160	AGGGTGGCGGATATTCCAATAAAGCCA (906)
401	TRPM1	ENSG00000134160	TCTGTTGCCAAGCACACCCAGAGCTAC (907)

402	SLC24A5	ENSG00000188467	CAGACAAAAGGGGGCCAAACATGGGCGAGA (908)
403	LINC00518	ENSG00000183674	GAAACAGGAAGTTTCATTTCATGAGTTTT (909)
404	SLC45A2	ENSG00000164175	TCACTTTATTCTTACTTTTCAGAAAGTT (910)
405	SLC24A5	ENSG00000188467	CAGACAAAAGGGGGCCAAACATGGGCGAGAAGG (911)
406	SLC45A2	ENSG00000164175	ACTGTTGTAGCAGCTTTGATTGCTAACCCAAGG (912)
407	TRPM1	ENSG00000134160	CATCTCATGGTGAAAGATTGGCAGCTG (913)
408	TRPM1	ENSG00000134160	AACCCTCTAAGTAAGCTCTCTGTGCTC (914)
409	TRPM1	ENSG00000134160	TTTGTAAATCCTAGCACGAAAGACTCTAACAGG (915)
410	MITF	ENSG00000187098	CACTATCAGGTGCAGACCCACCTC (916)
411	TRPM1	ENSG00000134160	GCCTCGGACATCCTGTCTTTGCGCACAAGTAC (917)
412	TRPM1	ENSG00000134160	AGACTGGGGCAGGGCGTGCCCTCGTG (918)
413	TRPM1	ENSG00000134160	AGTGTACCAGACCATGTCCAACCCTCTAAG (919)
414	TRPM1	ENSG00000134160	AGGCTGCTGGAAGACACATCTCCCTG (920)
415	LINC00520	ENSG00000258791	TCCCTCTTTGGGGTCTCAGAGAGATTG (921)
416	MITF	ENSG00000187098	AATCACTATCAGGTGCAGACCCACCTC (922)
417	TRPM1	ENSG00000134160	GACCTGGTTGGAAGGATGTACAAGAGTGTAC (923)
418	MLANA	ENSG00000120215	TCTCTCAGTCCTCCAACACTACCAAGA (924)
419	TRPM1	ENSG00000134160	CTGGCTGACAATGGCACCTGGGCAAGTAT (925)
420	TRPM1	ENSG00000134160	AAAGCCATGTATATCCGTGTATCCTAT (926)
421	TRPM1	ENSG00000134160	ATGCAGCCCAAGCTGAAACAAGTCTTT (927)
422	MLANA	ENSG00000120215	GCAATTATTCAGGATGGCATCTTGCTG (928)
423	LINC00518	ENSG00000183674	GCGTTTGACAGAGCTGTTCACTTC (929)
424	LINC00518	ENSG00000183674	AATACTCCTAACATTGTCTCTTTAAGA (930)
425	TRPM1	ENSG00000134160	AGGGTGGCGGATATTCCAATAAAGCCATGG (931)
426	MOK	ENSG00000080823	CACTATATAATCCCACTGCAAAACAATA (932)
427	LHFPL3-AS1	ENSG00000226869	GTCATGAAGGGCATTAAATCAAGGTTAT (933)
428	GPR143	ENSG00000101850	GCGACGTCCCCGCCGCGCTCGGTCCGC (934)
429	ABCB5	ENSG00000004846	GCACTGGAGAAGGATACCCCCAGGTAT (935)
430	LHFPL3-AS1	ENSG00000226869	CAAGTCATGAAGGGCATTAAATCAAGGTTAT (936)
431	LINC00518	ENSG00000183674	GCAGCGTTTGACAGAGCTGTTCACTTC (937)
432	LINC00518	ENSG00000183674	AGACCGCTGAGGATCAAAGGGGTTTTTC (938)
433	LHFPL3-AS1	ENSG00000226869	AGGCAAGTCATGAAGGGCATTAAATCAAGGTTAT (939)
434	TRPM1	ENSG00000134160	AAACTGGACACCACTGTAAAGAACATC (940)
435	KU-MEL-3	ENSG00000205444	CTTCCGCGAACTCCTCGCCCCGACCTC (941)
436	NA	NA	ATAACTTACACCGAAAGCAACTCAAGG (942)
437	AL162457.2	ENSG00000225106	CGACTTCAGGGATCTGTCACCCTCGTC (943)
438	LHFPL3-AS1	ENSG00000226869	TCTCAATTCCCAAGTAAAAATCTTCTGCTTTT (944)
439	KU-MEL-3	ENSG00000205444	CTTCCGCGAACTCCTCGCCCCGACCTCATCCTT (945)
440	LINC00520	ENSG00000258791	GACACTGCCCCACAATCCCATCAAGTC (946)
441	CHCHD6	ENSG00000159685	ATGGCTATCCTGGGCACAGCGGGGCGG (947)
442	SUGCT-AS1	ENSG00000203446	TCTGTGTCCTCTCACCTCATTATAGTA (948)
443	TRPM1	ENSG00000134160	TCCACGTCACCAGGGACAGGAGTCAGGAAA (949)
444	LHFPL3-AS1	ENSG00000226869	GAAGTGGCTGAAGTCCTTGGGAGTGTGAAG (950)
445	NA	NA	GAGATACCACGAACCCCTCAGAAGGAAGA (951)
446	LINC00520	ENSG00000258791	GTGTTTTTAAATTTCTCCAGAAGATTT (952)
447	SUGCT-AS1	ENSG00000203446	TCTGTGTCCTCTCACCTCATTATAGATAC (953)
448	LINC01320	ENSG00000228262	ACACATCTAGAAGACCCTCACCTTATG (954)
449	KIAA1549L	ENSG00000110427	AGTGTCTTTCCAGGACCTCCTCCAGA (955)

450	PAX3	ENSG00000135903	GGGCAGTATGGACAAAGTAAGCCTTGGACTTTT (956)
451	TRIM51	ENSG00000124900	GTTCCAAGACCTACCAGCAGTAGGATTA (957)
452	SUGCT-AS1	ENSG00000203446	AATTCTGTGTCTCTCACCTCATTATAGATAC (958)
453	LINC00520	ENSG00000258791	CAAGAAGAAGACAACCTTCTAAGATACTTT (959)
454	LINC01320	ENSG00000228262	ACACATCTAGAAGACCCTCACCTTATGCTT (960)
455	DCT	ENSG00000080166	GCTACAACAAACATCCTTGAACATGTA (961)
456	LINC00504	ENSG00000248360	ATGACTCTGAGGCCTACACAGCCACGT (962)
457	MSRB3-AS1	ENSG00000250748	GAAACAAGACCGAACAACCTCCAAGTTC (963)
458	TYR	ENSG00000077498	CACTCAATCACGGAGCCTCTGCTCTAT (964)
459	NA	NA	CATTTATTCTTACAACCTCCAAGCAAAAGA (965)
460	FCRLA	ENSG00000132185	GAGACAGTTAGATTTACTTCTCTTTT (966)
461	AC011294.1	ENSG00000233539	TCCCCAATGCCTATACCCCATTTGTATCTT (967)
462	ABCB5	ENSG00000004846	GAATCTTATGGTAGGTATACTTTTAC (968)
463	LHFPL3-AS1	ENSG00000226869	AAATCACAAGGTTTCAATTTATTTCTTTT (969)
464	SLC24A5	ENSG00000188467	GGTACTATCTTGACATAGGTGTATTT (970)
465	C10orf90	ENSG00000154493	AAAGTATTTTCTGGAAGCAGCAAGAGG (971)
466	LINC02099	ENSG00000253490	TCAAGCTTCAGCACCCCTTGCATCTCTGGATAAA (972)
467	CA14	ENSG00000118298	ACCACCCAGGGAGCTGCTCCTCAGAGG (973)
468	CA14	ENSG00000118298	CATACCACCCAGGGAGCTGCTCCTCAGAGG (974)
469	SHC4	ENSG00000185634	AAGATCTTCCAAGAGAGGGCAGCCTTT (975)
470	SLC6A15	ENSG00000072041	GGGCAAATCACACATAACACTTCATTC (976)
471	PAX3	ENSG00000135903	ATTAGTCTCAAGCCTTTGATAGCACGGTAT (977)
472	NLGN1	ENSG00000169760	AAGCATTCTGATTTGATTTATTCTGG (978)
473	AC011294.1	ENSG00000233539	ATGGTATGGGAGGGGCATCCAGAGAAAGA (979)
474	C5orf22	ENSG00000082213	TCAACTGATTTGCCCATTTCTTCTTAA (980)
475	NA	NA	GAGGTAATTTCTATCAACACTGGACATTTT (981)
476	BFSP1	ENSG00000125864	GAGACAGAGCGGGTCTGGAGAAGTCTTCTTAC (982)
477	LHFPL3-AS1	ENSG00000226869	AAGATAAAACTATAAACTCTGAGATAT (983)
478	TRPM1	ENSG00000134160	TATGTGAGTCAGAAAGTTTCAGACTTT (984)
479	ANO4	ENSG00000151572	GATGCAGGCATCCCTGTGTACCACCGA (985)
480	MIR3681HG	ENSG00000224184	ACCATCTTGGAAGCAGAGATCCTTCACCAGGCA (986)
481	VPS53	ENSG00000141252	GAATATGCTCAGAAAACACCTCTCTTT (987)
482	LHFPL3-AS1	ENSG00000226869	ACATGGACACCACATGGTATCAGAAATC (988)
483	PRTG	ENSG00000166450	GAGGTCCACGAAGGTGGAGTTGCTCGATTT (989)
484	MIR3681HG	ENSG00000224184	AGAGAAATAGAAATAGAGGGAAGATTA (990)
485	PRTG	ENSG00000166450	TCCTGGCTGCCAATCCCAGCCAAATAT (991)
486	MDGA2	ENSG00000139915	CGCTACTCCGAAAGGGTCTACACTATC (992)
487	SLC45A2	ENSG00000164175	TTCACAGACTCGCAGGGCAATGACATTTAA (993)
488	NA	NA	TCAGTGCCAAGCGACTTCTCTGAGTCTCAGG (994)
489	DLGAP1	ENSG00000170579	CGGCAGATGAGTCTGGAGTTTCAGGGCA (995)
490	AL138885.2	ENSG00000228478	GAAACCATCTCCCCAGGCCTTCAATA (996)
491	IGSF11	ENSG00000144847	GGGCCAGCAGGAGGAAGGGGAGTCATC (997)
492	AC010894.3	ENSG00000236449	CTGACTGACCATCACATAAAAGAATAC (998)
493	TEX41	ENSG00000226674	GAAGCAGTACCTTATAATGGTTCTTGTTCAAA (999)
494	DPYSL4	ENSG00000151640	AATCTGCTGGCGGAGATCCACGGTGTG (1000)
495	CCDC140	ENSG00000163081	AAAGAGGGGCCAGTGACGCGAGGAGCA (1001)
496	LHFPL3-AS1	ENSG00000226869	GTACACGTGGATTTGAATCTTGGCTTC (1002)
497	DCT	ENSG00000080166	CACACTGTACAGGGACTAGCTGGATTT (1003)
498	novel_gene	ENSG00000286873	ATGCGTATAGAGGACAGCCACACTAAGCTT (1004)
499	IGSF11	ENSG00000144847	AGTGCCCTGTCTTCAGCCCAGCCCAGG (1005)

500	PRDM7	ENSG00000126856	TCCCCTTCCATCAAAAGTCTACTAGTTTAT (1006)
501	TICRR	ENSG00000140534	CCAACTGATGCCACTTTAAACCGTTTGCTCTAC (1007)
502	MIR3681HG	ENSG00000224184	TGGACTTCCCAGCCCCAACTATGAGAAA (1008)
503	MLANA	ENSG00000120215	CCCGCCCCCGCCCCGTGGCACCACCCCTG (1009)
504	NA	NA	GTATATCTCCATTCTAACAGCACATTA (1010)
505	NA	NA	TCTTTGTATGCCTGGACTCAGAGCCAC (1011)

Table 2C: characteristics of the TSAs, TAAs and LSAs identified herein (continued)

Peptide (SEQ ID NO:)	ERE	MCS_strand	MCS_alignment
1	no	+	chr13:18232805-18232831
2	no	-	chr9:102611399-102611425
3	no	+	chr17:30422918-30422947
4	no	+	chr11:64320868-64320894
5	no	-	chr16:67183758-67183784
6	no	+,+	chrX:49533350-49533376;chrX:49571573-49571599
7	no	-	chrX:52516983-52517009
8	no	-	chrX:152766787-152766813
9	no	-	chrX:152767231-152767254
10	no	+	chrX:152701499-152701525
11	no	-,+	chrX:152766877-152766903;chrX:152701580-152701606
12	no	+	chrX:55221461-55221463 55221767-55221790
13	no	+, -	chrX:152736870-152736896;chrX:152750629-152750655
14	no	+	chrX:152701034-152701063
15	no	+	chrX:55221461-55221463 55221767-55221793
16	no	+	chrX:152701043-152701069
17	no	+	chrX:151924454-151924480
18	no	-	chrX:142202917-142202940
19	no	+	chrX:151924523-151924546
20	no	+	chrX:152701334-152701360
21	no	+	chrX:152701412-152701435
22	no	+	chrX:151924520-151924546
23	no	+	chrX:151924445-151924471
24	no	-	chrX:142203169-142203195
25	no	+	chrX:55222707-55222736
26	no	-	chrX:152767048-152767074
27	no	-	chrX:152767123-152767149
28	no	-	chrX:154652568-154652594
29	no	+	chrX:152701331-152701360
30	no	-	chrX:142202875-142202901
31	no	-	chrX:142202992-142203018
32	no	-	chrX:142203445-142203471
33	no	-	chrX:152767123-152767152
34	no	+	chrX:151924376-151924402
35	no	+	chrX:55222686-55222712
36	no	+	chrX:151924355-151924381
37	no	+	chrX:152701328-152701360
38	no	-	chrX:142203439-142203471
39	no	-	chrX:152766934-152766966
40	no	+	chrX:151924352-151924381
41	no	-,+	chrX:152750836-152750862;chrX:152717608-152717634
42	no	-	chrX:142203202-142203228
43	no	-	chrX:154652631-154652631 154653247-154653272

44	no	-	chrX:152750623-152750655
45	no	-;	chrX:152750647-152750679;chrX:152717791-152717823
46	no	-	chr16:35478345-35478371
47	no	-	chr3:177622656-177622685
48	no	+	chrX:152737005-152737031
49	no	+	chrX:141908507-141908533
50	no	+	chrX:152736495-152736521
51	no	+	chr2:232520644-232520673
52	no	-	chrX:142203190-142203219
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58	no	-	chrX:152766748-152766774
59	no	-	chr9:65485652-65485684
60	no	+	chrX:30219271-30219300
61	no	-	chrX:152766748-152766777
62	no	-	chr16:35477621-35477650
63	no	-	chrX:54790958-54790984
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65	no	+	chrX:153183221-153183247
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67	no	+	chrX:153183290-153183316
68	no	+	chrX:153182585-153182611
69	no	+	chrX:153183077-153183103
70	no	+	chr2:232521994-232522020
71	no	+	chrX:153182573-153182599
72	no	+	chrX:153182681-153182707
73	no	+	chrX:30218794-30218820
74	no	+	chrX:153182579-153182605
75	no	-	chrX:52700447-52700473
76	no	-	chrX:152134835-152134861
77	no	+	chr2:232521994-232522026
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87	no	-	chr19:9470435-9470464
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153	yes	-	chr5:12574525-12574551
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155	no	+	chr19:55862131-55862157
156	yes	-	chr4:54603955-54603981
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163	no	-	chr7:26196913-26196939
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226	no	-	chr22:22550202-22550231
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240	no	-	chr22:22548298-22548324
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242	no	-	chr22:22550904-22550936
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422	no	+	chr9:5891152-5891178
423	yes	-	chr6:10434321-10434344
424	no	-	chr6:10434579-10434605
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426	no	-	chr14:102246059-102246085
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431	yes	-	chr6:10434321-10434347
432	no	-	chr6:10434421-10434426 10434513-10434533
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446	no	-	chr14:55782521-55782547
447	yes	-	chr7:40539397-40539426
448	yes	+	chr2:33855692-33855718
449	no	+	chr11:33544273-33544299

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454	yes	+	chr2:33855692-33855721
455	no	-	chr13:94452609-94452635
456	yes	-	chr4:14888103-14888129
457	no	-	chr12:65642085-65642111
458	no	+	chr11:89242935-89242961
459	no	+	chrX:130827948-130827977
460	no	+	chr1:161707170-161707196
461	yes	-	chr7:46688406-46688435
462	no	+	chr7:20671857-20671883
463	no	-	chr7:104767903-104767929
464	no	+	chr15:48134416-48134442
465	no	-	chr10:126464952-126464978
466	no	+	chr8:29790336-29790368
467	no	+	chr1:150257481-150257507
468	no	+	chr1:150257478-150257507
469	no	-	chr15:48963604-48963630
470	no	-	chr12:84883748-84883774
471	no	-	chr2:222201534-222201563
472	no	+	chr3:174285640-174285666
473	no	-	chr7:46689289-46689318
474	no	+	chr5:31538210-31538236
475	no	-	chr6:10428732-10428761
476	no	-	chr20:17498906-17498938
477	no	-	chr7:104768197-104768223
478	no	-	chr15:31063812-31063838
479	no	+	chr12:100739961-100739987
480	yes	+	chr2:12315544-12315576
481	no	-	chr17:601915-601941
482	no	-	chr7:104743312-104743338
483	no	-	chr15:55683867-55683896
484	no	+	chr2:12397807-12397833
485	no	-	chr15:55673591-55673617
486	no	-	chr14:47301468-47301494
487	no	-	chr5:33954482-33954504 33982236-33982242
488	no	-	chr6:164900690-164900719
489	no	-	chr18:4248611-4248637
490	no	-	chr6:10424768-10424794
491	no	-	chr3:118981885-118981911
492	no	+	chr2:174649757-174649783
493	no	+	chr2:145070829-145070861
494	no	+	chr10:132202111-132202116 132203762-132203782
495	no	+	chr2:222303863-222303889
496	no	-	chr7:104783468-104783494
497	no	-	chr13:94443041-94443067
498	no	+	chr2:127892353-127892382
499	no	-	chr3:118904788-118904798 118905668-118905683
500	no	-	chr16:90064099-90064128
501	no	+	chr15:89582869-89582901
502	yes	+	chr2:12315601-12315630
503	no	+	chr9:5893905-5893934
504	no	-	chr2:37379139-37379165
505	no	-	chr15:47991164-47991190

* ERE = endogenous retroviral element

Example 2: Evidence that aeTSAs contribute to ICB response

Method

Predicted TA presentation. HLA alleles for melanoma samples from previous studies on ICB were inferred from RNA-seq using Optitype. Promiscuous binders for a given MAP (all HLA alleles capable of presenting the MAP) were obtained using NetMHCpan-4.1b. They corresponded to HLA alleles for which the given MAP had an eluted ligand likelihood prediction rank < 2%. A given TA was considered as presented in a sample if it had an expression > 0 RPHM and at least one of the patient's HLA allotypes was a potential binder. If the patient expressed more than one HLA allele capable of presenting a TA, the TA was counted multiple times. Only cutaneous melanoma samples from previous studies were analyzed.

Number of T cell clones expanded on-therapy in patients from Riaz et al⁸. The TCRB clonotypes from Riaz et al.⁸ were downloaded from (https://www.github.com/riazn/bms038_analysis). Then, the TCRB clones expanded per patient were determined using the FEST web tool (www.stat-apps.onc.jhmi.edu/FEST) with the following parameters per patient: 1) pre-therapy sample as a reference, 2) nTemplates_threshold = 1, 3) ignore_baseline_threshold = TRUE, 4) Nucleotide_level = FALSE, 5) FDR 5% and OR 5.

Results

Despite their high abundance in cancer cells, little is known about the role of unmutated TAs in spontaneous or treatment-induced anti-tumor immunity *in vivo*. To evaluate this, the number of unmutated TAs in pre-treatment biopsies from melanoma patients treated with ICB (anti-PD-1, anti-PD-L1, and/or anti-CTLA) was predicted. TA presence in individual tumors was inferred based on two criteria: expression at the RNA level of both the TA and a cognate HLA allotype (i.e., presence of TA-HLA pairs)⁴. In all datasets tested, patients presented high numbers of TA-HLA pairs. Still, no significant difference in the number of TA-HLA pairs was seen in pre-treatment samples between responders and non-responders (FIGs. 1A, 2A, 2B). A recent meta-analysis suggests that the lack of correlation between TA load and response to ICB commonly results from a threshold effect: when one or a few TAs are immunogenic, having more TAs does not confer any advantage¹⁰. For now, the lack of immunopeptidomic data and complete sets of unmutated TAs from these patients prevents drawing definitive conclusions on the value of unmutated TA numbers in predicting response to ICB.

In their previous study of anti-PD-1 therapy in melanoma, Riaz and colleagues reported a linear correlation between the number of expanded T-cell clones and the number of predicted mTSAs lost on-therapy in responders (partial and complete response patients, PRCR) but not in non-responders (stable or progressive disease patients, SD or PD)⁸. Notably, using the Riaz et al. data⁸, it was found that responders, but not non-responders, showed a marked decrease in

the number of unmutated TA-HLA pairs on-therapy (FIGs. 1B, 2C, 2D), which could not be explained solely by decreased tumor purity (FIG. 2E). The positive correlation between unmutated TA disappearance and response to ICB was validated in one out of two additional datasets with pre- and on-ICB samples^{11,12} (FIGs. 2C, 2D). Furthermore, the loss of aeTSA-HLA numbers in responders had a strong linear correlation with the number of T cell clones expanded on-therapy, whereas a positive but non-significant correlation with T cell expansion was observed for TAAs and LSAs (FIG. 1C).

To determine whether the loss of aeTSAs in responders was directly due to their recognition and elimination by certain T cell clonotypes, experiments were performed to identify the cognate antigens for the expanded T cell receptor V β (TCRB) sequences. To this end, the overlap between the expanded TCRB sequences from Riaz et al.⁸ and the database of aeTSA-specific CD8 TCRB clonotypes obtained using functional expansion of specific T cells (FEST) assays⁹ in previous studies was first checked^{4,15,16}. In the FEST assays, TCRB sequencing is performed on T cells isolated from healthy donor PBMCs and stimulated or not with individual synthetic aeTSAs. TCR clonotypes responsive to aeTSAs are then identified based on their significant expansion in the aeTSA-stimulated condition compared to the control. Remarkably, it was found that one TCRB clone expanded in a responder from Riaz et al.⁸ was specific to an exonic aeTSA derived from oncofetal IGF2BP1¹⁷, which was previously identified in ovarian cancer¹⁶. The expansion of this CD8 T-cell clonotype was associated with a complete loss of the IGF2BP1-derived aeTSA on-therapy, strongly indicating direct recognition and elimination (FIG. 1D).

Example 3: Immunogenicity of selected melanoma tumor antigen candidates

A functional expansion of specific T cells (FEST) assay was performed on melanoma aeTSAs identified herein.

Method

aeTSA selection for Immunogenicity assay. Melanoma aeTSAs to be tested in T cell-based immunogenicity assays were selected based on the following criteria: 1) complete loss of expression (RPHM) on-therapy in at least one responder from the Riaz et al.⁸ cohort capable to present the respective aeTSAs (at least one HLA allele with rank elution <2% in NetMHCpan4.1b⁵), 2) elevated mean expression in TCGA-SKCM, 3) the HLA allotype presenting the aeTSA (HLA-A*02:01 or HLA-B*68:01 shared by the melanoma samples and PBMCs donors), 4) the aeTSA biotype (25% canonical, 75% non-canonical), 5) novel MAP status.

Peptide-specific T cell functional expansion (FEST). T cells were cultured as previously described⁹, with minor modifications. Briefly, on day 0, thawed PBMCs from D36 (Miltenyi Biotec) were T cell-enriched using the Human Pan T cell isolation kit (Miltenyi Biotec). T cells were resuspended at 2×10^6 /mL in AIM V media supplemented with 50 μ g/mL gentamicin (ThermoFisher Scientific) and 1% HEPES. The T cell-negative fraction was irradiated at 30 Gy,

washed, and resuspended at 2×10^6 /mL in AIM V media supplemented with 50 µg/mL gentamicin and 1% HEPES. 2.5 ml per well of both T cells and irradiated T cell-depleted cells were added to a 12-well plate, along with each peptide (GLS Biochem) (1 µg/mL final concentration) or without peptide. Cells were cultured for 10 days at 37°C, 5% CO₂. On day 3 and 7, half the culture media was replaced with fresh culture media containing 100 IU/mL IL-2, 50 ng/mL IL-7, and 50 ng/mL IL-15 (day 3) and 200 IU/mL IL-2, 50 ng/mL IL-7, and 50 ng/mL IL-15 (day 7). On day 10, thawed PBMCs from the same donor were used to generate a new batch of T cell-depleted cells. These cells were irradiated at 30 Gy and loaded with 1 µg/mL of relevant peptide or without peptide during 2h at 37°C. These cells were washed and added to cultures at a 1:1 T cell:non-T cell ratio. On day 13 and 17, at least half the culture media was replaced with fresh culture media (final concentrations: 100 IU/mL IL-2, 25 ng/mL IL-7, and 25 ng/mL IL-15). On day 20, cells were harvested to perform FEST assays.

Functional Expansion of Specific T cells (FEST) assay. For FEST assays, CD8⁺ cells were further isolated using the Human CD8⁺ T Cell Isolation Kit (Miltenyi Biotec). As a negative control, CD8⁺ T cells were also isolated from freshly thawed uncultured PBMCs of the same healthy donor. DNA was extracted from CD8⁺ T cells using a QIAGEN DNA blood mini kit (QIAGEN). TCR Vβ CDR3 sequencing was performed using the ultradeep resolution of the immunoSEQ platform (Adaptive Biotechnologies). Raw data exported from the immunoSEQ portal were processed with the FEST web tool⁹ (www.stat-apps.onc.jhmi.edu/FEST).

Results

The ability of 12 selected aeTSAs to stimulate the expansion of specific T cell clonotypes *in vitro* was assessed in a FEST assay. The aeTSAs were able to induce specific T cell expansion (FIG. 3). The TCRβ clonotypes expanded by each of the aeTSAs are depicted in Table 3.

Table 3

aeTSA	Amino acid sequences of the CDR3 of the TCRβ chain of the clonotypes expanded
AAAGVSSTK (SEQ ID NO:73)	CASHPAGADMNTEAFF (SEQ ID NO:1012) CASSLAGRETQYF (SEQ ID NO:1013) CASSVWGEPYNEQFF (SEQ ID NO:1014) CASSRTDSYEQYF (SEQ ID NO:1015) CASSLQGANGYTF (SEQ ID NO:1016) CASSPTNTYEQYF (SEQ ID NO:1017)
ATFLQRKVLRL (SEQ ID NO:47)	CASSLSYTGELFF (SEQ ID NO:1018) CASSRTGNQPQHF (SEQ ID NO:1019) CASSSSGEQYF (SEQ ID NO:1020) CASSVEEGSYEQYF (SEQ ID NO:1021) CASRDYGYTF (SEQ ID NO:1022) CASSYSGDYNEQFF (SEQ ID NO:1023) CASSFEAYSNQPQHF (SEQ ID NO:1024) CASSGGDSPYEQYF (SEQ ID NO:1025) CASSLDTGVGANVLTF (SEQ ID NO:1026) CASSQLGVTEAFF (SEQ ID NO:1027) CASSPGTAQETQYF (SEQ ID NO:1028)

	CASSLDRGDYEQYF (SEQ ID NO:1029)
DSFSATETR (SEQ ID NO:7)	CASSLGGLYEQYF (SEQ ID NO:1030) CASSQDLANTGELFF (SEQ ID NO:1031) CSVEQLGEMNTEAFF (SEQ ID NO:1032) CASSQGEIDGYTF (SEQ ID NO:1033) CASSLTGDGYTF (SEQ ID NO:1034) CASSPRDGYEQYF (SEQ ID NO:1035) CASSLDRAYEQYF (SEQ ID NO:1036) CASSQDLGSSYEQYF (SEQ ID NO:1037) CASGTGGSTDTQYF (SEQ ID NO:1038) CASSETDTQYF (SEQ ID NO:1039) CASSVGQFSNQPQHF (SEQ ID NO:1040) CASSPRTNQPQHF (SEQ ID NO:1041) CASSLGGTGPYEQYF (SEQ ID NO:1042)
DTAPATFLR (SEQ ID NO:138)	CAISGDGYGYTF (SEQ ID NO:1043) CASSLTGGTEAFF (SEQ ID NO:1044) CASSLSDSYEQYF (SEQ ID NO:1045) CASSQEGREVDGYTF (SEQ ID NO:1046) CASSEVSQNPQHF (SEQ ID NO:1047) GNTIYF (SEQ ID NO:1048) CASQGAYEQYF (SEQ ID NO:1049) CASSFKPGLKWRDEQFF (SEQ ID NO:1050) CASSIGTANSYEQYF (SEQ ID NO:1051) CASSIGTNTEAFF (SEQ ID NO:1052) CASSVGDSGNTIYF (SEQ ID NO:1053) CASSSGVTNEKLFF (SEQ ID NO:1054) CASSATGDTEAFF (SEQ ID NO:1055)
ETMETLRTSR (SEQ ID NO:98)	CASSLRTGRGYGYTF (SEQ ID NO:1056) CAIQRGRTGELFF (SEQ ID NO:1057) CASSLATGYNEQFF (SEQ ID NO:1058) CASSFTERGYEKLFF (SEQ ID NO:1059) CASSPRTGMNTEAFF (SEQ ID NO:1060) CASSQDSEQGLVQPQHF (SEQ ID NO:1061) CASSRSTSGRADEQFF (SEQ ID NO:1062) CASSRASSGLSYEQYF (SEQ ID NO:1063) CASSVAGSTEAFF (SEQ ID NO:1064) CASSQEGGMNTEAFF (SEQ ID NO:1065) CASSSSDRVGEQYF (SEQ ID NO:1066) CASSLGQNSYNEQFF (SEQ ID NO:1067) CASSPRSSYNEQFF (SEQ ID NO:1068) CASSLLGGGQPQHF (SEQ ID NO:1069) CASSRGLAVSYNEQFF (SEQ ID NO:1070)
EVFNVKNTFPK (SEQ ID NO:134)	CASSLLARSSYEQYF (SEQ ID NO:1071) CASSPTENTEAFF (SEQ ID NO:1072) CASSVGGGRNYEQYF (SEQ ID NO:1073) CASSYSGGPYEQYF (SEQ ID NO:1074) CASSLGDGQPQHF (SEQ ID NO:1075) CASSQGDYGYTF (SEQ ID NO:1076) CASSYQGTNTEAFF (SEQ ID NO:1077) CASSFIGGQPQHF (SEQ ID NO:1078) CASSLGLAGTNTGELFF (SEQ ID NO:1079)
EVVPISHLY (SEQ ID NO:41)	CASSVGPETQYF (SEQ ID NO:1080) CASSQGLSSGNTIYF (SEQ ID NO:1081) CASSSATEAFF (SEQ ID NO:1082) CASSLKGVTYEQYF (SEQ ID NO:1083)

	CASSPDGGEQYF (SEQ ID NO:1084) CASSLFPDTQYF (SEQ ID NO:1085) CASSLGDSYTGELFF (SEQ ID NO:1086) CASSVEGYTEAFF (SEQ ID NO:1087) CASSPPESYEQYF (SEQ ID NO:1088)
GVDDLVR (SEQ ID NO:64)	CASSPDPEGGEQYF (SEQ ID NO:1089) CASSLQGHGYTF (SEQ ID NO:1090) CASNVARTGGDISGDYEQYF (SEQ ID NO:1091) CASSLGLAGSYEQYF (SEQ ID NO:1092) CASSDSSYNSPLHF (SEQ ID NO:1093)
GVPGPLLILPR (SEQ ID NO:59)	CASSEWQGQDSNNYGYTF (SEQ ID NO:1094) CASSNLAGLNEQFF (SEQ ID NO:1095) CASSPPSGGFQFF (SEQ ID NO:1096) CASSFDGWNTAEFF (SEQ ID NO:1097) CASSLGGQGYGYTF (SEQ ID NO:1098) CASSPGQGNNEKLFF (SEQ ID NO:1099) CASSIVFGSRNSPLHF (SEQ ID NO:1100) CASKESTAEFF (SEQ ID NO:1101) CSANTRDISYEQYF (SEQ ID NO:1102)
HTLPALSRR (SEQ ID NO:66)	CASSFQGLNTEAFF (SEQ ID NO:1103) CASSPGQGNEKLFF (SEQ ID NO:1104) CASSLGSGYEQYF (SEQ ID NO:1105) CASSLGLYNEQFF (SEQ ID NO:1106) CASSPGTDYNEQFF (SEQ ID NO:1107) CATRPGAIRGYTF (SEQ ID NO:1108) CASSLIGGADTEAFF (SEQ ID NO:1109)
ITSGVKVKK (SEQ ID NO:110)	CASSLLTGNYGYTF (SEQ ID NO:1110) CASYNRGERGGYTF (SEQ ID NO:1111) CASSPGTSGSSYNEQFF (SEQ ID NO:1112) CASSPVPRGDVPYEQYF (SEQ ID NO:1113) CASSADPNTEAFF (SEQ ID NO:1114) CSARDTRGGQPQHF (SEQ ID NO:1115) CASSLTSGSRNEQFF (SEQ ID NO:1116) CASSSGRFYEQYF (SEQ ID NO:1117) CASSVLAGGSYEQYF (SEQ ID NO:1118) CASSYGTGVEQYF (SEQ ID NO:1119) CASSQPGTSGYNEQFF (SEQ ID NO:1120) CASSRLAGGQETQYF (SEQ ID NO:1121) CASRPGTGGRMDIQYF (SEQ ID NO:1122) CAIRSTDTQYF (SEQ ID NO:1123)
VLMMKLEDL (SEQ ID NO:120)	CASSLGGNQPQHF (SEQ ID NO:1124) CASSSGPSGGNTIYF (SEQ ID NO:1125) CASSLGTGGYEQFF (SEQ ID NO:1126) CASSLGGGGYGYTF (SEQ ID NO:1127) CASRTGGANTEAFF (SEQ ID NO:1128) CASSGDRGHEQYF (SEQ ID NO:1129) CAISETGLVGEKLFF (SEQ ID NO:1130) CASSLGQGSEKLFF (SEQ ID NO:1131) CASSLGRMNTEAFF (SEQ ID NO:1132) CASSLLGPGELFF (SEQ ID NO:1133) CASSSRDRESGNTIYF (SEQ ID NO:1134) CASSPEGGSSYNEQFF (SEQ ID NO:1135) CASSQSGQGYGYTF (SEQ ID NO:1136) CASSGTSGAYNEQFF (SEQ ID NO:1137)

These results show that the representative aeTSAs tested induce polyclonal T cell expansion following *in vitro* stimulation, providing evidence that they may be useful for immunotherapy against melanoma.

The TCR recognition propensity of 200 representative aeTSAs and 5 mTSAs described
5 herein was also assessed using the PRedictor of Immunogenic Epitope PRIME2.0 web tool (<http://ec2-18-188-210-66.us-east-2.compute.amazonaws.com:3000>, Gfeller, D., et al., *Improved predictions of antigen presentation and TCR recognition with MixMHCpred2.2 and PRIME2.0 reveal potent SARS-CoV-2 CD8+ T-cell epitopes*. Cell Systems, 2023. **14**(1): p. 72-83.e5). PRIME2.0 is based on a neural network and uses as input features (1) the predicted HLA-I
10 presentation score ($-\log(\%rank)$ of MixMHCpred2.2), (2) the amino acid frequency at positions with minimal impact on binding to HLA-I and more likely to face the TCR, and (3) the length of the peptide. The PRIME2.0 scores of the aeTSAs and mTSAs was compared to that of 590 known immunogenic peptides (binding 53 HLA alleles) and 5887 non-immunogenic peptides (binding 62 HLA alleles) used to train PRIME2.0. The results reported in FIG. 3B show that the tested aeTSAs
15 have a PRIME2.0 score that is (1) comparable (and even better) to that of mTSAs; (2) comparable to that of a set of known immunogenic control peptides (neoantigens) used to train the PRIME 2.0 algorithm; and (3) significantly higher than that of a set of non-immunogenic control peptides used to train the PRIME 2.0 algorithm. The aeTSA of SEQ ID NO:1 described herein was shown to have a very high PRIME 2.0 immunogenicity score of 0.31991. This data provides further
20 evidence that the aeTSAs described herein are immunogenic and may be useful for immunotherapy against melanoma.

Example 4: Further evidence that aeTSAs are good candidates for immunotherapy

A therapeutically attractive feature of unmutated TAs is their sharing between patients. In
25 contrast to mTSAs which were patient-specific, aeTSAs from melanoma were abundant and shared at the peptide and RNA levels (FIGs. 4A-B). Nevertheless, TAs showed a TA type-, cancer type- and cancer subtype-specific expression pattern and regulation. Specifically, it was found that aeTSAs coded by oncofetal (or cancer-germline) genes and TAAs coded by cell cycle genes were enriched in melanoma samples from TCGA, consistent with an increased stemness of these
30 tumors (FIGs. 4B, 5).

Using TCGA multi-omics data, a pronounced correlation between the expression of TAs and their corresponding source genes was found, suggesting a gene-level regulation (FIG. 4C). Expression of aeTSAs was often correlated with hypomethylation of the source gene promoters in melanoma. By contrast, TAAs and LSAs showed a prevalent association with both the focal
35 DNA copy number (CNV) and the hypomethylation of source-gene promoters, whereas no TA type was correlated with the TMB (FIG. 4D). In summary, these results indicate that, in agreement with the role of MAPs in mirroring the internal cell state, TA expression reflects cancer cell

programs shared between patients and regulated, at least in part, at the mutational and/or epigenetic level. The association with cancer (sub)type suggests that unmutated TA prioritization is possible and likely important for effective therapy.

MAPs obtained from MHC I immunoprecipitation of bulk tumor lysates are “contaminated”
5 by peptides from tumor-infiltrating immune cells and other stromal cells in the microenvironment¹³. Hence it was aimed to validate that the unmutated TA expression is associated with malignant cells (or with the cell lineage of origin for LSAs) using published single-cell RNA-seq datasets from melanoma¹⁴ (FIGs. 6A, B). It was found that TAs were highly and primarily expressed by cancer cells (FIGs. 7A, B). Among the aeTSAs detected, most were expressed in cancer cells
10 only (72%). When detected in annotated non-cancer cells, TA expression was associated with up to 100% cell doublet formation between non-cancer and cancer cells (FIG. 8A). Indeed, melanoma TA-positive non-cancer cell populations showed increased expression of melanoma (and melanocyte) markers *MLANA* (FIG. 8B, upper panel) and *PMEL* (FIG. 8B, lower panel) relative to TA-negative non-cancer cells. Hence, aeTSAs were cancer cell-specific and their
15 detection in other cell populations resulted from technical limitations in the single-cell sample preparation.

Altogether, the results presented in this study strongly support the immune targeting of unmutated TAs across cancers with varying TMB levels. aeTSAs are particularly attractive targets for immunotherapy considering their cancer specificity, immunogenicity, high abundance, and
20 sharing between patients.

Although the present invention has been described hereinabove by way of specific embodiments thereof, it can be modified, without departing from the spirit and nature of the subject invention as defined in the appended claims. In the claims, the word “comprising” is used as an open-ended term, substantially equivalent to the phrase “including, but not limited to”. The
25 singular forms “a”, “an” and “the” include corresponding plural references unless the context clearly dictates otherwise.

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WHAT IS CLAIMED IS:

1. A tumor antigen peptide (TAP) comprising or consisting of one of the amino acid sequences set forth in SEQ ID NOs: 1-505.
2. The TAP of claim 1, wherein the TAP binds to an HLA-A*01:01 molecule and comprises or
5 consists of the sequence of SEQ ID NO: 11, 14, 20, 27, 29, 37, 86, 87, 121, 150, 165, 173, 279, 288, 299, 308, 312, 316, 319, 331, 340, 352, 362, 363, 384, 395, 398, 411, 419, 429, 458, 474, 476, 487, 492, 500, or 501.
3. The TAP of claim 1, wherein the TAP binds to an HLA-A*02:01 molecule and comprises or
10 consists of the sequence of SEQ ID NO: 1, 2, 4, 19, 22, 25, 40, 50, 52, 54, 60, 65, 67, 76, 81, 89, 91, 103, 107, 120, 124, 128, 135, 157, 175, 179, 186, 188, 201, 208, 218, 219, 228, 232, 233, 240, 250, 257, 261, 263, 265, 266, 282, 286, 298, 311, 315, 317, 325, 333, 337, 349, 367, 373, 387, 388, 393, 399, 404, 412, 414, 415, 422, 434, 437, 455, 480, 489, or 494.
4. The TAP of claim 1, wherein the TAP binds to an HLA-A*02:09 molecule and comprises or
15 consists of the sequence of SEQ ID NO: 22, 40, 50, 62, 83, 89, 232, 265, 282, 311, 315, 317, 337, 349, 367, 399, 407, 412, or 494.
5. The TAP of claim 1, wherein the TAP binds to an HLA-A*03:01 molecule and comprises or consists of the sequence of SEQ ID NO: 209, 247, 272, 347, or 505.
6. The TAP of claim 1, wherein the TAP binds to an HLA-A*23:01 molecule and comprises or
20 consists of the sequence of SEQ ID NO: 48, 84, 129, 151, 152, 171, 174, 182, 223, 237, 245, 290, 358, 397, 426, 446, 481, 482, or 486.
7. The TAP of claim 1, wherein the TAP binds to an HLA-A*24:02 molecule and comprises or consists of the sequence of SEQ ID NO: 31, 244 or 481.
8. The TAP of claim 1, wherein the TAP binds to an HLA-A*25:01 molecule and comprises or consists of the sequence of SEQ ID NO: 11, 31, 249, 289, 403, 425, 464, or 490.
- 25 9. The TAP of claim 1, wherein the TAP binds to an HLA-A*26:01 molecule and comprises or consists of the sequence of SEQ ID NO: 11, 20, 27, 39, 41, 42, 45, 114, 116, 122, 168, 181, 268, 284, 329, 364, 398, 417, 430, 440, 447, 452, 457, 460, 462, 475, 490, or 497.
10. The TAP of claim 1, wherein the TAP binds to an HLA-A*30:01 molecule and comprises or consists of the sequence of SEQ ID NO: 26, 304 or 376.

11. The TAP of claim 1, wherein the TAP binds to an HLA-A*30:02 molecule and comprises or consists of the sequence of SEQ ID NO: 117, 185, 190, 193, 197, 256, 294, 323, 471, or 485.
12. The TAP of claim 1, wherein the TAP binds to an HLA-A*33:01 molecule and comprises or consists of the sequence of SEQ ID NO: 248.
- 5 13. The TAP of claim 1, wherein the TAP binds to an HLA-A*68:01 molecule and comprises or consists of the sequence of SEQ ID NO: 6-8, 12, 15, 23, 28, 41, 42, 47, 51, 53, 56, 59, 64, 66, 68, 70, 73-75, 77, 79, 80, 82, 85, 88, 92, 93, 96-99, 101, 102, 108-112, 118, 119, 123, 130, 131, 134, 137, 138, 141, 142, 144-147, 149, 153, 154, 156, 158, 160, 161, 166, 169, 172, 176, 184, 198, 202, 203, 212, 214, 216, 217, 220, 224, 226, 229, 234, 236, 239, 248, 254, 269, 270, 275, 280, 283, 287,
10 293, 300, 301, 303, 306, 310, 314, 320, 328, 332, 348, 354, 355, 359, 360, 366, 369, 370, 372, 381, 382, 386, 389, 390, 392, 394, 402, 405, 406, 409, 413, 418, 424, 428, 436, 441-445, 449, 456, 459, 465-468, 473, 479, 483, 488, 493, 499, or 502.
14. The TAP of claim 1, wherein the TAP binds to an HLA-B*07:02 molecule and comprises or consists of the sequence of SEQ ID NO: 35, 36, 43, 104, 125, 127, 139, 140, 187, 191, 196, 206,
15 231, 243, 246, 251, 252, 260, 281, 291, 292, 321, 330, 361, 408, 432, 435, 439, 451, 461, 491, or 503.
15. The TAP of claim 1, wherein the TAP binds to an HLA-B*08:01 molecule and comprises or consists of the sequence of SEQ ID NO: 21, 162, 189, 286, 307, 309, 317, 339, 343, 349, or 414.
16. The TAP of claim 1, wherein the TAP binds to an HLA-B*13:02 molecule and comprises or
20 consists of the sequence of SEQ ID NO: 207, 311, 393, 400, or 455.
17. The TAP of claim 1, wherein the TAP binds to an HLA-B*14:01 molecule and comprises or consists of the sequence of SEQ ID NO: 396.
18. The TAP of claim 1, wherein the TAP binds to an HLA-B*15:01 molecule and comprises or consists of the sequence of SEQ ID NO: 11, 26, 30, 63, 113, 132, 148, 192, 195, 200, 207, 210, 222,
25 235, 238, 258, 262, 267, 276, 295, 297, 305, 309, 318, 326, 336, 342, 374, 377, 383, 401, 421, 427, 433, 438, 450, 463, 470, or 477.
19. The TAP of claim 1, wherein the TAP binds to an HLA-B*18:01 molecule and comprises or consists of the sequence of SEQ ID NO: 3, 10, 33, 225 or 396.
20. The TAP of claim 1, wherein the TAP binds to an HLA-B*37:01 molecule and comprises or
30 consists of the sequence of SEQ ID NO: 302.

21. The TAP of claim 1, wherein the TAP binds to an HLA-B*38:01 molecule and comprises or consists of the sequence of SEQ ID NO: 26, 180, 338, 341, 378, 380, 416, 448, 454, 496, or 498.
22. The TAP of claim 1, wherein the TAP binds to an HLA-B*40:01 molecule and comprises or consists of the sequence of SEQ ID NO: 215 or 322.
- 5 23. The TAP of claim 1, wherein the TAP binds to an HLA-B*40:02 molecule and comprises or consists of the sequence of SEQ ID NO: 213, 215, 339, or 351.
24. The TAP of claim 1, wherein the TAP binds to an HLA-B*44:02 molecule and comprises or consists of the sequence of SEQ ID NO: 346, 353, 356, or 453.
25. The TAP of claim 1, wherein the TAP binds to an HLA-B*49:01 molecule and comprises or
10 consists of the sequence of SEQ ID NO: 9, 57, 78, 115, 136, 167, 255, 273, 274, 278, 313, 339, 480, 484, or 495.
26. The TAP of claim 1, wherein the TAP binds to an HLA-B*51:01 molecule and comprises or consists of the sequence of SEQ ID NO: 227 or 259.
27. The TAP of claim 1, wherein the TAP binds to an HLA-C*03:03 molecule and comprises or
15 consists of the sequence of SEQ ID NO: 24, 69, 204 or 388.
28. The TAP of claim 1, wherein the TAP binds to an HLA-C*03:04 molecule and comprises or consists of the sequence of SEQ ID NO: 24, 49, 69, 159, 241, 242 or 334.
29. The TAP of claim 1, wherein the TAP binds to an HLA-C*06:02 molecule and comprises or consists of the sequence of SEQ ID NO: 13, 34 or 72.
- 20 30. The TAP of claim 1, wherein the TAP binds to an HLA-C*07:01 molecule and comprises or consists of the sequence of SEQ ID NO: 13, 75, 133, 163, 183, 199, 205, 285, 334, 391 or 472.
31. The TAP of claim 1, wherein the TAP binds to an HLA-C*07:02 molecule and comprises or consists of the sequence of SEQ ID NO: 13, 32, 36, 105, 177, 339, 371 or 478.
32. The TAP of claim 1, wherein the TAP binds to an HLA-C*08:02 molecule and comprises or
25 consists of the sequence of SEQ ID NO: 18, 54 or 379.
33. The TAP of claim 1, wherein the TAP binds to an HLA-C*12:03 molecule and comprises or consists of the sequence of SEQ ID NO: 24, 49, 58, 71, 94, 162, 178, 242, 289, 344, 345, 357, 367, 368, 375, 423 or 431.

34. The TAP of claim 1, wherein the TAP binds to an HLA-C*14:02 molecule and comprises or consists of the sequence of SEQ ID NO: 105, 271, 350, 365, 385, 410, 423, or 504.
35. The TAP of any one of claims 1-34, which is encoded by a sequence located a non-protein coding region of the genome or by a long non-coding RNA.
- 5 36. The TAP of claim 35, wherein said non-protein coding region of the genome is an intergenic region.
37. The TAP of claim 35, wherein said non-protein coding region of the genome is an intron.
38. The TAP of any one of claims 1 to 37, wherein said TAP is conjugated to a molecule that increases protease resistance, plasma protein binding, plasma half-life and/or intracellular
10 penetration of the TAP.
39. A combination comprising at least two of the TAPs or nucleic acids defined in any one of claims 1-38.
40. A synthetic long peptide (SLP) comprising at least one of the amino acid sequences defined in claim 1.
- 15 41. A nucleic acid encoding one or more of the TAPs of claims 1 to 38, the combination of claim 39, or the SLP of claim 40.
42. The nucleic acid of claim 41, wherein the nucleic acid is an mRNA, and wherein the mRNA optionally comprises one or more 5'-end modifications, 3'-end modifications, and/or modified nucleosides to increase stability, improve translation and/or reduce immunogenicity of the mRNA.
- 20 43. The nucleic acid of claim 41, wherein the nucleic acid is a DNA.
44. The nucleic acid of any one of claims 41-43, wherein the nucleic acid is a component of a viral vector.
45. A vesicle or particle comprising the TAP of any one of claims 1-38, the combination of claim 39, the SLP of claim 40, or the nucleic acid of any one of claims 41-44.
- 25 46. The vesicle or particle of claim 45, wherein the vesicle is a lipid nanoparticle (LNP).
47. The vesicle or particle of claim 45 or 46, which comprises a cationic lipid.
48. A composition comprising the TAP of any one of claims 1-38, the combination of claim 39, the SLP of claim 40, the nucleic acid of any one of claims 41-44, or the vesicle or particle of any one of claims 45-47, and a pharmaceutically acceptable carrier.

49. A vaccine comprising the TAP of any one of claims 1-38, the combination of claim 39, the SLP of claim 40, the nucleic acid of any one of claims 41-44, the vesicle or particle of any one of claims 45-47, or the composition of claim 48, and an adjuvant.
50. An isolated major histocompatibility complex (MHC) class I molecule comprising the TAP of
5 any one of claims 1-38 in its peptide binding groove.
51. The isolated MHC class I molecule of claim 50, which is in the form of a multimer.
52. The isolated MHC class I molecule of claim 51, wherein said multimer is a tetramer.
53. An isolated cell comprising (i) the TAP of any one of claims 1-38; (ii) the combination of claim 39; (iii) the SLP of claim 40; (iv) the nucleic acid of any one of claims 41-44; or (v) a vector comprising
10 a nucleotide sequence encoding the TAP of any one of claims 1-38, the combination of claim 39 or the SLP of claim 40.
54. An isolated cell expressing at its surface major histocompatibility complex (MHC) class I molecules comprising the TAP or combination of any one of claims 1-38 in their peptide binding groove.
- 15 55. The cell of claim 53 or 54, which is an antigen-presenting cell (APC).
56. The cell of claim 55, wherein said APC is a dendritic cell.
57. A T-cell receptor (TCR) that specifically recognizes the isolated MHC class I molecule of any one of claims 50-52 and/or MHC class I molecules expressed at the surface of the cell of any one of claims 54-56, or a nucleic acid encoding said TCR.
- 20 58. The TCR of claim 57, which is a soluble TCR.
59. An antibody or an antigen-binding fragment thereof that specifically binds to the isolated MHC class I molecule of any one of claims 50-52 and/or MHC class I molecules expressed at the surface of the cell of any one of claims 54-56, or a nucleic acid encoding said antibody or antigen-binding fragment thereof.
- 25 60. The TCR of claim 57 or 58, or the antibody or antigen-binding fragment thereof according to claim 59, which is a bispecific TCR or a bispecific antibody or antigen-binding fragment thereof.
61. The TCR, antibody or antigen-binding fragment thereof according to claim 60, wherein the bispecific antibody or antigen-binding fragment thereof is a single-chain diabody (scDb).

62. The TCR, antibody or antigen-binding fragment thereof according to claim 60 or 61, wherein the bispecific TCR, antibody or antigen-binding fragment thereof also specifically binds to a T cell signaling molecule.
63. The TCR, antibody or antigen-binding fragment thereof according to claim 62, wherein the T
5 cell signaling molecule is a CD3 chain.
64. A chimeric antigen receptor (CAR) comprising the antibody or an antigen-binding fragment thereof of claim 59, or a nucleic acid encoding said CAR.
65. An isolated cell expressing at its cell surface the TCR of claim 57 or the CAR of claim 64.
66. The isolated cell of claim 65, which is a CD8⁺ T lymphocyte.
- 10 67. A cell population comprising at least 0.5% of the isolated cell as defined in claim 65 or 66.
68. A method of treating cancer in a subject comprising administering to the subject an effective amount of:
- (a) a TAP comprising or consisting of any one of the sequences set forth in SEQ ID NOs: 1-505 or any combination thereof, or a synthetic long peptide (SLP) comprising at least one of
15 the sequences set forth in SEQ ID NOs: 1-505;
- (b) at least one nucleic acid encoding the TAP, combination thereof or SLP defined in (a);
- (c) a vesicle or particle comprising the TAP, combination thereof or SLP defined in (a) or the at least one nucleic acid defined in (b);
- (d) a composition comprising the TAP, combination thereof or SLP defined in (a), the at least
20 one nucleic acid defined in (b), or the vesicle or particle defined in (c), and a pharmaceutically acceptable carrier;
- (e) a vaccine comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), the vesicle or particle defined in (c), or the composition defined in (d), and an adjuvant;
- 25 (f) a cell expressing at its surface major histocompatibility complex (MHC) class I molecules comprising the TAP or combination thereof defined in (a) in their peptide binding groove;
- (g) a cell expressing at its cell surface a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) that specifically recognizes MHC class I molecules expressed at the surface of the cell defined in (f); or
- 30 (h) a soluble TCR, an antibody or an antigen-binding fragment thereof, or a CAR, that specifically binds to the MHC class I molecules expressed at the surface of the cell defined in

(f), or a nucleic acid encoding said soluble TCR, antibody, antigen-binding fragment thereof, or CAR.

69. The method of claim 68, wherein the cancer is melanoma.

70. The method of claim 68 or 69, further comprising administering at least one additional antitumor agent or therapy to the subject.

71. The method of claim 70, wherein said at least one additional antitumor agent or therapy is a chemotherapeutic agent, immunotherapy, an immune checkpoint inhibitor, radiotherapy or surgery.

72. Use of:

(a) a TAP comprising or consisting of any one of the sequences set forth in SEQ ID NOs: 1-505 or any combination thereof, or a synthetic long peptide (SLP) comprising at least one of the sequences set forth in SEQ ID NOs: 1-505;

(b) at least one nucleic acid encoding the TAP, combination thereof or SLP defined in (a);

(c) a vesicle or particle comprising the TAP, combination thereof or SLP defined in (a) or the at least one nucleic acid defined in (b);

(d) a composition comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), or the vesicle or particle defined in (c), and a pharmaceutically acceptable carrier;

(e) a vaccine comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), the vesicle or particle defined in (c), or the composition defined in (d), and an adjuvant;

(f) a cell expressing at its surface major histocompatibility complex (MHC) class I molecules comprising the TAP or combination thereof defined in (a) in their peptide binding groove;

(g) a cell expressing at its cell surface a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) that specifically recognizes MHC class I molecules expressed at the surface of the cell defined in (f); or

(h) a soluble TCR, an antibody or an antigen-binding fragment thereof, or a CAR, that specifically binds to the MHC class I molecules expressed at the surface of the cell defined in (f), or a nucleic acid encoding said soluble TCR, antibody, antigen-binding fragment thereof, or CAR;

for treating cancer in a subject, or for the manufacture of a medicament for treating cancer in a subject.

73. The use of claim 72, wherein said cancer is melanoma.

74. The use of claim 72 or 73, further comprising the use at least one additional antitumor agent or therapy to the subject.
75. The use of claim 74, wherein said at least one additional antitumor agent or therapy is a chemotherapeutic agent, immunotherapy, an immune checkpoint inhibitor, radiotherapy or surgery.
- 5 76. An agent for use in treating cancer in a subject, wherein the agent is:
- (a) a TAP comprising or consisting of any one of the sequences set forth in SEQ ID NOs: 1-505 or any combination thereof, or a synthetic long peptide (SLP) comprising at least one of the sequences set forth in SEQ ID NOs: 1-505;
 - (b) at least one nucleic acid encoding the TAP, combination thereof or SLP defined in (a);
 - 10 (c) a vesicle or particle comprising the TAP, combination thereof or SLP defined in (a) or the at least one nucleic acid defined in (b);
 - (d) a composition comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), or the vesicle or particle defined in (c), and a pharmaceutically acceptable carrier;
 - 15 (e) a vaccine comprising the TAP, combination thereof or SLP defined in (a), the at least one nucleic acid defined in (b), the vesicle or particle defined in (c), or the composition defined in (d), and an adjuvant;
 - (f) a cell expressing at its surface major histocompatibility complex (MHC) class I molecules comprising the TAP or combination thereof defined in (a) in their peptide binding groove;
 - 20 (g) a cell expressing at its cell surface a T-cell receptor (TCR) or a chimeric antigen receptor (CAR) that specifically recognizes MHC class I molecules expressed at the surface of the cell defined in (f); or
 - (h) a soluble TCR, an antibody or an antigen-binding fragment thereof, or a CAR, that specifically binds to the MHC class I molecules expressed at the surface of the cell defined in (f), or a nucleic acid encoding said soluble TCR, antibody, antigen-binding fragment thereof, or CAR.
 - 25
77. The agent for use according to claim 76, wherein said cancer is melanoma.
78. The agent for use according to claim 76 or 77, further comprising the use at least one additional antitumor agent or therapy to the subject.
- 30 79. The agent for use according to claim 78, wherein said at least one additional antitumor agent or therapy is a chemotherapeutic agent, immunotherapy, an immune checkpoint inhibitor, radiotherapy or surgery.