

CLAIMS

What is claimed is:

1. A method of targeting a tumor antigen, comprising:
 - obtaining omics data from a tumor tissue sample of a patient, and identifying, using the omics data, a presence of at least one mutation in a cancer driver gene that gives rise to the tumor antigen;
 - determining a HLA allele type of the patient;
 - matching the allele type of the patient and the tumor antigen with a majority allele type having a minimum affinity to the same tumor antigen; and
 - upon matching, a cancer vaccine targeting the tumor antigen is to be administered.
2. The method of claim 1, wherein the majority allele type is a represented allele type among different ethnicities, different geographic locations, different gender, or family provenance.
3. The method of claim 2, wherein the majority allele type has a population frequency of at least 0.1% in at least one of the ethnicities.
4. The method of any of claims 2-3, wherein the majority allele type has a population frequency that is in a top quartile in at least one of the ethnicities.
5. The method of any of the preceding claims, wherein the minimum affinity is determined by comparing affinities to the tumor antigen with respect to a plurality of HLA alleles.
6. The method of any of the preceding claims, wherein the minimum affinity is determined by a K_d of equal of less than 100nM.
7. The method of any of the preceding claims, further comprising ranking the HLA allele type of the patient among a plurality of HLA allele types based on binding affinities to the tumor antigen.
8. A method of targeting a tumor antigen, comprising:
 - obtaining omics data from a tumor tissue sample of a patient, and identifying a presence of at least one mutation in a cancer driver gene that gives rise to the tumor antigen using the omics data;
 - determining a HLA allele type of the patient;

matching the allele type of the patient and the tumor antigen with HLA allele types and mutation sequences of a plurality of patients who had been diagnosed with at least one type of cancer and treated with at least one cancer treatment; and upon matching, a cancer treatment is to be administered to the patient based on the matching.

9. The method of claim 8, wherein the matching further comprises ranking the tumor antigen based on the HLA allele type and a treatment outcome of the at least one cancer treatment.

10. The method of any of claims 8-9, wherein the cancer treatment is a cancer vaccine targeting the tumor antigen.

11. The method of any of claims 8-10, wherein the plurality of patients is stratified by at least one of gender, ethnicity, and geographical location.

12. The method of any of the preceding claims, wherein the omics data comprise at least one omics data selected from the group consisting of whole genome sequencing data, whole exome sequencing data, RNAseq data, and quantitative proteomics data.

13. The method of any of the preceding claims, further comprising a step of filtering the at least one mutation by at least one of an *a priori* known molecular variation selected from the group consisting of a single nucleotide polymorphism, a short deletion and insertion polymorphism, a microsatellite marker, a short tandem repeat, a heterozygous sequence, a multinucleotide polymorphism, and a named variant.

14. The method of any of the preceding claims, wherein the cancer driver gene is in a cancer selected from the group consisting of ALL, AML, BLCA, BRCA, CLL, CM, COREAD, ESCA, GBM, HC, HNSC, LUAD, LUSC, MB, NB, NSCLC, OV, PRAD, RCCC, SCLC, STAD, THCA, and UCEC.

15. The method of any of the preceding claims, wherein the cancer driver gene is one of the genes listed in Table 1.

16. The method of any of the preceding claims, wherein the tumor antigen has a length of between 7 and 20 amino acids.

17. The method of any of the preceding claims, wherein the cancer vaccine is one of a recombinant virus vaccine, a recombinant bacterial vaccine, a recombinant yeast vaccine, a nucleic acid encoding the tumor antigen, the tumor antigen coupled with a carrier molecule, and a genetically modified immune cell composition.
18. The method of claim 17, wherein the genetically modified immune cell composition comprises at least one of a genetically modified T cell, a genetically modified NK cell, a genetically modified NKT cells, which express a chimeric antigenic receptor specific to the tumor antigen.
19. The method of any of claims 17-18, wherein the recombinant virus vaccine, the recombinant bacterial vaccine, and the recombinant yeast vaccine comprise a recombinant nucleic acid encoding the tumor antigen.
20. The method of any of the preceding claims, wherein at least one of a co-stimulatory molecule, an immune stimulatory cytokine, and a protein that interferes with or down-regulates checkpoint inhibition is to be coadministered.
21. The method of claim 20, wherein the co-stimulatory molecule is selected from the group consisting of CD80, CD86, CD30, CD40, CD30L, CD40L, ICOS-L, B7-H3, B7-H4, CD70, OX40L, 4-1BBL, GITR-L, TIM-3, TIM-4, CD48, CD58, TL1A, ICAM-1, and LFA3.
22. The method of any of claims 20-21, wherein the immune stimulatory cytokine is selected from the group consisting of IL-2, IL-12, IL-15, IL-15 super agonist (ALT803), IL-21, IPS1, and LMP1.
23. The method of any of claims 20-22, wherein the protein that interferes is an antibody or an antagonist of CTLA-4, PD-1, TIM1 receptor, 2B4, or CD160.