

CLAIMS

1. A method for selecting at least one immunogenic mutated peptide, comprising:
 - (a) obtaining a plurality of mutant sequences;
 - (b) identifying at least one epitope that derived from a disease-associated mutation;
 - (c) incorporating a plurality of factors associated with the immunogenicity of said at least one epitope;
 - (d) weighing said plurality of factors;
 - (e) assigning an immunogenicity score to said at least one epitope based on the weights of the plurality of factors;
 - (f) ranking said at least one epitope; and
 - (g) selecting said immunogenic mutated peptide(s) based on an ranking result in step (f),wherein said immunogenic mutated peptide(s) includes at least one epitope that may elicit T-cell response.
2. The method of claim 1, wherein one of steps (c)-(e) is achieved utilizing a machine learning model.
3. The method of any of claims 1-2, wherein 100 or less epitopes are selected.
4. The method of claim 3, wherein 50 or less epitopes are selected.
5. The method of claim 4, wherein 30 or less epitopes are selected.
6. The method of claim 5, wherein 10 or less epitopes are selected.
7. The method of claim 5, wherein 10 to 30 epitopes are selected.
8. The method of any of claims 1-7, wherein said plurality of factors accounts for the presentation of said epitopes by MHC class I and class II.
9. The method of claim 8, wherein binding affinities of the selected epitopes with MHC class I have IC50 values less than 1500 nM.
10. The method of any of claims 8-9, wherein said plurality of factors comprise MHC class I binding stability.
11. The method of any of claims 8-10, wherein said plurality of factors include protein abundance, gene expression or a combination thereof.
12. The method of any of claims 1-11, wherein said plurality of factors accounts for the ability for said epitopes to elicit immune response in cytotoxic T cells.
13. The method of any of claims 1-12, wherein said plurality of factors accounts for the ability for said epitopes to elicit immune response in helper T cell

14. The method of any of claims 12-13, wherein said plurality of factors comprise similarity of said epitope to self peptides.
15. The method of any of claims 12-14, wherein said plurality of factors comprise homology of said epitope to known antigens.
16. The method of any of claims 1-15, wherein the variant frequency of said mutation is at least 10%.
17. The method of claim 16, wherein the variant frequency of said mutation is at least 30%.
18. The method of any of claims 1-17, wherein said mutation is present with at least two copies.
19. The method of any of claims 1-18, wherein one of said plurality of factors is loss of heterozygosity.
20. The method of any of claims 1-19, wherein one of said plurality of factors is allele dosage.
21. The method of any of claims 1-20, wherein one of said plurality of factors is clonality of said disease-associated mutation.
22. The method of any of claims 1-21, wherein said immunogenicity score is integrated from the plurality of factors including a factor that can be used to calculate a peptide-level score and a factor that can be used to calculate a sample-level score.
23. The method of claim 1, wherein said immunogenicity score is integrated from a plurality of factors including MHC class I and class II presentation of said epitopes, the ability for said epitopes to elicit immune response in both helper and cytotoxic T cells, and the clonality of said disease-associated mutation.
24. A system for selecting at least one immunogenic mutated peptide, comprising:
 - a hardware memory storing computer-executable means of:
 - (a) obtaining a plurality of mutant sequences;
 - (b) identifying at least one epitope that derived from a disease-associated mutation;
 - (c) incorporating a plurality of factors associated with the immunogenicity of said at least one epitope;
 - (d) weighing said plurality of factors;
 - (e) assigning an immunogenicity score to said at least one epitope based on the weights of the plurality of factors;
 - (f) ranking said at least one epitope; and
 - (g) selecting said immunogenic mutated peptide(s) based on an ranking result in step (f),
 - wherein said immunogenic mutated peptide(s) includes at least one epitope that may elicit

T-cell response.