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~~ the at least one epitope, wherein the plurality of factors comprises a first factor that can be used to calculate a peptide-level score and a second factor that can be used to calculate a sample-level score, wherein the second factor for calculating said sample-level score comprises the clonality of the disease-associated mutation;

(d) weighing ~~said~~ the plurality of factors;

(e) assigning an immunogenic~~ity~~ score to ~~said~~ the at least one epitope based on the weights of the plurality of factors;

(f) ranking ~~said~~ the at least one epitope; and

(g) selecting ~~said~~ at least one immunogenic mutated peptide~~(s)~~ based on ~~an~~ a ranking result in step (f),

wherein ~~said~~ the immunogenic mutated peptide~~(s) includes~~ comprises the 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~~2. The method of ~~any of claims 1-2~~claim 1, wherein 100 or less epitopes are selected.

~~4~~3. The method of claim ~~3~~1, wherein 50 or less epitopes are selected.

~~5~~4. The method of claim ~~4~~1, wherein 30 or less epitopes are selected.

~~6~~5. The method of claim ~~5~~1, wherein 10 or less epitopes are selected.

~~7. The method of claim 5, wherein 10 to 30 epitopes are selected.~~

~~8~~6. The method of ~~any of claims 1-7~~ claim 1, wherein ~~said~~the plurality of factors accounts for the presentation of ~~said~~ the at least one epitopes by MHC class I and class II.

~~9~~7. The method of claim ~~8~~5, wherein the binding ~~affinities~~ affinity of the selected at least one epitopes with MHC class I ~~have~~ has an IC50 values less than 1500 nM.

~~10~~8. The method of ~~any of claims 8-9~~ claim 5, wherein ~~said~~ the plurality of factors comprises MHC class I binding stability.

~~11~~9. The method of ~~any of claims 8-10~~ claim 5, wherein ~~said~~ the plurality of factors ~~include~~ comprises protein abundance, gene expression or a combination thereof.

~~12~~10. The method of ~~any of claims 1-11~~ claim 1, wherein ~~said~~ the plurality of factors accounts for the ability for ~~said~~ the at least one epitope~~s~~ to elicit immune response in cytotoxic T cells.

~~13~~11. The method of ~~any of claims 1-12~~ claim 8, wherein ~~said~~ the plurality of factors accounts for the ability for ~~said~~ the at least one epitope~~s~~ to elicit immune response in helper T cell.

~~14~~12. The method of ~~any of claims 12-13~~ claim 9, wherein ~~said~~ the plurality of factors comprises the similarity of ~~said~~ the at least one epitope to self-peptide~~s~~.

~~15~~13.The method of ~~any of claims 12-14~~ claim 9, wherein ~~said~~ the plurality of factors comprises the homology of ~~said~~ the at least one epitope to a known antigen~~s~~.

~~16~~14. The method of ~~any of claims 1-15~~ claim 1, wherein the variant frequency of ~~said~~ the mutation is at least 10%.

~~17~~15. The method of claim ~~16~~ 1, wherein the variant frequency of ~~said~~ the mutation is at least 30%.

~~18~~16. The method of ~~any of claims 1-17~~ claim 1, wherein ~~said mutation is present with at least two copies~~the plurality of factors comprises a copy number, tumor purity, or both copy number and tumor purity.

~~19~~17. The method of ~~any of claims 1-18~~claim 1, wherein one of ~~said~~ the plurality of factors is the status of loss of heterozygosity.

~~20~~18. The method of ~~any of claims 1-19~~claim 1, wherein one of ~~said~~ the 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 immunogenic 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~~19.The method of claim 1, wherein ~~said~~ the immunogenic~~ity~~ score is integrated from a plurality of factors including MHC class I and class II presentation of ~~said~~ the at least one epitope~~s~~, the ability for ~~said~~ the at least one epitope~~s~~ to elicit immune response in both helper and cytotoxic T cells, and the clonality of ~~said~~ the disease-associated mutation.

~~24~~20. 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~~ the at least one epitope, wherein the plurality of factors comprises a first factor that can be used to

calculate a peptide-level score and a second factor that can be used to calculate a sample-level score, wherein the second factor for calculating said sample-level score comprises the clonality of the disease-associated mutation;

(d) weighing ~~said~~ the plurality of factors;

(e) assigning an immunogenic~~ity~~ score to ~~said~~ the at least one epitope based on the weights of the plurality of factors;

(f) ranking ~~said~~ the at least one epitope; and

(g) selecting ~~said~~ at least one immunogenic mutated peptide~~(s)~~ based on a~~n~~ ranking result in the step (f), wherein ~~said~~ the immunogenic mutated peptide~~(s) includes~~ comprises the at least one epitope that may elicit T-cell response.