**Claims**

1. A method for selecting a number A of neoepitopes for an individual suffering from or suspected of suffering from cancer, said method comprising the steps of:

a. Obtaining one or more neoepitopes from said individual, each neoepitope comprising at least one minimal epitope, wherein each neoepitope comprises at least one mutation such as an immunogenic mutation compared to a reference sequence, wherein the minimal epitope consists of a number of amino acids equal to or smaller than the number of amino acids of the neoepitope and comprises said at least one mutation; wherein preferably obtaining the neoepitopes comprises the step of identifying mutations in nucleic acid sequences which are specific for the tumor;

b. Determining MHC I and/or MHC II binding affinity for at least one minimal epitope, such as at least two, three or four minimal epitopes within each of said neoepitopes, optionally wherein the binding affinity is determined by *in silico* prediction;

c. Selecting neoepitopes comprising at least one minimal epitope predicted to bind to MHC I and/or to MHC II, thereby obtaining MHC binding neoepitopes;

d. Ranking the MHC binding neoepitopes with respect to their likelihood of clinical utility as follows:

I. the number of minimal epitopes, by determining the number of minimal epitopes comprised in the neoepitopes, and wherein neoepitopes comprising a high number of minimal epitopes are ranked higher than neoepitopes comprising a lower number of minimal epitopes, preferably wherein the minimal epitope is an MHC I binding minimal epitope;

II. their MHC I rank wherein neoepitopes with a low %Rank score are ranked above neoepitopes with a higher %Rank score, wherein the %Rank score (MHC I) of a neoepitope comprising one or more minimal epitopes predicted to bind to MHC I is equal to the lowest %Rank score (MHC I) of said one or more minimal epitopes;

III. their MHC II rank, wherein neoepitopes with a low %Rank score are ranked above neoepitopes with a higher %Rank score, wherein the %Rank score (MHC II) of a neoepitope comprising one or more minimal epitopes predicted to bind to MHC II is equal to the lowest %Rank score (MHC II) of said one or more minimal epitopes;

IV. their MHC I binding differential, including determining the MHC I binding differential of the MHC I binding neoepitope obtained in step c, wherein the MHC I binding differential is given by the formula (%Rank score (MHC I) for reference) / (%Rank score (MHC I) for neoepitope), wherein neoepitopes with a high MHC I binding differential are ranked higher than neoepitopes with a lower MHC I binding differential, and/or wherein neoepitopes binding to MHC I are selected in step e only if the plurality of neoepitopes does not comprise any neoepitope binding to MHC II;

V. their MHC II binding differential, including determining the MHC II binding differential of the MHC II binding neoepitope obtained in step c, wherein the MHC II binding differential is given by the formula (%Rank score (MHC II) for reference) / (%Rank score (MHC II) for neoepitope), wherein neoepitopes with a high MHC II binding differential are ranked higher than neoepitopes with a lower MHC II binding differential;

VI. the position of the mutation, including determining whether the mutation is in an anchoring position or a non-anchoring position of the minimal neoepitope for each minimal epitope comprised within the neoepitope and prioritizing minimal neoepitopes with the mutation in an anchoring position; and

the BLOSUM score, wherein the neoepitopes are prioritized with respect to their BLOSUM score in a descending order, wherein the BLOSUM score of a neoepitope is equal to the BLOSUM score of the best ranking minimal epitope it comprises, wherein a minimal epitope with a BLOSUM score < 1 is ranked higher than a minimal epitope with a BLOSUM score ≥ 1; and

e. Selecting A neoepitopes among the highest ranking MHC binding neoepitopes of step d, thereby selecting A neoepitopes likely to have clinical utility.

2. The method according to claim 1, wherein A is an integer of from 1 to 100, such as from 5 to 50, such as from 5 to 30, such as from 10 to 20, such as 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25.

3. The method according to any one of the preceding claims, wherein step a comprises identifying mutations in nucleic acid sequences in one or more sample

derived from the individual compared to a reference sample, preferably wherein the one or more sample is a sample derived from tumor cells of the individual.

4. The method according to claim 3, wherein the mutations are found in at least two samples derived from tumor cells of the individual.

5. The method according to any one of the preceding claims, wherein the at least one minimal epitope is between 1 and 50 minimal epitopes, such as between 1 and 40 minimal epitopes, such as between 1 and 30 minimal epitopes, such as between 1 and 20 minimal epitopes.

6. The method according to any one of the preceding claims, wherein step c comprises selecting neoepitopes comprising at least one minimal epitope predicted to bind to MHC I and at least one minimal epitope predicted to bind to MHC II.

7. The method according to any one of the preceding claims, wherein step e comprises selecting neoepitopes having a %Rank score (MHC I) below 2.0, such as below 1.5, such as below 1, preferably equal to or below 0.5.

8. The method according to any one of the preceding claims, wherein step c comprises selecting neoepitopes having a %Rank score (MHC II) below 10, such as below 2.

9. The method according to any one of the preceding claims, wherein said neoepitopes have a length of from 7 to 40 amino acids, such as from 15 to 30 amino acids, such as from 25 to 30 amino acids, such as 27 amino acids.

10. The method according to any one of the preceding claims, wherein the neoepitopes of step d, VI are ranked by assigning to each neoepitope the highest score of the minimal epitopes they comprise, and wherein the ranking of the neoepitopes is performed in a descending order 1) to 7) as follows:
    1) if the mutation is in an anchoring position and the binding differential of the minimal epitope is equal to or greater than 20, the minimal epitope has the highest score;

2) if the mutation is in a non-anchoring position and the binding differential of the minimal epitope is equal to or greater than 20, the score of the minimal epitope is lower than the score for the minimal epitopes of 1);

3) if the mutation is in an anchoring position and the binding differential of the minimal epitope is lower than 20 and equal to or greater than 3, the score of the minimal epitope is lower than the score the minimal epitopes of 2);

4) if the mutation is in a non-anchoring position and the binding differential of the minimal epitope is lower than 20 and equal to or greater than 3, the score of the minimal epitope is lower than the score the minimal epitopes of 3);

5) if the mutation is in an anchoring position and the binding differential of the minimal epitope is less than 3 and equal to or greater than 1, the score of the minimal epitope is lower than the score of the minimal epitopes of 4);

6) if the mutation is in a non-anchoring position and the binding differential of the minimal epitope is less than 3 and equal to or greater than 1, the score of the minimal epitope is lower than the score of the minimal epitopes of 5;

7) if the minimal epitope has a mutation with a binding differential lower than 1, regardless of the position of the mutation, the minimal epitope has the lowest score.