CLAIMS

Now, therefore, the following is claimed:

1. A method for developing a diagnostic test for a particular disease, the method comprising the steps of:

amplifying and sequencing the immune repertoire in a sample, wherein the sample is collected from each of multiple subjects in a patient group and a control group, wherein the patient group comprises subjects who have the same disease and the control group comprises subjects who are healthy, wherein the amplifying and sequencing the immune repertoire is in the sample of each subject in each of the two groups to identify each unique CDR3 sequence present in the samples and to determine the frequency of occurrence of each unique CDR3 sequence;

identifying CDR3 sequences that are shared between at least two subjects in each of the control group and the patient group;

ranking the CDR3 sequences by order of frequency of occurrence;

identifying the Linklets from each group; and

identifying the Linklets that are associated to a statistically significant degree with the patient group to provide a disease signature.

2. The method of claim 1, wherein the sample is blood.

3. The method of claim 1, wherein the sample is tissue.

4. The method of claim 1, wherein at least about 1,000 CDR3 sequences are identified that are shared between at least two subjects in each of the control group and the patient group.

5. The method of claim 1, wherein at least about 10^6 Linklets from each group are identified.

6. The method of claim 1, wherein a minimum number of Linklets associated with the disease signature is established as a diagnostic number, so when at least that

number of Linklets are identified in a subject's blood sample, that subject is diagnosed as having the disease.

7. The method of claim 6, wherein the diagnostic number is at least about 500.

8. A method for developing a diagnostic test for a particular disease, the method comprising the steps of:

amplifying and sequencing the immune repertoire in a blood sample, wherein the blood sample is collected from each of multiple subjects in a patient group and a control group, wherein the patient group comprises subjects who have the same disease and the control group comprises subjects who are categorized as healthy, wherein the amplifying and sequencing the immune repertoire is in the blood sample of each subject in each of the two groups to identify each unique CDR3 sequence present in the blood samples and to determine the frequency of occurrence of each unique CDR3 sequence;

identifying at least about 1,000 CDR3 sequences that are shared between at least two subjects in each of the control group and the patient group;

ranking the at least about 1,000 CDR3 sequences by order of frequency of occurrence;

identifying at least about 10^6 Linklets from each group; and

identifying the Linklets that are associated to a statistically significant degree with the patient group to provide a disease signature;

wherein a minimum number of Linklets associated with the disease signature is established as a diagnostic number, so when at least that number of Linklets are identified in a subject's blood sample, that subject is diagnosed as having the disease.