CLAIMS

What Is Claimed Is:

1. A method of detecting Lyme disease in a subject, the method comprising detecting a presence of one or more of the *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11, and/or a presence of one or more amino acids that encode one or more of the *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11, in a sample obtained from the subject, thereby detecting Lyme disease in the subject.

2. The method of claim 1, wherein detecting the presence of the one or more of the *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11 comprises detecting a presence of one or more antibodies in the sample that bind to the one or more *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11.

3. The method of claim 1, wherein detecting the presence of the one or more of the *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11 comprises the use of antibodies raised against the one or more of the *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11 in the sample.

4. The method of claim 1, wherein detecting the presence of the one or more amino acids that encode the one or more *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11 comprises sequencing the one or more nucleic acids that encode the antigenic peptides or proteins in the sample.

5. Use of an effective amount of an antibiotic selected from oxytetracycline, doxycycline, minocycline, amoxicillin, penicillin, cefaclor, cefbuperazone, cefminox, cefotaxime, cefotetan, cefmetazole, cefoxitin, cefuroxime axetil, cefuroxime acetyl, ceftin, ceftriaxone, azithromycin, clarithromycin, erythromycin, and combination thereof, in the manufacture of a medicament for treating Lyme disease in a subject, wherein a presence of one or more of the *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11, and/or a presence of one or more amino acids that encode one or more of the *B. burgdorferi* antigenic peptides or proteins listed in TABLE 7, 8, 9, 10, and/or 11, is deleted in a sample obtained from the subject.

6. A reaction mixture comprising reagents for performing the method of claim 1.

7. A kit comprising reagents for performing the method of claim 1.

8. A computer-implemented method of generating predicted binding intensities from a microarray peptide data set, the method comprising:

passing the microarray peptide data set through an electronic neural network model, wherein the microarray peptide data set is obtained from a microarray that comprises a quasi-random set of peptides using one or more antibodies or donor serum sample and wherein the electronic neural network model has been trained to predict binding intensities of peptides not present on the microarray; and,

outputting from the electronic neural network the predicted binding intensities of peptides not represented on the microarray using the microarray peptide data set.

9. The computer-implemented method of claim 8, wherein the electronic neural network model is trained on binding intensities associated with the microarray peptide data set is utilized to predict binding intensities of donor's circulating antibodies to one or more proteomes selected from the group consisting of: a proteome associated with a vector of a disease, a proteome associated with a carrier of a vector of a disease, and a human proteome.

10. The computer-implemented method of claim 9, wherein predicted strong binding targets in the proteome(s) are used to identify immunogenic full proteins that can further be used as biomarkers in orthogonal assays.

11. The computer-implemented method claim 8, further comprising:

passing the predicted binding intensities of peptides that are not present on the microarray set to one or more classifiers that have been trained using one or more potential biomarkers to distinguish between a disease state and a non-disease state.

12. The computer-implemented method of claim 8, further comprising:

ranking at least a subset of a set of peptides not represented on the array based upon the predicted binding intensities obtained using a machine learning model trained on the microarray peptide data set to produce a set of ranked peptides;

using statistical methods, identifying protein biomarkers from proteomes of the pathogen and/or other associated organisms;

producing a classification model using predicted intensity values of the set of ranked peptides that are not represented on the microarray, which classification model classifies a sample from a test subject as being positive or negative for a disease;

assessing a performance of the classification model to produce a classification model performance assessment measure; and,

determining whether the set of ranked peptides comprises candidate biomarkers for detecting a presence of the disease in test subjects based on the classification model performance assessment measure.

13. The computer-implemented method of claim 12, wherein the disease is Lyme disease.

14. The computer-implemented method of claim 12, wherein the classification model is selected from the group consisting of: a general linear model, a support vector machine, an extreme gradient boosting model, an electronic neural network model, and a combination thereof.

15. The computer-implemented method of claim 12, wherein the disease is associated with a pathogen and a carrier and wherein the method further comprises:

filtering, from the subset of the quasi-random set of peptides, carrier-related peptides, wherein the carrier-related peptides are associated with other pathogens associated with the carrier.

16. The computer-implemented method of claim 15, wherein the pathogen is *Borrelia burgdorferi* and the carrier is the blacklegged tick *Ixodes scapularis*.

17. The computer-implemented method of claim 12, wherein the subset of the set of peptides not represented on the microarray is ranked according to p-values associated with corresponding predicted binding intensities.

18. The computer-implemented method of claim 12, wherein the subset of peptides not represented on the microarray corresponds to a set of n-highest ranked peptides, wherein n is an integer greater than one.

19. The computer-implemented method of claim 12, wherein assessing the performance of the classification model comprises generating a ROC curve corresponding to the performance of the classification model.

20. A system for generating predicted binding intensities from a microarray peptide data set using an electronic neural network, the system comprising:

a processor; and

a memory communicatively coupled to the processor, the memory storing instructions which, when executed on the processor, perform operations comprising:

passing the microarray peptide data set through the electronic neural network, wherein the microarray peptide data set is obtained from a microarray that comprises a quasi-random set

of peptides using one or more antibodies or donor serum sample and wherein the electronic neural network has been trained to predict binding intensities of peptides not present on the microarray using the microarray peptide data set; and,

outputting from the electronic neural network the predicted binding intensities of the peptides not represented on the microarray.

21. The system of claim 20, wherein the instructions which, when executed on the processor, further perform operations comprising:

passing the predicted binding intensities of the peptides not represented on the microarray to one or more classifiers that have been trained using one or more potential biomarkers to distinguish between a disease state and a non-disease state.

22. The system of claim 20, wherein the instructions which, when executed on the processor, further perform operations comprising:

mapping, using an electronic neural network amino language model, the microarray peptide data set to a set of embeddings; and

passing the set of embeddings to a machine learning model to determine the predicted binding intensities of peptides not represented on the array.

23. The system of claim 20, wherein the instructions which, when executed on the processor, further perform operations comprising:

ranking at least a subset of a set of peptides not represented on the microarray based upon the predicted binding intensities from the microarray peptide data set to produce a set of ranked peptides;

producing a classification model using the set of ranked peptides, which classification model classifies a sample from a test subject as being positive or negative for a disease;

assessing a performance of the classification model to produce a classification model performance assessment measure; and,

determining whether the set of ranked peptides comprises candidate biomarkers for detecting a presence of the disease in test subjects based on the classification model performance assessment measure.