METHODS FOR IDENTIFYING EPITOPES AND PARATOPES

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 62/784,617, filed December 24, 2018. The contents of the aforesaid application are hereby incorporated by reference in its entirety.

BACKGROUND

Antibodies bind target antigens with high specificity and affinity. Molecularly, binding is facilitated by the set of amino acids in the antibody (paratope) and the antigen (epitope) which contribute to energetically favorable interactions for binding to occur. Determining the structural features governing antibody-antigen interactions is important for understanding an antibody's mechanism of action and as a reference to aid antibody engineering efforts. X-ray co-crystallography is a leading method to determine the structure of antibody-antigen complexes, detailing both the structural paratope and epitope with high resolution. However, achievement of high resolution co-crystal structures has considerable resource, throughput, and specialized technical expertise requirements. Other methods to characterize paratopes and epitopes provide greater throughput and experimental accessibility but typically come with a tradeoff of resolution. Epitope binning by competition binding or epitope characterization by alanine scanning each provide greater speed and throughput than crystallography but cannot provide the molecular detail nor the comprehensiveness of characterization as in crystallography. Thus, there exists a need in the art for improved methods of identifying epitope and paratope regions between an antibody and its recognized antigen.

SUMMARY

In an aspect, there is provided a method of identifying an epitope on a target polypeptide, the method comprising:

(a) binding an antibody molecule to a plurality of variants of the target polypeptide;

(b) obtaining a plurality of variants exhibiting reduced binding to the antibody molecule, wherein the plurality of variants comprise:

(i) mutations on one or more surface residues of the target polypeptide;

(ii) distinct mutations of a selected surface residue of the target polypeptide; and/or

(iii) distinct mutations of each of a plurality of selected surface residues of the target polypeptide;

and wherein the reduced binding comprises a reduction of binding detected for a variant of the plurality of variants and the antibody molecule, relative to the binding detected for a wild-type target polypeptide and the antibody molecule, and wherein the reduced binding is at least about 20% of the binding exhibited by the wild-type target polypeptide;

(c) determining an enrichment score for each of the plurality of the obtained variants;

(d) generating an antibody molecule-target polypeptide docking model, wherein the antibody molecule-target polypeptide docking model is constrained according to the enrichment scores, and wherein the antibody molecule-target polypeptide docketing model does not exhibit a mode of engagement atypical for a known antibody-antigen complex according to a structural filter derived from antibody-antigen crystal structure; and

(e) identifying a site on the target polypeptide that is capable of being directly bound by the antibody molecule based on the antibody molecule-target polypeptide docking model;

thereby identifying an epitope on a target polypeptide.

In an example, step (a) further comprises removing an antibody molecule-target polypeptide docketing model that exhibits a mode of engagement atypical for a known antibody-antigen complex, *e.g.*, according to a structural filter derived from antibody-antigen crystal structure.

In an example, step (a) comprises generating a plurality of antibody molecule-target polypeptide models.

In an example, step (b) comprises identifying a plurality of sites on the target polypeptide that is capable of being bound by the antibody molecule.

In an example, the site comprises or consists of one or more non-consecutive regions on the target polypeptide. In an example, the site comprises or consists of a consecutive region on the target polypeptide.

In another aspect, the disclosure features a method of identifying a paratope on an antibody molecule, the method comprising:

(a) binding the antibody molecule to a plurality of variants of the target polypeptide;

(b) obtaining a plurality of variants exhibiting reduced binding to the antibody molecule, wherein the plurality of variants comprise:

(i) mutations on one or more surface residues of the target polypeptide;

(ii) distinct mutations of a selected surface residue of the target polypeptide; and/or

(iii) distinct mutations of each of a plurality of selected surface residues of the target polypeptide;

and wherein the reduced binding comprises a reduction of binding detected for a variant of the plurality of variants and the antibody molecule, relative to the binding detected for a wild-type target polypeptide and the antibody molecule, and wherein the reduced binding is at least about 20% of the binding exhibited by the wild-type target polypeptide;

(c) determining enrichment scores for each of the plurality of the enriched variants;

(d) generating an antibody molecule-target polypeptide docking model, wherein the antibody-target polypeptide docking model is constrained according to the enrichment scores, and wherein the antibody molecule-target polypeptide docketing model does not exhibit a mode of engagement atypical for a known antibody-antigen complex, according to a structural filter derived from antibody-antigen crystal structure; and

(e) identifying one or more sites on the antibody molecule that is capable of being directly bound by the target polypeptide based on the antibody-target polypeptide docking model;

thereby identifying a paratope on an antibody molecule.

In yet another example, the disclosure features a method of identifying a paratope on an antibody molecule, the method comprising:

(a) binding the antibody molecule to a plurality of variants of the target polypeptide;

(b) obtaining (*e.g.*, enriching) a plurality of variants exhibiting reduced binding to the antibody molecule;

(c) determining (*e.g.*, calculating) enrichment scores for each of the plurality of the enriched variants;

(d) generating an antibody molecule-target polypeptide docking model, wherein the antibody-target polypeptide docking model is constrained according to the enrichment scores; and

(e) identifying one or more sites on the antibody molecule that is capable of being bound by the target polypeptide based on the antibody-target polypeptide docking model;

thereby identifying a paratope on an antibody molecule.

In an example, the altered binding comprises altered binding affinity, *e.g.*, reduced binding affinity.

In an example, step (a) comprises binding the antibody molecule to a library displaying a plurality of variants of the target polypeptide. In an example, step (a) comprises binding the antibody molecule to a library comprising a plurality of cells expressing (*e.g.*, displaying) a plurality of variants of the target polypeptide. In an example, each of the plurality of cells expresses about one distinct variant of the target polypeptide. In an example, the cell is a eukaryotic cell, *e.g.*, a yeast cell.

In an example, the plurality of variants comprise mutations on one or more surface residues of the target polypeptide. In an example, the plurality of variants comprise distinct mutations of a selected surface residue of the target polypeptide. In an example, the plurality of variants comprise distinct mutations of each of a plurality of selected surface residues of the target polypeptide.

In an example, the disclosure features an antibody molecule for which the epitope on a target polypeptide or the paratope on the antibody molecule for the target polypeptide is identified according to a method described herein.

In an example, the disclosure features a nucleic acid molecule encoding an antibody molecule described herein or one or more chains (*e.g.*, VH and/or VL) of an antibody molecule described herein. In another example, the disclosure features a vector comprising a nucleic acid molecule described herein. In yet another example, the disclosure features a host cell comprising a nucleic acid molecule described herein or a vector described herein. In an example, the disclosure features a method of making an antibody molecule, comprising culturing a host cell described herein under conditions suitable for expression of an antibody molecule.

BRIEF DESCRIPTION OF THE DRAWINGS

FIGS. 1A-1B are a series of diagrams showing positions interrogated on surface of APRIL. (A) Alignment of mouse and human APRIL, with positions interrogated in the deep mutational scanning library highlighted in gray. The chimeric form of APRIL was generated by mutating the 5 positions underlined in red in muAPRIL to the corresponding amino acid found in huAPRIL. (B) Structure of APRIL homotrimer with positions chosen for diversification in the library shaded gray, selected for even coverage of the antigen surface. Nine N-terminal amino acids of APRIL present in the library design but not observed in the APRIL crystal structure are represented (box below structure); two Lys residues were selected for diversification.

FIG. 2 is a graph showing antibody and TACI affinity to APRIL expressed on the surface of yeast. A set of purified anti-APRIL antibodies (2419, 4035, 4540, and 3530), isotype control and TACI were assessed for approximate affinity to APRIL expressed on the surface of yeast. Binding isotherms were used to estimate concentration yielding 80% maximal binding for each antibody, which was used for library enrichment.

FIG. 3 is a series of diagrams showing an overview of epitope mapping with computational docking workflow. A site-saturation library of the APRIL antigen library was generated and expressed by yeast surface display. Antibodies were applied to the yeast library, and FACS enrichment was performed to enrich non-binding members of the library. The enriched library was subjected to NGS to ascertain and count the underlying mutations. Mutation enrichment scores were mapped onto the surface of APRIL to determine putative epitope regions of mapped antibodies. These data were used to constrain antibody-antigen docking, resulting in a cluster of models that are consistent with the mutational profile data. The resultant high-confidence models provide molecular definition of epitope and paratope residues.

FIGS. 4A-4B are a series of graphs showing FACS enrichment of library against multiple antibodies and TACI. Flow cytometry analyses of either WT APRIL or library yeast populations are shown before or after enrichment. X-axis represents APRIL surface expression (c-myc) and Y-axis

What is claimed is:

1. A method of identifying an epitope on a target polypeptide, the method comprising:

(a) binding an antibody molecule to a plurality of variants of the target polypeptide;

(b) obtaining a plurality of variants exhibiting reduced binding to the antibody molecule, wherein the plurality of variants comprise:

(i) mutations on one or more surface residues of the target polypeptide;

(ii) distinct mutations of a selected surface residue of the target polypeptide; and/or

(iii) distinct mutations of each of a plurality of selected surface residues of the target polypeptide;

and wherein the reduced binding comprises a reduction of binding detected for a variant of the plurality of variants and the antibody molecule, relative to the binding detected for a wild-type target polypeptide and the antibody molecule, and wherein the reduced binding is at least about 20% of the binding exhibited by the wild-type target polypeptide;

(c) determining an enrichment score for each of the plurality of the obtained variants;

(d) generating an antibody molecule-target polypeptide docking model, wherein the antibody molecule-target polypeptide docking model is constrained according to the enrichment scores, and wherein the antibody molecule-target polypeptide docketing model does not exhibit a mode of engagement atypical for a known antibody-antigen complex according to a structural filter derived from antibody-antigen crystal structure; and

(e) identifying a site on the target polypeptide that is capable of being directly bound by the antibody molecule based on the antibody molecule-target polypeptide docking model;

thereby identifying an epitope on a target polypeptide.

2. A method of identifying a paratope on an antibody molecule, the method comprising:

(a) binding the antibody molecule to a plurality of variants of the target polypeptide;

(b) obtaining a plurality of variants exhibiting reduced binding to the antibody molecule, wherein the plurality of variants comprise:

(i) mutations on one or more surface residues of the target polypeptide;

(ii) distinct mutations of a selected surface residue of the target polypeptide; and/or

(iii) distinct mutations of each of a plurality of selected surface residues of the target polypeptide;

and wherein the reduced binding comprises a reduction of binding detected for a variant of the plurality of variants and the antibody molecule, relative to the binding detected for a wild-type target polypeptide and the antibody molecule, and wherein the reduced binding is at least about 20% of the binding exhibited by the wild-type target polypeptide;

(c) determining enrichment scores for each of the plurality of the enriched variants;

(d) generating an antibody molecule-target polypeptide docking model, wherein the antibody-target polypeptide docking model is constrained according to the enrichment scores, and wherein the antibody molecule-target polypeptide docketing model does not exhibit a mode of engagement atypical for a known antibody-antigen complex, according to a structural filter derived from antibody-antigen crystal structure; and

(e) identifying one or more sites on the antibody molecule that is capable of being directly bound by the target polypeptide based on the antibody-target polypeptide docking model;

thereby identifying a paratope on an antibody molecule.

3. The method of claim 1 or 2, wherein step (a) comprises:

(i) binding the antibody molecule to a library displaying a plurality of variants of the target polypeptide; and/or

(ii) binding the antibody molecule to a library comprising a plurality of cells expressing a plurality of variants of the target polypeptide.

4. The method of claim 3, wherein:

(i) each of the plurality of cells expresses about one distinct variant of the target polypeptide and/or

(ii) the cell is a eukaryotic cell.

5. The method of any of the preceding claims, wherein each of the plurality of variants comprises a single amino acid substitution relative to a wild-type amino acid sequence of the target polypeptide.

6. The method of claim 5, wherein the single amino acid substitution occurs at a surface residue of the target polypeptide.

7. The method of any of the preceding claims, wherein step (b) comprises obtaining variants exhibiting less than about 80% of the binding to the antibody molecule exhibited by a wild-type target polypeptide.

8. The method of any of the preceding claims, wherein step (b) comprises obtaining cells exhibiting less than about 80% of the binding to the antibody molecule exhibited by a cell comprising a wild-type target polypeptide.

9. The method of any of the preceding claims, wherein step (b) comprises performing one or more enrichments for variants exhibiting reduced binding to the antibody molecule.

10. The method of any of the preceding claims, further comprising, prior to step (c), identifying the variants exhibiting reduced binding to the antibody molecule by sequencing the genes encoding the variants.

11. The method of claim 10, wherein the variants are sequenced by next generation sequencing.

12. The method of any of the preceding claims, wherein step (c) comprises determining the frequency of occurrence for each of the plurality of the obtained variants.

13. The method of claim 12, wherein step (c) further comprises aggregating the frequency of occurrence of each variant comprising a distinct mutation at a particular residue and/or heavily weighting variants with higher frequencies of occurrence.

14. The method of any of the preceding claims, wherein:

(i) the enrichment score is specific to a single residue of the amino acid sequence of the target polypeptide; and/or

(ii) each enrichment score is specific to a different single residue of the amino acid sequence of the target polypeptide.

15. The method of any of the preceding claims, further comprising repeating steps (a)-(c) at least once with replicates of the plurality of the variants of the target polypeptide, and wherein step (c) further comprises omitting one or more promiscuous mutations, wherein promiscuous mutations comprise mutations for which more than 50% of replicates had an enrichment score of greater than 30% and for which more than 75% of replicates had an enrichment score greater than 15%.

16. The method of any of the preceding claims, wherein the antibody molecule-target polypeptide docking model is constrained by adding one or more attractive constraints, wherein the attractive constraint is for a residue having an enrichment score greater than a first preselected value;

and wherein the first preselected value is between 20% and 40%.

17. The method of claim 16, wherein the attractive constraint comprises a linearly scaled bonus based on the enrichment score.

18. The method of any of the preceding claims, wherein the antibody molecule-target polypeptide docking model is constrained by adding a repulsive constraint for a residue having an enrichment score less than a second preselected value;

and wherein the second preselected value is between 5% and 20%.

19. The method of any of the preceding claims, wherein step (d) comprises:

(i) generating a docked pose between a model of the antibody molecule and a model of the target polypeptide;

(ii) generating a plurality of docked poses between a model of the antibody molecule and a model of the target polypeptide;

(iii) scoring the plurality of docked poses according to a docking algorithm; and/or

(iv) selecting a subset of the plurality of docked poses having the highest scores;

wherein the model of the antibody molecule comprises an ensemble antibody homology model derived from a plurality of homology models of the antibody.

20. The method of any of the preceding claims, wherein step (d) comprises:

(i) generating a plurality of antibody molecule-target polypeptide models; and/or

(ii) identifying a plurality of sites on the target polypeptide that is capable of being bound by the antibody molecule.