

What is claimed is:

1. A method for producing a combination of peptides or proteins with target physico-chemical properties, comprising:
 - receiving a plurality of amino acid sequences of the peptides or proteins,
 - selecting the peptides or proteins having desired amino acid sequences,
 - determining a profile of protein-protein interactions of the peptides or proteins having desired amino acid sequences,
 - selecting a target profile of the protein-protein interactions of the peptides or proteins having desired amino acid sequences, and
 - producing a combination of peptides or proteins having desired amino acid sequences according to the target profile of the protein-protein interactions.
2. The method of claim 1, wherein the profile of the protein-protein interactions is determined by measuring interaction parameters of the peptides or proteins having desired amino acid sequences.
3. The method of claim 1 further comprising determining a profile of physico-chemical properties of the peptides or proteins having desired amino acid sequences, wherein the combination of peptides or proteins having desired amino acid sequences is produced according to the target profile of the protein-protein interaction and the profile of the physico-chemical properties.
4. The method of claim 3, wherein the physico-chemical property is a theoretical isoelectric point, an experimental isoelectric point, surface hydrophobicity, relative surface hydrophobicity, a hydrophobicity index, surface charges, charge heterogeneity, second osmotic vial coefficient, agitation stability, opalescence, viscosity, or interfacial sensitivity.
5. The method of claim 4, wherein the surface hydrophobicity or surface charges is determined by conducting a structural modeling of the peptides or proteins having desired amino acid sequences.
6. The method of claim 1, wherein the protein-protein interactions are repulsive or attractive protein-protein interactions.

7. The method of claim 2, wherein the combination of the peptides or proteins having desired amino acid sequences is a bispecific antibody or a multi-specific antibody.
8. The method of claim 7, further comprising determining a hydrophobicity index, surface charges, or charge heterogeneity of a variable region of the bispecific antibody or the multi-specific antibody for producing the bispecific antibody or the multi-specific antibody.
9. The method of claim 1, wherein a concentration of the combination of the peptides or proteins having desired amino acid sequences is from about 20 mg/mL to about 200 mg/mL.
10. The method of claim 1, wherein a concentration of the combination of the peptides or proteins having desired amino acid sequences is at least about 70 mg/mL.
11. A system for producing a combination of peptides or proteins with target physico-chemical properties, comprising:
 - a first data storage including a plurality of amino acid sequences of the peptides or proteins,
 - a first processor coupled to the first data storage capable of making a selection of the peptides or proteins having desired amino acid sequences, and
 - a second processor capable of generating a profile of protein-protein interactions of the peptides or proteins having desired amino acid sequences, selecting a target profile of the protein-protein interactions of the peptides or proteins having desired amino acid sequences, and identifying a combination of peptides or proteins having desired amino acid sequences, wherein the combination of the peptides or proteins having desired amino acid sequences are selected according to the target profile of the protein-protein interactions.
12. The system of claim 11, wherein the profile of the protein-protein interactions is determined by measuring interaction parameters of the peptides or proteins having desired amino acid sequences.
13. The system of claim 11, further comprising a profile of physico-chemical properties of the peptides or proteins having desired amino acid sequences, wherein the combination of peptides or proteins having desired amino acid sequences is selected according to the target profile of the protein-protein interaction and the profile of the physico-chemical properties.
14. The system of claim 13, wherein the physico-chemical property is a theoretical isoelectric point, an experimental isoelectric point, surface hydrophobicity, relative surface hydrophobicity, a

hydrophobicity index, surface charges, charge heterogeneity, second osmotic vial coefficient, agitation stability, opalescence, viscosity, or interfacial sensitivity.

15. The system of claim 14, wherein the surface hydrophobicity or surface charges is determined by conducting a structural modeling of the peptides or proteins having desired amino acid sequences.

16. The system of claim 11, wherein the protein-protein interactions are repulsive or attractive protein-protein interactions.

17. The system of claim 11, wherein the combination of the peptides or proteins having desired amino acid sequences is a bispecific antibody or a multi-specific antibody.

18. The system of claim 17 further comprising a profile of a hydrophobicity index, surface charges, or charge heterogeneity of a variable region of the bispecific antibody or the multi-specific antibody.

19. The system of claim 11, wherein a concentration of the combination of the peptides or proteins having desired amino acid sequences is from about 20 mg/mL to about 200 mg/mL.

20. The system of claim 11, wherein a concentration of the combination of the peptides or proteins having desired amino acid sequences is at least about 70 mg/mL.

21. A method for optimizing or selecting at least one component in a formulation, wherein the formulation comprises the combination of the peptides or proteins having desired amino acid sequences of claim 1, the method comprising:

adjusting ionic strength of the formulation based on the target profile of the protein-protein interactions of the peptides or proteins having desired amino acid sequences, and

adjusting a pH value of the formulation based on the target profile of the protein-protein interactions of the peptides or proteins having desired amino acid sequences.

22. The method of claim 21 further comprising adding a salt to the formulation based on the target profile of the protein-protein interactions of the peptides or proteins having desired amino acid sequences.

23. The method of claim 21 further comprising adding a hydrophobic excipient to the formulation based on the target profile of the protein-protein interactions of the peptides or proteins having desired amino acid sequences.
24. The method of claim 21, wherein the at least one component is sodium chloride, acetate, histidine, or arginine hydrochloride.
25. A method for optimizing or selecting at least one component in a formulation, wherein the formulation comprises a bispecific antibody or a multi-specific antibody, the method comprising:
- determining a profile of protein-protein interactions of the bispecific antibody or the multi-specific antibody, and
- optimizing or selecting the at least one component in the formulation based on the profile of the protein-protein interactions of the bispecific antibody or the multi-specific antibody.
26. The method of claim 25, wherein the profile of the protein-protein interactions is determined by measuring interaction parameters of the bispecific antibody or the multi-specific antibody.
27. The method of claim 25, further comprising, adjusting ionic strength of the formulation based on the profile of the protein-protein interactions of the bispecific antibody or the multi-specific antibody.
28. The method of claim 25, further comprising, adjusting a pH value of the formulation based on the profile of the protein-protein interactions of the bispecific antibody or the multi-specific antibody.
29. The method of claim 25, further comprising determining a profile of physico-chemical properties of the bispecific antibody or the multi-specific antibody, wherein optimizing or selecting the at least one component in the formulation is based on the profile of the protein-protein interactions of the bispecific antibody or the multi-specific antibody and the profile of the physico-chemical properties of the bispecific antibody or the multi-specific antibody.
30. The method of claim 25, further comprising adding a salt to the formulation based on the profile of protein-protein interactions of the bispecific antibody or the multi-specific antibody.

31. The method of claim 25, further comprising adding a hydrophobic excipient to the formulation based on the profile of protein-protein interactions of the bispecific antibody or the multi-specific antibody.
32. The method of claim 25, wherein at least one component is sodium chloride, acetate, histidine, or arginine hydrochloride.
33. The method of claim 29, wherein the physico-chemical property is a theoretical isoelectric point, an experimental isoelectric point, surface hydrophobicity, relative surface hydrophobicity, a hydrophobicity index, surface charges, charge heterogeneity, second osmotic vial coefficient, agitation stability, opalescence, viscosity, or interfacial sensitivity.
34. The method of claim 33, wherein the surface hydrophobicity or surface charges is determined by conducting a structural modeling of the bispecific antibody or the multi-specific antibody.
35. The method of claim 25, wherein the protein-protein interactions are repulsive or attractive protein-protein interactions.
36. The method of claim 29, further comprising determining a hydrophobicity index, surface charges, or charge heterogeneity of a variable region of the bispecific antibody or the multi-specific antibody.
37. The method of claim 25, wherein a concentration of the bispecific antibody or the multi-specific antibody is from about 20 mg/mL to about 200 mg/mL.
38. The method of claim 25, wherein a concentration of the bispecific antibody or the multi-specific antibody is at least about 70 mg/mL.