CLAIMS

1. A method, comprising:

growing amino acid sequences on a surface, wherein at least one of the amino acids within the amino acid sequence is an isobaric amino acid, and wherein, when the isobaric amino acid is added to a medium exposed to the sequences for addition thereto, the medium containing the isobaric amino acid further contains an entity, incorporatable in an amino acid sequence, that has a molecular weight different than the isobaric amino acid, wherein the amino acid sequences on the surface are formed from a plurality of amino acids that define amino acid sequences having the same length.

2. The method of claim 1, wherein at least some of the amino acid sequences are attached to the surface by a cleavable linker.

3. The method of any one of claims 1 or 2, further comprising analyzing the amino acid sequence by mass spectrometry.

4. The method of claim 3, wherein the mass spectrometry comprises tandem mass spectrometry.

5. The method of claim 3, wherein the mass spectrometry comprises ESI.

6. The method of claim 3, wherein the mass spectrometry comprises MALDI-TOF/TOF.

7. The method of any one of claims 3-6, wherein analyzing the amino acid sequences comprises sequencing the amino acid sequences.

8. The method of any one of claims 1-7, wherein isobaric amino acid is an unnatural amino acid.

9. The method of any one of claims 1-8, wherein the entity comprises an unnatural amino acid.

10. A composition, comprising:

a substrate having attached thereto amino acid sequences, the amino acid sequences consisting of a first amino acid sequence and a second amino acid sequence, each defined by a plurality of amino acids forming the respective sequences, the second amino acid sequence having the same number of amino acid residues as the first sequence, wherein the second amino acid sequence is identical to the first amino acid sequence except at one or more locations where the first amino acid sequence contains a first, isobaric amino acid, and the second amino acid sequence contains at a corresponding position, a second amino acid structurally different from the first amino acid and having a molecular weight different than the first amino acid.

11. The composition of claim 10, further comprising a particle comprising the first amino acid sequence and the second amino acid sequence.

12. The composition of claim 11, wherein the first amino acid sequence and the second amino acid sequence are each attached to the particle by a cleavable linker.

13. The composition of claim 12, wherein the cleavable linker is a methionine residue.

14. The composition of any one of claims 10-13, wherein the isobaric amino acid is leucine or isoleucine.

15. The composition of any one of claims 10-14, wherein the isobaric amino acid is lysine or glutamine.

16. The composition of any one of claims 10-15, wherein the isobaric amino acid is an unnatural amino acid.

17. The composition of any one of claims 10-16, wherein the second amino acid is an unnatural amino acid.

18. A surface to which is attached amino acid sequences, the amino acid sequences consisting of a first amino acid sequence and a second amino acid

sequence, each via a cleavable moiety, the first amino acid sequence and the second amino acid sequence each defined by a plurality of amino acids forming the respective sequences, the second amino acid sequence having the same number of amino acid residues as the first sequence, wherein the second amino acid sequence is identical to the first amino acid sequence except at one or more locations where the first amino acid sequence contains a first, isobaric amino acid, and the second amino acid sequence contains at a corresponding position, a second amino acid with a molecular weight different from the first amino acid.

19. The surface of claim 18, wherein the cleavable moiety is a methionine residue.

20. The surface of any one of claims 18 or 19, wherein the isobaric amino acid is leucine or isoleucine.

21. The surface of any one of claims 18 or 19, wherein the isobaric amino acid is lysine or glutamine.

22. The surface of any one of claims 18-21, wherein the isobaric amino acid is an unnatural amino acid.

23. The surface of any one of claims 18-22, wherein the second amino acid is an unnatural amino acid.

24. A method comprising:

distinguishing, using mass spectrometry, a first amino acid sequence from a second amino acid sequence having the same number of amino acid residues as the first sequence, the first amino acid sequence and the second amino acid sequence each being defined by a plurality of amino acids forming the respective sequences, wherein the second amino acid sequence is identical to the first amino acid sequence except at one or more locations where the first amino acid sequence contains a first, isobaric amino acid, the second amino acid sequence contains at a corresponding position, a second amino acid that has a molecular weight different than the first amino acid, and wherein the first and second amino acid sequences are attached to a same substrate.

25. The method of claim 24, the method further comprising essentially simultaneously cleaving the first and second amino acid sequences from a common particle prior to subjecting the first and second amino acid sequences to mass spectrometry.

26. The method of claim 25, wherein the mass spectrometry comprises tandem mass spectrometry.

27. The method of claim 25, wherein the mass spectrometry comprises ESI.

28. The method of claim 25, wherein mass spectrometry comprises MALDI-TOF/TOF.

29. The method of any one of claims 24-28, wherein the second amino acid sequence has a parent peak m/z value different than the parent peak m/z value of the first amino acid sequence.

30. The method of any one of claims 24-29, wherein mass spectrometry comprises tandem mass spectrometry.

31. The method of any one of claims 24-30, wherein the isobaric amino acid is an unnatural amino acid.

32. The method of any one of claims 24-31, wherein the second amino acid is an unnatural amino acid.

33. A method, comprising:

exposing an amino acid sequence, attached to a surface, to a solution containing an isobaric amino acid, the isobaric amino acid being a member of an isobaric group consisting of a first amino acid species and a second amino acid species, wherein, when the isobaric amino acid incorporated into the amino acid sequence is the first amino acid species, the solution further comprises an entity, incorporatable in an amino acid sequence, that has a molecular weight different than the isobaric amino acid, and when the isobaric amino acid incorporated into the amino acid sequence is the second amino acid species, the solution is substantially free of the incorporatable entity, wherein the amino acid sequences on the surface are formed

from a plurality of amino acids that define amino acid sequences having the same length.

34. The method of claim 33, wherein at least some of the amino acid sequences are attached to the surface by a cleavable linker.

35. The method of any one of claims 33 or 34, further comprising analyzing the amino acid sequence by mass spectrometry.

36. The method of claim 35, wherein the mass spectrometry comprises tandem mass spectrometry.

37. The method of claim 35, wherein the mass spectrometry comprises ESI.

38. The method of claim 35, wherein the mass spectrometry comprises MALDI-TOF/TOF.

39. The method of any one of claims 35-38, wherein analyzing the amino acid sequences comprises sequencing the amino acid sequences.

40. The method of any one of claims 33-39, wherein isobaric amino acid is an unnatural amino acid.

41. The method of any one of claims 33-40, wherein the entity comprises an unnatural amino acid.

CLAIMS

1. A method, comprising:

growing amino acid sequences on a surface, wherein at least one of the amino acids within the amino acid sequence is an isobaric amino acid, and wherein, when the isobaric amino acid is added to a medium exposed to the sequences for addition thereto, the medium containing the isobaric amino acid further contains an entity, incorporatable in an amino acid sequence, that has a molecular weight different than the isobaric amino acid, wherein the amino acid sequences on the surface are formed from a plurality of amino acids that define amino acid sequences having the same length.

2. The method of claim 1, wherein at least some of the amino acid sequences are attached to the surface by a cleavable linker.

3. The method of any one of claims 1 or 2, further comprising analyzing the amino acid sequence by mass spectrometry.

4. The method of claim 3, wherein the mass spectrometry comprises tandem mass spectrometry.

5. The method of claim 3, wherein the mass spectrometry comprises ESI.

6. The method of claim 3, wherein the mass spectrometry comprises MALDI-TOF/TOF.

7. The method of any one of claims 3-6, wherein analyzing the amino acid sequences comprises sequencing the amino acid sequences.

8. The method of any one of claims 1-7, wherein isobaric amino acid is an unnatural amino acid.

9. The method of any one of claims 1-8, wherein the entity comprises an unnatural amino acid.

10. A composition, comprising:

a substrate having attached thereto amino acid sequences, the amino acid sequences consisting ~~essentially~~ of a first amino acid sequence and a second amino acid sequence, each defined by a plurality of amino acids forming the respective sequences, the second amino acid sequence having the same number of amino acid residues as the first sequence, wherein the second amino acid sequence is identical to the first amino acid sequence except at one or more locations where the first amino acid sequence contains a first, isobaric amino acid, and the second amino acid sequence contains at a corresponding position, a second amino acid structurally different from the first amino acid and having a molecular weight different than the first amino acid.

11. The composition of claim 10, further comprising a particle comprising the first amino acid sequence and the second amino acid sequence.

12. The composition of claim 11, wherein the first amino acid sequence and the second amino acid sequence are each attached to the particle by a cleavable linker.

13. The composition of claim 12, wherein the cleavable linker is a methionine residue.

14. The composition of any one of claims 10-13, wherein the isobaric amino acid is leucine or isoleucine.

15. The composition of any one of claims 10-14, wherein the isobaric amino acid is lysine or glutamine.

16. The composition of any one of claims 10-15, wherein the isobaric amino acid is an unnatural amino acid.

17. The composition of any one of claims 10-16, wherein the second amino acid is an unnatural amino acid.

18. ~~An article, comprising:~~

~~a~~A surface to which is attached amino acid sequences, the amino acid sequences consisting ~~essentially~~ of a first amino acid sequence and a second amino acid

sequence, each via a cleavable moiety, the first amino acid sequence and the second amino acid sequence each defined by a plurality of amino acids forming the respective sequences, the second amino acid sequence having the same number of amino acid residues as the first sequence, wherein the second amino acid sequence is identical to the first amino acid sequence except at one or more locations where the first amino acid sequence contains a first, isobaric amino acid, and the second amino acid sequence contains at a corresponding position, a second amino acid with a molecular weight different from the first amino acid.

19. The ~~article~~ surface of claim 18, wherein the cleavable moiety is a methionine residue.

20. The ~~article~~ surface of any one of claims 18 or 19, wherein the isobaric amino acid is leucine or isoleucine.

21. The ~~article~~ surface of any one of claims 18 or 19, wherein the isobaric amino acid is lysine or glutamine.

22. The ~~method~~ surface of any one of claims 18-21, wherein the isobaric amino acid is an unnatural amino acid.

23. The ~~method~~ surface of any one of claims 18-22, wherein the second amino acid is an unnatural amino acid.

24. A method comprising:

distinguishing, using mass spectrometry, a first amino acid sequence from a second amino acid sequence having the same number of amino acid residues as the first sequence, the first amino acid sequence and the second amino acid sequence each being defined by a plurality of amino acids forming the respective sequences, wherein the second amino acid sequence is identical to the first amino acid sequence except at one or more locations where the first amino acid sequence contains a first, isobaric amino acid, the second amino acid sequence contains at a corresponding position, a second amino acid that has a molecular weight different than the first amino acid, and wherein the first and second amino acid sequences are attached to a same substrate.

25. The method of claim 24, the method further comprising essentially simultaneously cleaving the first and second amino acid sequences from a common particle prior to subjecting the first and second amino acid sequences to mass spectrometry.

26. The method of claim 25, wherein the mass spectrometry comprises tandem mass spectrometry.

27. The method of claim 25, wherein the mass spectrometry comprises ESI.

28. The method of claim 25, wherein mass spectrometry comprises MALDI-TOF/TOF.

29. The method of any one of claims 24-28, wherein the second amino acid sequence has a parent peak m/z value different than the parent peak m/z value of the first amino acid sequence.

30. The method of any one of claims 24-29, wherein mass spectrometry comprises tandem mass spectrometry.

31. The method of any one of claims 24-30, wherein the isobaric amino acid is an unnatural amino acid.

32. The method of any one of claims 24-31, wherein the second amino acid is an unnatural amino acid.

33. A method, comprising:

exposing an amino acid sequence, attached to a surface, to a solution containing an isobaric amino acid, the isobaric amino acid being a member of an isobaric group consisting of a first amino acid species and a second amino acid species, wherein, when the isobaric amino acid incorporated into the amino acid sequence is the first amino acid species, the solution further comprises an entity, incorporatable in an amino acid sequence, that has a molecular weight different than the isobaric amino acid, and when the isobaric amino acid incorporated into the amino acid sequence is the second amino acid species, the solution is substantially free of the incorporatable entity, wherein the amino acid sequences on the surface are formed

from a plurality of amino acids that define amino acid sequences having the same length.

34. The method of claim 33, wherein at least some of the amino acid sequences are attached to the surface by a cleavable linker.

35. The method of any one of claims 33 or 34, further comprising analyzing the amino acid sequence by mass spectrometry.

36. The method of claim 35, wherein the mass spectrometry comprises tandem mass spectrometry.

37. The method of claim 35, wherein the mass spectrometry comprises ESI.

38. The method of claim 35, wherein the mass spectrometry comprises MALDI-TOF/TOF.

39. The method of any one of claims 35-38, wherein analyzing the amino acid sequences comprises sequencing the amino acid sequences.

40. The method of any one of claims 33-39, wherein isobaric amino acid is an unnatural amino acid.

41. The method of any one of claims 33-40, wherein the entity comprises an unnatural amino acid.