## CLAIMS

1. A composition comprising a peptide and a moiety, wherein the peptide comprises an amino acid sequence that can bind to a carbohydrate receptor on a cell.

2. The composition of claim 1, wherein the carbohydrate receptor is annexin 1, wherein the amino acid sequence can selectively bind the carbohydrate receptor.

3. The composition of any one of claims 1-2, wherein the cell is a tumor cell.

4. The composition of any one of claims 1-3, wherein the amino acid sequence comprises SEQ ID NO:2 having none, one, or more conservative amino acid substitutions.

5. The composition of any one of claims 1-4, wherein the amino acid sequence comprises IFLLWQRX (amino acids 1 to 8 of SEQ ID NO:20), IFLLWQRXX (amino acids 1 to 9 of SEQ ID NO:20), IFLLWQRXXX (amino acids 1 to 10 of SEQ ID NO:20), IFLLWQRXXXX (amino acids 1 to 11 of SEQ ID NO:20), or IFLLWQRXXXXX (SEQ ID NO:20), wherein each X is independently a polar or charged amino acid, wherein the amino acid sequence has none, one, or more conservative amino acid substitutions in IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20).

6. The composition of claim 5, wherein each X can independently be selected from all, any set of 10, any set of 9, any set of 8, any set of 7, any set of 6, any set of 5, any set of 4, any set of 3, any set of 2, or any 1 of the amino acids C, R, K, S, T, H, D, E, N, Q, and M.

7. The composition of claim 5, wherein each X can independently be selected from the set of three amino acids C, R, and K.

8. The composition of claim 5, wherein each X can independently be selected from the set of two amino acids C and R.

9. The composition of any one of claims 5-8, wherein a single one of the X in the amino acid sequence is C, two of the X in the amino acid sequence are C, two of the X in the amino acid sequence are R, three of the X in the amino acid sequence are R, four of the X in the amino acid sequence are R, or a compatible combination thereof.

10. The composition of any one of claims 5-9, wherein the amino acid sequence consists of IFLLWQRX (amino acids 1 to 8 of SEQ ID NO:20), IFLLWQRXX (amino acids 1 to 9 of SEQ ID NO:20), IFLLWQRXXX (amino acids 1 to 10 of SEQ ID NO:20), IFLLWQRXXXX (amino acids 1 to 11 of SEQ ID NO:20), or IFLLWQRXXXXX (SEQ ID NO:20).

11. The composition of any one of claims 5-8, wherein the portion of the amino acid sequence corresponding to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) can have at least 55% sequence identity to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID

NO:20), wherein differences between the annexin 1-binding compound and IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) consist of conservative amino acid substitutions.

12. The composition of any one of claims 5-8, wherein the portion of the amino acid sequence corresponding to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) can have at least 70% sequence identity to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20).

13. The composition of any one of claims 5-8, wherein the portion of the amino acid sequence corresponding to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) can have at least 80% sequence identity to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20).

14. The composition of any one of claims 5-8, wherein the annexin 1-binding compound has at least 5 consecutive amino acids of the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20).

15. The composition of any one of claims 5-8, wherein the annexin 1-binding compound has at least 6 consecutive amino acids of the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20).

16. The composition of claim 5, wherein the amino acid sequence comprises IFLLWQRCR (SEQ ID NO:17), IFLLWQRCRR (SEQ ID NO:19), IFLLWQRCRRR (SEQ ID NO:18), or IFLLWQRCRRRR (SEQ ID NO:22).

17. The composition of claim 5, wherein the amino acid sequence consists of IFLLWQRCR (SEQ ID NO:17), IFLLWQRCRR (SEQ ID NO:19), IFLLWQRCRRR (SEQ ID NO:18), or IFLLWQRCRRRR (SEQ ID NO:22).

18. The composition of any one of claims 1-4, wherein the amino acid sequence has at least 55% sequence identity to SEQ ID NO:2, wherein differences between the amino acid sequence and SEQ ID NO:2 consist of conservative amino acid substitutions.

19. The composition of any one of claims 1-4, or 18, wherein the amino acid sequence has at least 70% sequence identity to SEQ ID NO:2.

20. The composition of any one of claims 1-4, 18, or 19, wherein the amino acid sequence has at least 80% sequence identity to SEQ ID NO:2.

21. The composition of any one of claims 1-4 or 18-20, wherein the amino acid sequence comprises SEQ ID NO:2.

22. The composition of any one of claims 1-4 or 18-21, wherein the peptide comprises SEQ ID NO:2.

23. The composition of any one of claims 1-4 or 18-22, wherein the amino acid sequence consists of SEQ ID NO:2.

24. The composition of any one of claims 1-4, wherein the amino acid sequence comprises at least 5 consecutive amino acids of SEQ ID NO:2.

25. The composition of any one of claims 1-4, wherein the amino acid sequence comprises at least 6 consecutive amino acids of SEQ ID NO:2.

26. The composition of any one of claims 1-4, wherein the peptide comprises at least 6 amino acids.

27. The composition of any one of claims 1-4 or 18-26, wherein the peptide comprises at least 7 amino acids.

28. The composition of any one of claims 1-15 or 18-27, wherein the peptide comprises at least 8 amino acids.

29. The composition of any one of claims 1-28, wherein the peptide comprises at least 9 amino acids.

30. The composition of any one of claims 1-29, wherein the moiety is a small molecule, pharmaceutical drug, toxin, fatty acid, detectable marker, conjugating tag, nanoshell, or enzyme.

31. The composition of any one of claims 1-30, wherein the moiety is covalently linked to the peptide.

32. The composition of claim 31, wherein the moiety is linked to the amino terminal end of the peptide.

33. The composition of claim 31, wherein the moiety is linked to the carboxy terminal end of the peptide.

34. The composition of claim 31, wherein the moiety is linked to an amino acid within the peptide.

35. The composition of any one of claims 1-34, further comprising a linker connecting the moiety and the peptide.

36. The composition of any one of claims 1-35, wherein the moiety is SN-38, wherein the amino acid sequence does not consist of SEQ ID NO:2.

37. The composition of any one of claims 1-35, wherein the moiety is SN-38, wherein the peptide does not consist of SEQ ID NO:2.

38. The composition of any one of claims 1-35, wherein the moiety is a cancer chemotherapeutic agent.

39. The composition of any one of claims 1-38, wherein the amino acid sequence consists of SEQ ID NO:2.

40. The composition of any one of claims 1-38, wherein the peptide consists of SEQ ID NO:2.

41. The composition of any one of claims 1-40, further comprising a pharmaceutically acceptable carrier.

42. The composition of any one of claims 1-41, wherein the moiety comprises a therapeutic agent.

43. The composition of any one of claims 1-42, wherein the composition further comprises a therapeutic agent.

44. The composition of any one of claims 1-43, wherein the moiety comprises a detectable agent.

45. The composition of any one of claims 1-44, wherein the moiety comprises a therapeutic agent.

46. The composition of any one of claims 1-45, wherein the composition further comprises a detectable agent.

47. The composition of any one of claims 1-46, wherein the composition further comprises a therapeutic agent.

48. The composition of any one of claims 1-47, wherein the composition further comprises an anti-cancer agent.

49. An isolated nucleic acid comprising a nucleic acid sequence encoding a peptide and moiety according to any one of claims 1-48.

50. Use of a composition according to any one of claims 1-48 in the manufacture of a medicament for the treatment of cancer.

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52. A method of diagnosing cancer in a subject; the method comprises:

detecting a composition according to any one of claims 1-48, in a sample derived from a subject that has been administered said composition;

wherein detecting the composition thereby detects a tumor in the subject; and wherein detecting the composition thereby diagnoses cancer in the subject.

53. The method of claim 52, wherein detecting the composition comprises detecting the level, amount, concentration, or a combination of binding of the composition to cancer tissue in the subject, wherein the level, amount, concentration, or a combination of binding of the composition to cancer tissue in the subject indicates the prognosis of the cancer in the subject.

54. The method of claim 52, further comprising:

repeating the detection of the composition, wherein the subject has been administered a repeated dose of the composition at a later time; and

wherein a change in the level, amount, concentration, or a combination of binding of the composition to cancer tissue in the subject indicates the progress of the endometriosis in the subject.

55. The method of claim 52, further comprising repeating the detection of the composition, wherein the subject has been administered the composition following treatment; and wherein a change in the level, amount, concentration, or a combination of binding of the composition to cancer tissue in the subject indicates the progress the treatment of the cancer in the subject.

## Claims

1. A composition comprising a peptide and a moiety, wherein the peptide encompasses an amino acid sequence that can bind to a carbohydrate receptor on a cell,

wherein the amino acid sequence comprises IFLLWQRX (amino acids 1 to 8 of SEQ ID NO:20), IFLLWQRXX (amino acids 1 to 9 of SEQ ID NO:20), IFLLWQRXXX (amino acids 1 to 10 of SEQ ID NO:20), IFLLWQRXXXX (amino acids 1 to 11 of SEQ ID NO:20), or IFLLWQRXXXXX (SEQ ID NO:20),

wherein each X is independently a polar or charged amino acid, wherein the amino acid sequence has none, one, or more conservative amino acid substitutions in IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20), and further wherein the carbohydrate receptor is annexin 1 wherein the amino acid sequence can selectively bind the carbohydrate receptor.

2. The composition of any one of claims 1, wherein the cell is a tumor cell.

3. The composition of any of claims 1 or 2, wherein the amino acid sequence comprises SEQ ID NO:2 having none, one, or more conservative amino acid substitutions.

4. The composition of claim 1, wherein each X can independently be selected from all, any set of 10, any set of 9, any set of 8, any set of 7, any set of 6, any set of 5, any set of 4, any set of 3, any set of 2, or any 1 of the amino acids C, R, K, S, T, H, D, E, N, and Q.

5. The composition of claim 1, wherein each X can independently be selected from the set of three amino acids C, R, and K.

6. The composition of claim 1, wherein each X can independently be selected from the set of two amino acids C and R.

7. The composition of any one of claims 4-6, wherein a single one of the X in the amino acid sequence is C, two of the X in the amino acid sequence are C, two of the X in the amino acid sequence are R, three of the X in the amino acid sequence are R, or four of the X in the amino acid sequence are R.

8. The composition of any one of claims 4-7, wherein the amino acid sequence comprises IFLLWQRX (amino acids 1 to 8 of SEQ ID NO:20), IFLLWQRXX (amino acids 1 to 9 of SEQ ID NO:20), IFLLWQRXXX (amino acids 1 to 10 of SEQ ID NO:20), IFLLWQRXXXX (amino acids 1 to 11 of SEQ ID NO:20), or IFLLWQRXXXXX (SEQ ID NO:20).

9. The composition of any one of claims 4-6, wherein the portion of the amino acid sequence corresponding to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) can have at least 55% sequence identity of the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20), wherein differences between the annexin 1-binding compound and IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) consist of conservative amino acid substitutions.

10. The composition of any one of claims 4-6, wherein the portion of the amino acid sequence corresponding to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) can have at least 70% sequence identity of the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20), wherein differences between the annexin 1-binding compound and IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) consist of conservative amino acid substitutions.

11. The composition of any one of claims 4-6, wherein the portion of the amino acid sequence corresponding to the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) can have at least 80% sequence identity of the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID

NO:20), wherein differences between the annexin 1-binding compound and IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20) consist of conservative amino acid substitutions.

12. The composition of any one of claims 4-6, wherein the annexi 1-binding compound has at least 5 consecutive amino acids of the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20).

13. The composition of any one of claims 4-6, wherein the annexi 1-binding compound has at least 6 consecutive amino acids of the sequence IFLLWQR (amino acids 1 to 7 of SEQ ID NO:20).

14. The composition of claim 1, wherein the amino acid sequence comprises IFLLWQRCR (SEQ ID NO:17), IFLLWQRCRR (SEQ ID NO:19), IFLLWQRCRRR (SEQ ID NO:18), or IFLLWQRCRRRR (SEQ ID NO:22).

15. The composition of claim 1, wherein the amino acid sequence consists of IFLLWQRCR (SEQ ID NO:17), IFLLWQRCRR (SEQ ID NO:19), IFLLWQRCRRR (SEQ ID NO:18), or IFLLWQRCRRRR (SEQ ID NO:22).

16. The composition of any one of claims 1-3, wherein the amino acid sequence has at least 55% sequence identity to SEQ ID NO:2, wherein differences between the amino acid sequence and SEQ ID NO:2 consist of conservative amino acid substitutions.

17. The composition of any one of claims 1-3, or 16, wherein the amino acid sequence has at least 70% sequence identity to SEQ ID NO:2.

18. The composition of any one of claims 1-3, 16 or 17, wherein the amino acid sequence has at least 80% sequence identity to SEQ ID NO:2.

19. The composition of any one of claims 1-3 or 16-18, wherein the amino acid sequence comprises SEQ ID NO:2.

20. The composition of any one of claims 1-3 or 16-19, wherein the peptide comprises SEQ ID NO:2.

21. The composition of any one of claims 1-3, or 16-20, wherein the amino acid sequence consists of SEQ ID NO:2.

22. The composition of any one of claims 1-3, wherein the amino acid sequence comprises at least 5 consecutive amino acids of SEQ ID NO:2.

23. The composition of any one of claims 1-3, wherein the amino acid sequence comprises at least 6 consecutive amino acids of SEQ ID NO:2.

24. The composition of any one of claims 1-3, wherein the peptide comprises at least 6 amino acids.

25. The composition of any one of claims 1-3 or 16-24, wherein the peptide comprises at least 7 amino acids.

26. The composition of any one of claims 1-3 or 16-25, wherein the peptide comprises at least 8 amino acids.

27. The composition of any one of claims 1-26, wherein the peptide comprises at least 9 amino acids.

28. The composition of any one of claims 1-27, wherein the moiety is a small molecule, pharmaceutical drug, toxin, fatty acid, detectable marker, conjugating tag, nanoshell, or enzyme.

29. The composition of any one of claims 1-28, wherein the moiety is covalently linked to the peptide.

30. The composition of claim 29, wherein the moiety is linked to the amino terminal end of the peptide.

31. The composition of claim 29, wherein the moiety is linked to the carboxy terminal end of the peptide.

32. The composition of claim 29, wherein the moiety is linked to an amino acid within the peptide.

33. The composition of any of claims 1-32, further comprising a linker connecting the moiety and the peptide.

34. The composition of any one of claims 1-33, wherein the moiety is SN-38, wherein the amino acid sequence does not consist of SEQ ID NO:2.

35. The composition of any one of claims 1-33, wherein the moiety is SN-38, wherein the peptide does not consist of SEQ ID NO:2.

36. The composition of any one of claims 1-33, wherein the moiety is a cancer chemotherapeutic agent.

37. The composition of any one of claims 1-36, wherein the amino acid sequence consists of SEQ ID NO:2.

38. The composition of any one of claims 1-36, wherein the peptide consists of SEQ ID NO:2.

39. The composition of any one of claims 1-38, further comprising a pharmaceutically acceptable carrier.

40. The composition of any one of claims 1-39, wherein the moiety comprises a therapeutic agent.

41. The composition of any one of claims 1-40, wherein the composition further comprises a therapeutic agent.

42. The composition of any one of claims 1-41, wherein the moiety comprises a detectable agent.

43. The composition of any one of claims 1-42, wherein the moiety comprises a therapeutic agent.

44. The composition of any one of claims 1-43, wherein the composition further comprises a detectable agent.

45. The composition of any one of claims 1-44, wherein the composition further comprises a therapeutic agent.

46. The composition of any one of claims 1-45, wherein the composition further comprises an anti-cancer agent.

47. An isolated nucleic acid comprising a nucleic acid sequence encoding a peptide and moiety according to any one of claims 1-46.

48. Use of a composition according to any one of claims 1-46 in the manufacture of a medicament for the treatment of cancer.

49. A method of diagnosing cancer in a subject: the method comprises:

detecting a composition according to any one of claims 1-46, in a sample derived from a subject that has been administered said composition;

wherein detecting the composition thereby detects a tumor in the subject; and

wherein detecting the composition thereby diagnoses cancer in the subject.

50. The method of claim 49, wherein detecting the composition comprises detecting the level, amount, concentration, or a combination of binding of the composition to cancer tissue in the subject, wherein the level, amount, concentration, or a combination of binding the composition to cancer tissue in the subject indicates the prognosis of the cancer in the subject.

51. The method of claim 49, further comprising:

repeating the detection of the composition, wherein the subject has been administered a repeated dose of the composition at a later time; and

wherein a change in the level, amount, concentration, or a combination of binding of the composition to cancer tissue in the subject indicates the progress of the endometriosis in the subject.

52. The method claim 49, further comprising repeating the detection of the composition, wherein the subject has been administered the composition following treatment; and wherein the change in the level, amount, concentration or a combination of binding of the composition to cancer tissue in the subject indicates the progress of the treatment of the cancer in the subject.