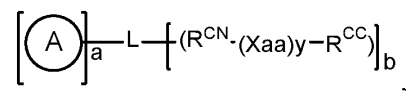


CLAIMS

1. An agent having the structure of:



or a pharmaceutically acceptable salt thereof, wherein:

the agent inhibits, kills or removes a cell infected by SARS-CoV-2

each of a and b is independently 1-200;

each A is chosen from ABT, AT, and PT, where

each ABT is independently an antibody binding moiety;

each AT is independently an antibody moiety;

each PT is independently a partner moiety;

L is a linker moiety;

each Xaa is independently a residue of an amino acid or an amino acid analog;

y is 5-50;

R^{CN} and R^{CC} are independently R^{C} ;

each R^{C} is independently $-\text{L}^a - \text{R}'$;

each L^a is independently a covalent bond, or an optionally substituted bivalent group selected from C_1 - C_{50} aliphatic or C_1 - C_{50} heteroaliphatic having 1-5 heteroatoms, wherein one or more methylene units of the group are optionally and independently replaced with $-\text{C}(\text{R}')_2-$, $-\text{Cy}-$, $-\text{O}-$, $-\text{S}-$, $-\text{S}-\text{S}-$, $-\text{N}(\text{R}')-$, $-\text{C}(\text{O})-$, $-\text{C}(\text{S})-$, $-\text{C}(\text{NR}')-$, $-\text{C}(\text{O})\text{N}(\text{R}')-$, $-\text{N}(\text{R}')\text{C}(\text{O})\text{N}(\text{R}')-$, $-\text{N}(\text{R}')\text{C}(\text{O})\text{O}-$, $-\text{S}(\text{O})-$, $-\text{S}(\text{O})_2-$, $-\text{S}(\text{O})_2\text{N}(\text{R}')-$, $-\text{C}(\text{O})\text{S}-$, or $-\text{C}(\text{O})\text{O}-$;

each $-\text{Cy}-$ is independently an optionally substituted bivalent monocyclic, bicyclic or polycyclic group wherein each monocyclic ring is independently selected from a C_{3-20} cycloaliphatic ring, a C_{6-20} aryl ring, a 5-20 membered heteroaryl ring having 1-10 heteroatoms, and a 3-20 membered heterocyclyl ring having 1-10 heteroatoms;

each R' is independently $-\text{R}$, $-\text{C}(\text{O})\text{R}$, $-\text{CO}_2\text{R}$, or $-\text{SO}_2\text{R}$;

each R is independently $-\text{H}$, or an optionally substituted group selected from C_{1-30} aliphatic, C_{1-30} heteroaliphatic having 1-10 heteroatoms, C_{6-30} aryl, C_{6-30} arylaliphatic, C_{6-30} arylheteroaliphatic having 1-10 heteroatoms, 5-30 membered heteroaryl having 1-10 heteroatoms, and 3-30 membered heterocyclyl having 1-10 heteroatoms, or

two R groups are optionally and independently taken together to form a covalent bond, or:

two or more R groups on the same atom are optionally and independently taken together with the atom to form an optionally substituted, 3-30 membered, monocyclic, bicyclic or polycyclic ring having, in addition to the atom, 0-10 heteroatoms; or

two or more R groups on two or more atoms are optionally and independently taken together with their intervening atoms to form an optionally substituted, 3-30 membered, monocyclic, bicyclic or polycyclic ring having, in addition to the intervening atoms, 0-10 heteroatoms;

wherein $-(Xaa)_y-$ is or comprises:

$-(Xaa^{T0})_{y0}-(Xaa^{T1})_{y1}-Xaa^{T2}-(Xaa^{T3})_{y3}-Xaa^{T4}-(Xaa^{T5})_{y5}-(Xaa^{T6})_{y6}-(Xaa^{T7})_{y7}-(Xaa^{T8})_{y8}-Xaa^{T9}-$
 $(Xaa^{T10})_{y10}-(Xaa^{T11})_{y11}-(Xaa^{T12})_{y12}-$,

or a salt form thereof, wherein:

$y0$ is 0-20;

each Xaa^{T0} is independently a residue of an amino acid or an amino acid analog;

$y1$ is 0-2;

each Xaa^{T1} is independently a residue of an amino acid or an amino acid analog;

Xaa^{T2} is a residue of an amino acid or an amino acid analog whose side chain comprises 3 or more non-hydrogen atoms;

$y3$ is 0-10;

each of Xaa^{T3} is independently a residue of an amino acid or an amino acid analog;

each of Xaa^{T4} and Xaa^{T9} is independently a residue of an amino acid or an amino acid analog,

wherein Xaa^{T4} is optionally connected to Xaa^{T9} through a linker;

$y5$ is 0-10;

each Xaa^{T5} is independently a residue of an amino acid or an amino acid analog;

$y6$ is 0-2;

each Xaa^{T6} is independently a residue of an amino acid or an amino acid analog;

$y7$ is 0-1;

Xaa^{T7} is a negatively-charged residue of an amino acid or an amino acid analog;

$y8$ is 0-10;

each Xaa^{T8} is independently a residue of an amino acid or an amino acid analog;

$y10$ is 0-10;

each of Xaa^{T10} is independently a residue of an amino acid or an amino acid analog;

$y11$ is 1-5;

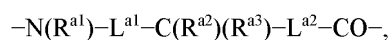
each Xaa^{T11} is independently a residue of an amino acid or an amino acid analog;

$y12$ is 0-20; and

each Xaa^{T12} is independently a residue of an amino acid or an amino acid analog.

2. The agent of claim 1, wherein each of Xaa^{T0} , Xaa^{T1} , Xaa^{T2} , Xaa^{T3} , Xaa^{T4} , Xaa^{T5} , Xaa^{T6} , Xaa^{T7} , Xaa^{T8} , Xaa^{T9} , Xaa^{T10} , Xaa^{T11} , and Xaa^{T12} is independently a residue of an amino acid having the structure

of formula A-I and formula A-I has the structure of:



or a salt thereof, wherein:

each of R^{a1} , R^{a2} , R^{a3} is independently $-L^a-R^*$;

each of L^{a1} and L^{a2} is independently L^a ;

each L^a is independently a covalent bond, or an optionally substituted bivalent group selected from C_1 - C_{20} aliphatic or C_1 - C_{20} heteroaliphatic having 1-5 heteroatoms, wherein one or more methylene units of the group are optionally and independently replaced with $-C(R')_2-$, $-Cy-$, $-O-$, $-S-$, $-S-S-$, $-N(R')-$, $-C(O)-$, $-C(S)-$, $-C(NR')-$, $-C(O)N(R')-$, $-N(R')C(O)N(R')-$, $-N(R')C(O)O-$, $-S(O)-$, $-S(O)_2-$, $-S(O)_2N(R')-$, $-C(O)S-$, or $-C(O)O-$;

each $-Cy-$ is independently an optionally substituted bivalent monocyclic, bicyclic or polycyclic group wherein each monocyclic ring is independently selected from a C_{3-20} cycloaliphatic ring, a C_{6-20} aryl ring, a 5-20 membered heteroaryl ring having 1-10 heteroatoms independently selected from oxygen, nitrogen, sulfur, phosphorus and silicon, and a 3-20 membered heterocyclyl ring having 1-10 heteroatoms independently selected from oxygen, nitrogen, sulfur, phosphorus and silicon;

each R^* is independently $-R$, $-C(O)R$, $-CO_2R$, or $-SO_2R$;

each R is independently $-H$, or an optionally substituted group selected from C_{1-30} aliphatic, C_{1-30} heteroaliphatic having 1-10 heteroatoms independently selected from oxygen, nitrogen, sulfur, phosphorus and silicon, C_{6-30} aryl, C_{6-30} arylaliphatic, C_{6-30} arylheteroaliphatic having 1-10 heteroatoms independently selected from oxygen, nitrogen, sulfur, phosphorus and silicon, 5-30 membered heteroaryl having 1-10 heteroatoms independently selected from oxygen, nitrogen, sulfur, phosphorus and silicon, and 3-30 membered heterocyclyl having 1-10 heteroatoms independently selected from oxygen, nitrogen, sulfur, phosphorus and silicon, or

two R groups are optionally and independently taken together to form a covalent bond, or:

two or more R groups on the same atom are optionally and independently taken together with the atom to form an optionally substituted, 3-30 membered, monocyclic, bicyclic or polycyclic ring having, in addition to the atom, 0-10 heteroatoms independently selected from oxygen, nitrogen, sulfur, phosphorus and silicon; or

two or more R groups on two or more atoms are optionally and independently taken together with their intervening atoms to form an optionally substituted, 3-30 membered, monocyclic, bicyclic or polycyclic ring having, in addition to the intervening atoms, 0-10 heteroatoms independently selected from oxygen, nitrogen, sulfur, phosphorus and silicon.

3. The agent of claim 1 or 2, wherein y_0 is 0, y_1 is 1 or 2; and $-(Xaa^{T1})_{y1}-$ is or comprises a

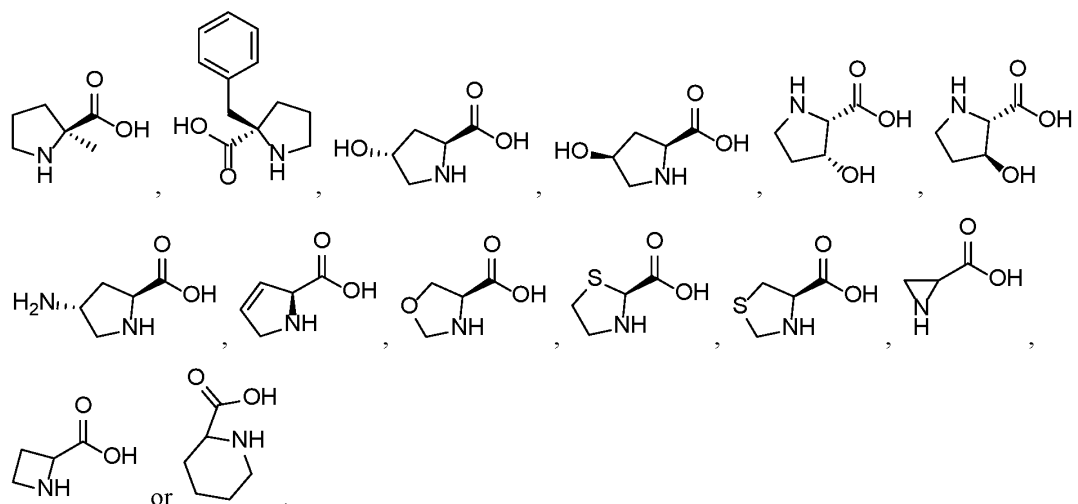
dipeptide residue or an amino acid residue that is suitable for forming a turn.

4. The agent of any one of claims 1 to 3, wherein $-(Xaa^{T1})_{y1}-$ is or comprises a residue of L-proline, D-proline, a proline derivative, L-serine, D-serine, glycine, L-pseudoproline, or D-psuedoproline.

5. The agent of any claims 1 to 3, wherein $-(Xaa^{T1})_{y1}-$ is or comprises a residue of an amino acid having the structure of formula A-I, wherein R^{a1} and R^{a2} are taken together with their intervening atoms to form an optionally substituted, saturated or partially unsaturated, 3-6 membered, monocyclic or bicyclic ring having, in addition to the intervening atoms, 0-1 heteroatoms selected from oxygen, nitrogen, and sulfur.

6. The agent of any one of claims 1 to 3, wherein $-(Xaa^{T1})_{y1}-$ is or comprises a L-proline residue.

7. The agent of any one of claims 1 to 3, wherein $-(Xaa^{T1})_{y1}-$ is or comprises a residue of



8. The agent of any one of claims 1 to 3, wherein $y1$ is 0.

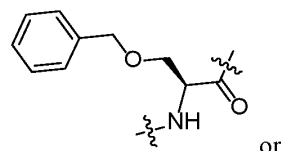
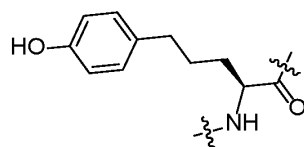
9. The agent of any one of claims 1 to 8, wherein $-Xaa^{T2}-$ is or comprises a residue of an amino acid having the structure of formula A-I, wherein R^{a2} is hydrophobic, neutral or negatively charged and is a group $-L^a-R'$, wherein L^a is an optionally substituted bivalent group selected from C_3-C_{10} aliphatic or C_3-C_{10} heteroaliphatic having 1-5 heteroatoms, wherein one or more methylene units of the group are optionally and independently replaced with $-C(R')_2-$, $-O-$, $-S-$, $-N(R')-$, $-C(O)-$, $-C(S)-$, $-C(NR')-$,

–S(O)–, or –S(O)₂–.

10. The agent of claim 9, wherein L^a is –CH₂–CH₂–CH₂–, –CH₂–O–CH₂–, or –CH₂–S–CH₂–.

11. The agent of claim 9 or 10, wherein R¹ is optionally substituted phenyl.

12. The agent of any one claims 9 to 11, wherein –Xaa^{T2}– is



13. The agent of any one claims 1 to 12, wherein y₃ is 1-10.

14. The agent of any one of the preceding claims, wherein

y₃ is 2 and –(Xaa^{T3})y₃– is or comprises TF;

y₃ is 4 and –(Xaa^{T3})y₃– is or comprises TFL; or

y₃ is 6 and –(Xaa^{T3})y₃– is or comprises TFLKY.

15. The agent of any one of the preceding claims, wherein Xaa^{T4} is connected to Xaa^{T9} through a linker, wherein the linker is L^a and is bonded to a backbone carbon atom of Xaa^{T4} and a backbone carbon atom of Xaa^{T9}; wherein L^a is or comprises –CH₂–CH₂–, –O–, –S– or –S–S–.

16. The agent of any one of the preceding claims, wherein Xaa^{T4} is Cys.

17. The agent of any one of the preceding claims, wherein –(Xaa^{T5})y₅– is or comprises YNK and –(Xaa^{T5})y₅– is connected to an antibody moiety or an antibody binding moiety optionally through a linker bound to the lysine (K) amino acid in –(Xaa^{T5})y₅.

18. The agent of any one of claims 1-17, wherein y₅ is 0 and –(Xaa^{T6})y₆– is or comprises a D-Ser residue.

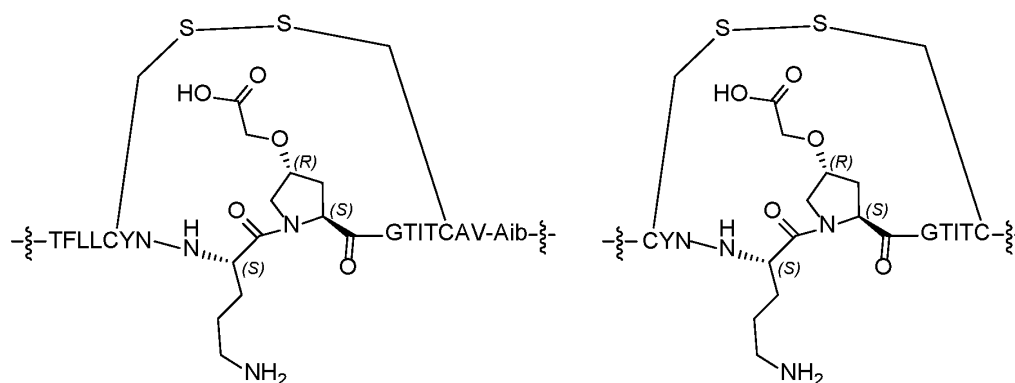
19. The agent of any one of the preceding claims, wherein y_6 is 1 or 2.
20. The agent of any one of the preceding claims, wherein $-(Xaa^{T6})_{y6}-$ is or comprises a dipeptide residue or an amino acid residue that is suitable for forming a turn.
21. The agent of any one of the preceding claims, wherein $-(Xaa^{T6})_{y6}-$ is or comprises a residue of L-proline, D-proline, a proline derivative, L-serine, D-serine, glycine, L-pseudoproline, or D-pseudoproline.
22. The agent of any one of claims 19-21, wherein $-(Xaa^{T6})_{y6}-$ is or comprises a D-Ser residue.
23. The agent of any one of claims 19-22, wherein $-(Xaa^{T6})_{y6}-$ is or comprises a residue that comprises or is further substituted with $-L^a-COOH$.
24. The agent of claim 23, wherein $-(Xaa^{T6})_{y6}-$ is or comprises a residue having the structure of
-
25. The agent of any one of the preceding claims, wherein y_7 is 1 and comprises $-COOH$ or y_7 is 0.
26. The agent of claim 25, wherein Xaa^{T7} is D or E.
27. The agent of any one of the preceding claims, wherein $-(Xaa^{T8})_{y8}-$ is or comprises GTI or $-G-Xaa^{T8}-IT-Xaa^{T8}-$, wherein each Xaa^{T8} is independently an alpha amino acid residue.
28. The agent of any one of the preceding claims, wherein $-(Xaa^{T8})_{y8}-$ is or comprises $GTI-Xaa^{T8}-$.
29. The agent of any one of the preceding claims, wherein Xaa^{T4} and Xaa^{T9} are independently Cys and form a disulfide bond $-S-S-$.
30. The agent of any one of the preceding claims, wherein $-(Xaa^{T10})_{y10}-$ is or comprises AV.

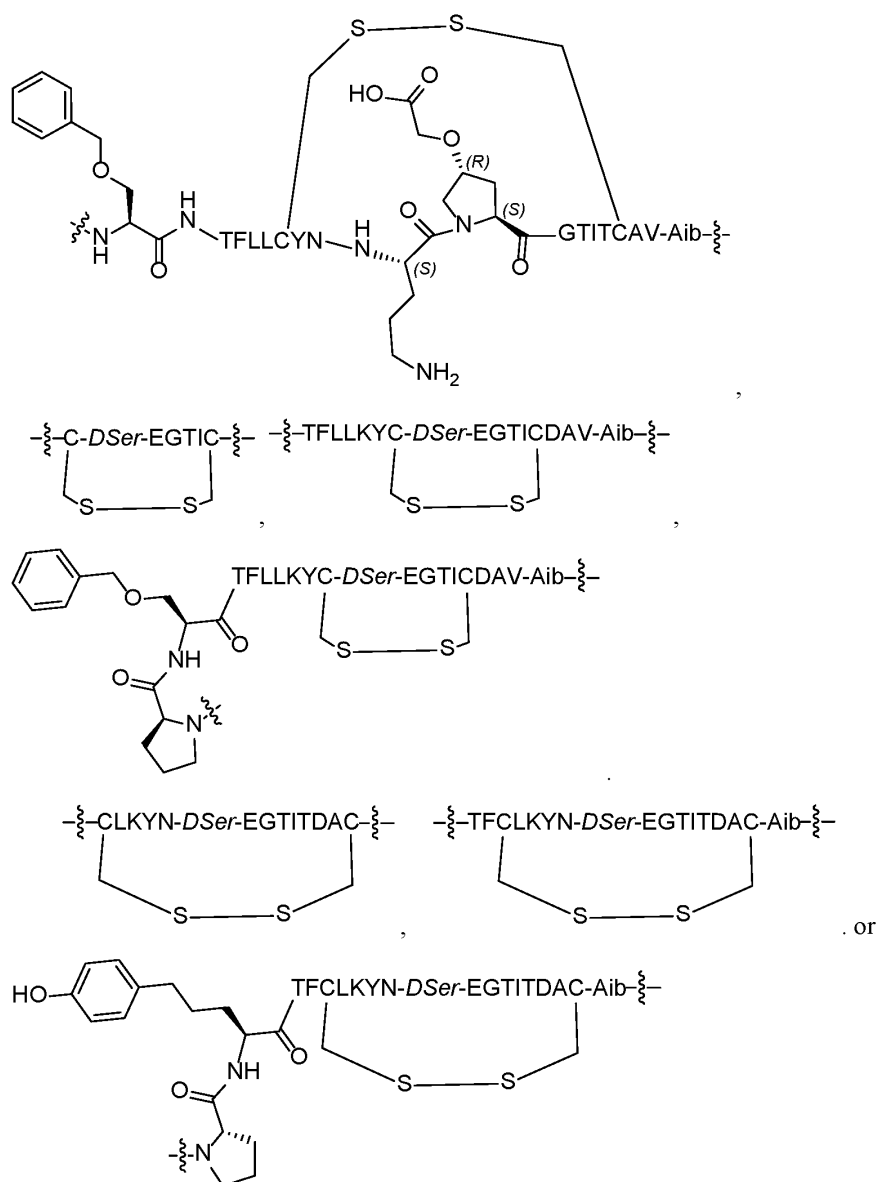
31. The agent of any one of the preceding claims, wherein y_{10} is 3 or 4.
32. The agent of claim 31, wherein $-(Xaa^{T2})_{y2}-$ is or comprises AVAD.
33. The agent of any one of the preceding claims, wherein $-(Xaa^{T11})_{y11}-$ is or comprises L-Ala, D-Ala, Aib, Gly, or negatively charged residue.
34. The agent of claim 1 or 2, wherein $-(Xaa)_y-$ is or comprises a sequence selected from, or a sequence designed based on a sequence selected from:

Number	Sequence
P1	FKLPLGIM(K)ITNFRAILTAFS(L)
P2	PT7(K)FMLKYDENGTTTDAVDC
P3	VLYNST7(S)FSTFKCYGVSATK
P4	PALNCYWPLM(K)DYGFTTSGI
P5	RDVSD7(I)TDSVRDPKTSEILD
P6	YQDVNCTDVS(P)TAIHADQLTP
P7	SNNTIAIPTNFS(L)ISITTEVM
P8	QYGSFCT7(A)QLNRALSGIAA(V)EQ
P9	GIGV7(A)QNVLYENQKQIANQF
P10	IQK7(E)EIDRLNEVAKNLNESLI

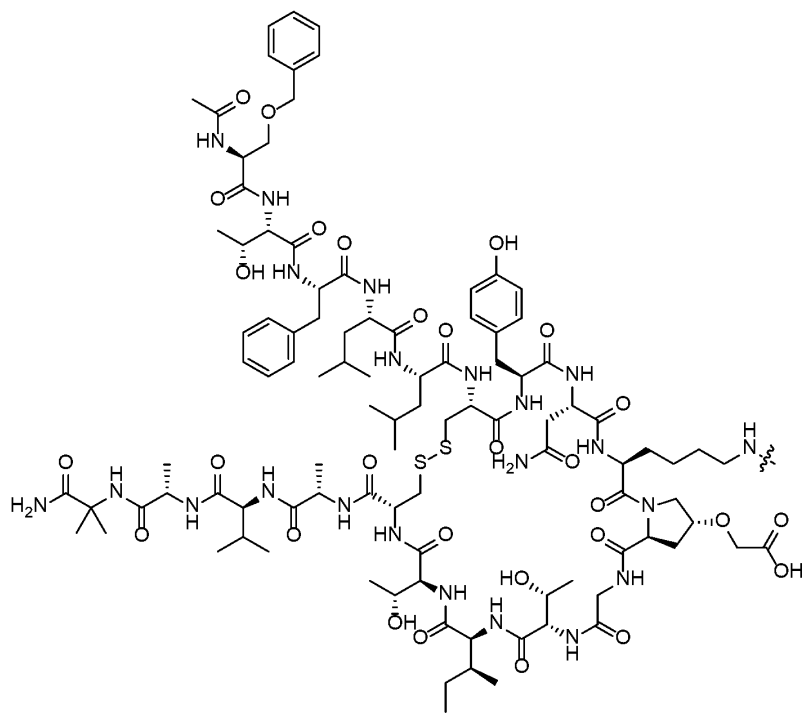
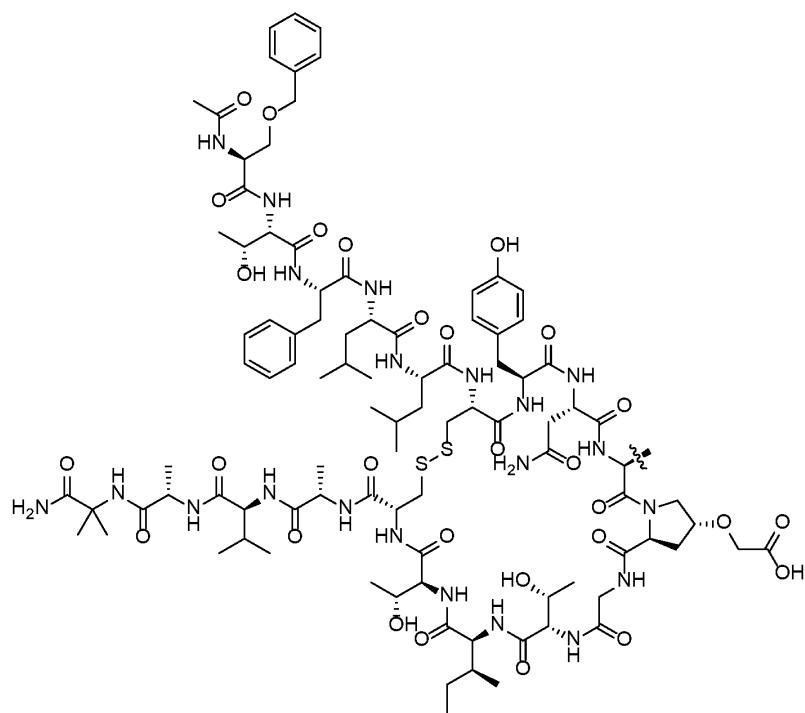
35. The agent of claim 1 or 2, wherein $-(X_{aa})_y-$ is or comprises IEEQAKTFLDKFNHEAEDLFYQS.

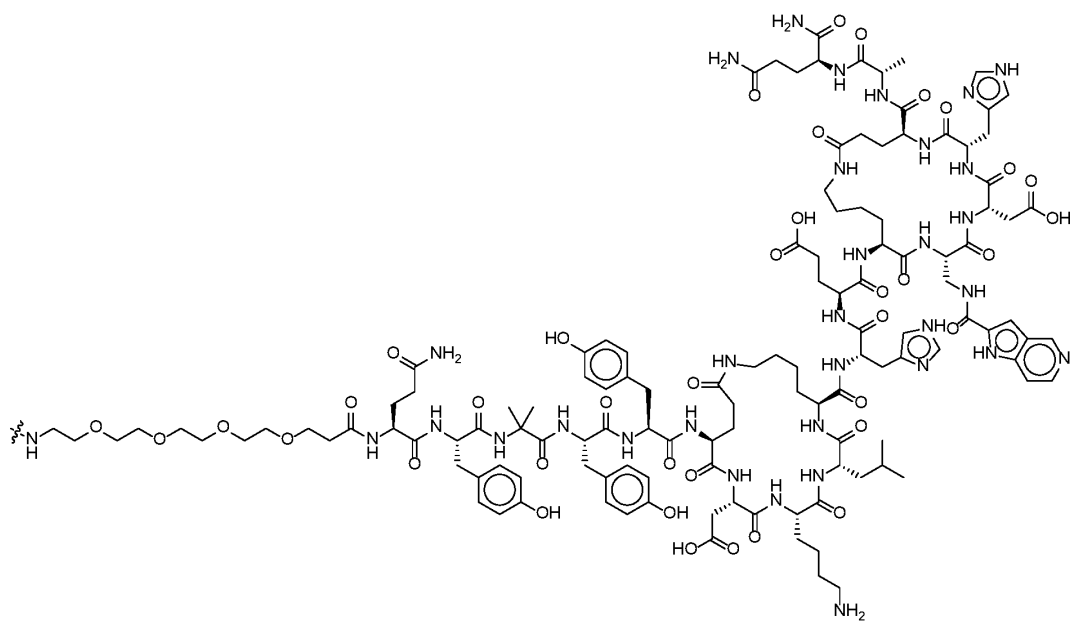
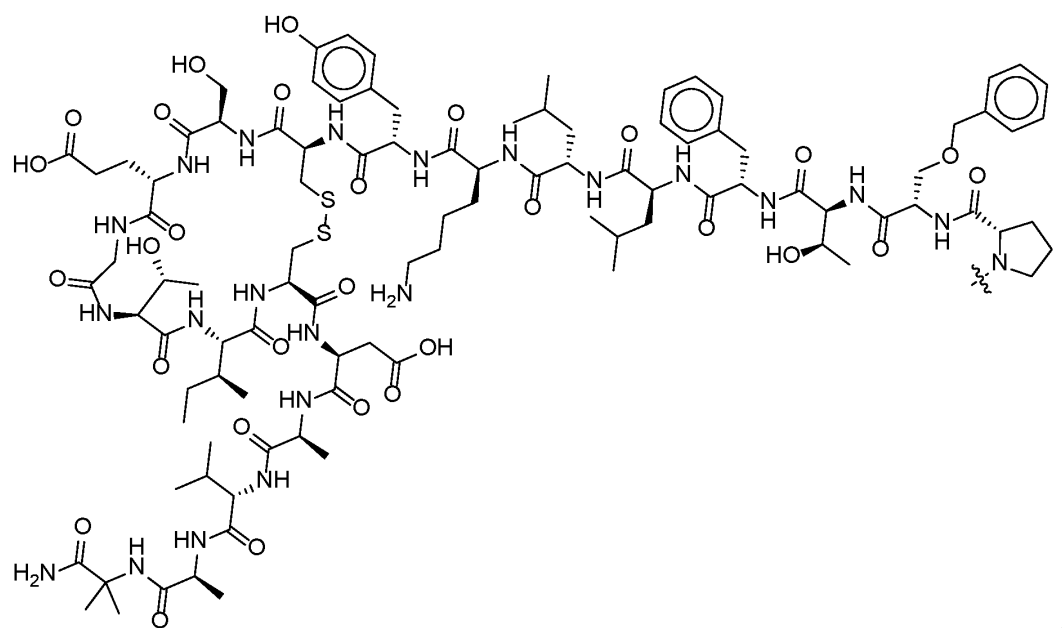
36. The agent of any one of claims 1-2, wherein $-(X_{aa})_y-$ is or comprises

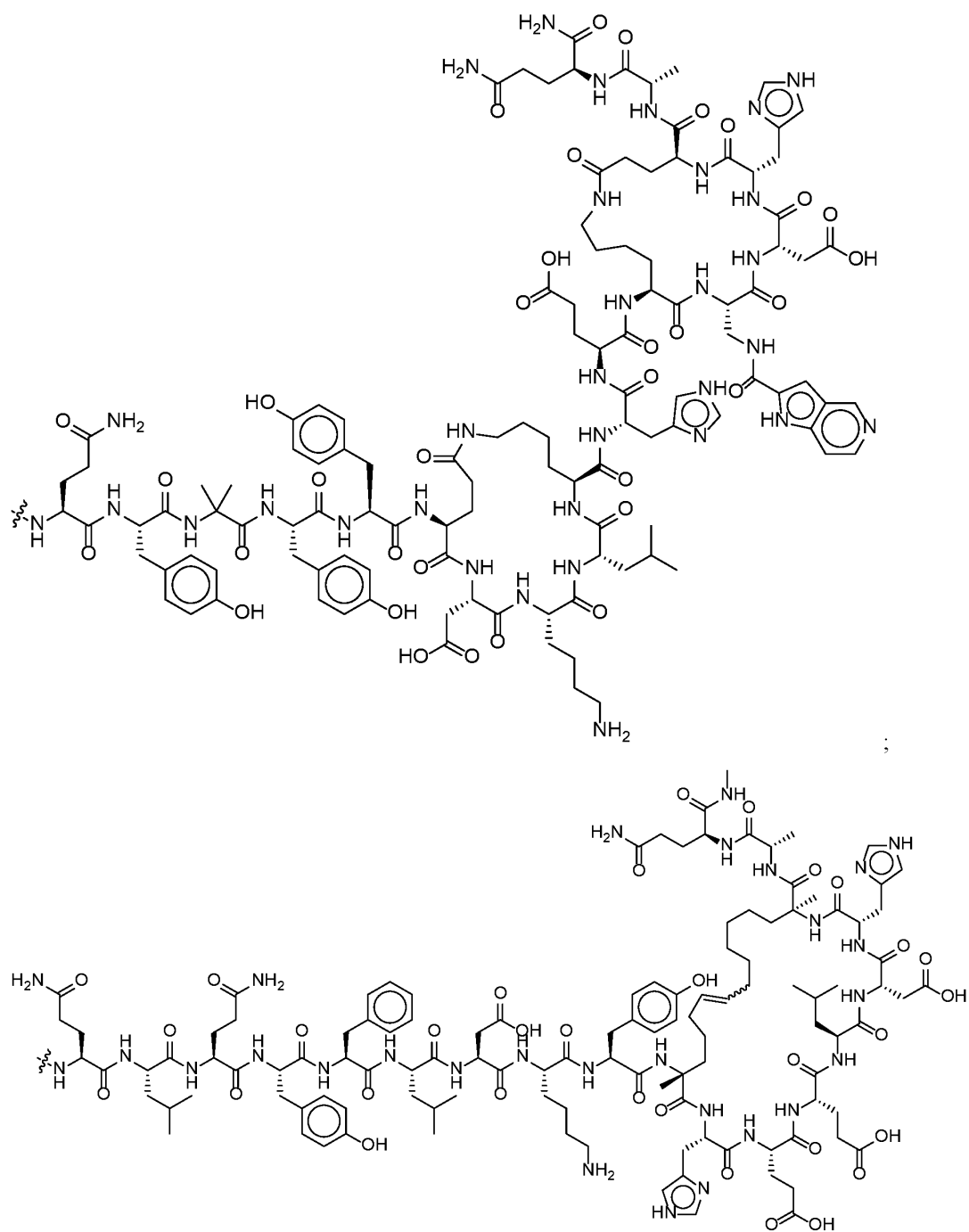


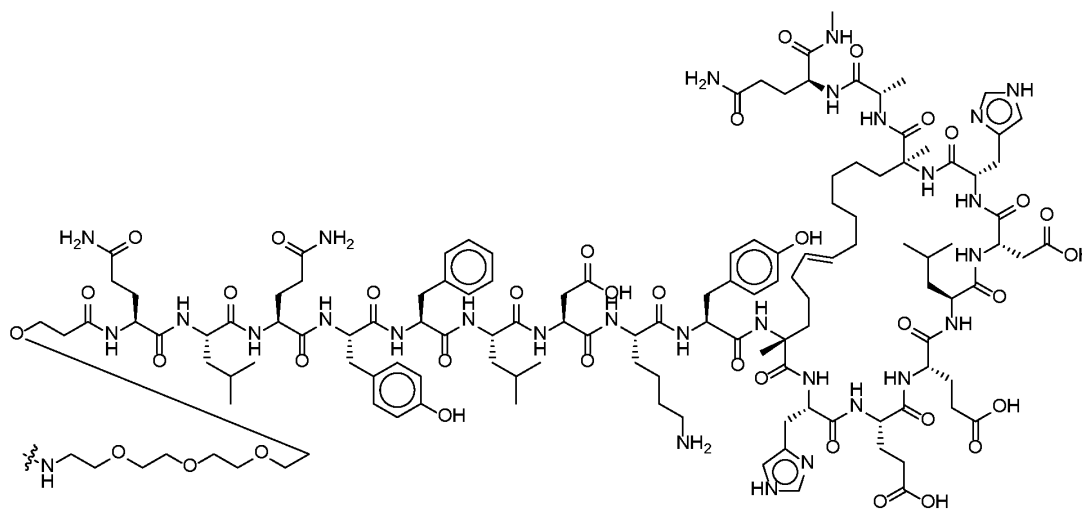
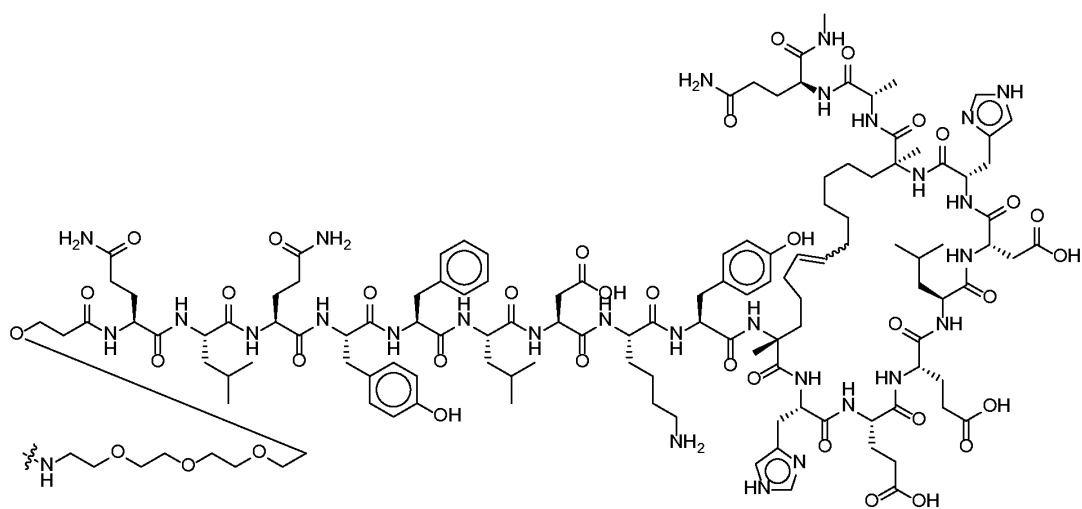


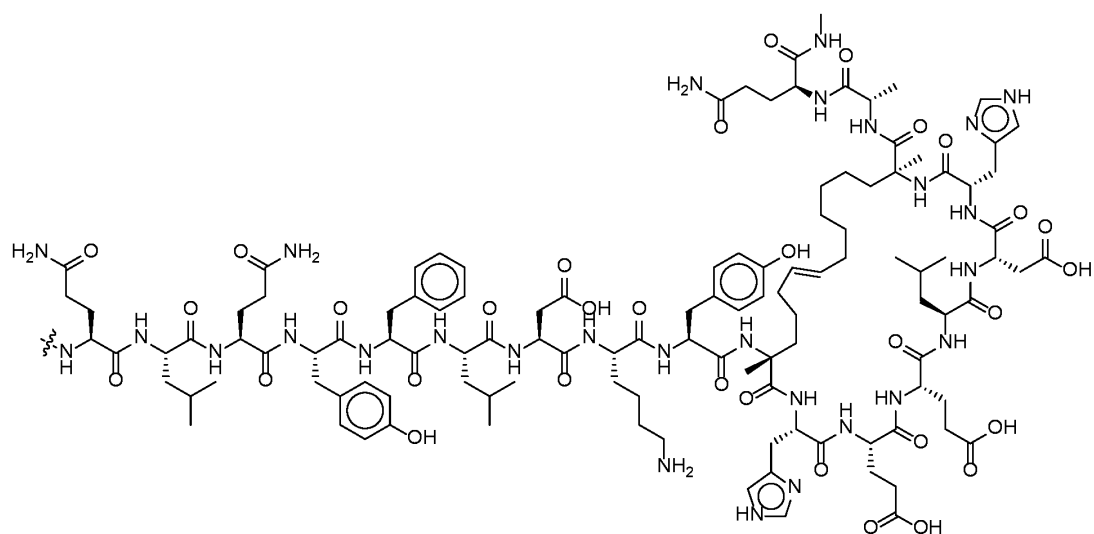
37. The agent of any one of claims 1-2, wherein $-(\text{Xaa})_y-$ is or comprises

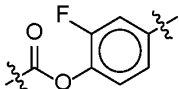


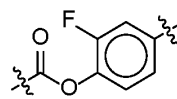




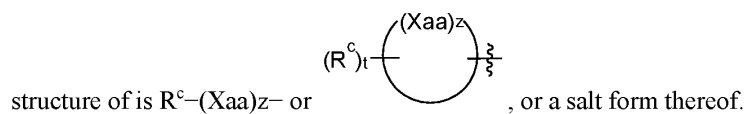




38. The agent of claim 1 or 2 where $-(Xaa)_y-$ is or comprises sequence designed based on, DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL, or a fragment thereof.
39. The agent of any one of the preceding claims, comprising a linker.
40. The agent of claim 39, wherein the linker comprises one or more $-[(CH_2)_2-O]_m-$, and m is 7 - 12.
41. The agent of any one of the preceding claims, wherein the linker comprises a reactive group, wherein upon contact with an antibody, the reactive group reacts with a group of the antibody and conjugates a target binding moiety, or a moiety comprising $-(Xaa)_y-$, to the antibody optionally through a linker.
42. The agent of claim 41, wherein the reactive group is or comprises , wherein $-C(O)-$ is connected to a target binding moiety, or a moiety comprising $-(Xaa)_y-$, optionally through a linker and the other end is connected to an antibody binding moiety.
43. The agent of any one of the preceding claims, comprising one and only one antibody binding moiety.



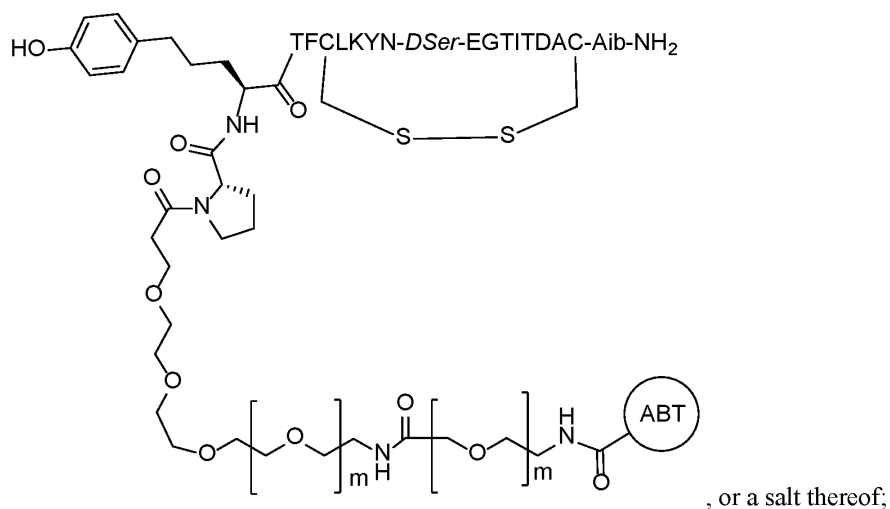
44. The agent of any one of the preceding claims, wherein the antibody binding moiety has the

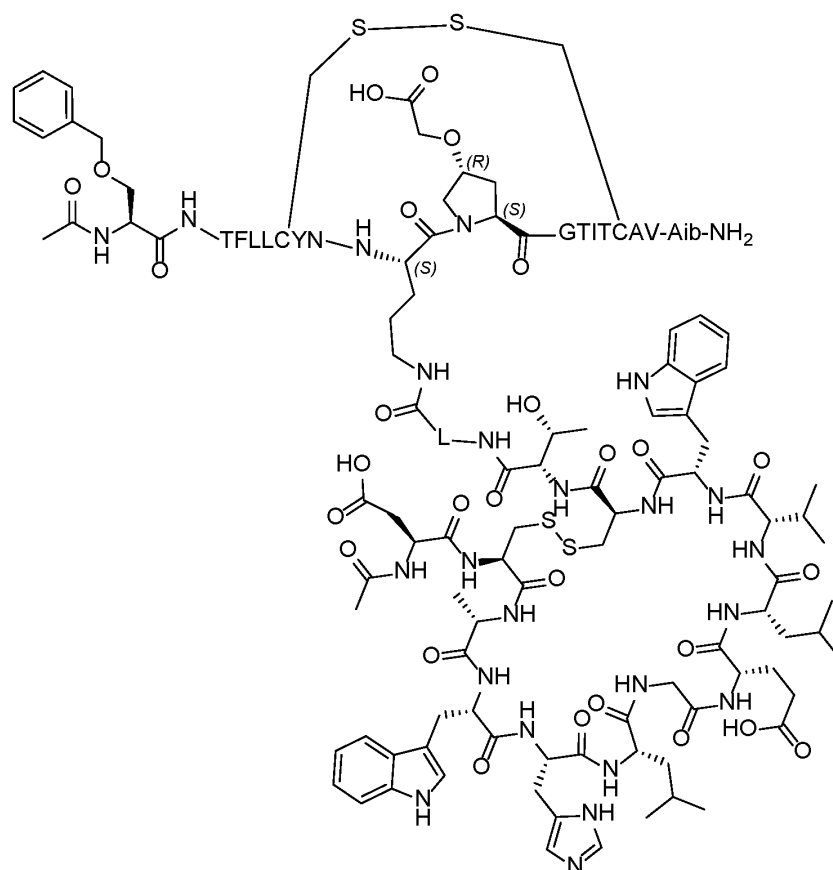
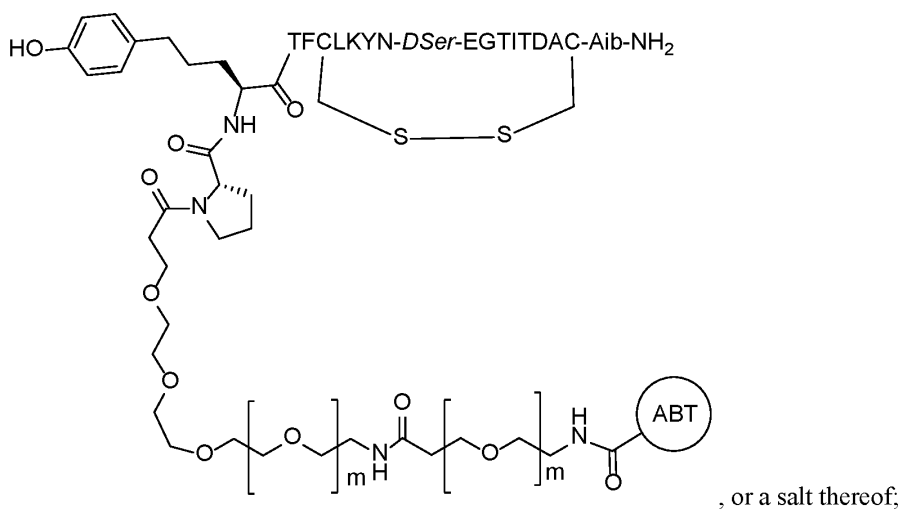


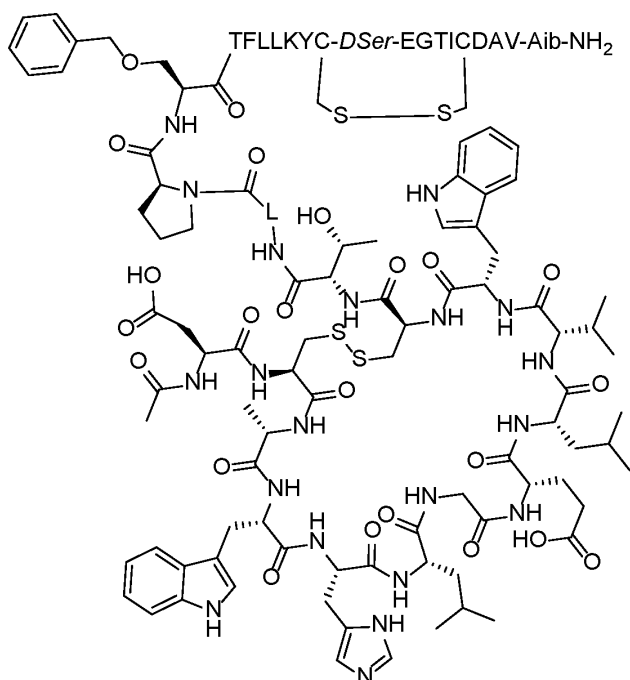
44. The agent of any one of the preceding claims, wherein the antibody binding moiety comprises or has the structure selected from A-1 to A-50, or a salt form thereof.

45. The agent of any one of the preceding claims, wherein the antibody binding moiety comprises or has the structure of DCAWHLGELVWCT or a salt form thereof, wherein the two C residues are linked by a $-S-S-$.

46. The agent of claim 1 or 2, wherein the agent has the structure of

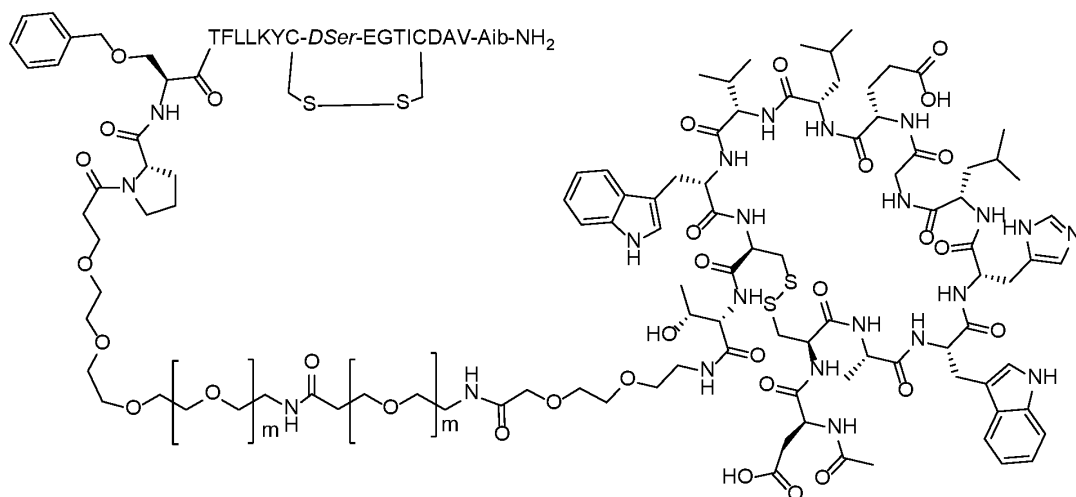






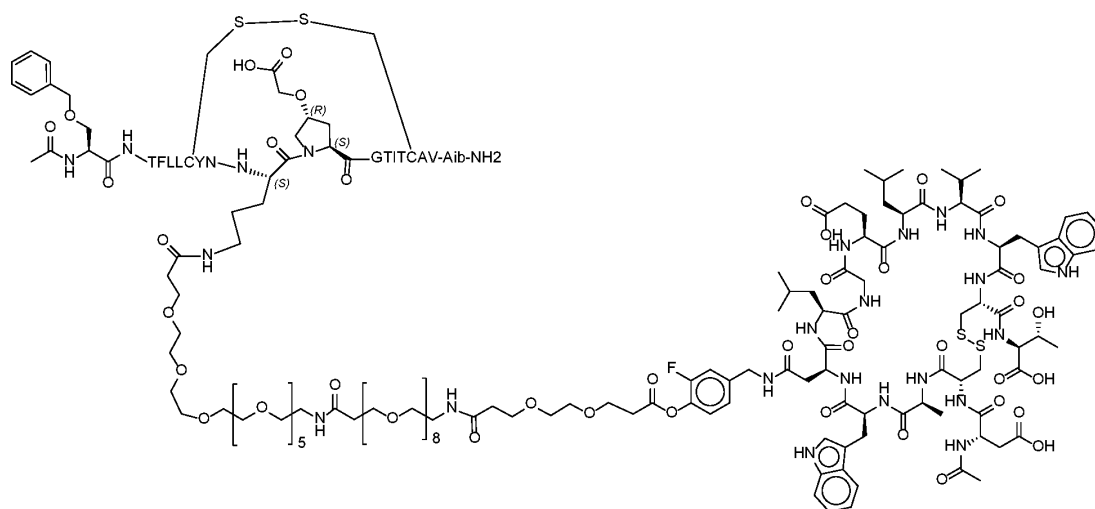
or a salt thereof, wherein L is a linker moiety.

47. The agent of claim 1 or 2, wherein the agent has the structure of



(I-1)

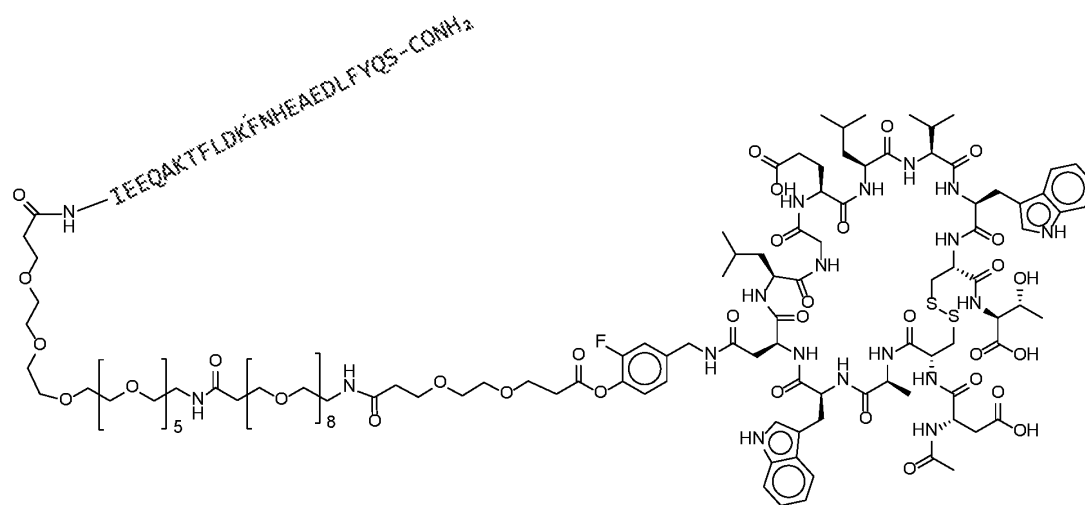
or a salt thereof;



(I-4)

or a salt thereof.

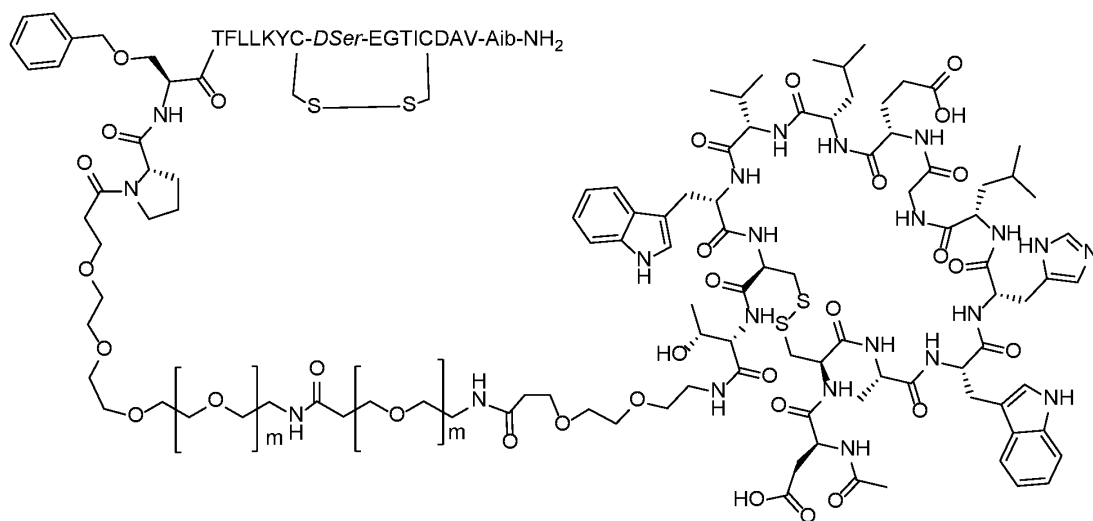
51. The agent of claim 1 or 2, wherein the agent has the structure of



(I-5)

or a salt thereof.

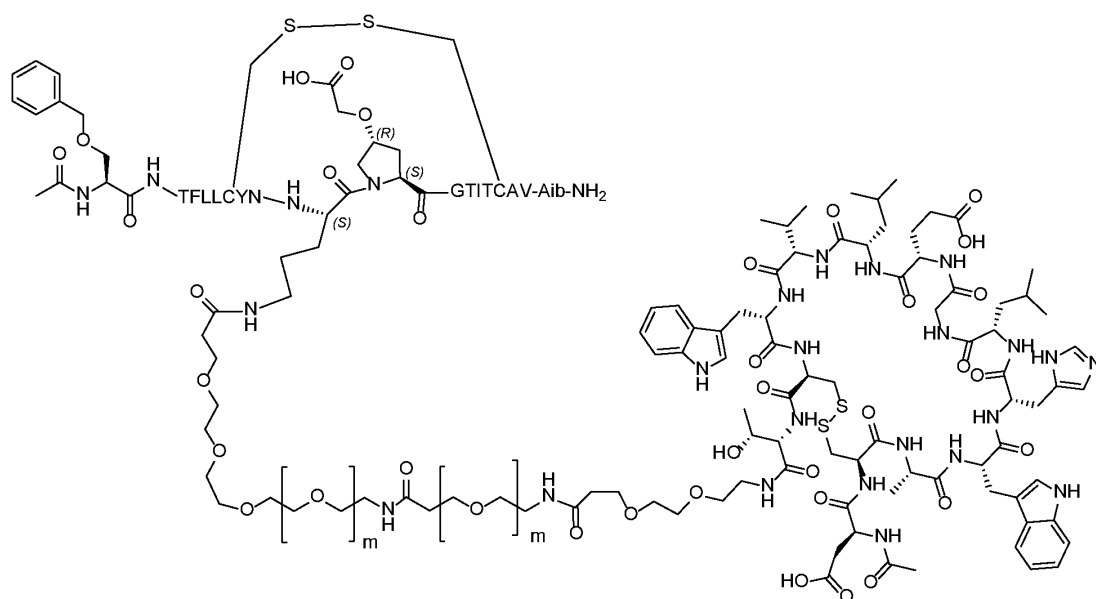
52. The agent of claim 1 or 2, wherein the agent has the structure of



(I-9)

or a salt thereof.

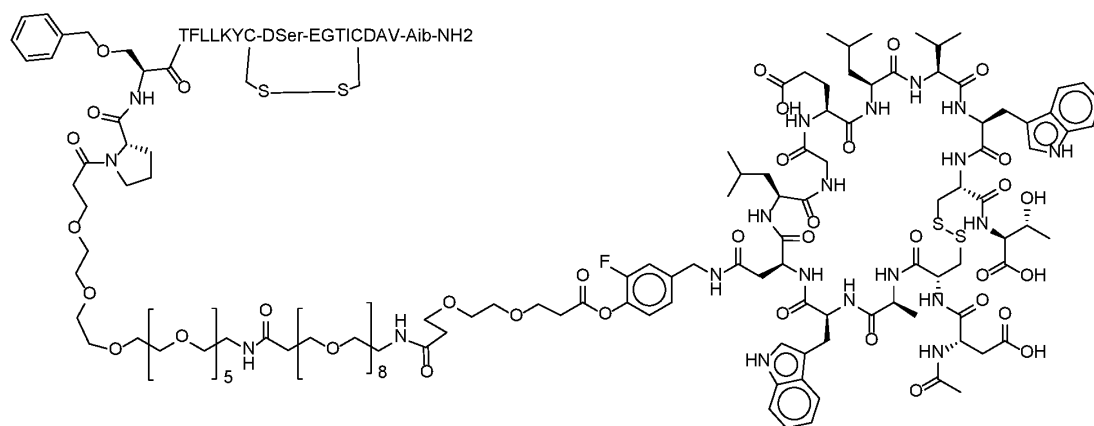
53. The agent of claim 1 or 2, wherein the agent has the structure of



(I-10)

or a salt thereof.

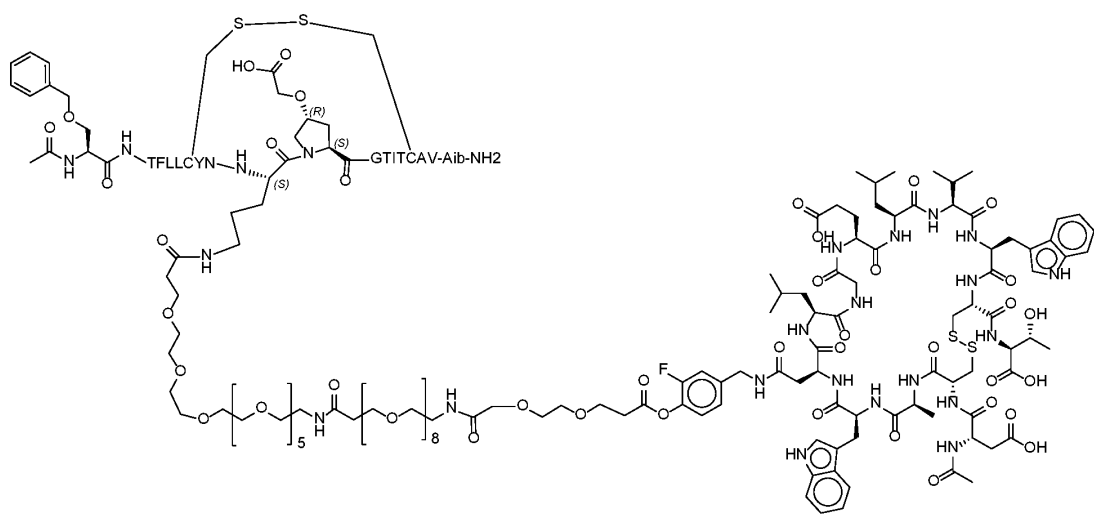
54. The agent of claim 1 or 2, wherein the agent has the structure of



(I-11)

or a salt thereof.

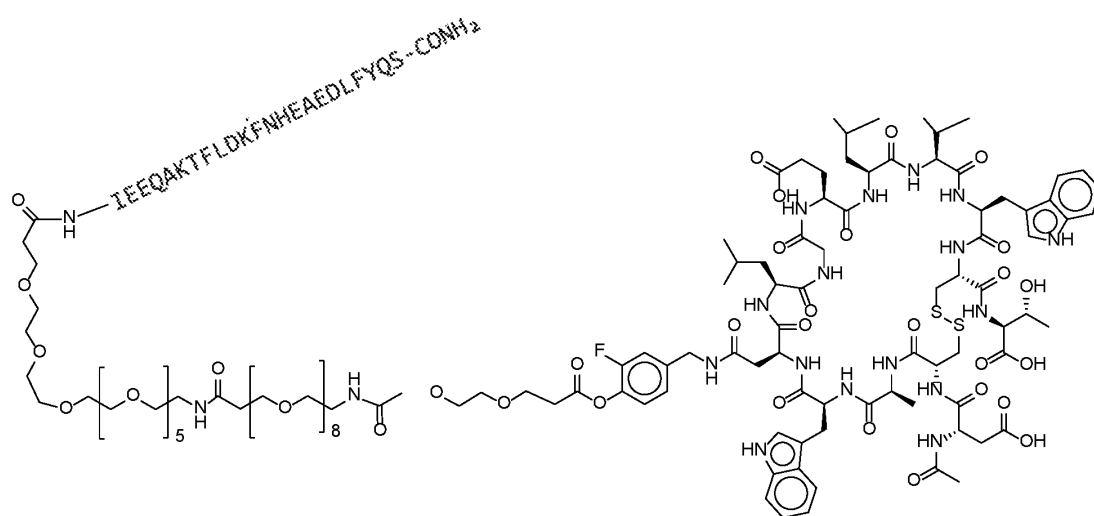
55. The agent of claim 1 or 2, wherein the agent has the structure of



(I-12)

or a salt thereof.

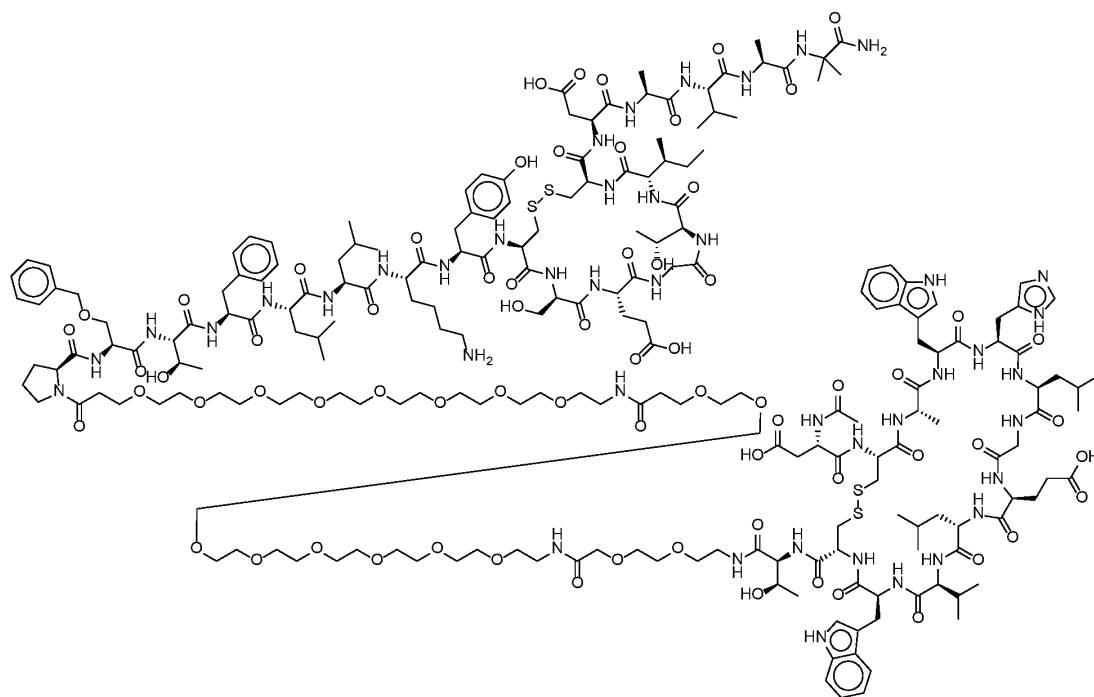
56. The agent of claim 1 or 2, wherein the agent has the structure of



(I-13)

or a salt thereof.

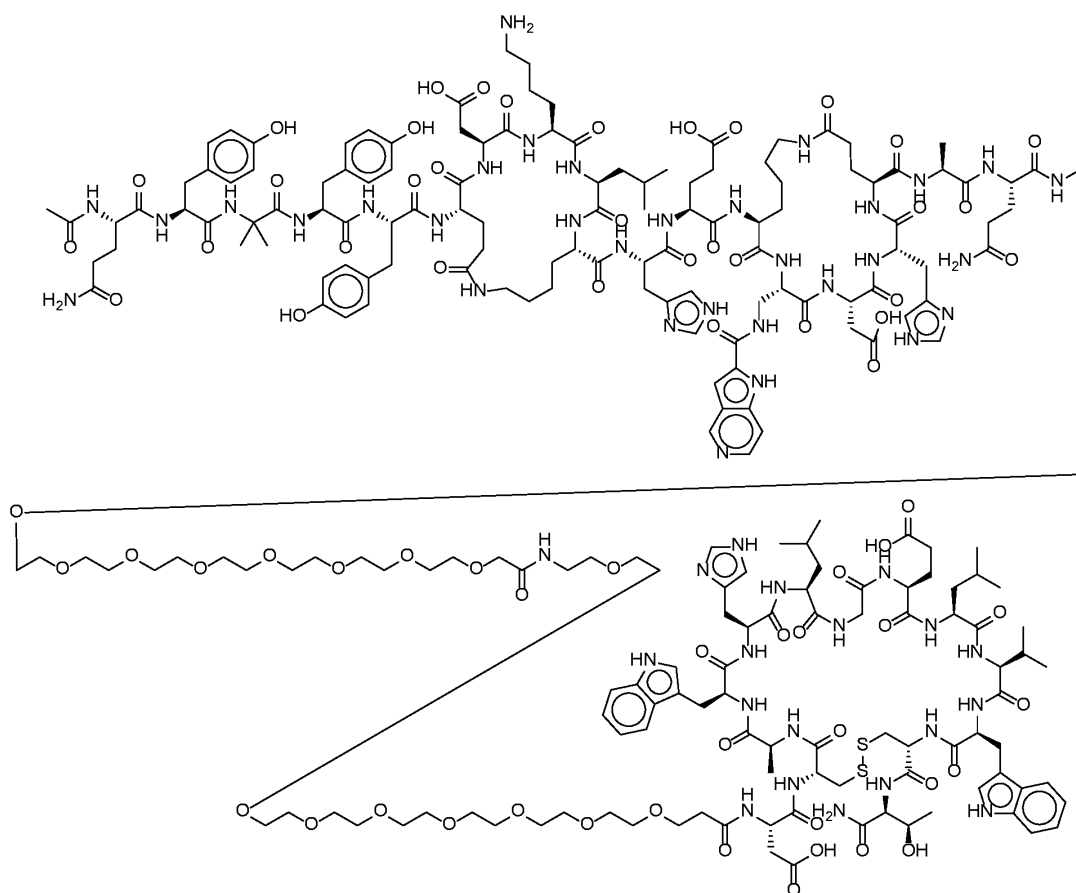
57. The agent of claim 1 or 2, wherein the agent has the structure of



(I-17)

or a salt thereof.

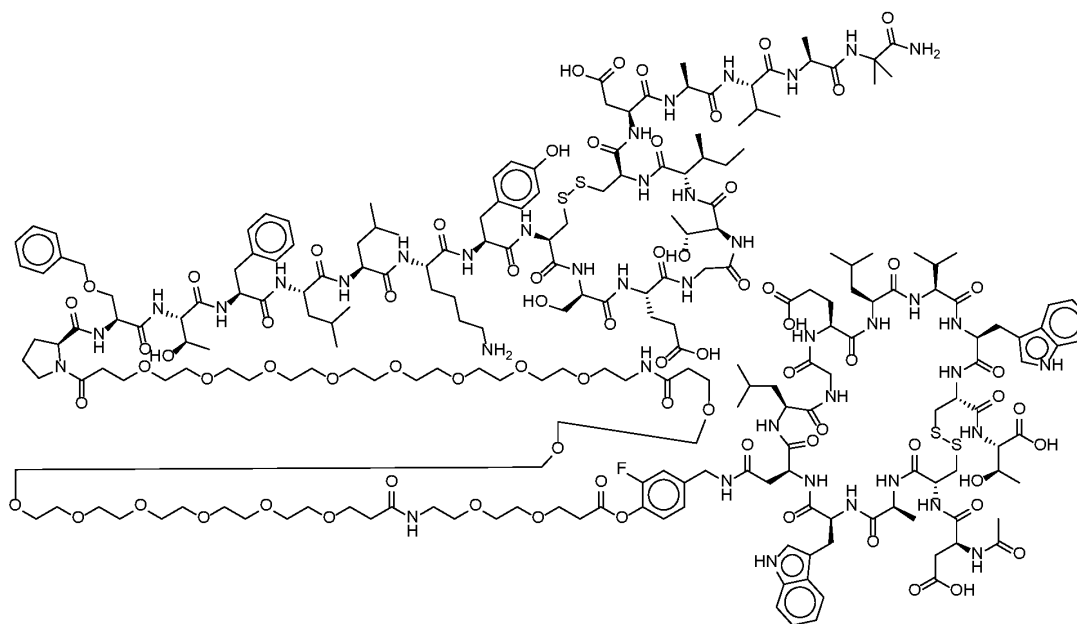
58. The agent of claim 1 or 2, wherein the agent has the structure of



(I-18)

or a salt thereof.

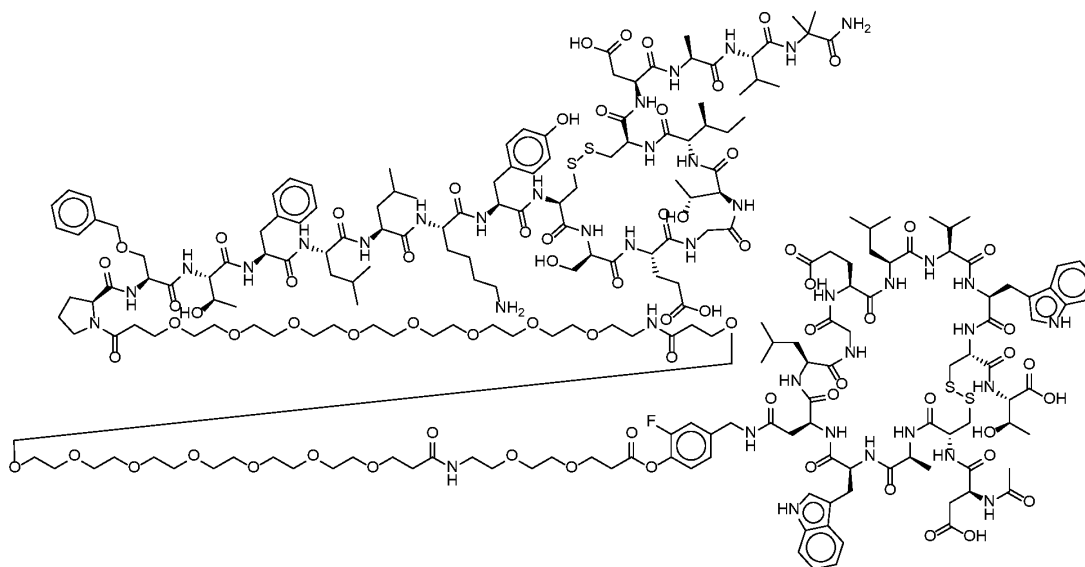
59. The agent of claim 1 or 2, wherein the agent has the structure of



(I-19)

or a salt thereof.

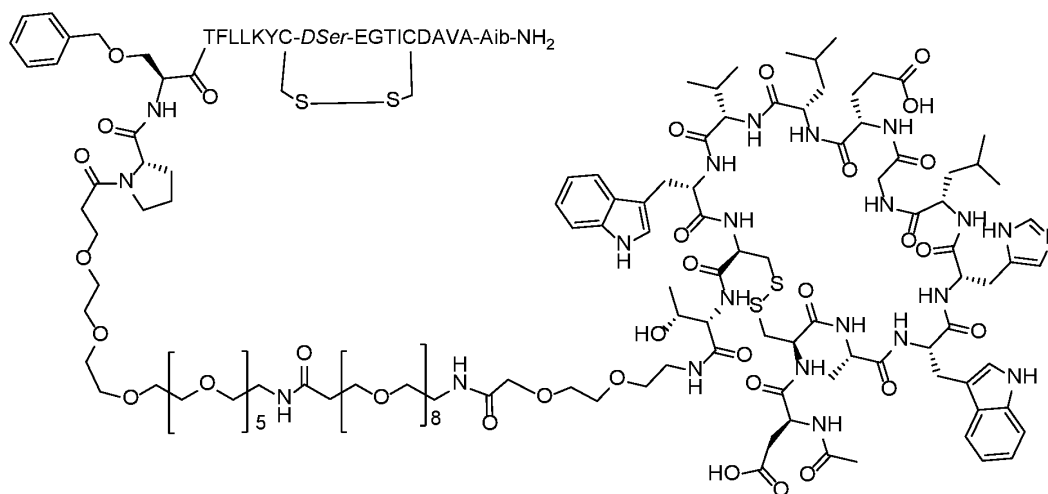
60. The agent of claim 1 or 2, wherein the agent has the structure of



(I-20)

or a salt thereof.

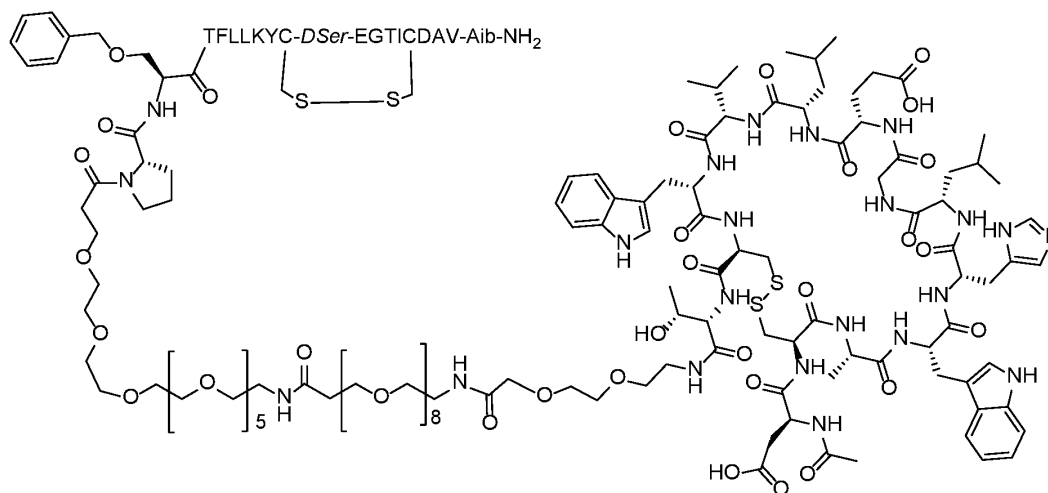
61. The agent of claim 1 or 2, wherein the agent has the structure of



(I-23)

or a salt thereof.

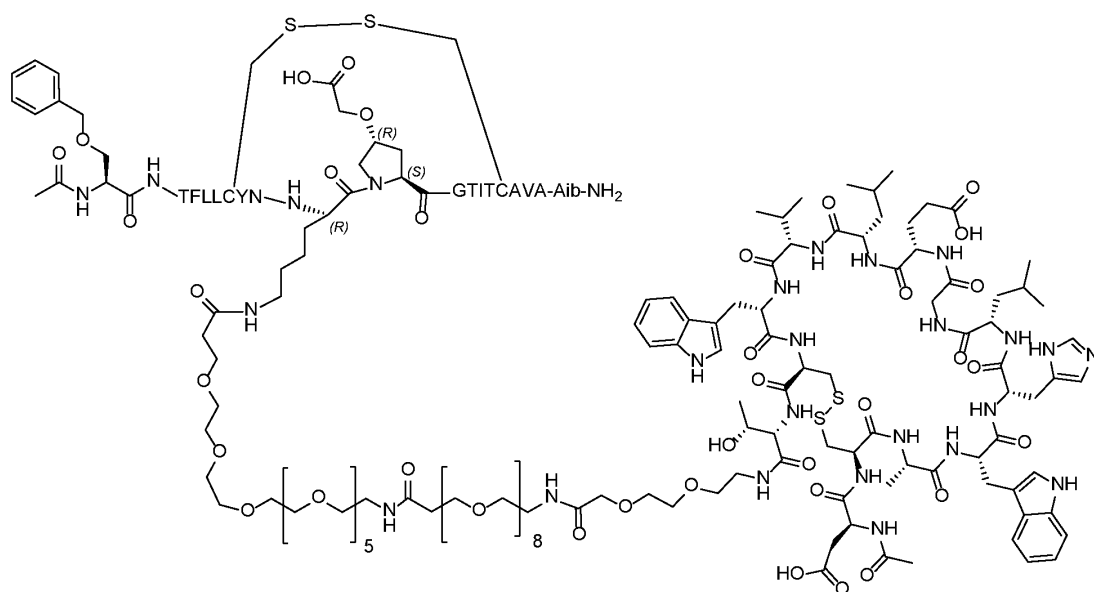
62. The agent of claim 1 or 2, wherein the agent has the structure of



(I-24)

or a salt thereof.

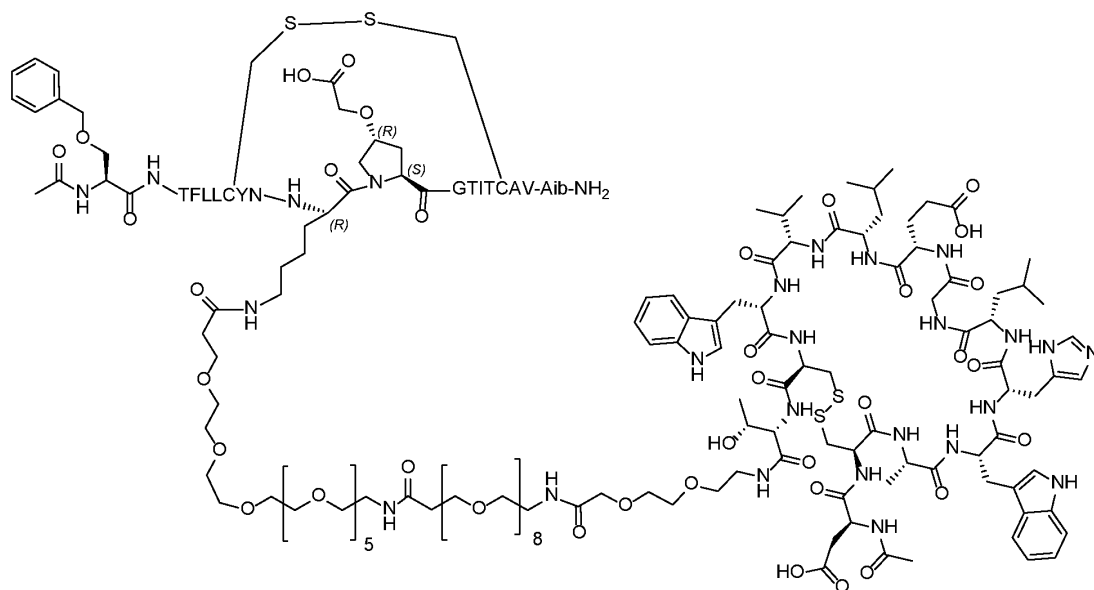
63. The agent of claim 1 or 2, wherein the agent has the structure of



(I-25)

or a salt thereof.

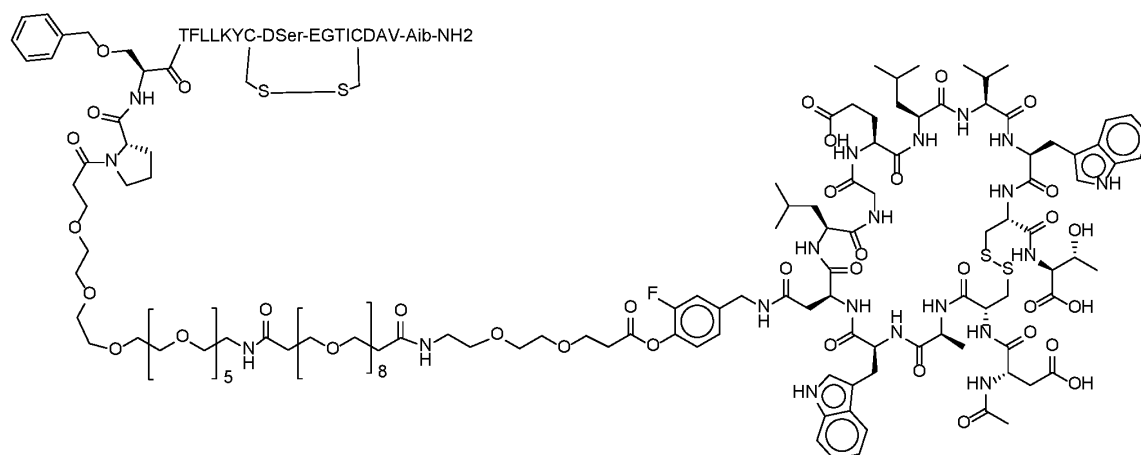
64. The agent of claim 1 or 2, wherein the agent has the structure of



(I-26)

or a salt thereof.

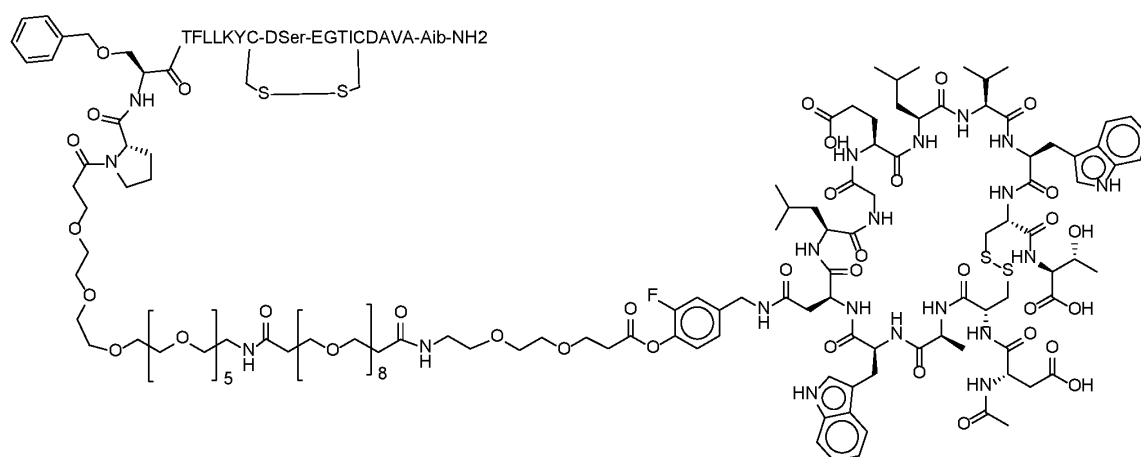
65. The agent of claim 1 or 2, wherein the agent has the structure of



(I-27)

or a salt thereof.

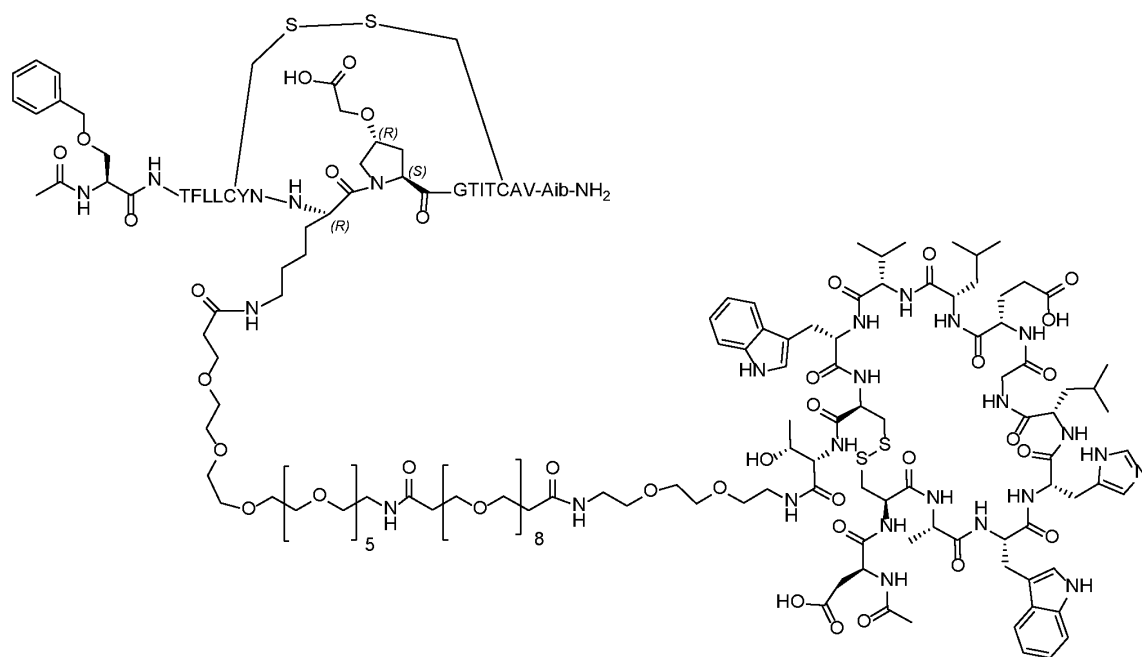
66. The agent of claim 1 or 2, wherein the agent has the structure of



(I-28)

or a salt thereof.

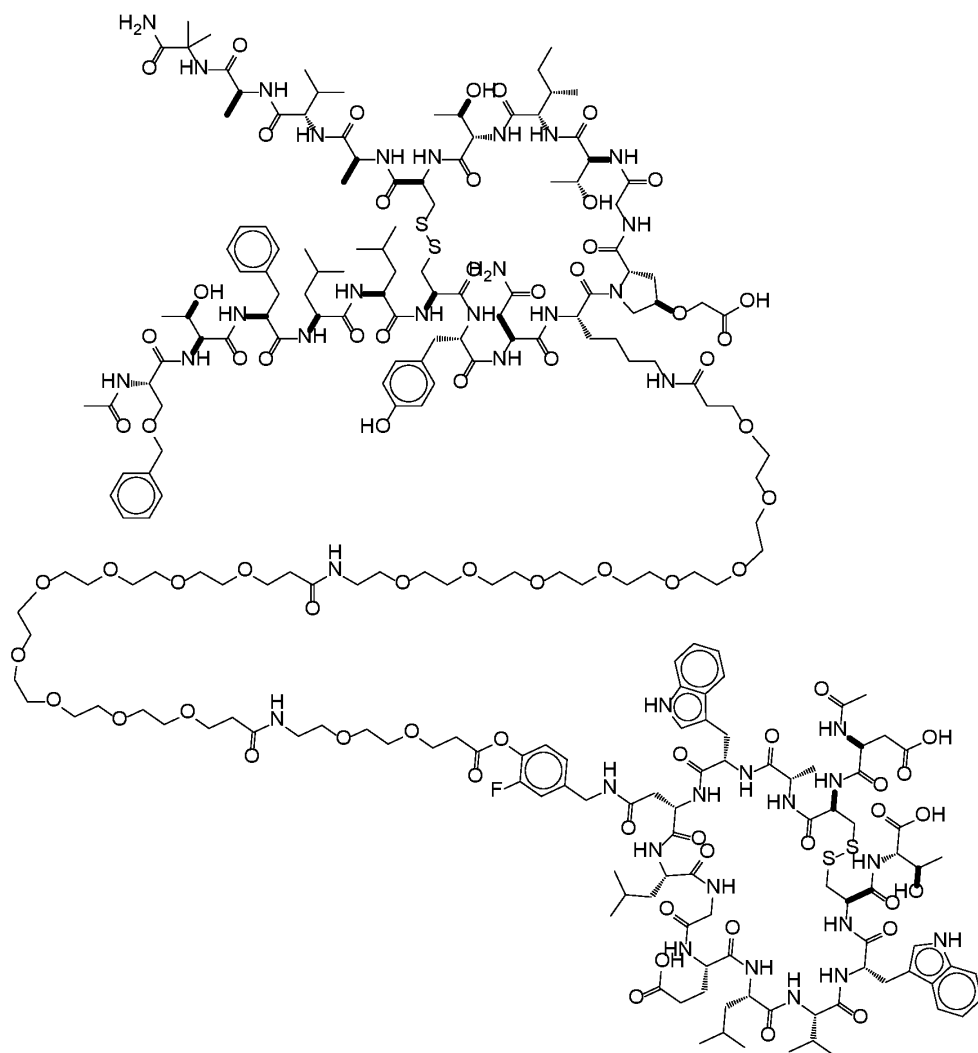
67. The agent of claim 1 or 2, wherein the agent has the structure of



(I-29)

or a salt thereof.

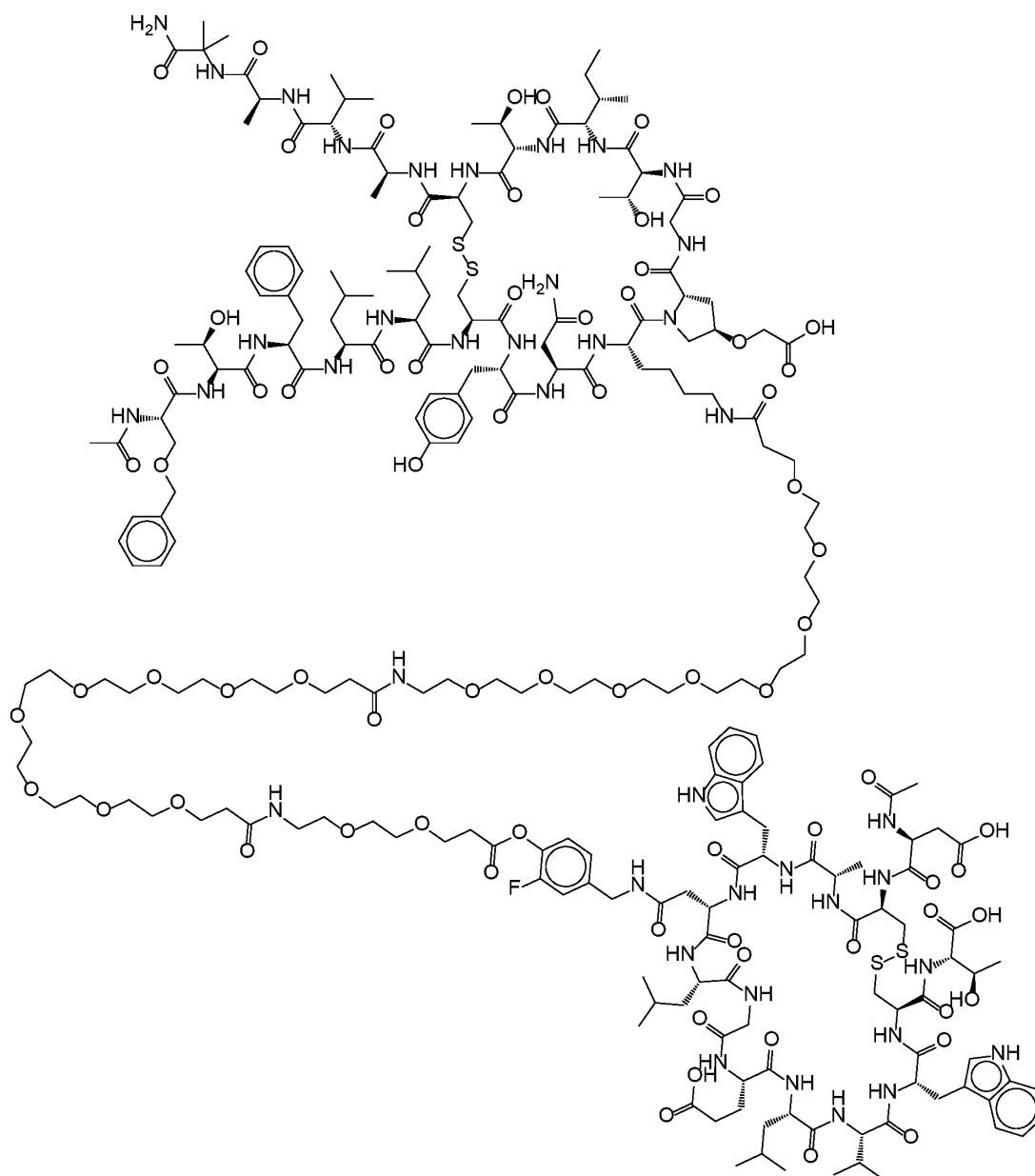
68. The agent of claim 1 or 2, wherein the agent has the structure of



(I-30)

or a salt thereof.

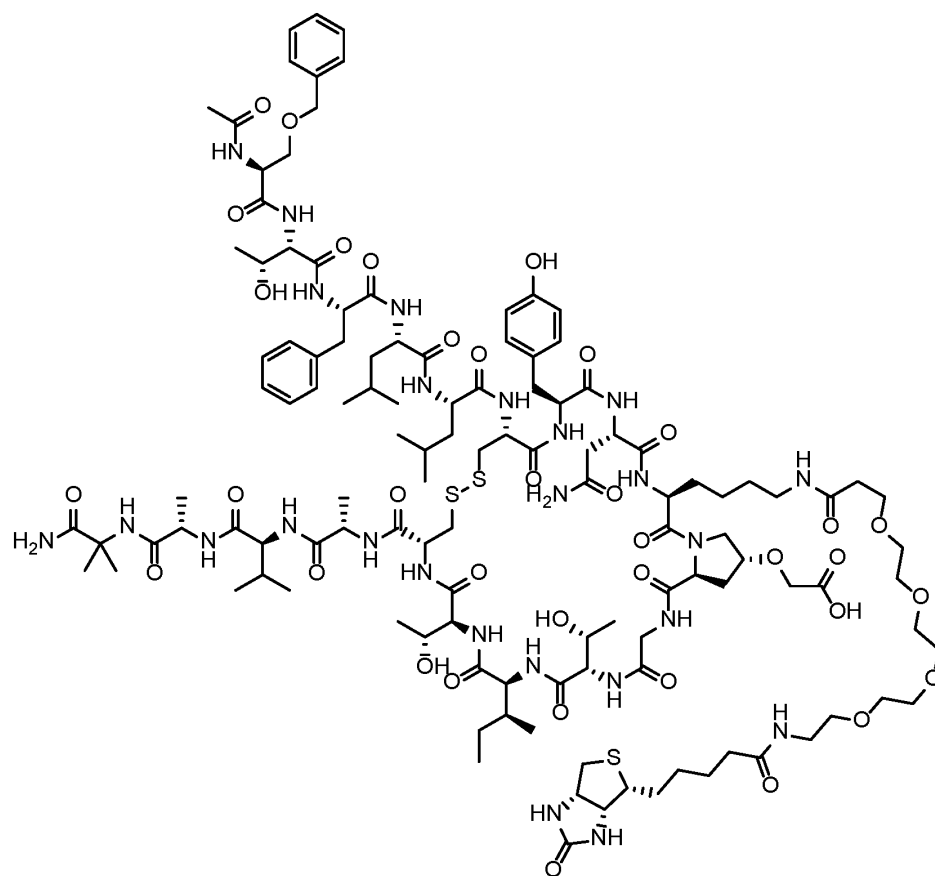
69. The agent of claim 1 or 2, wherein the agent has the structure of



(I-31)

or a salt thereof.

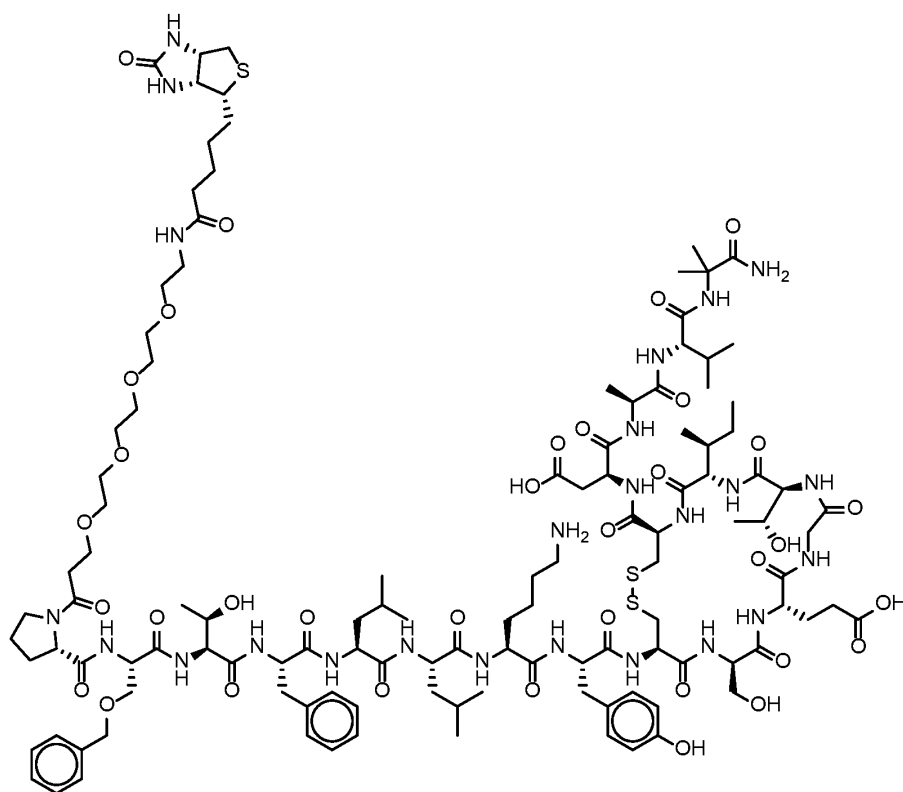
70. The agent of claim 1 or 2, wherein the agent has the structure of



(I-32)

or a salt thereof.

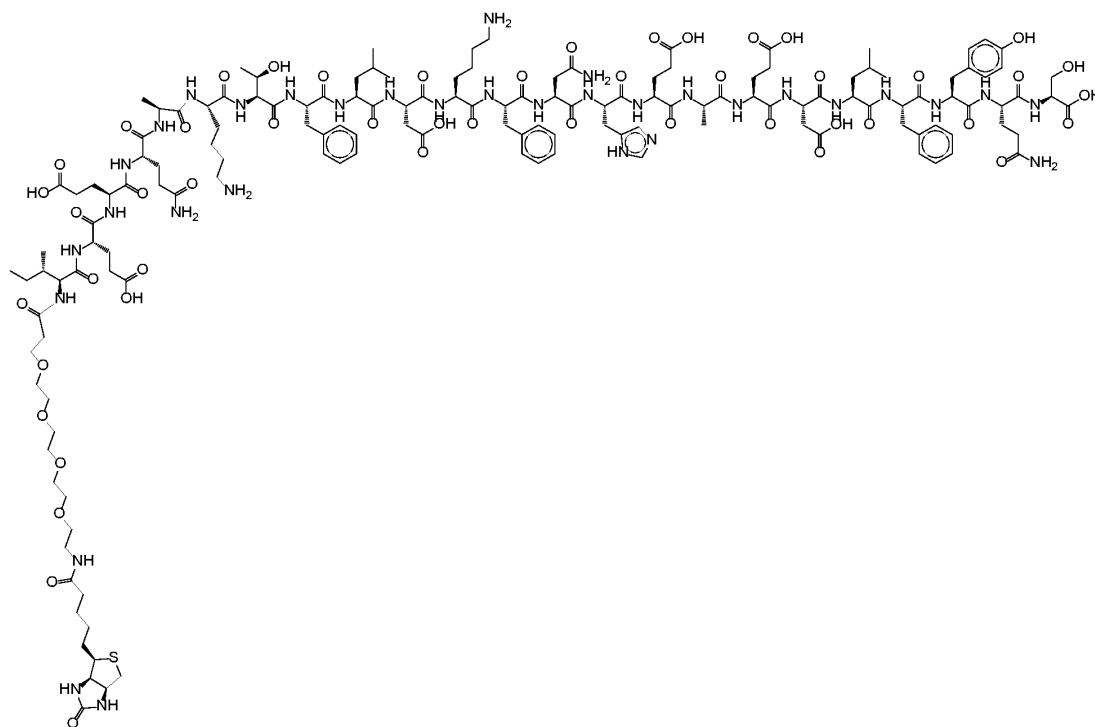
71. The agent of claim 1 or 2, wherein the agent has the structure of



(I-33)

Or a salt thereof.

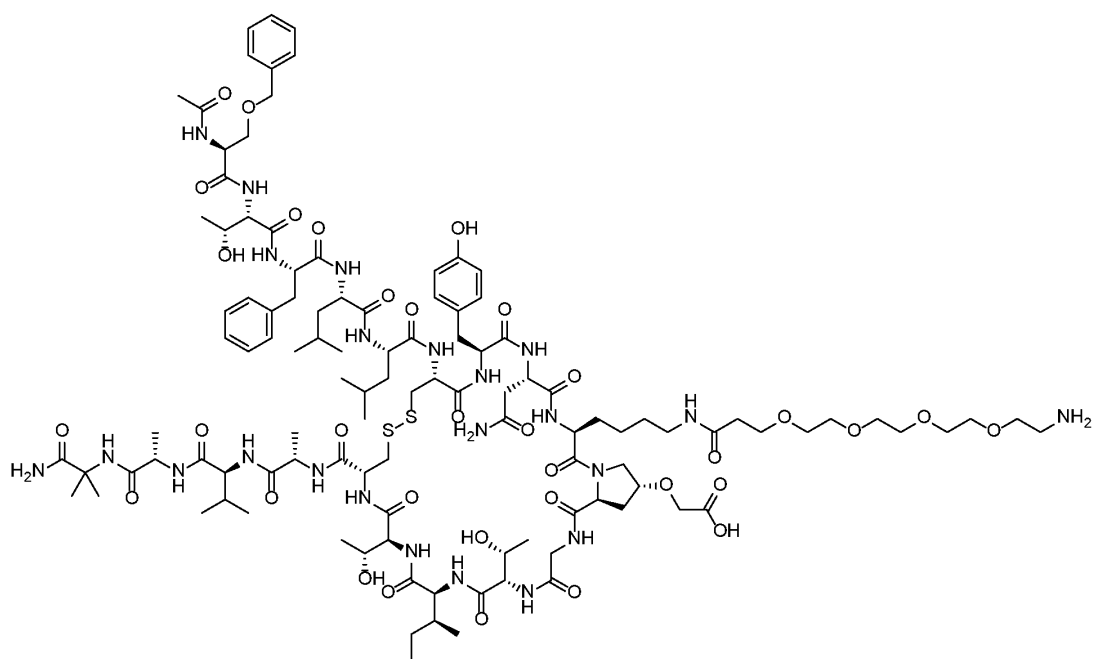
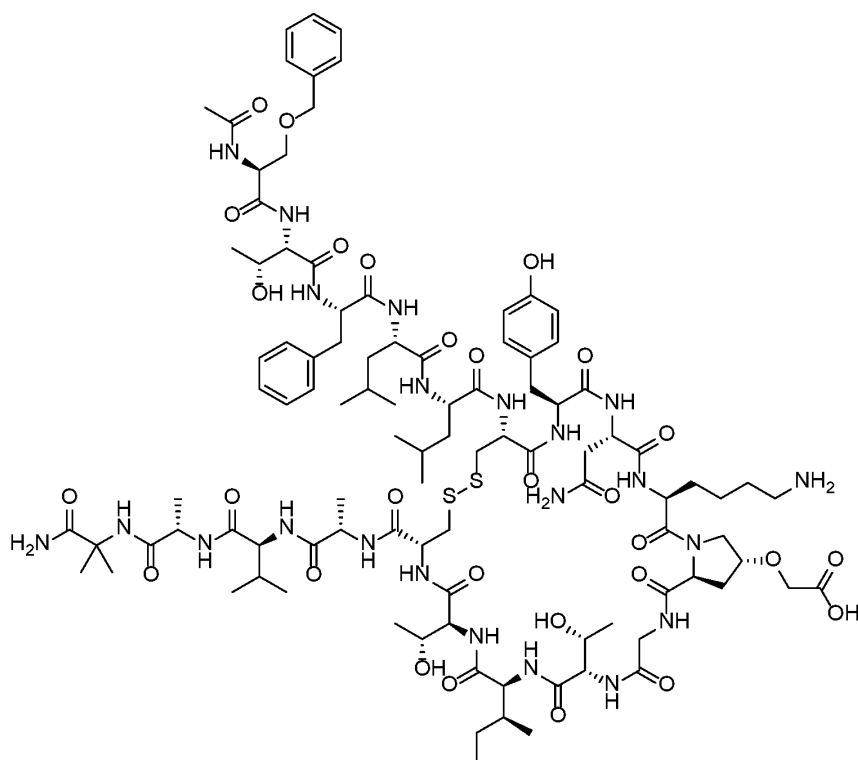
72. The agent of claim 1 or 2, wherein the agent has the structure of

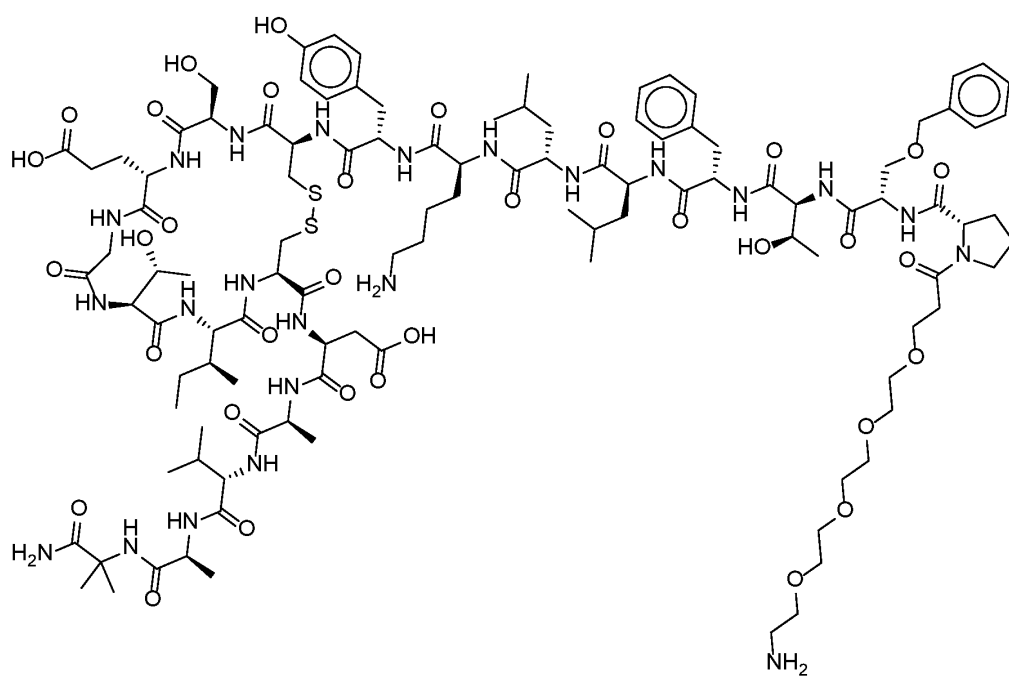
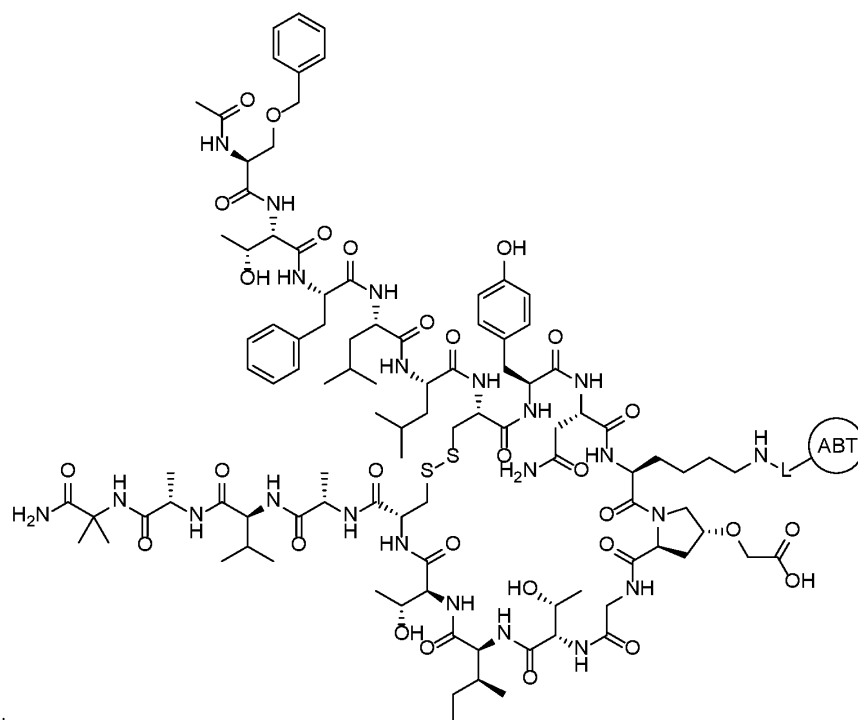


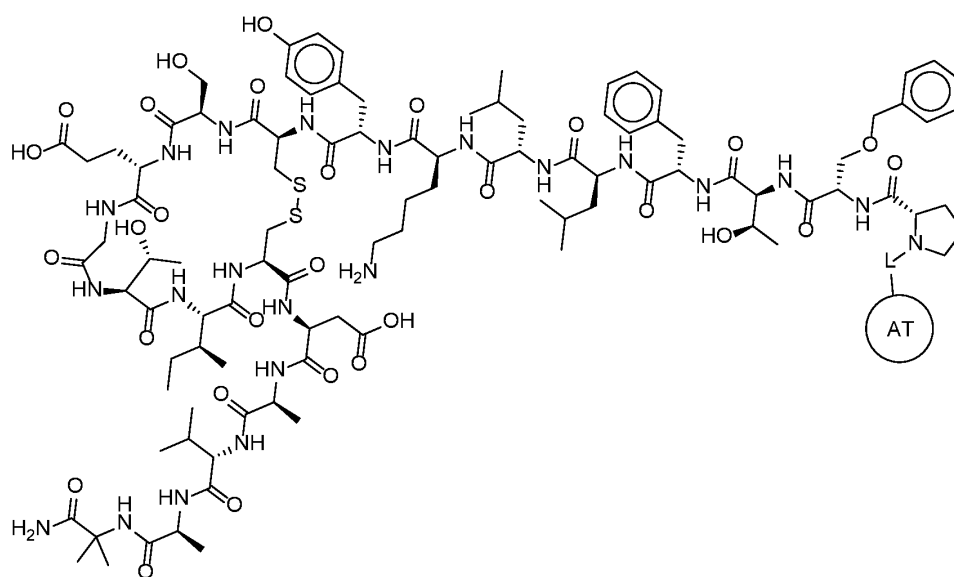
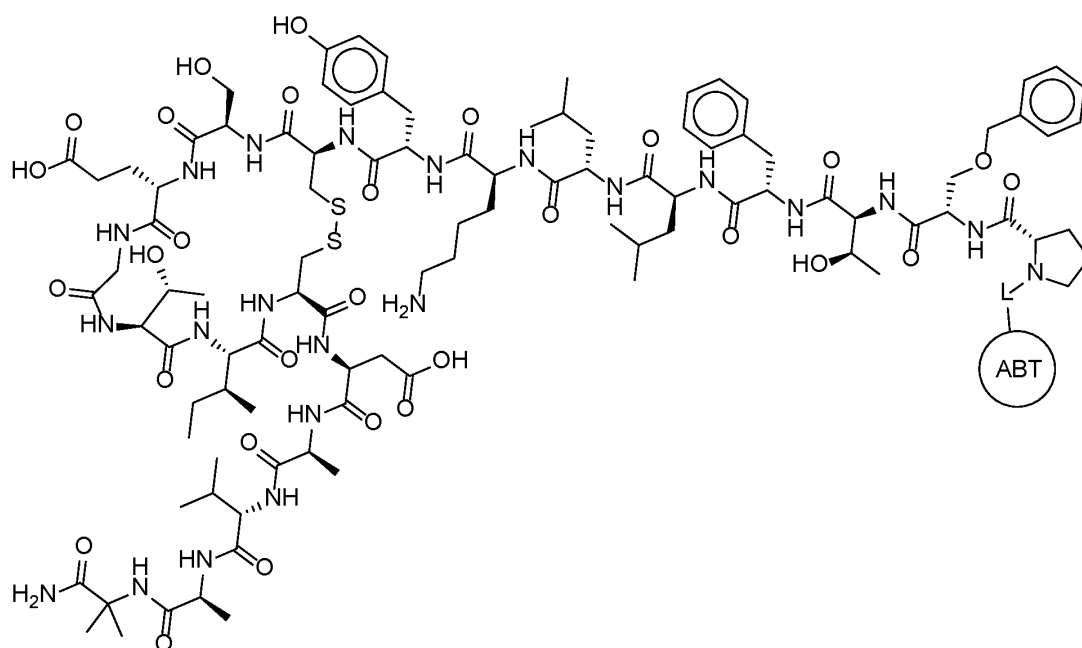
(I-34)

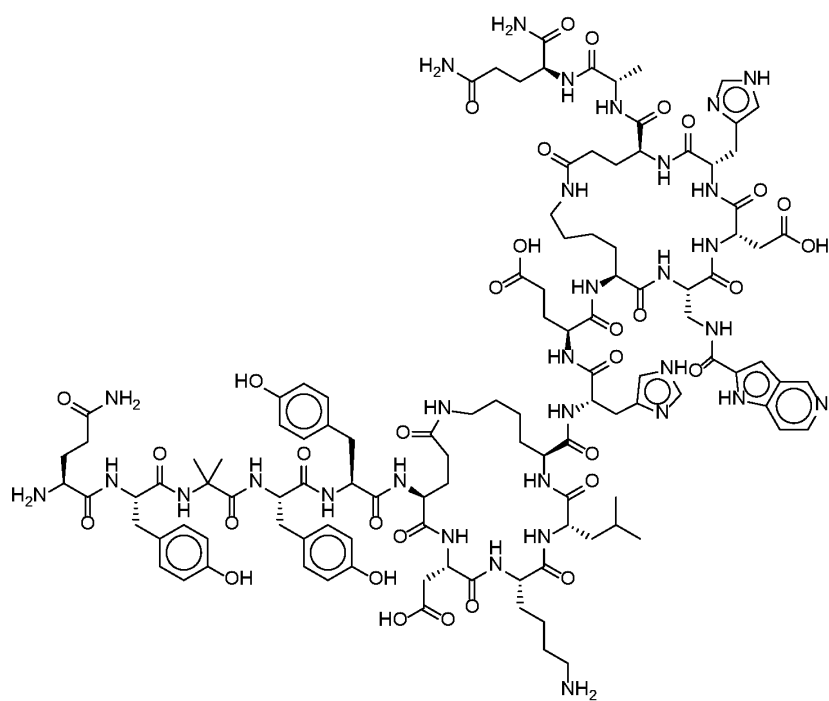
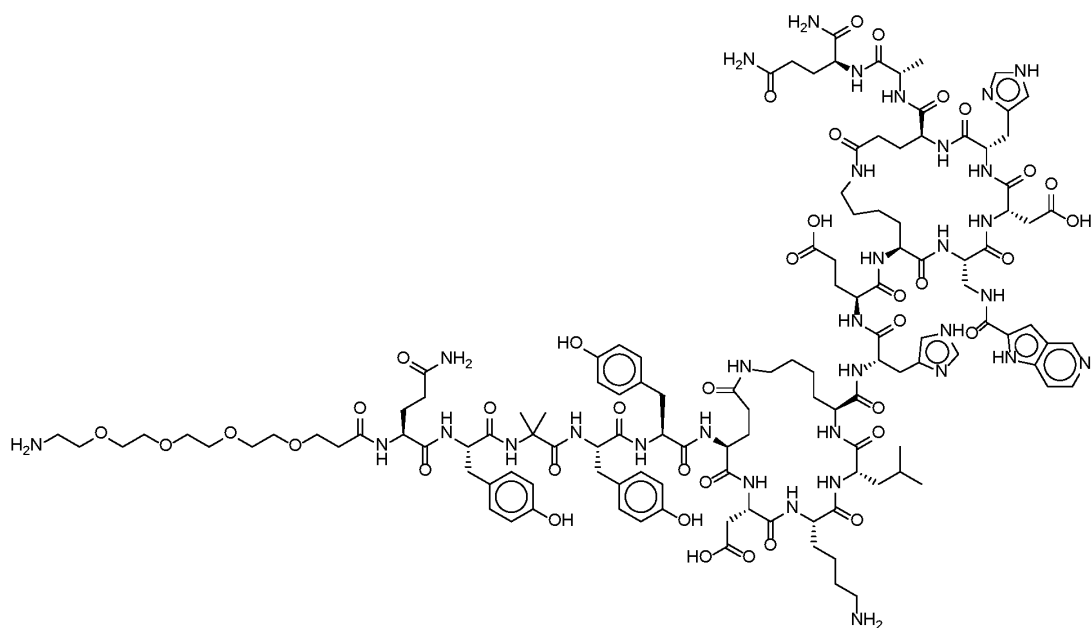
Or a salt thereof.

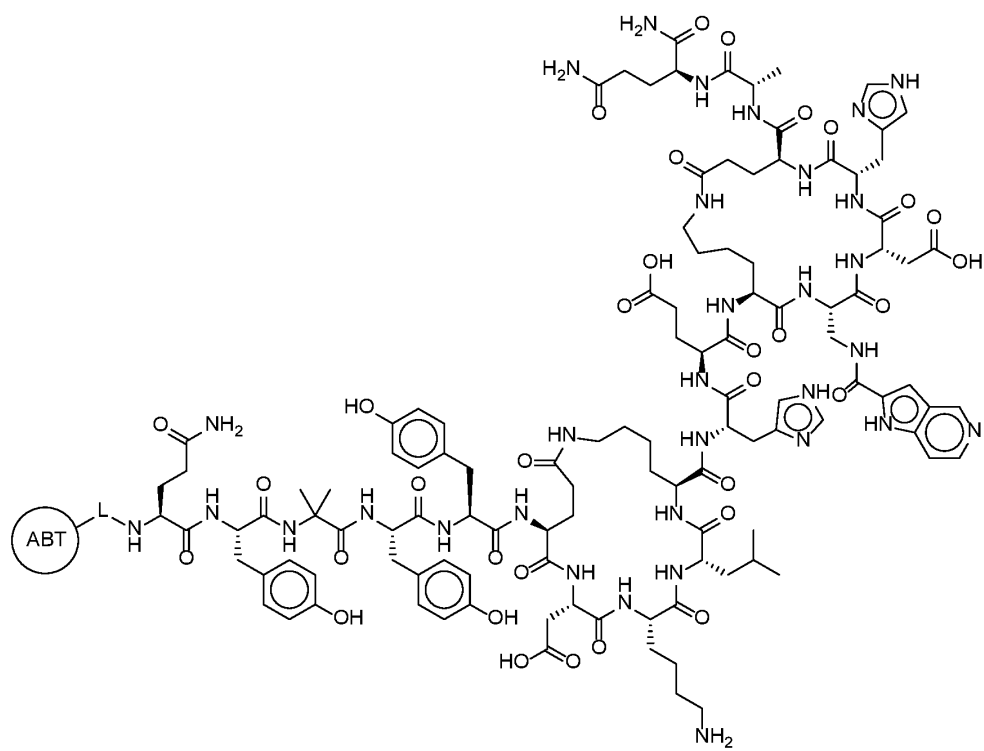
73. An agent, wherein the agent is any of the following or a salt thereof, in the following list of agents L is a Linker, ABT is an antibody binding moiety, and AT is an antibody moiety,

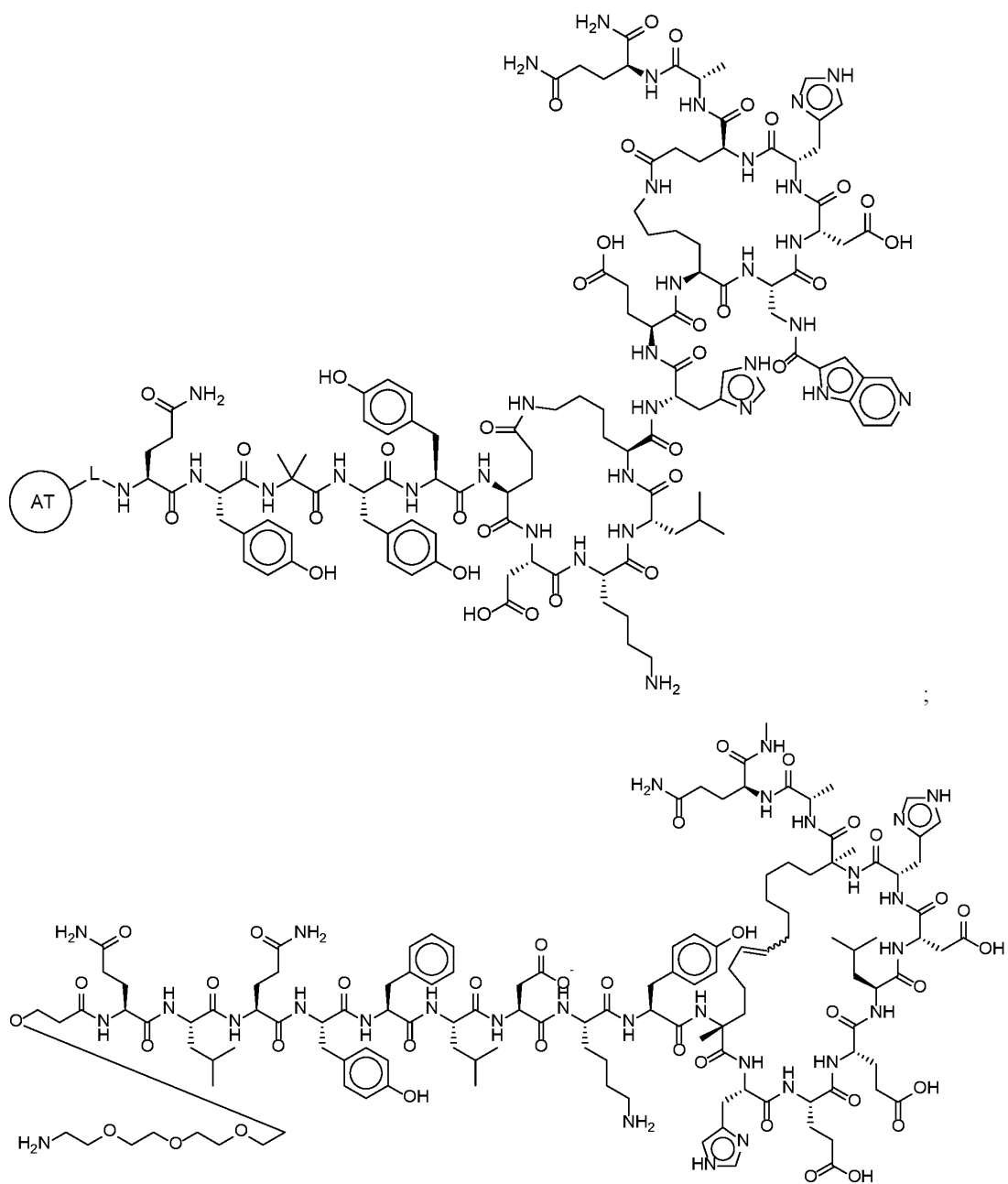


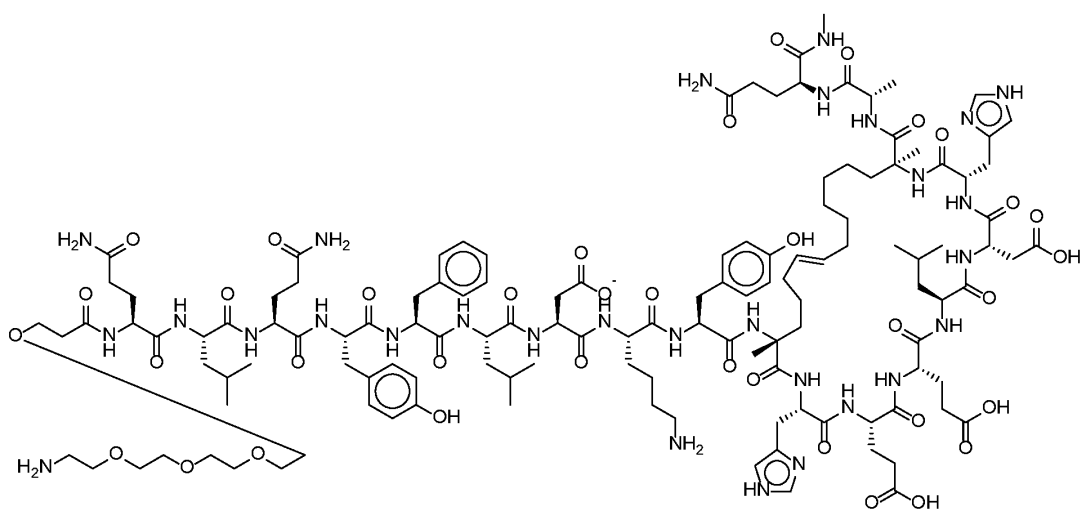




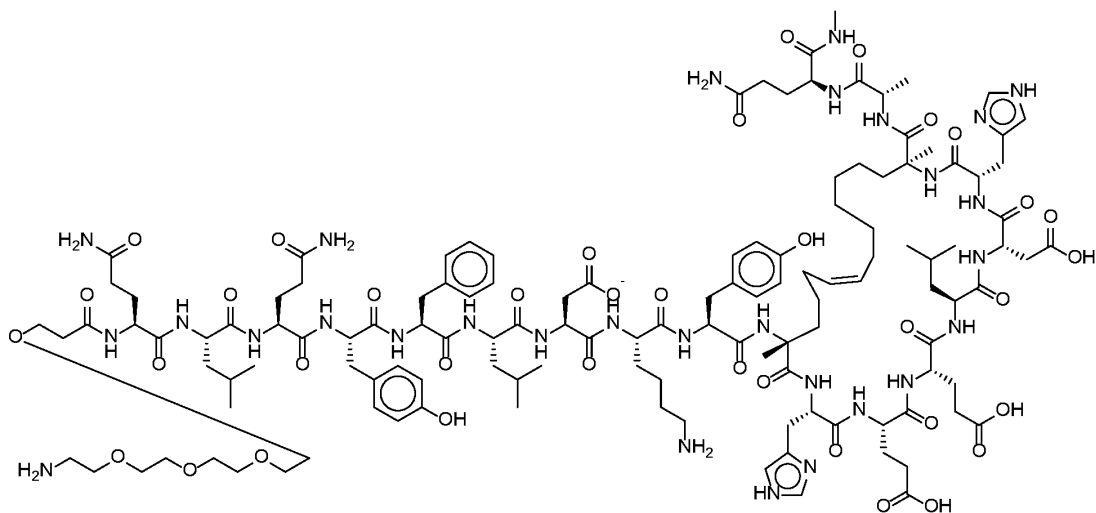




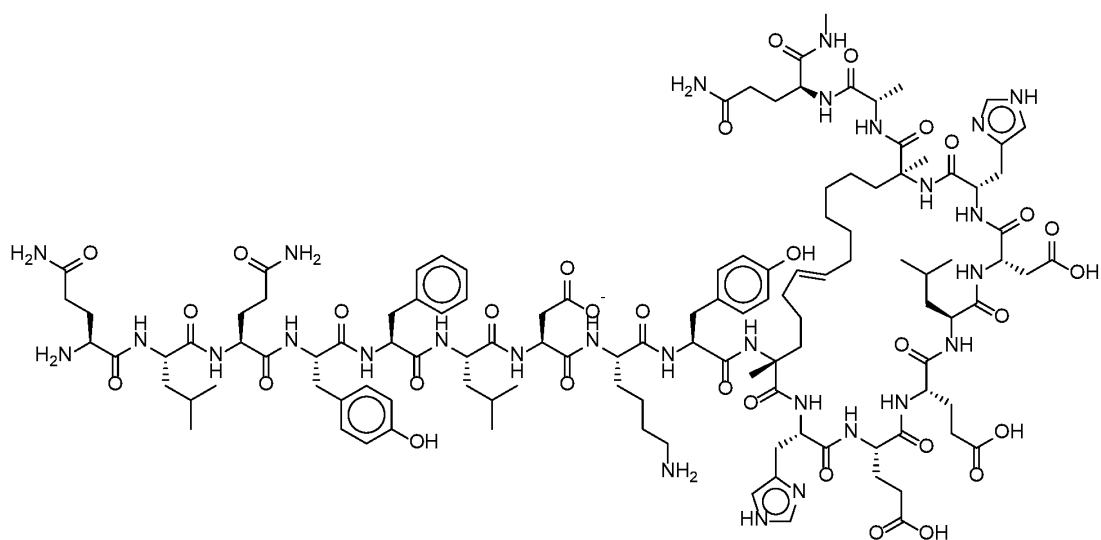
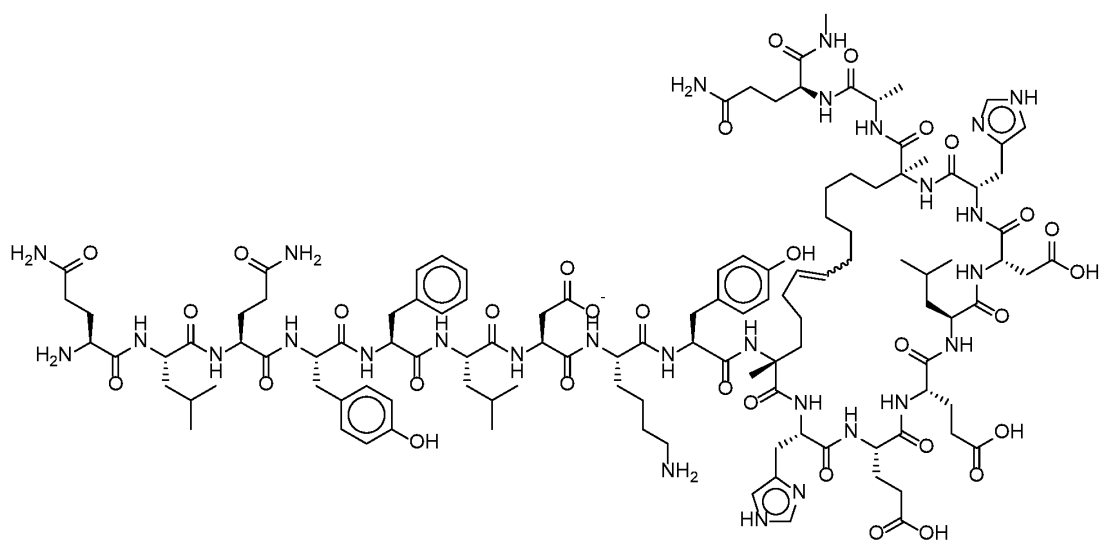


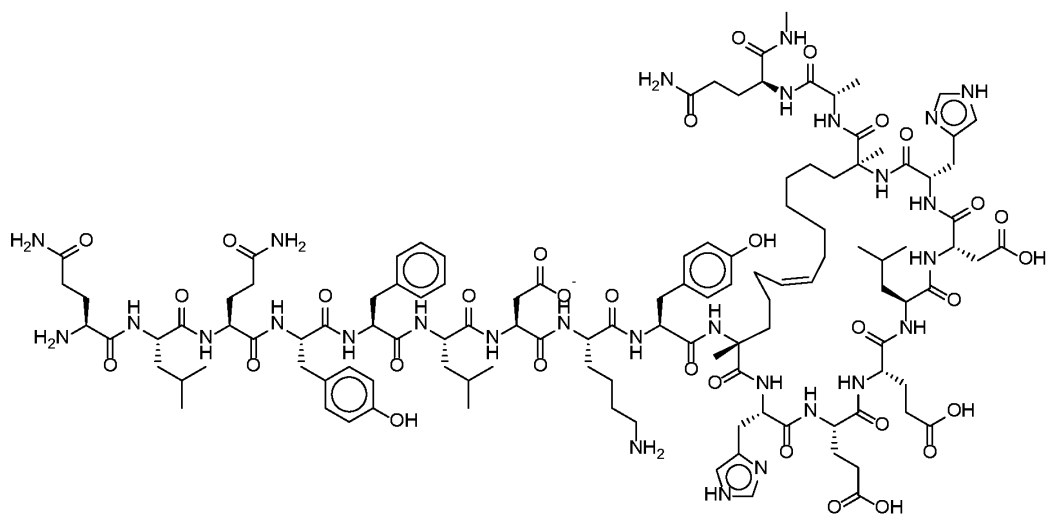


;

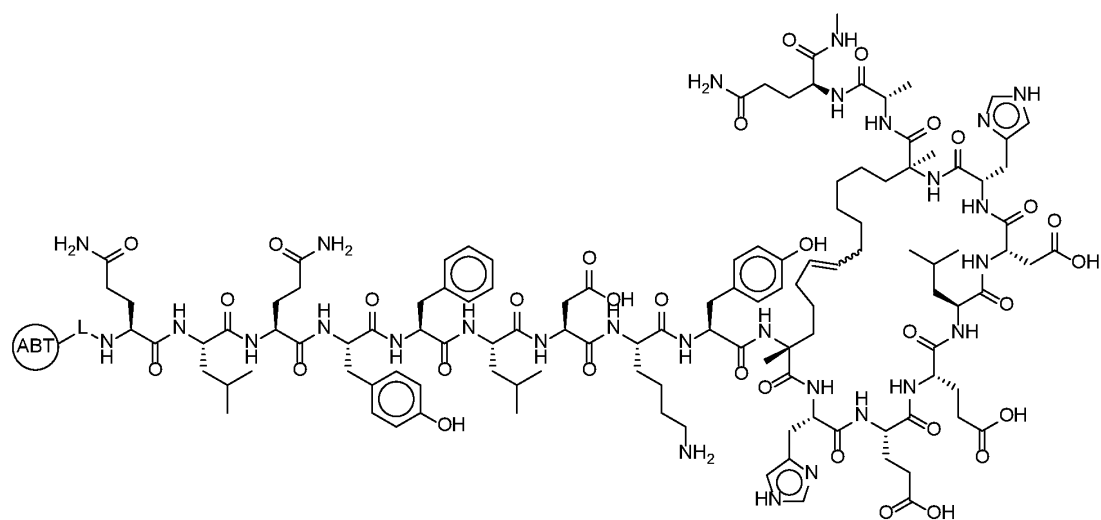


;

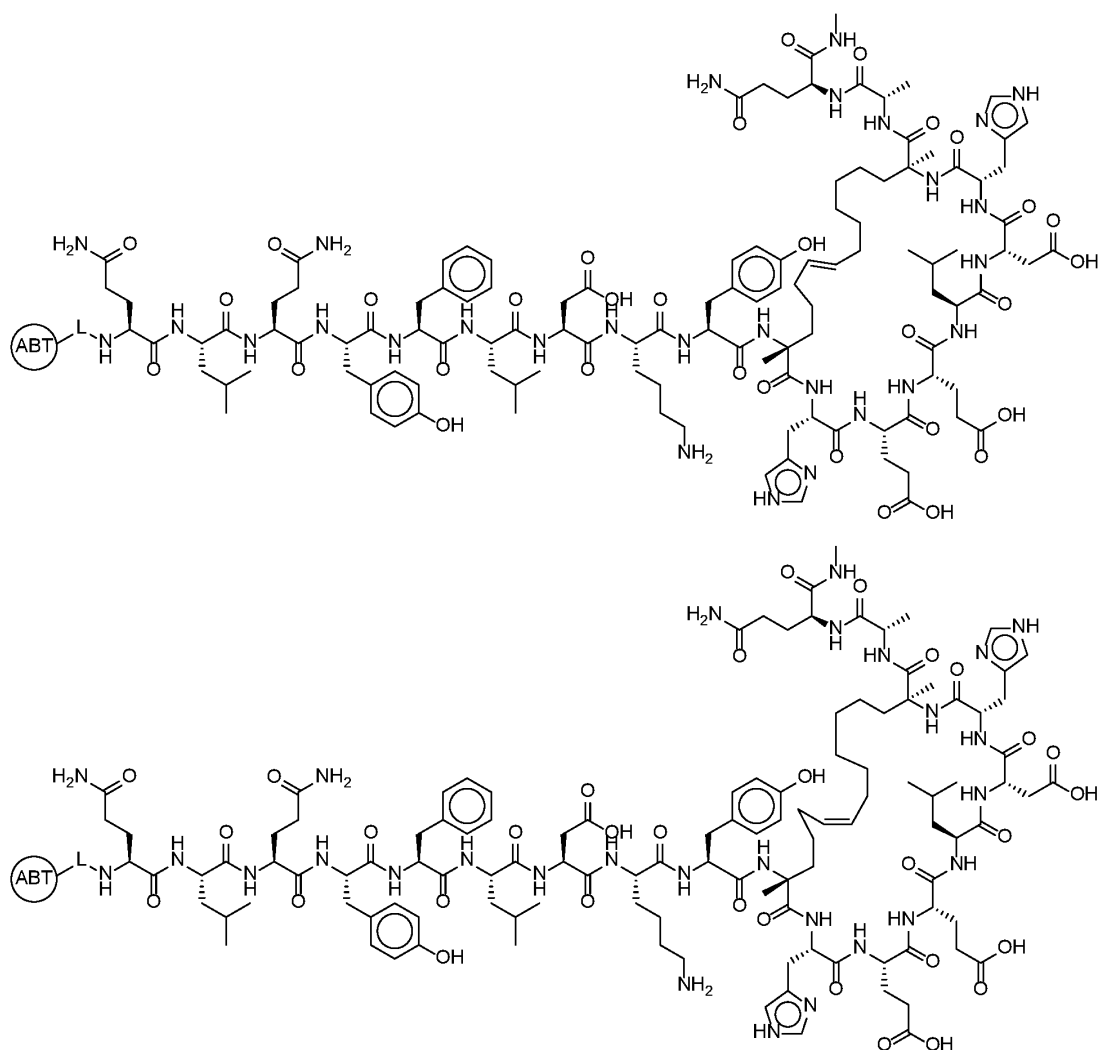




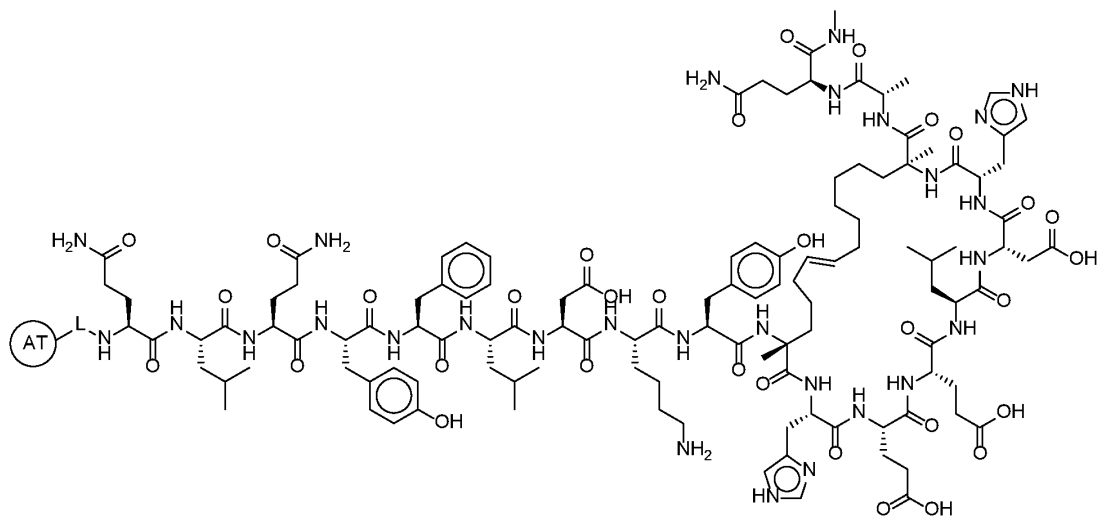
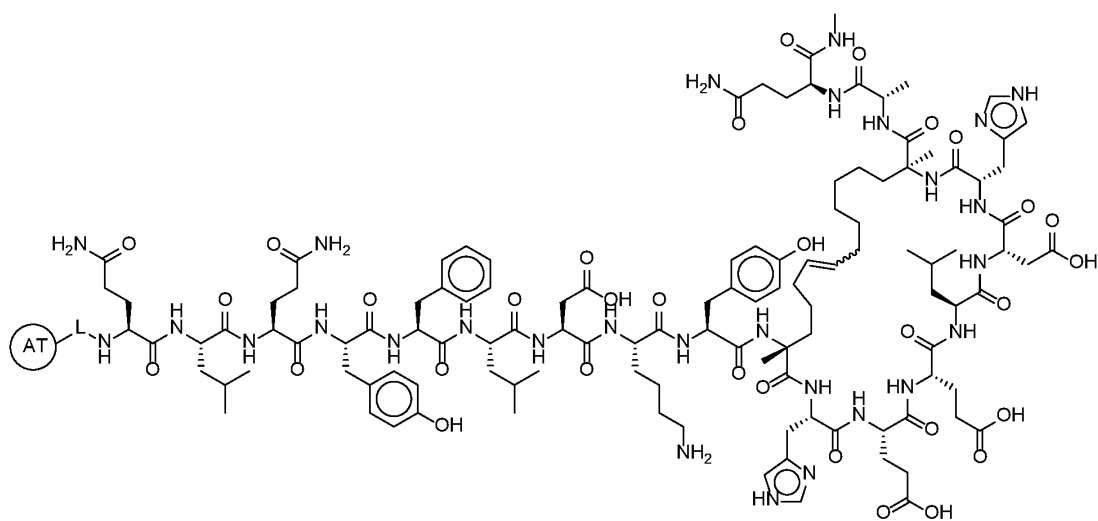
.

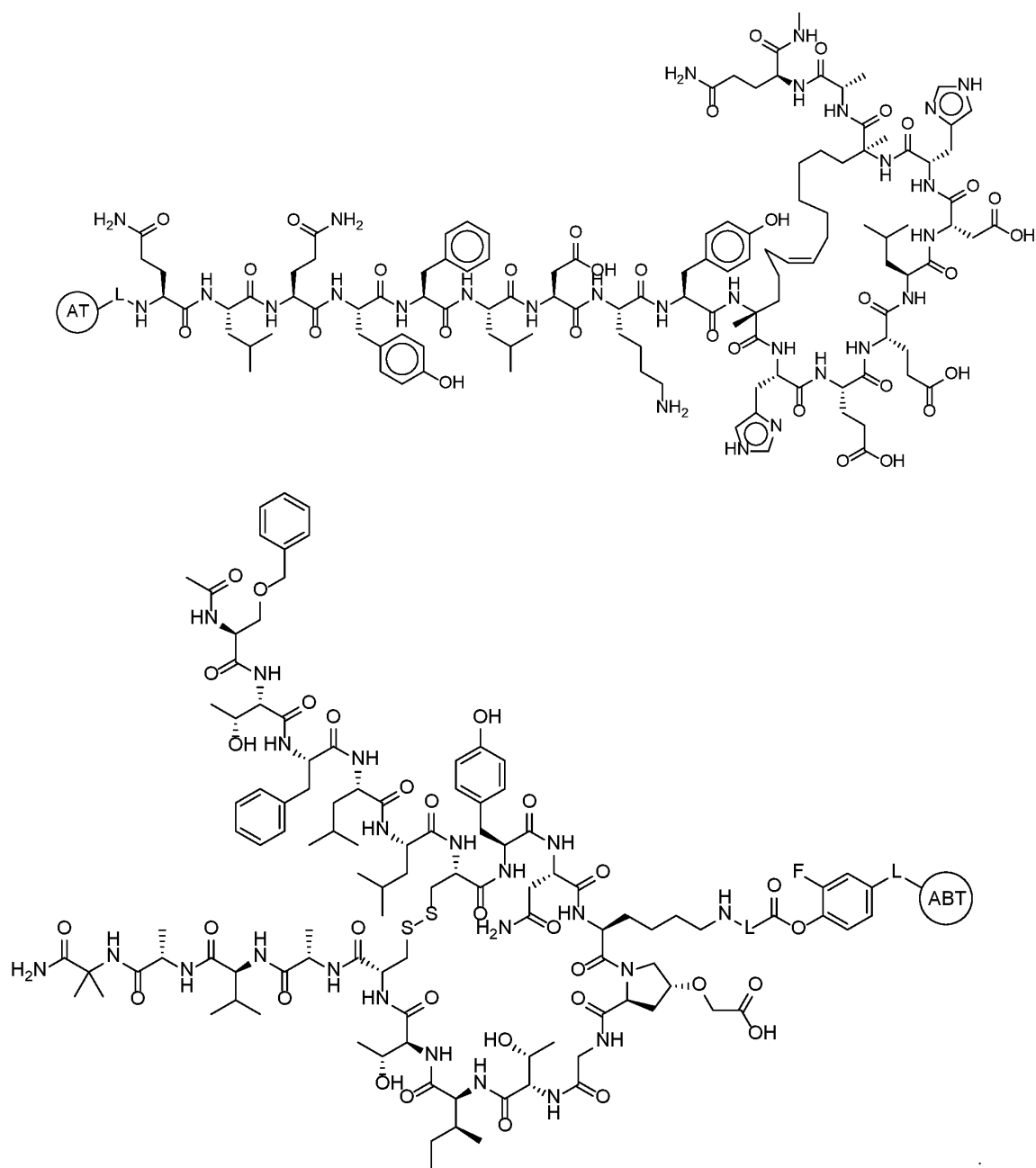


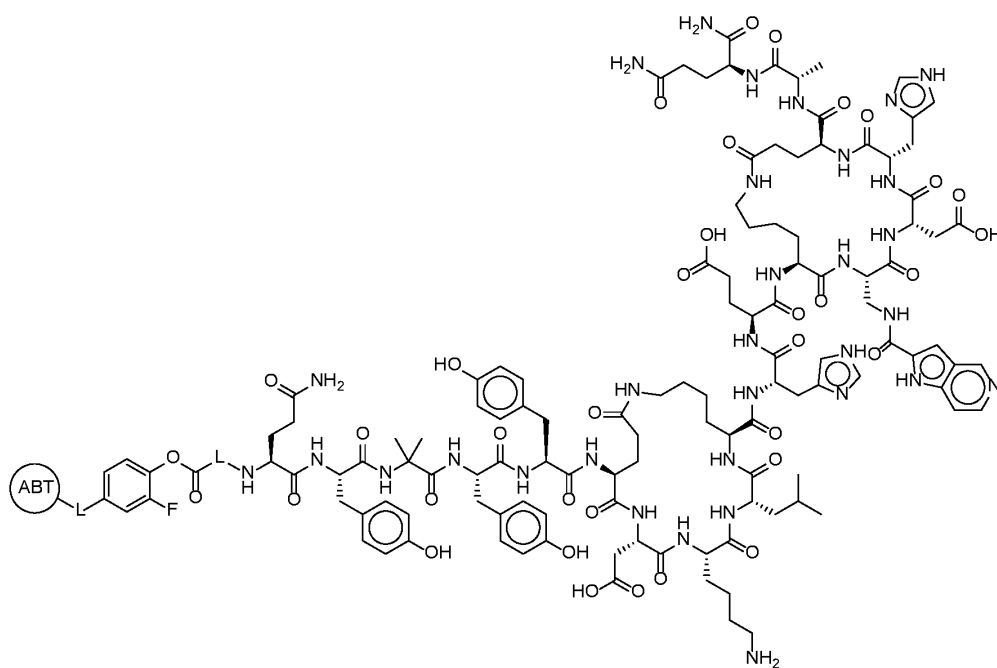
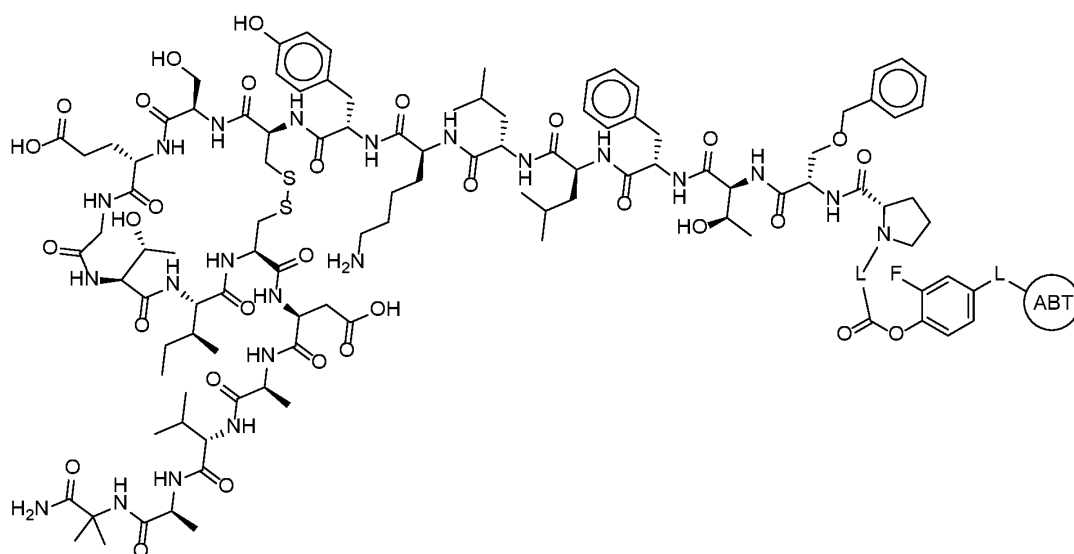
;



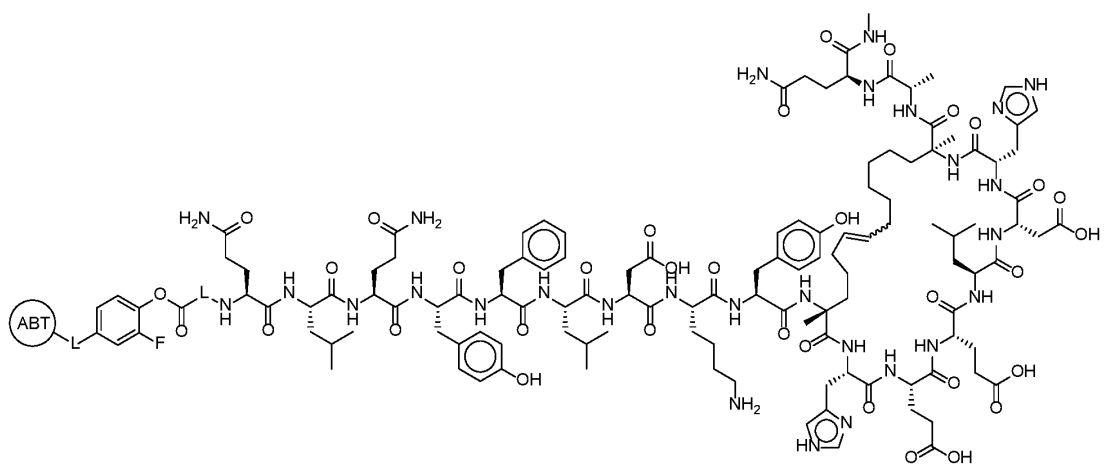
;





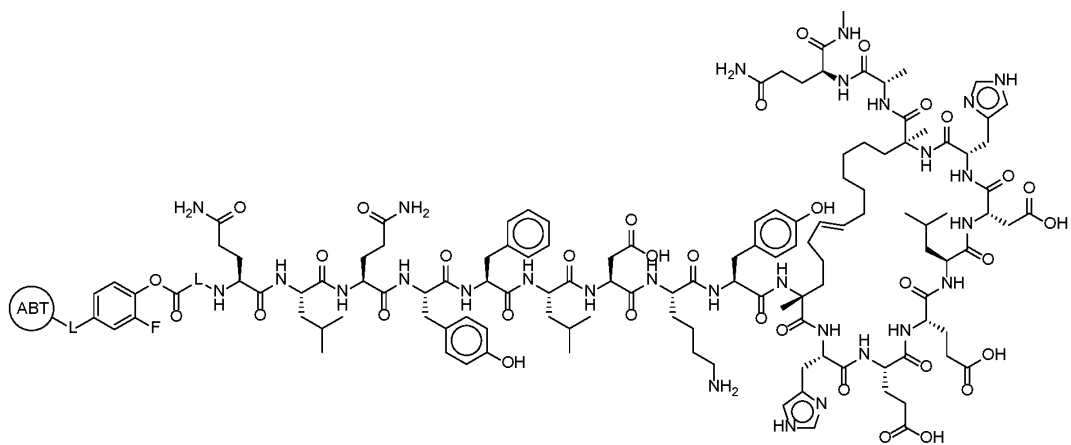


; or

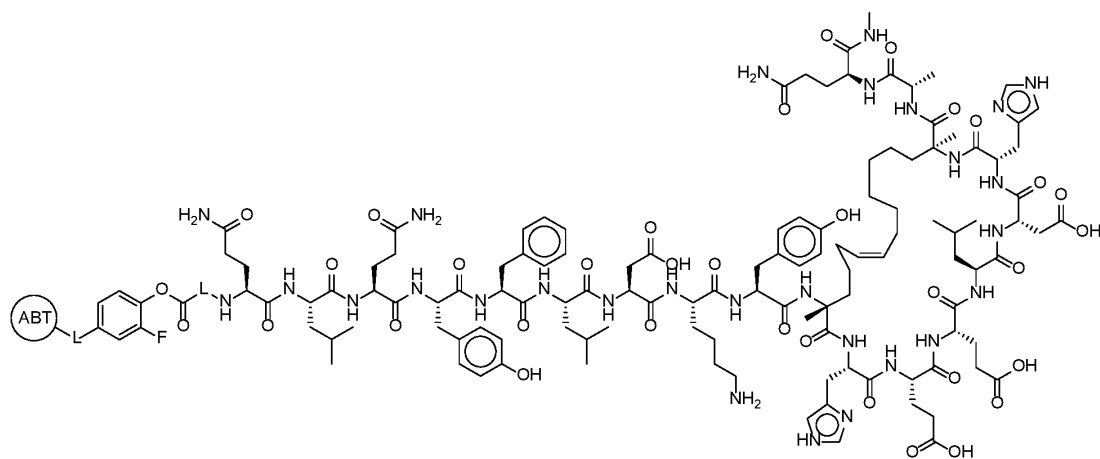


;

74. An agent, wherein the agent is



or



75. The agent of any one of claims 1-74, wherein the agent comprising an antibody moiety, which is or comprises an IgG or a fragment thereof.
76. A pharmaceutical composition, comprising an agent of a preceding claims or a pharmaceutically acceptable salt thereof, or a composition of a preceding claims, and a pharmaceutically acceptable carrier.
77. A method for preparing an agent of any one of the preceding claims which comprises an antibody moiety, comprising contacting an agent of any one of claims 41-42 or 47-72 or a salt thereof and with an antibody, wherein the antibody comprises IgG.
78. A method for treating a condition, disorder or disease associated with SARS-CoV-2 infection, comprising administering to a subject suffering therefrom an effective amount of an agent or a composition of any one of claims 1-74.
79. A method for inducing, promoting, encouraging, enhancing, triggering, or generating an immune response toward SARS-CoV-2, comprising administering to a subject infected thereby an effective amount of agent or a composition of any one of claims 1-51.
80. The method of claim 78, wherein the effective amount is an amount sufficient to
- (i) induce or generate ADCC or ADCP toward SARS-CoV-2;
 - (ii) induce or generate long-term immunity toward SARS-CoV-2; or
 - (iii) provide memory T and/or B cells against SARS-CoV-2 in the subject.
81. The method of any one of claim 78-79, comprising administering a population of immune cells.
82. The method of claim 81, wherein the population of immune cells comprises NK cells, selected from allogeneic NK cells, peripheral blood-derived NK cells, MG4101 NK cells, CB-NK NK cells, and cord blood-derived NK cells.