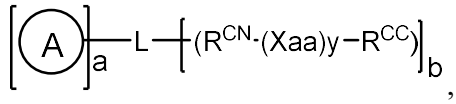
CLAIMS

1. An agent having the structure of:



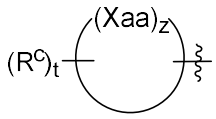
or a pharmaceutically acceptable salt thereof, wherein:

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

each of a and b is 1~~independently 1-200~~;

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

~~each~~ ABT is ~~independently~~ an antibody binding moiety that has the structure: R^c–(Xaa)z– or



, wherein t is an integer from 1 to 20, and z is an integer from 1 to 50;

~~each~~ AT is ~~independently~~ an antibody moiety that is immunoglobulin G (IgG), a derivative of IgG, pooled IgG, or intravenous immune globulin (IVIG);

~~each~~ PT is independently a partner moiety selected from a diagnostic agent or detectable 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 $-L^a-R'$;

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 aliphatic or heteroaliphatic 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, and a 3-20 membered heterocyclyl ring having 1-10 heteroatoms;

each R' is independently $-R$, $-C(O)R$, $-CO_2R$, or $-SO_2R$; and

each R is independently $-H$, 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 they are attached 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 an integer from 0 to 20~~0–20~~;

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

y1 is 0, 1, or 2~~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 an integer from 0 to 10~~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 an integer from 0 to 10~~0–10~~;

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

y6 is 0, 1, or 2~~0–2~~;

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

y7 is 0 or 1~~0–1~~;

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

y8 is an integer from 0 to 10~~0–10~~;

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

y10 is an integer from 0 to 10~~0–10~~;

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

y11 is 1, 2, 3, 4, or 5~~1–5~~;

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

y12 is an integer from 0 to 20~~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~~:

$$-N(R^{a1})-L^{a1}-C(R^{a2})(R^{a3})-L^{a2}-CO- \text{ (A-I)},$$

~~or a salt thereof,~~ wherein:

each of R^{a1}, R^{a2}, and 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 aliphatic or heteroaliphatic 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 $-SO_2R$; and

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

y0 is 0, y1 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;

−Xaa^{T2}− is or comprises 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)$_2$−;

y3 is 1-10;

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 −CH_2−CH_2−, −O−, −S− or −S−S−;

−(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;

y5 is 0 and −(Xaa^{T6})y6− is or comprises a D-Ser;

y6 is 1 or 2;

y7 is 1 and comprises -COOH or y7 is 0;

−(Xaa^{T8})y8− is or comprises GTI or −G−Xaa^{T8}−IT−Xaa^{T8}−, wherein each Xaa^{T8} is independently an alpha amino acid;

y10 is 3 or 4;

−(Xaa^{T11})y11− is or comprises L-Ala, D-Ala, Aib, Gly, or negatively charged; or

a combination thereof.

4. The agent of any one of claims 1 to 3, wherein

y1 is 0;

−(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;

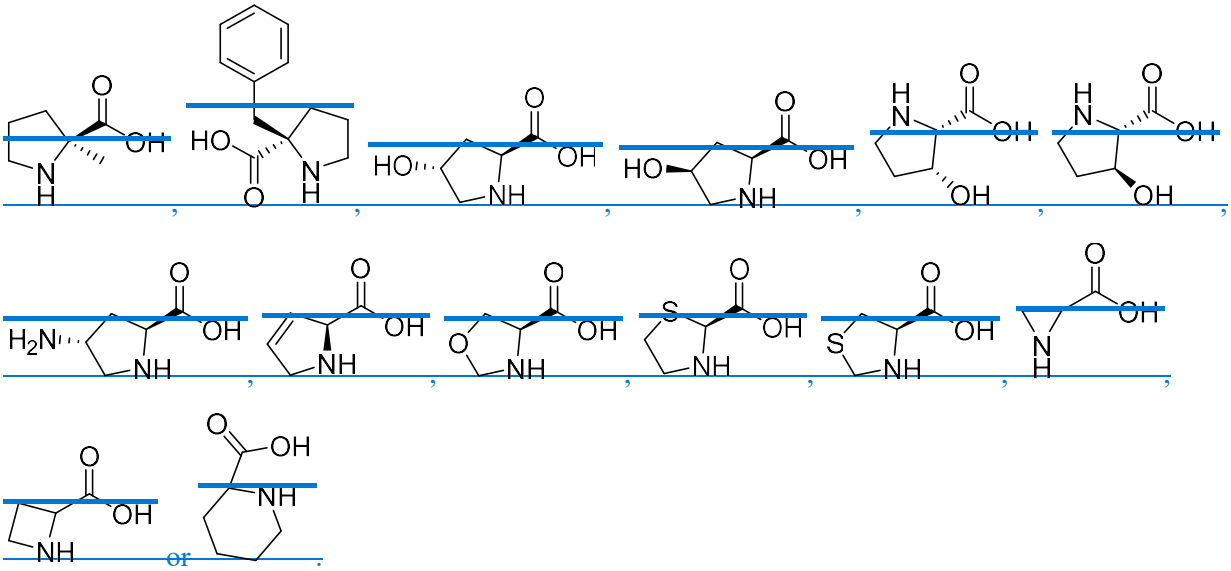
−(Xaa^{T1})y1− is or comprises an amino acid having the structure of formula A-I, wherein R^{a1} and R^{a2} are taken together with their intervening atoms to form an optionally substituted, saturated or partially unsaturated, 3-6 membered, monocyclic or bicyclic ring having, in addition to the intervening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

−(Xaa^{T1})y1− is or comprises a L-proline.

~~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~~



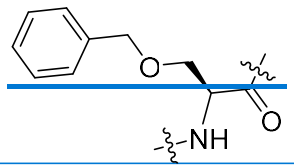
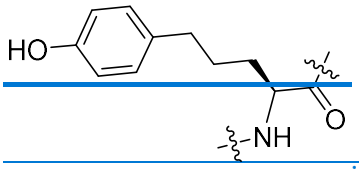
~~8. The agent of any one of claims 1 to 3, wherein y1 is 0.~~

~~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.~~5. The agent of claim ~~3-9~~, wherein L^{a} −Xaa^{T2}− is −CH$_2$−CH$_2$−CH$_2$−~~,~~ or −CH$_2$−O−CH$_2$−, or

−CH_2−S−CH_2−, R’ is optionally substituted phenyl, or a combination thereof.

~~11. The agent of claim 9 or 10, wherein R’ is optionally substituted phenyl.~~

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

~~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 TFLL; or~~

~~y3 is 6 and =(Xaa^{T3})y3= is or comprises TFLLKY.~~

~~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 =CH_2=CH_2=, =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 y6 is 1 or 2.~~

~~20.~~6. 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;

−(Xaa^{T6})y6− is or comprises L-proline, D-proline, a proline derivative, L-serine, D-serine, glycine, L-pseudoproline, or D-psuedoproline;

−(Xaa^{T6})y6− is or comprises an amino acid that comprises or is further substituted with −L^{a}−COOH; or

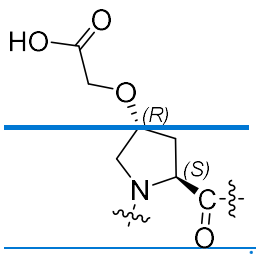
a combination thereof.

~~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-psuedoproline.~~

~~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 y7 is 1 and comprises −COOH or y7 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}−.~~

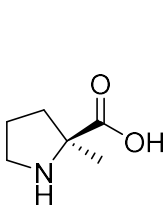
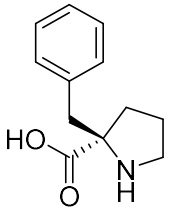
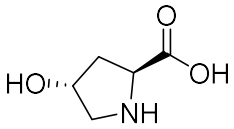
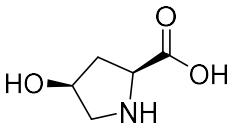
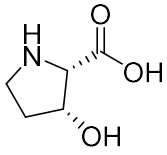
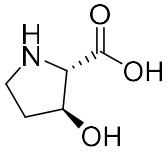
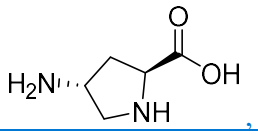
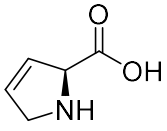
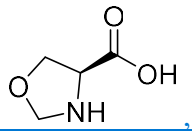
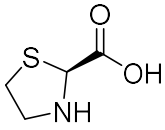
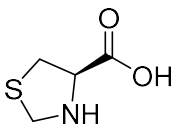
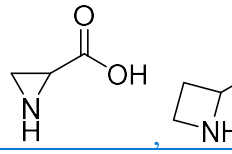
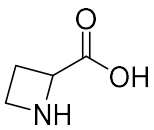
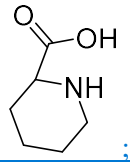
~~29. The agent of any one of the preceding claims, wherein Xaa^{T4} and Xaa^{T9} are independently Cys and form a disulfide bond −S−S−.~~

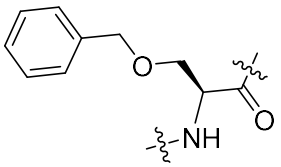
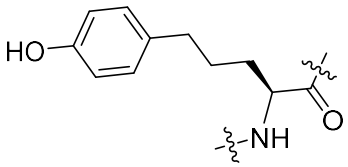
~~30. The agent of any one of the preceding claims, wherein −(Xaa^{T10})y10− is or comprises AV.~~

~~31. The agent of any one of the preceding claims, wherein y10 is 3 or 4.~~

~~32. The agent of claim 31, wherein −(Xaa^{T2})y2− is or comprises AVAD.~~

7. The agent of the preceding claims, wherein

−(Xaa^{T1})y1− is or comprises , , , , , , , , , , , , , ;

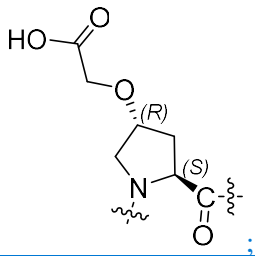
−Xaa^{T2}− is  or ;

−(Xaa^{T2})y2− is or comprises AVAD;

−(Xaa^{T3})y3− is or comprises TF, TFLL, or TFLLKY;

Xaa^{T4} is Cys;

−(Xaa^{T6})y6− is or comprises a D-Ser,



−(Xaa^{T6})y6− is or comprises has the structure ;

Xaa^{T7} is D or E;

−(Xaa^{T8})y8− is or comprises GTI−Xaa^{T8}−;

Xaa^{T4} and Xaa^{T9} are independently Cys and form a disulfide bond −S−S−;

−(Xaa^{T10})y10− is or comprises AV; or

a combination thereof.

~~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.~~8. The agent of claim 1 or 2, wherein

−(Xaa)y− is or comprises IEEQAKTFLDKFNHEAEDLFYQS;

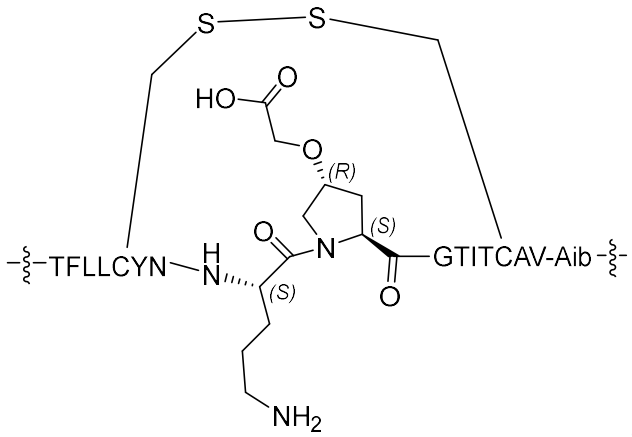
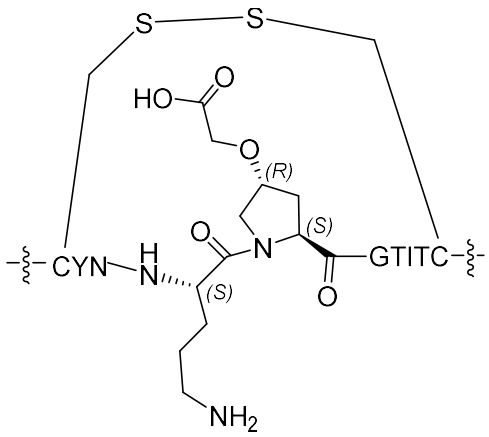
−(Xaa)y− is or comprises DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL, or a fragment thereof;

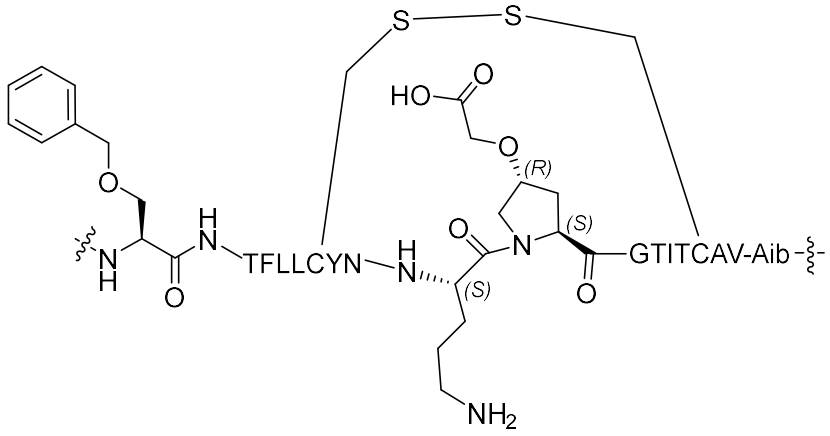
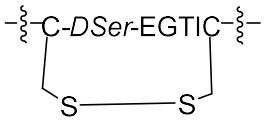
−(Xaa)y− is or comprises a sequence selected from, or a sequence designed based on a sequence selected from:

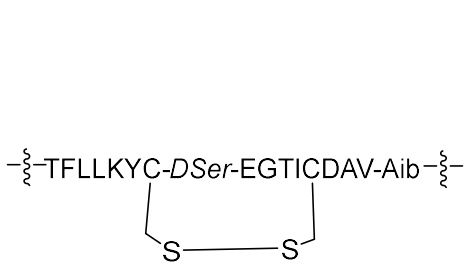
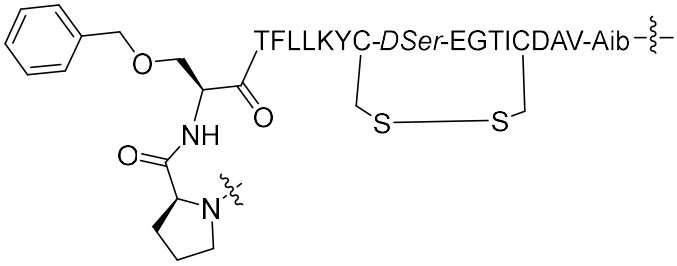
Number	Sequence
P1	FKLPLGI*N*(K)ITNFRAILTAF*S*(L)
P2	PT*T*(K)FMLKYDENGTITDAVDC
P3	VLYNST*F*(S)FSTFKCYGVSATK
P4	PALNCYWPL*N*(K)DYGFYTTSGI
P5	RDVSD*F*(I)TDSVRDPKTSEILD
P6	YQDVNCTDV*S*(P)TAIHADQLTP
P7	SNNTIAIPTNF*S*(L)ISITTEVM
P8	QYGSFC*T*(A)QLNRALSGIA*A*(V)EQ
P9	GIGV*T*(A)QNVLYENQKQIANQF
P10	IQ*K*(E)EIDRLNEVAKNLNESLI

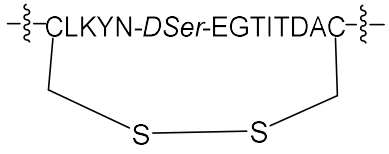
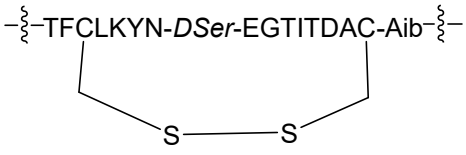
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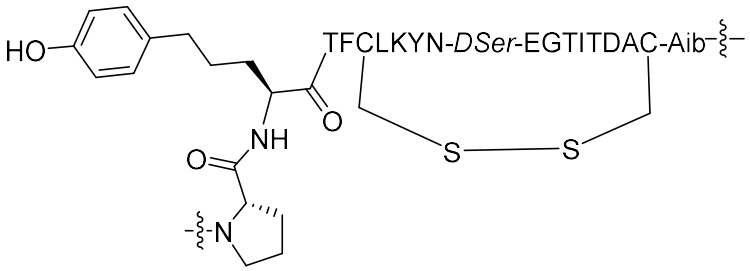
−(Xaa)y− is or comprises


S
S
HO
O
O
(R)
(S)
N
O
O
H
N
(S)
TFLLCYN
GTITCAV-Aib
NH2
,

S
S
HO
O
O
(R)
(S)
N
O
O
H
N
(S)
CYN
GTITC
NH2
,


S
S
HO
O
O
(R)
O
(S)
N
O
O
H
N
H
N
O
H
N
TFLLCYN
(S)
GTITCAV-Aib
NH2
,

C-DSer-EGTIC
S
S
,

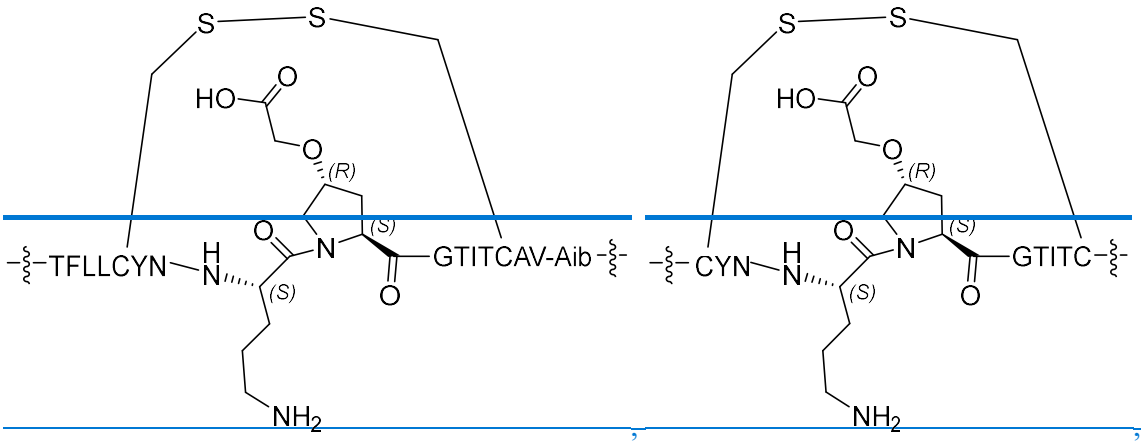

TFLLKYC-DSer-EGTICDAV-Aib
S
S
,

O
TFLLKYC-DSer-EGTICDAV-Aib
S
S
NH
O
N
,.


CLKYN-DSer-EGTITDAC
S
S
,

TFCLKYN-DSer-EGTITDAC-Aib
S
S
, or


HO
TFCLKYN-DSer-EGTITDAC-Aib
O
NH
O
S
S
N
.

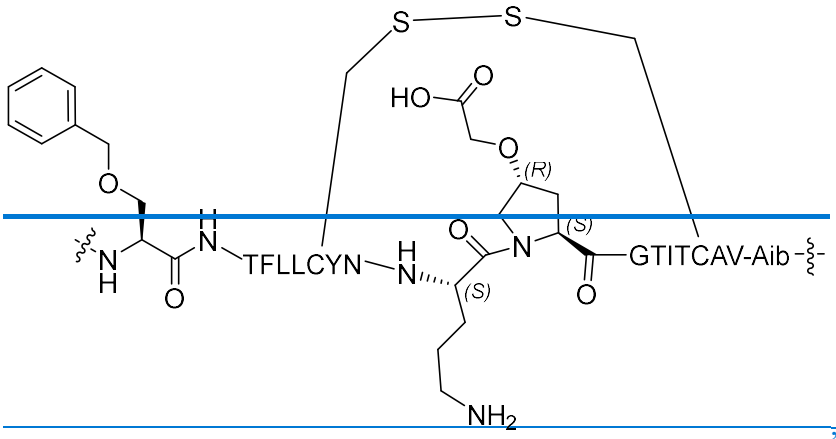
~~35. The agent of claim 1 or 2, wherein –(Xaa)y– is or comprises IEEQAKTFLDKFNHEAEDLFYQS.~~

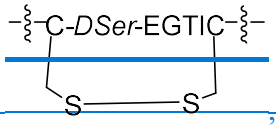
~~36. The agent of any one of claims 1-2, wherein –(Xaa)y– is or comprises~~



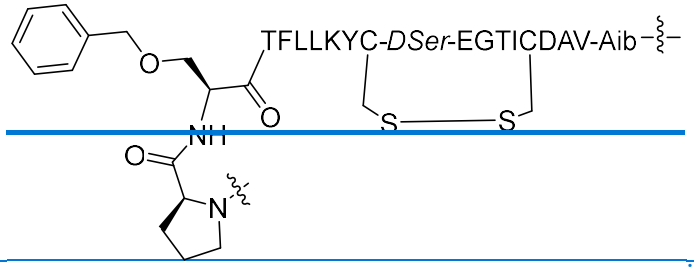
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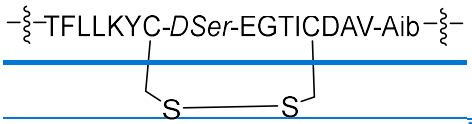
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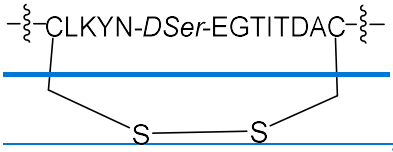
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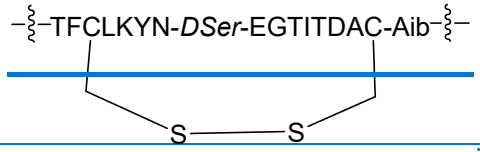


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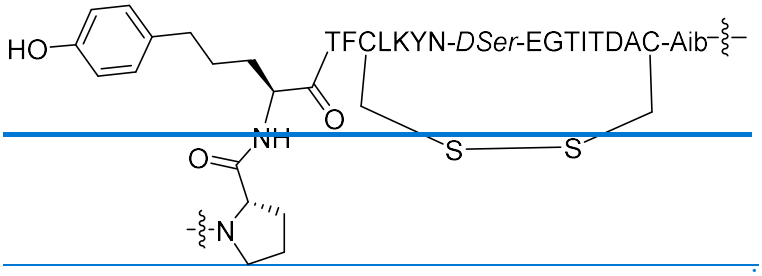
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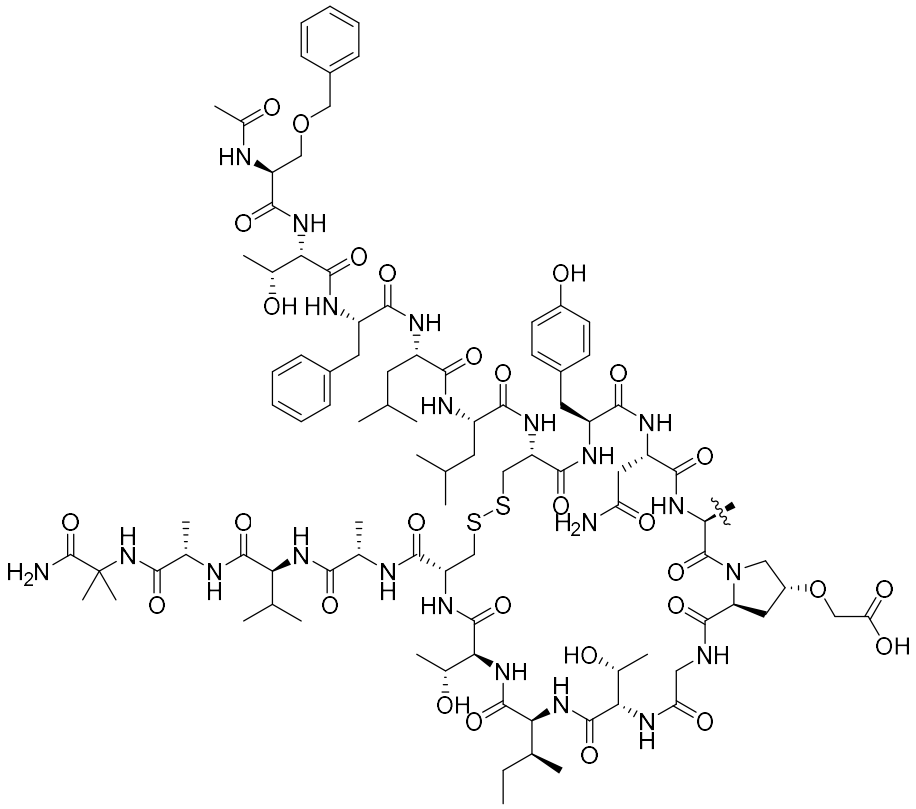
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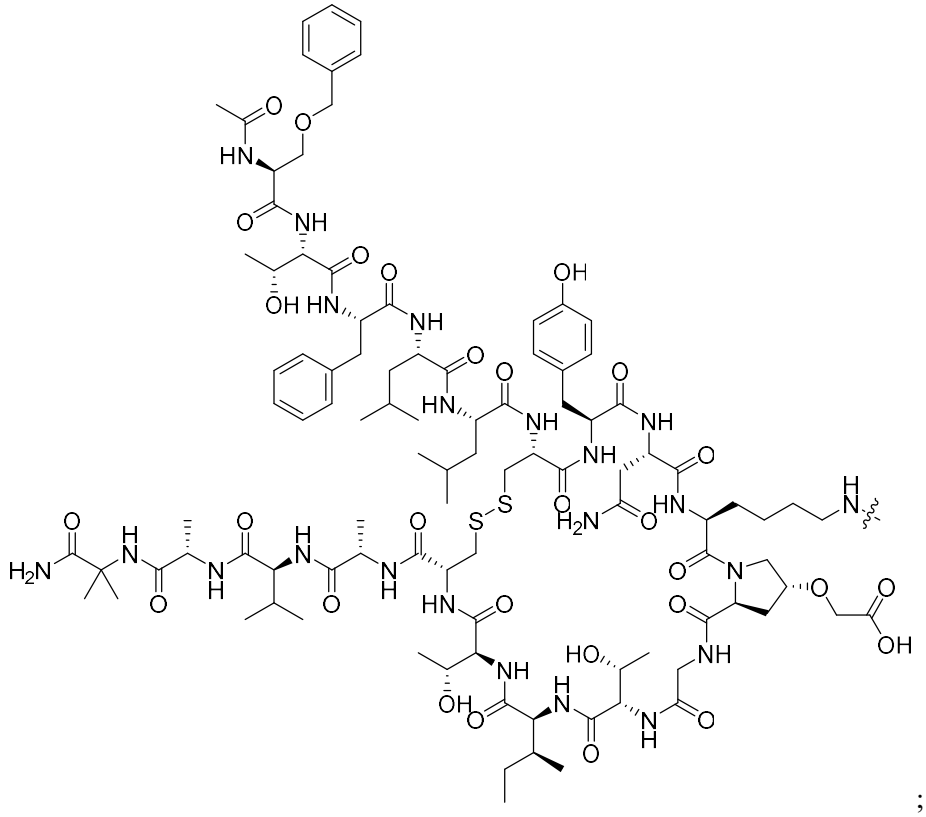
. ~~or~~



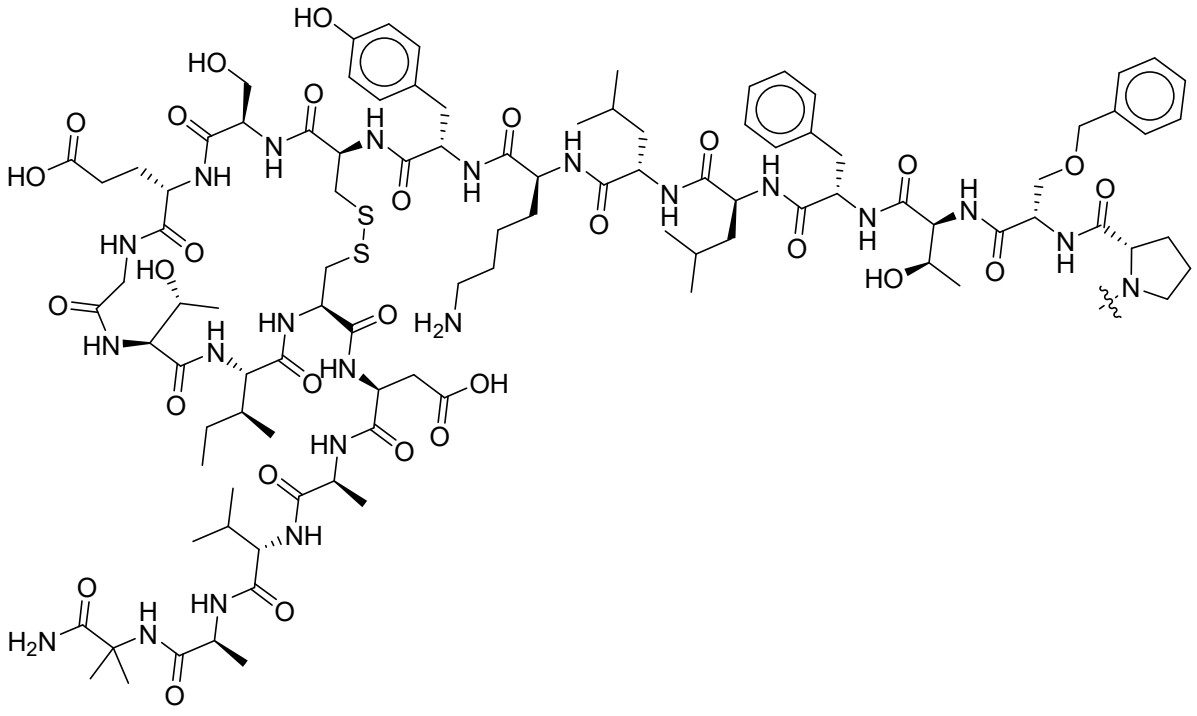
~~37.~~9. The agent of claim 1 or 2 ~~any one of claims 1-2~~, wherein –(Xaa)y–R^{CC} is or comprises



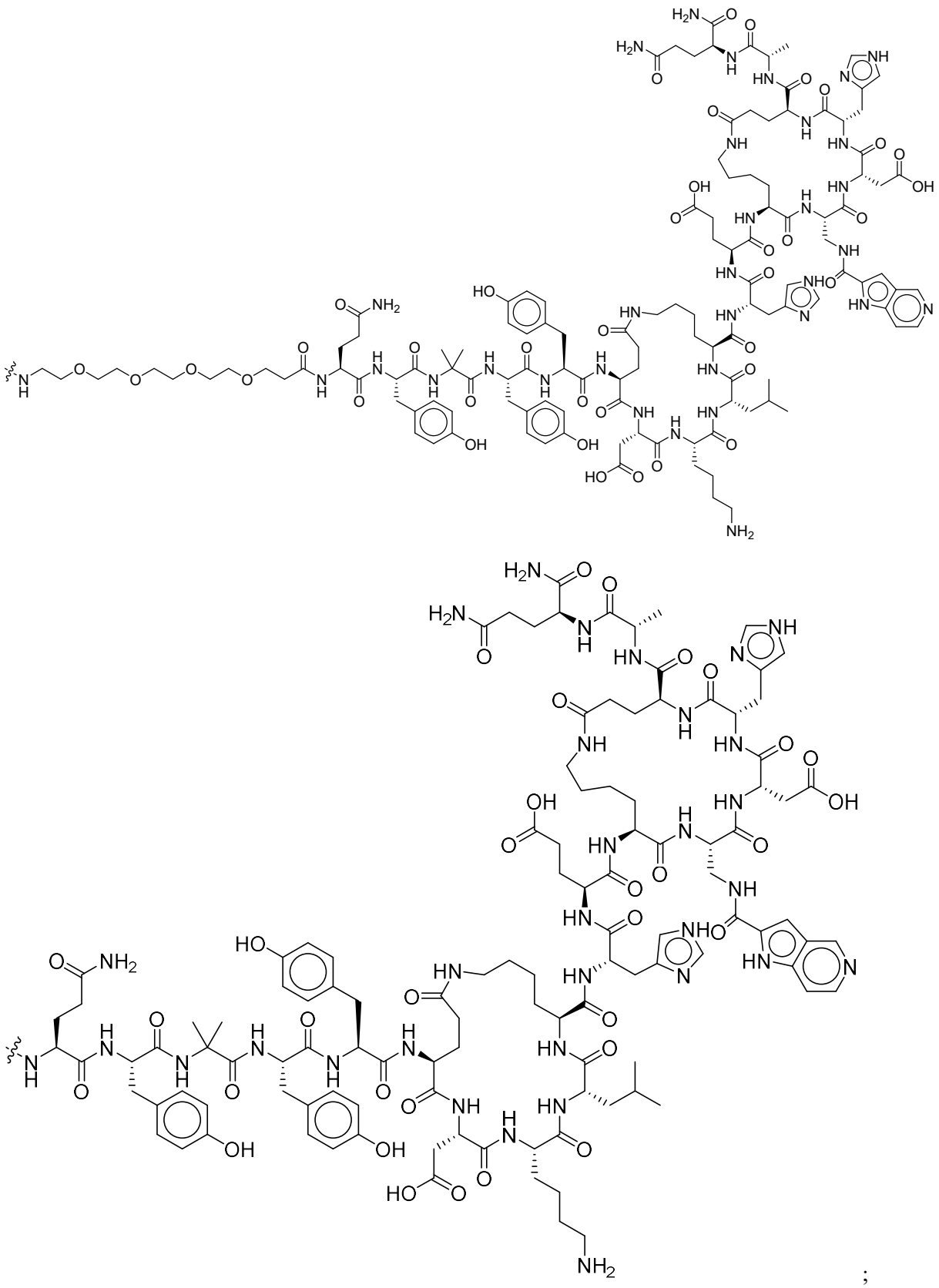
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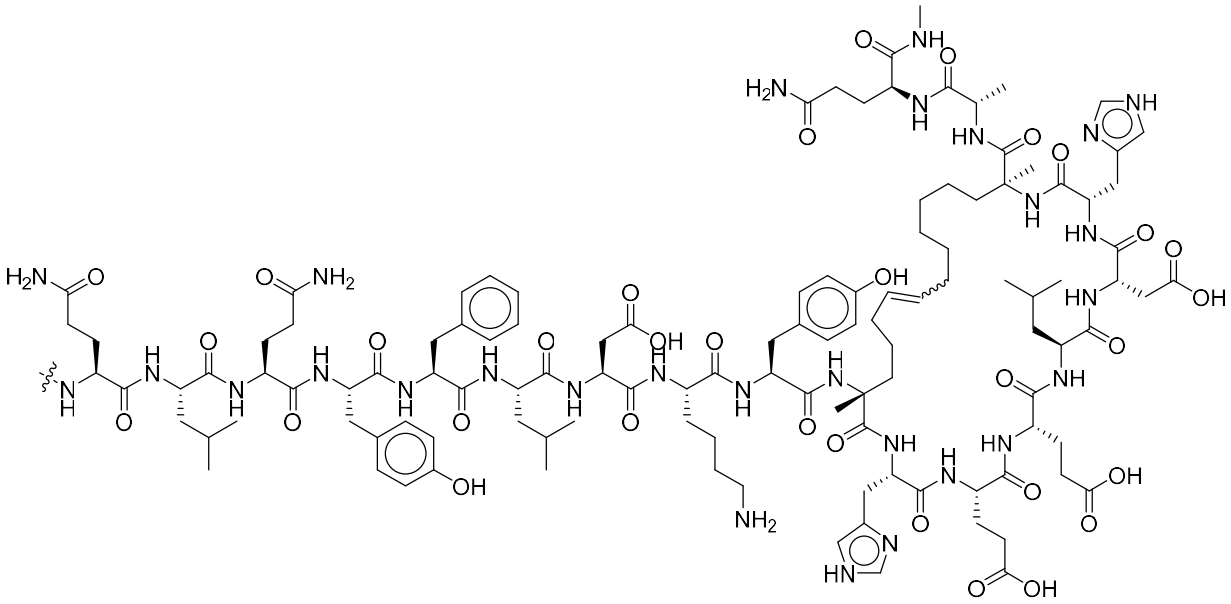
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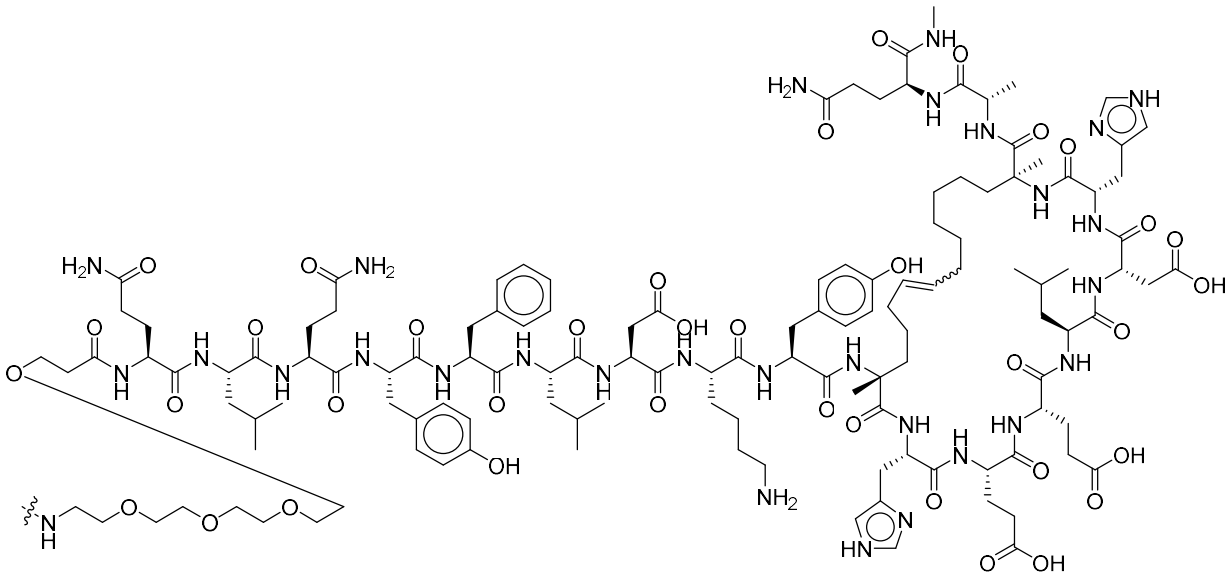


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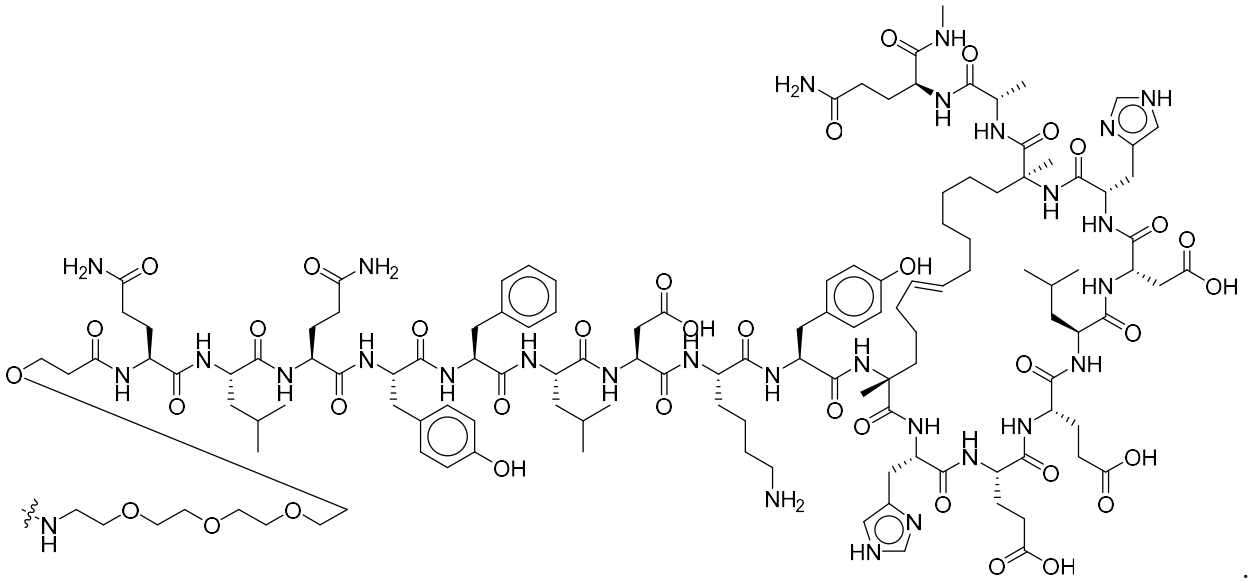


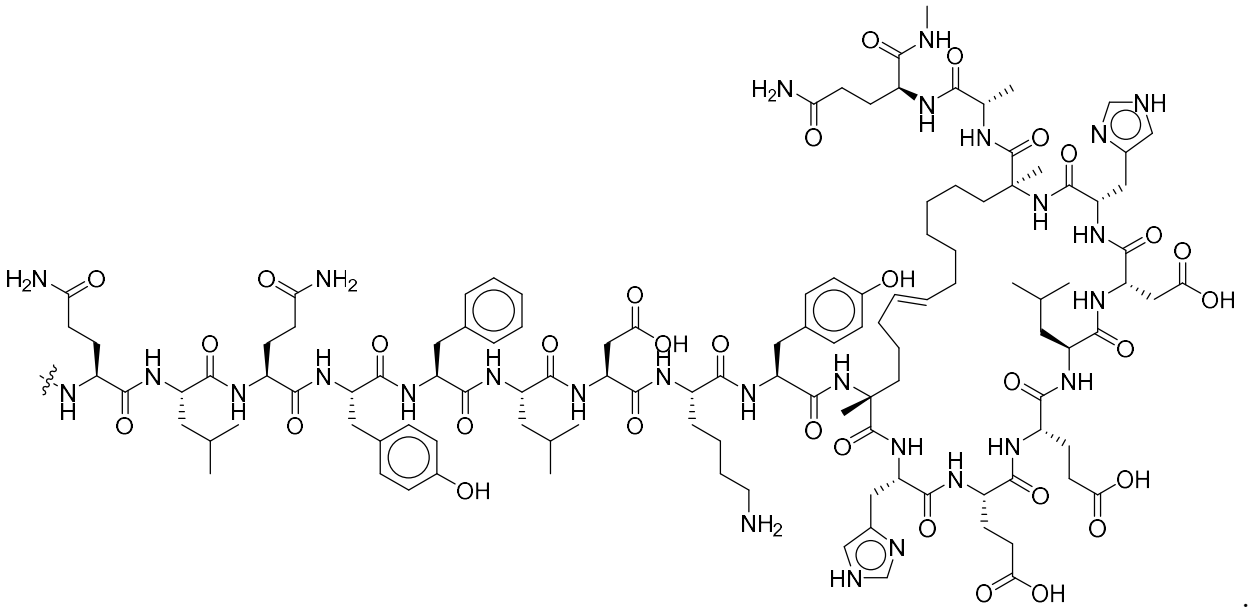
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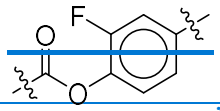
~~38. The agent of claim 1 or 2 where −(Xaa)y− is or comprisessequence designed based on, DISGINASVVNIQKEIDRLNEVAKNLNESLIDLQEL, or a fragment thereof.~~

~~39. The agent of any one of the preceding claims, comprising a linker.~~

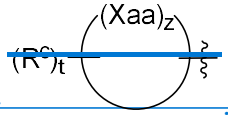
~~40.~~10. The agent of any one of the preceding claims~~claim 39~~, wherein the linker moiety comprises one or more −[$(CH_2)_2$−O]m− groups, ~~and~~ wherein m is an integer from 7 to 12~~7 – 12~~.

~~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.~~11. The agent of any one of the preceding claims, ~~comprising one and only one~~wherein the agent comprising a single A that is an antibody binding moiety.

~~44. The agent of any one of the preceding claims, wherein the antibody binding moiety has the structure of is R^e–(Xaa)z– or~~  ~~, or a salt form thereof.~~

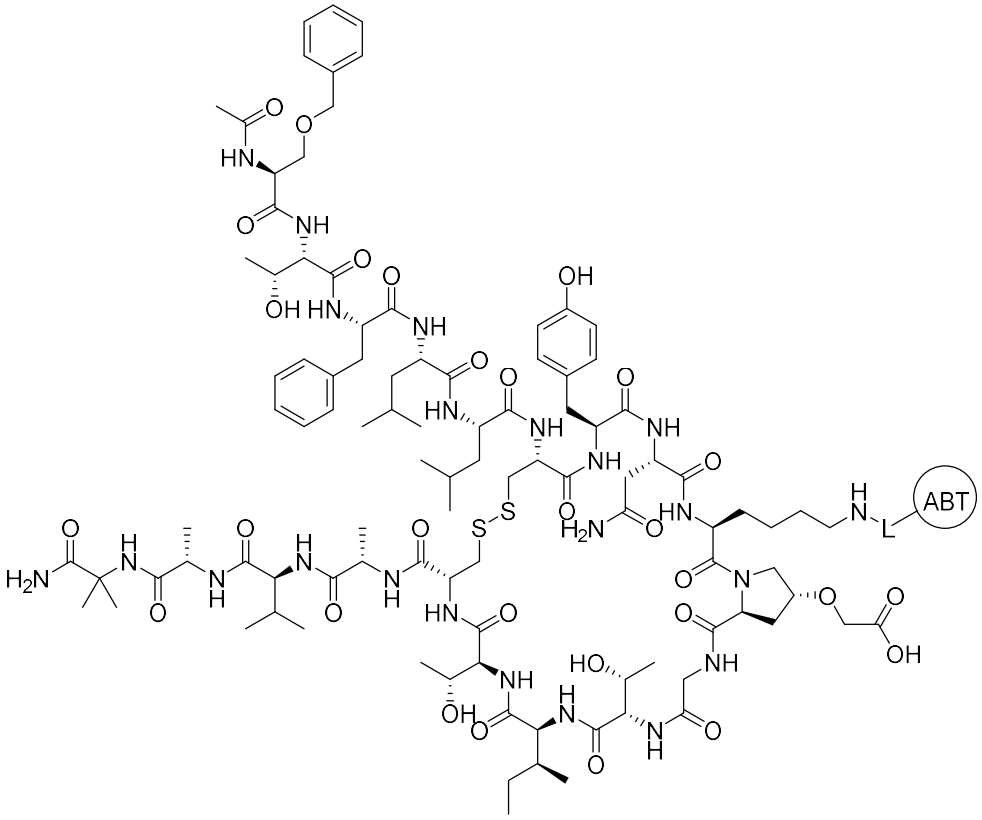
~~45.~~12. The agent of any one of the preceding claims, wherein

the antibody binding moiety comprises or has the structure selected from A-1 to A-50~~, or a salt form thereof~~; or

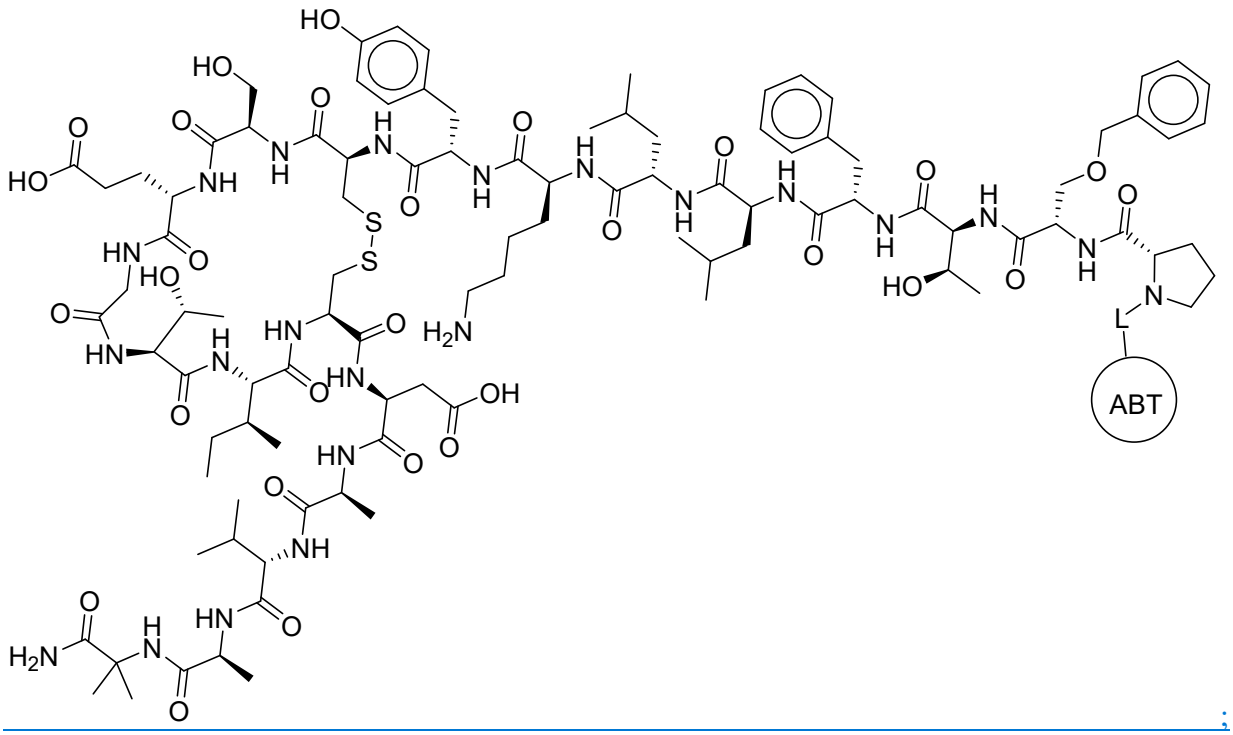
the antibody binding moiety comprises or has the amino acid sequence DCAWHLGELVWCT, wherein the two cystein amino acids are linked by a –S–S–.

~~46. 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–.~~

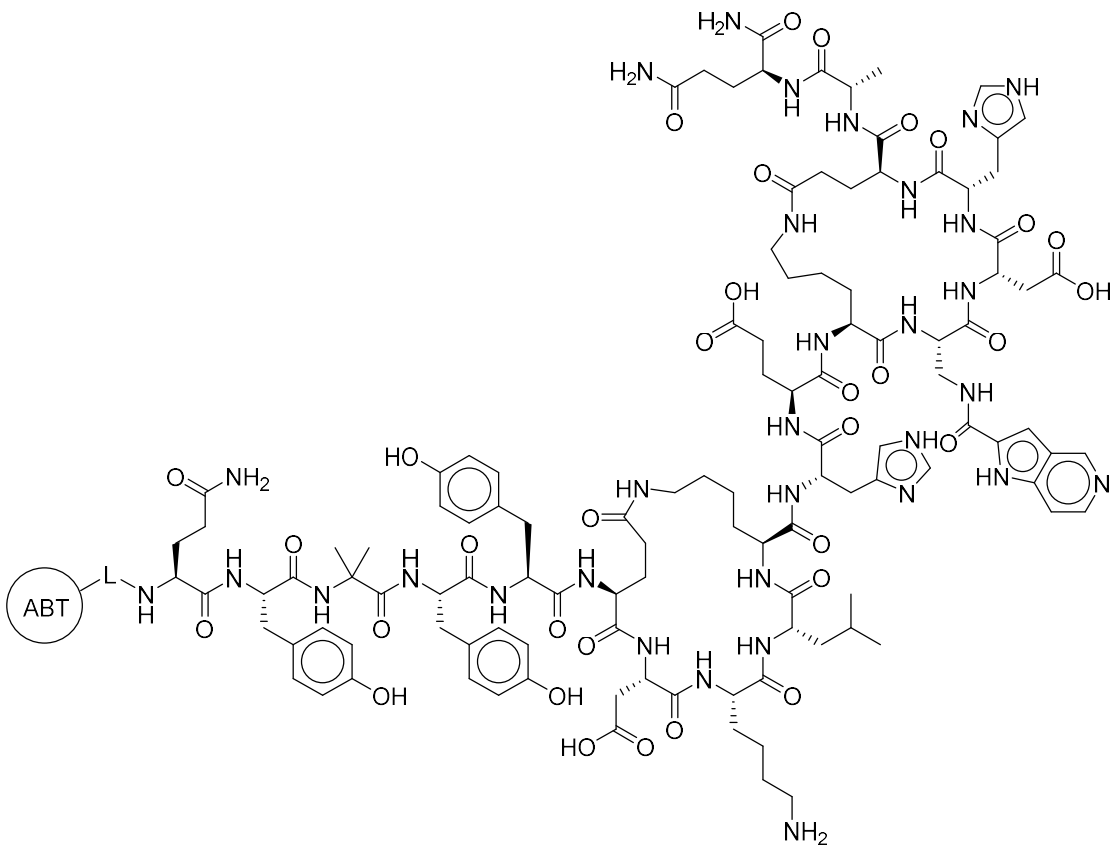
13. The agent of claim 1, 2, or 12, wherein the agent has the structure:


ABT

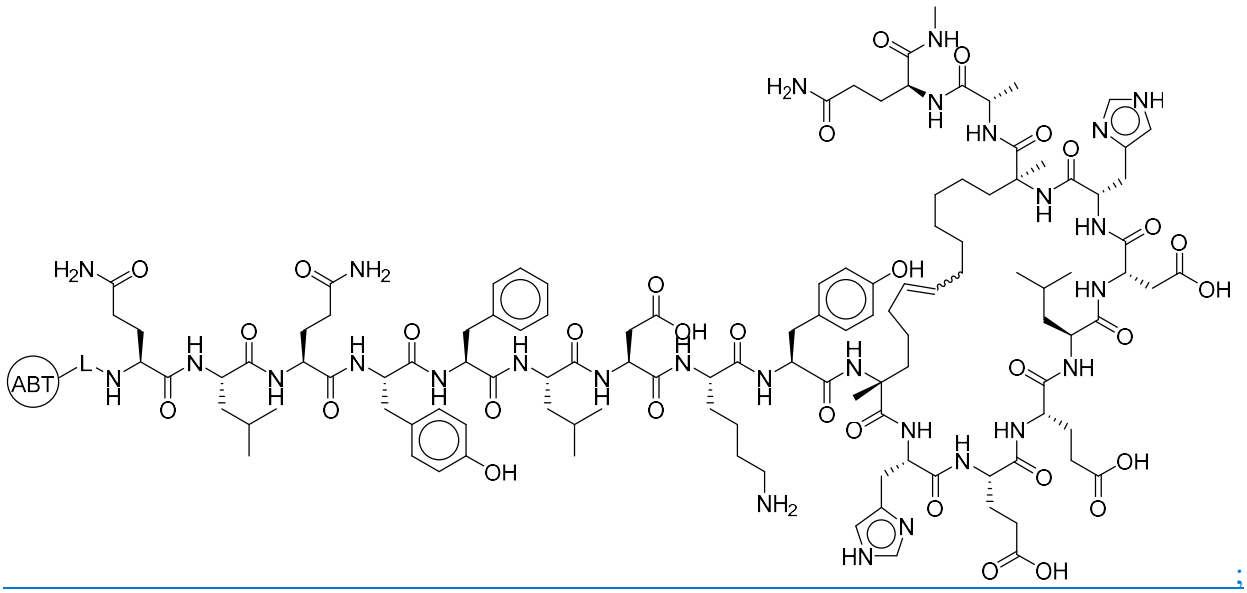
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ABT

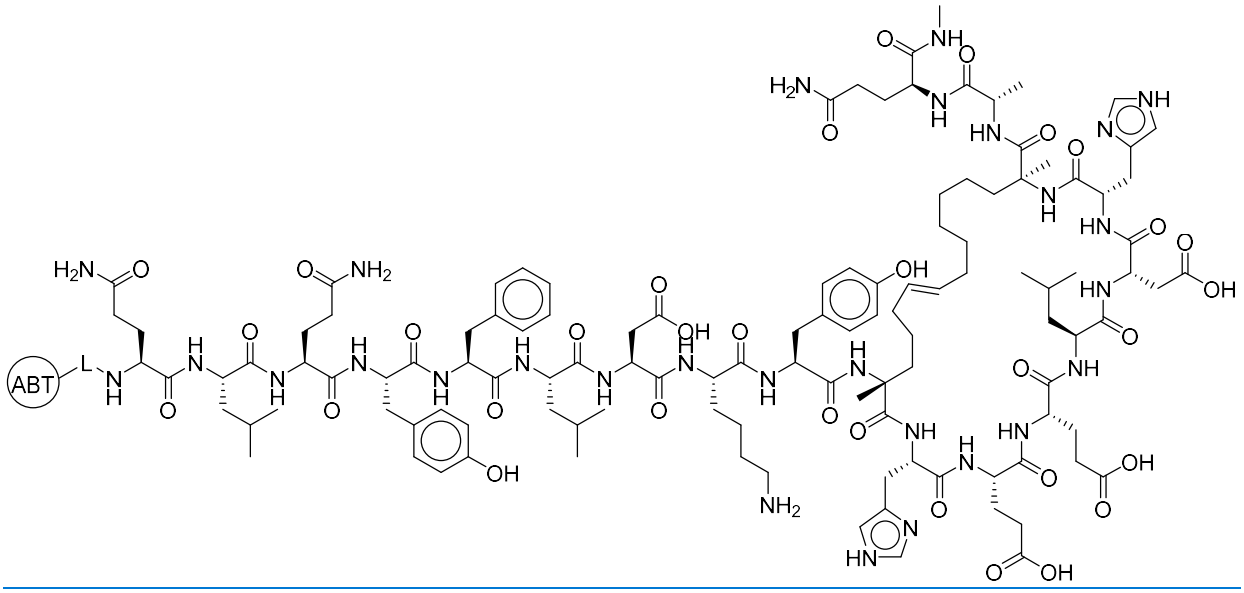
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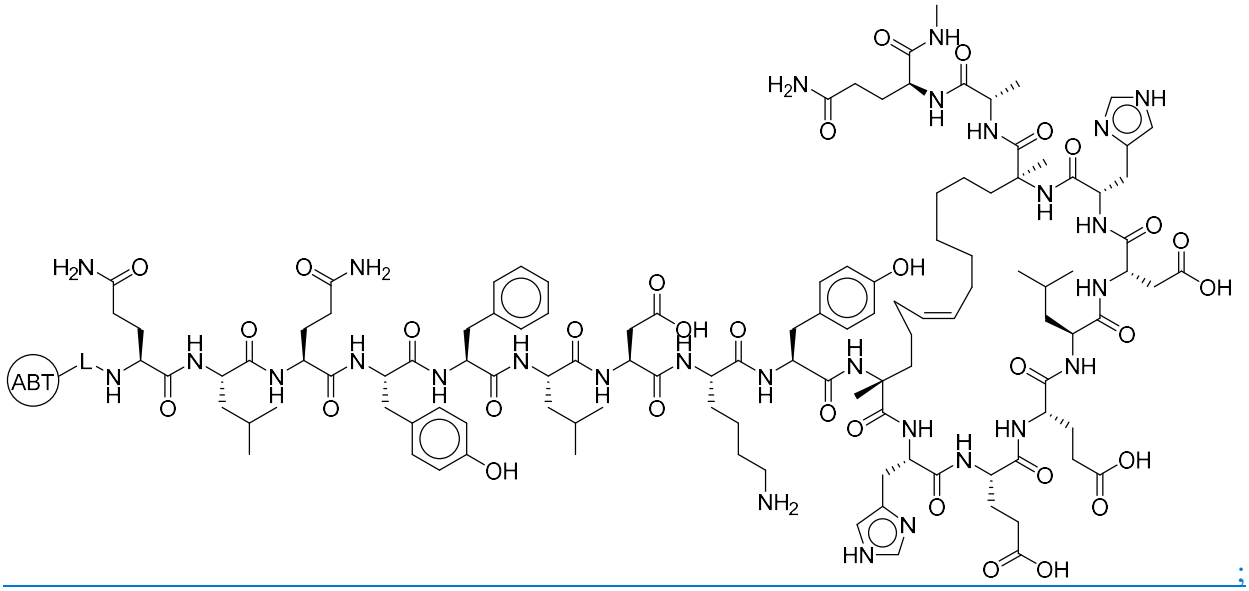

ABT
L
NH2
OH
HO
NH
HN
O
N
H

;

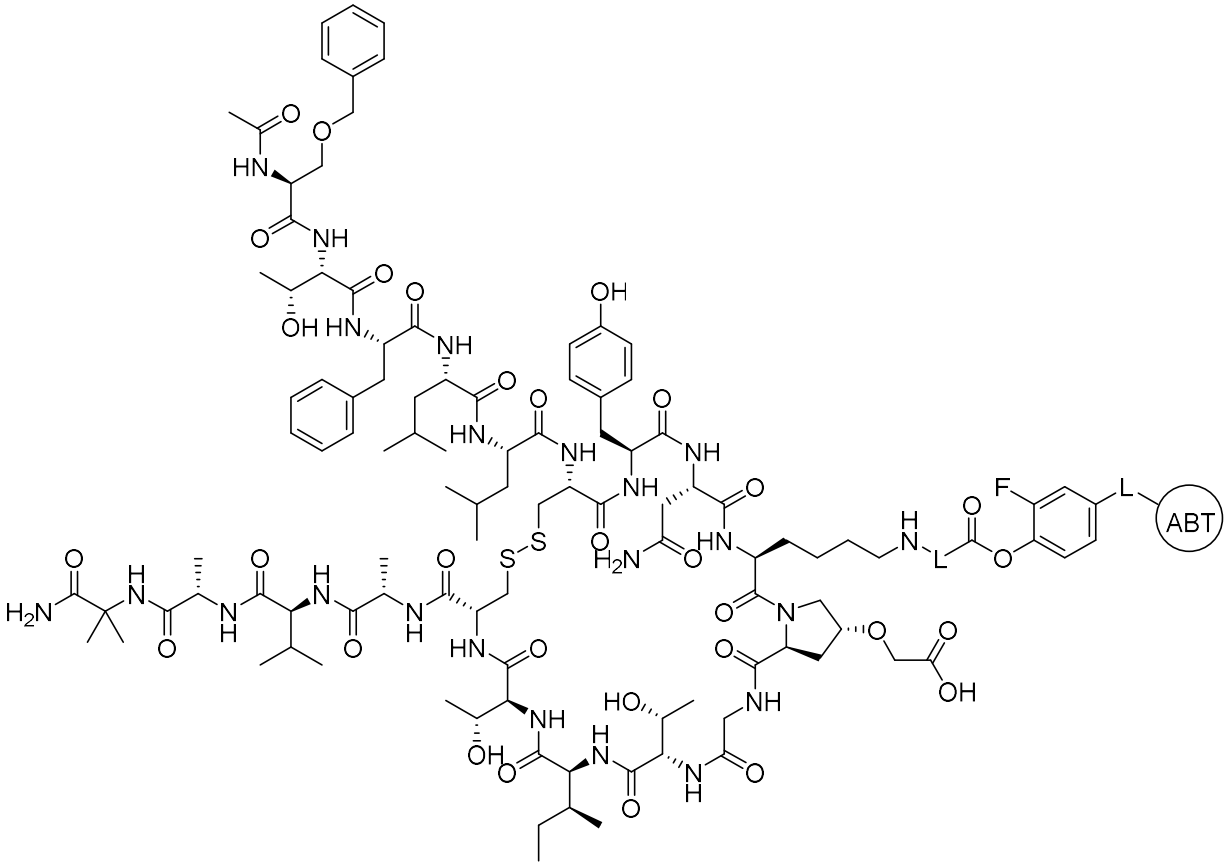

ABT
L
NH2
OH
HO
NH
HN
O
N
H

;

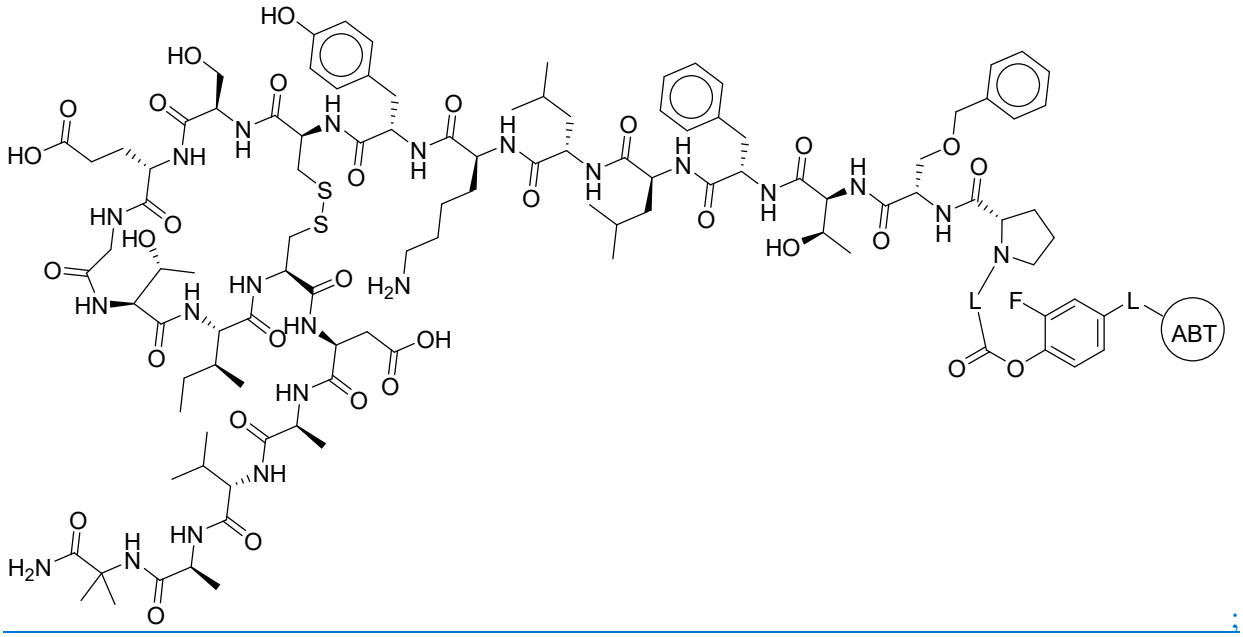




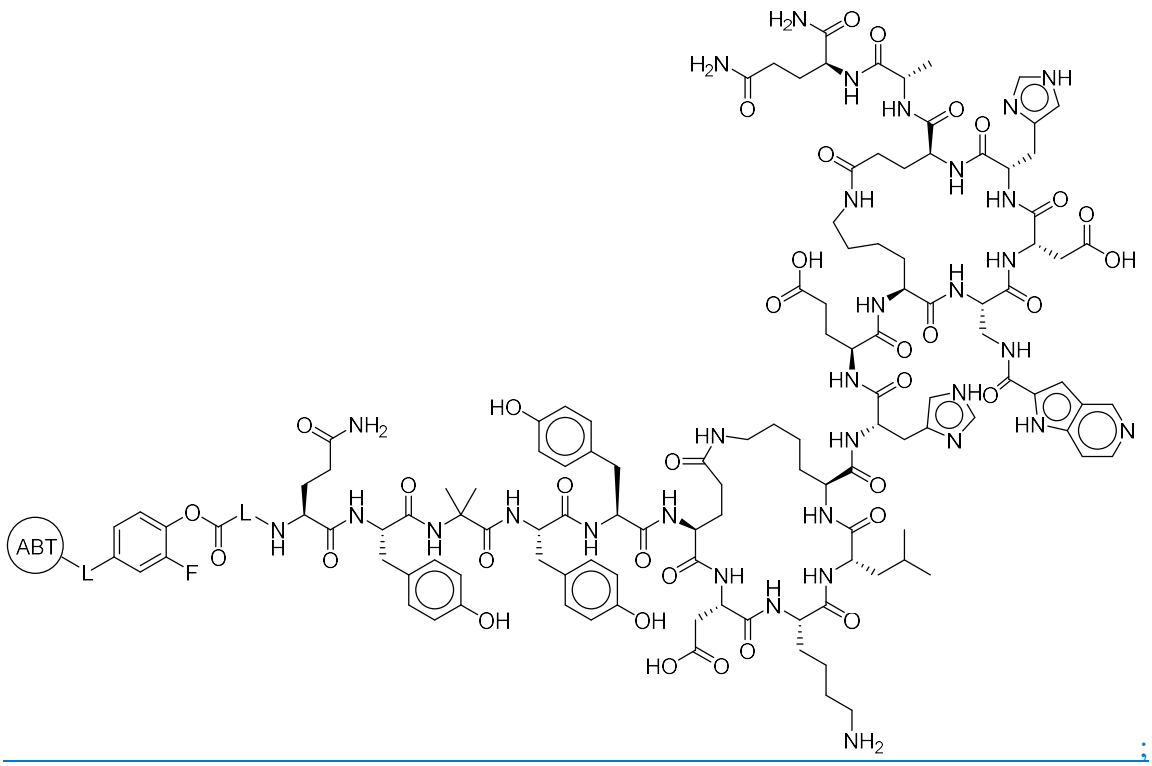
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ABT

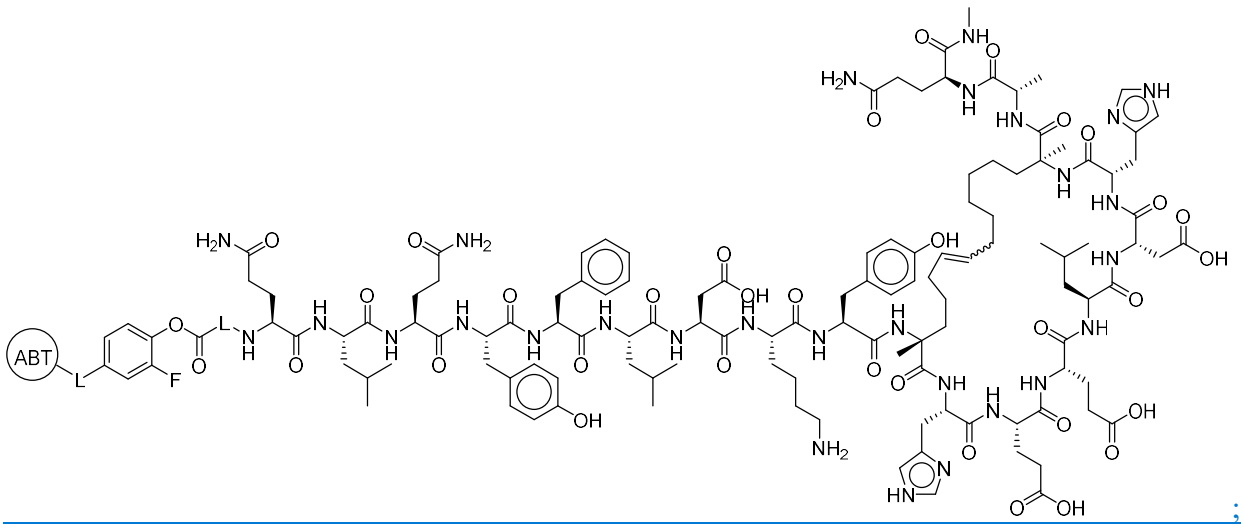
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ABT

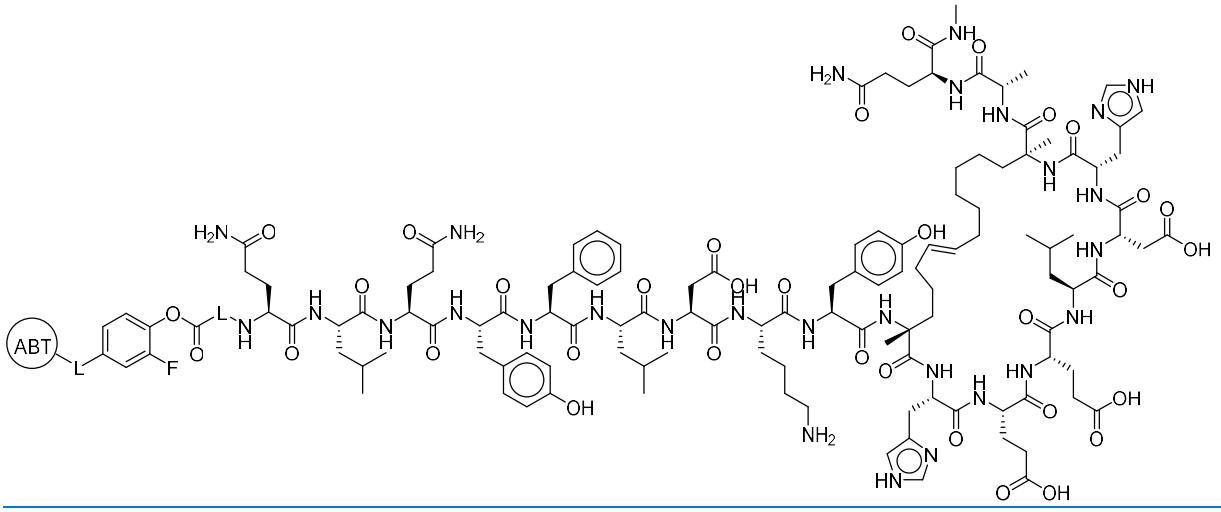
;


ABT
L
F
O
O
L
N
H
O
NH2
OH
HO
NH
HN
NH2

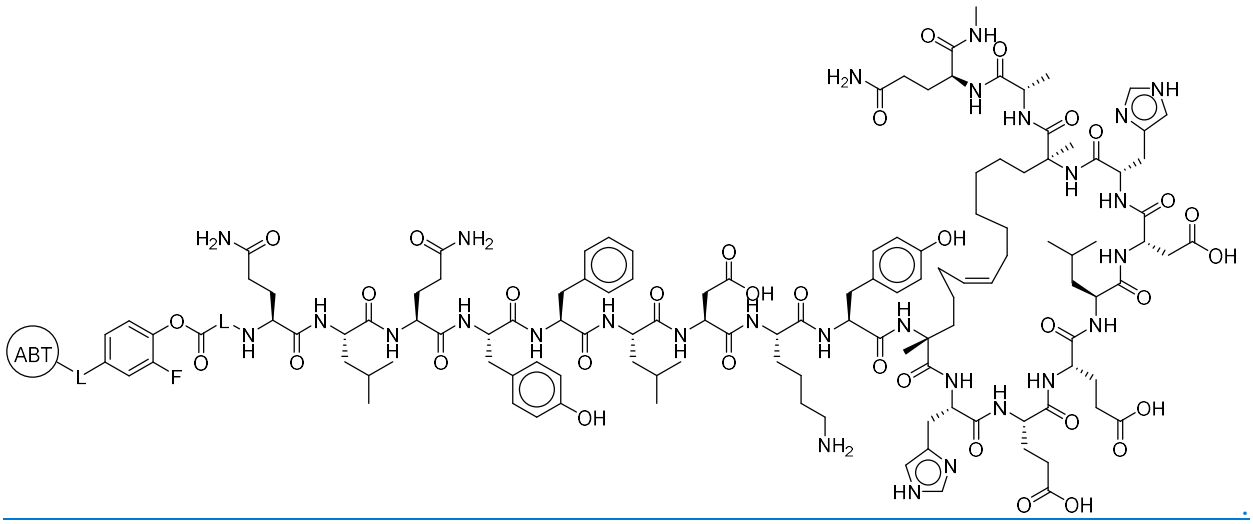
;


ABT
L
F
O
O
L
N
H
O
NH2
OH
HO
NH
HN
NH2

;

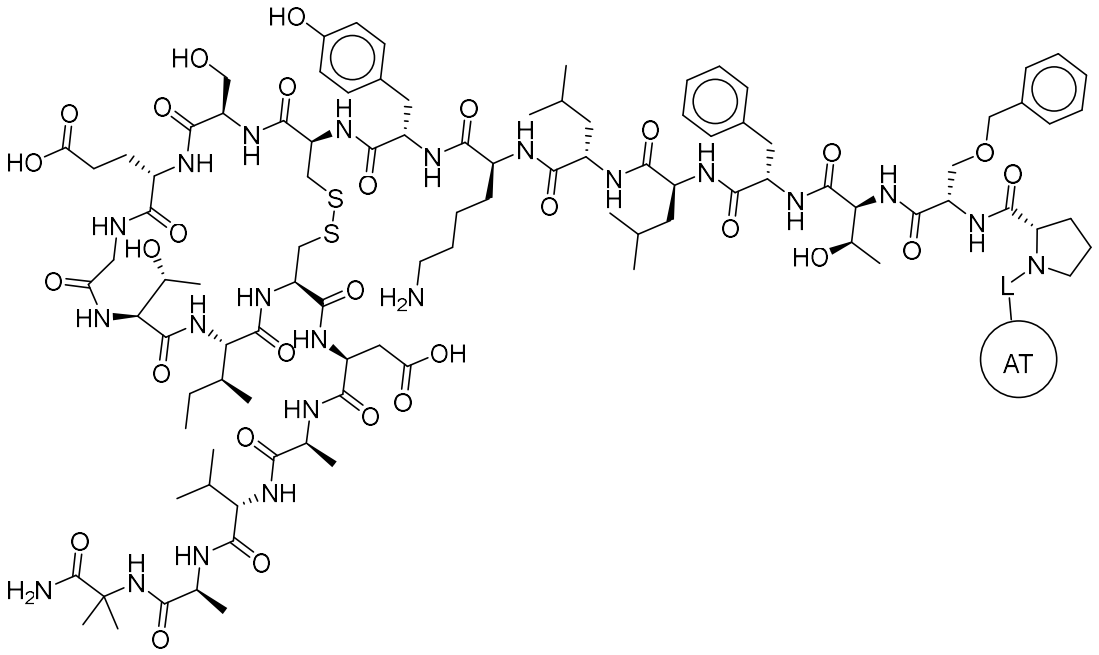


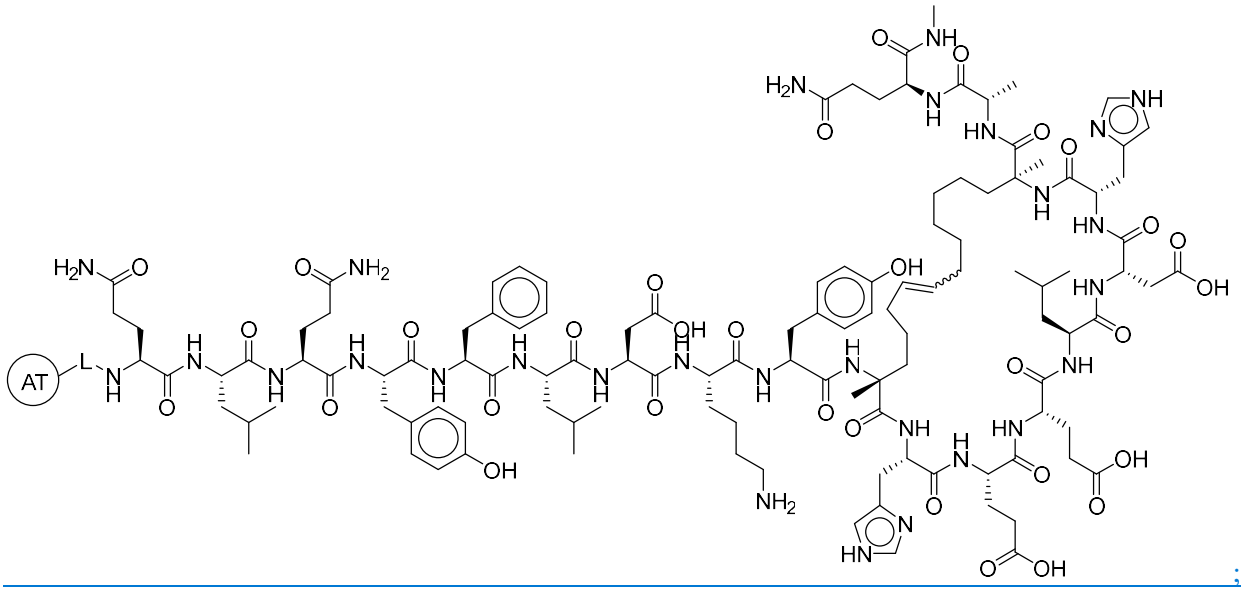
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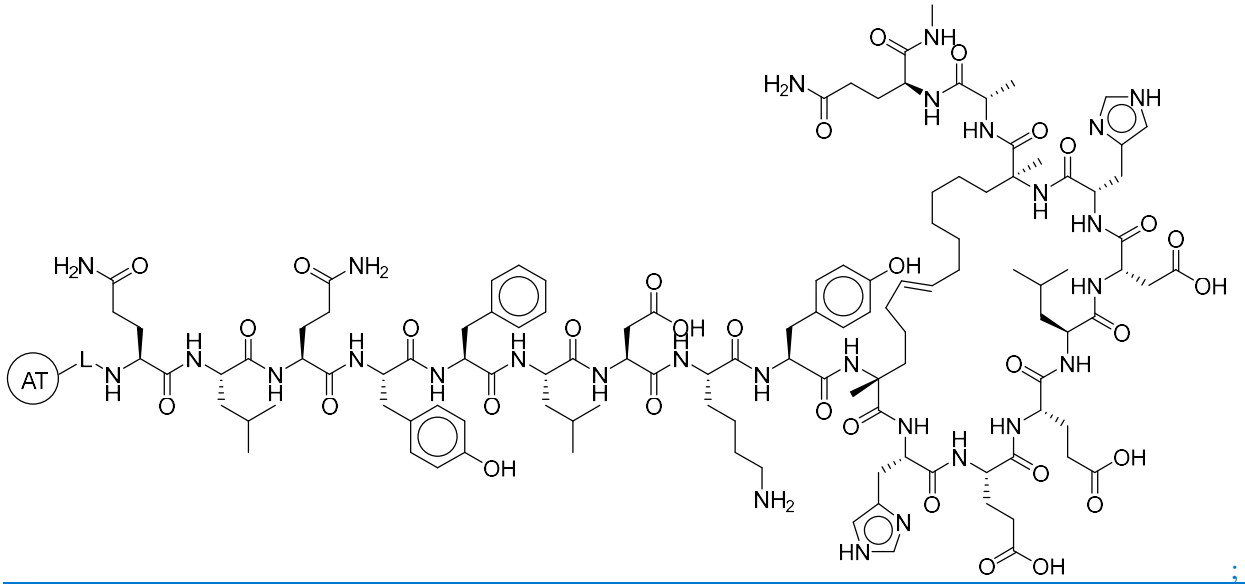
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14. The agent of claim 1 or 2, wherein the agent has the structure:

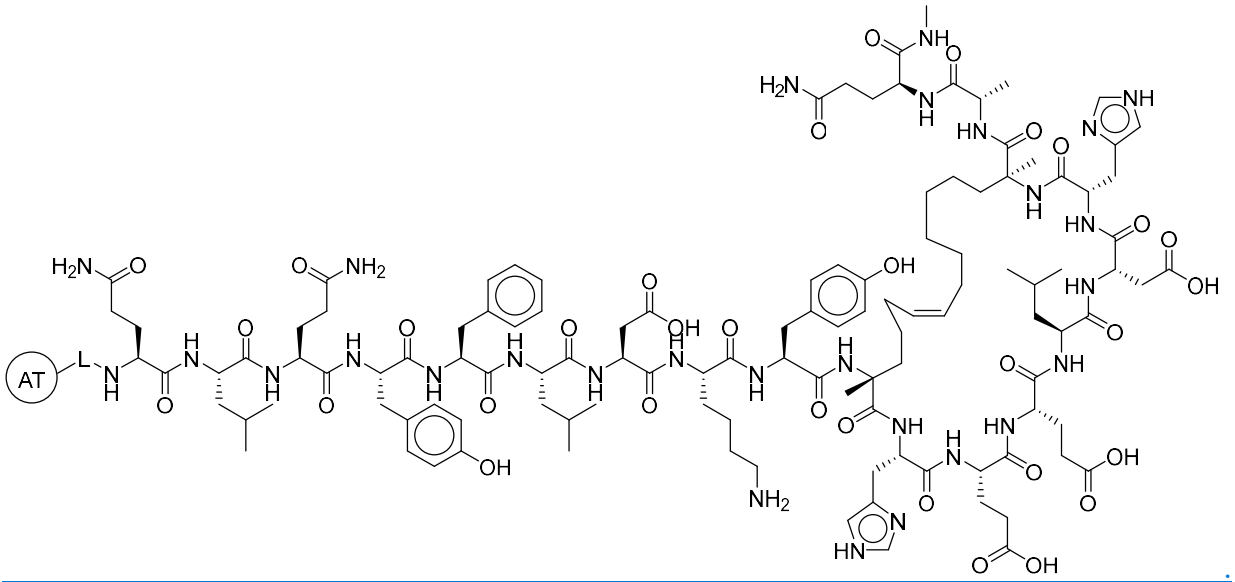

HO
HO
HO



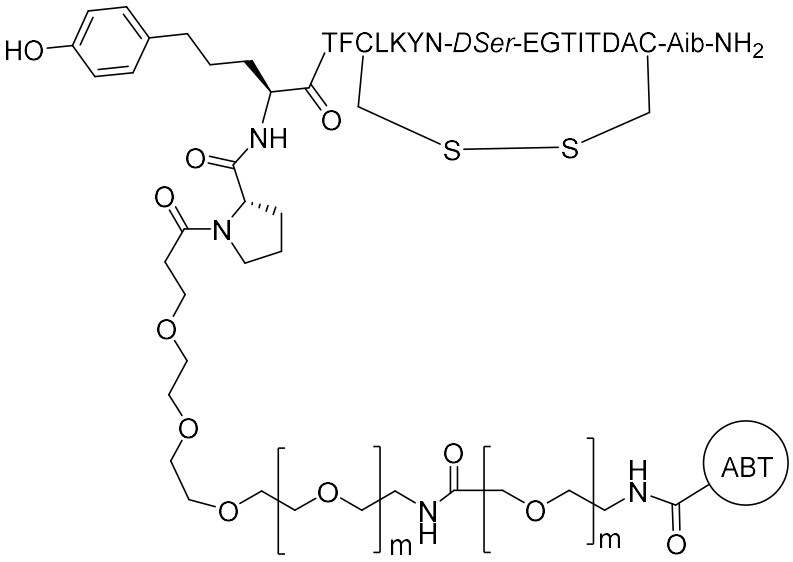
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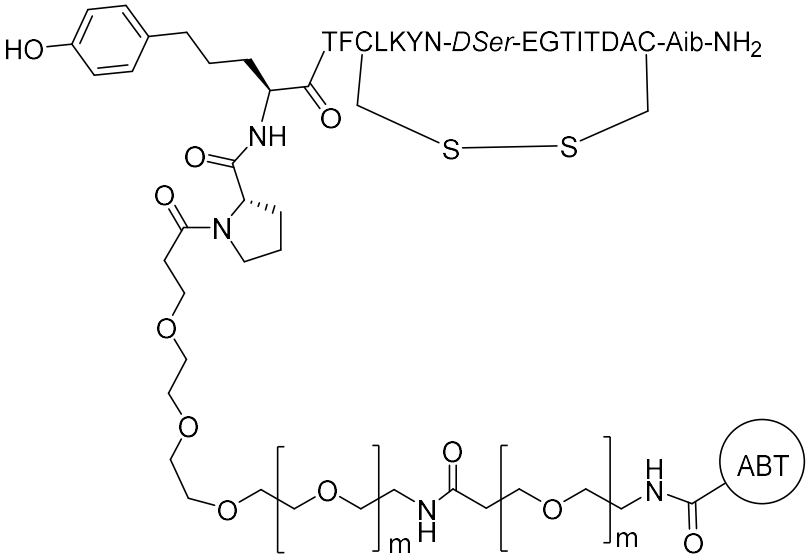
; or



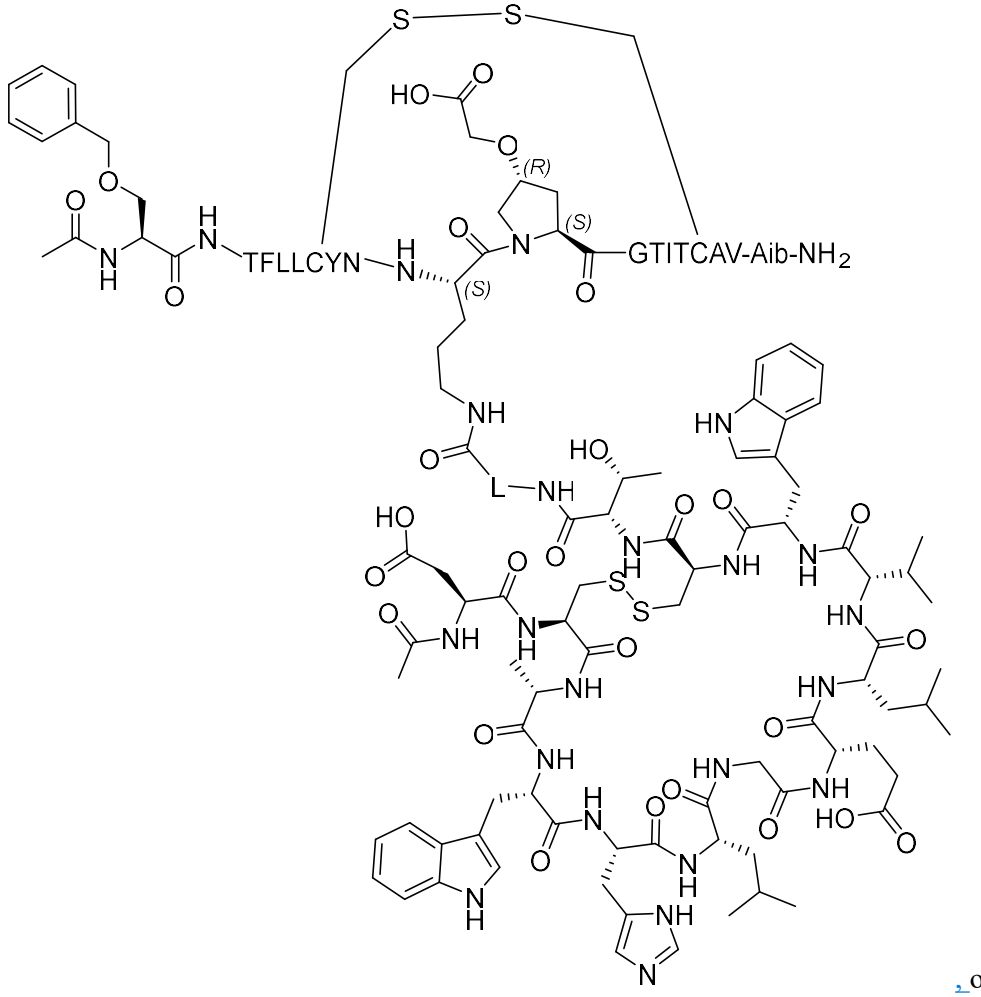
47.15. The agent of claim 1, 2, or 12, wherein the agent has the structure of



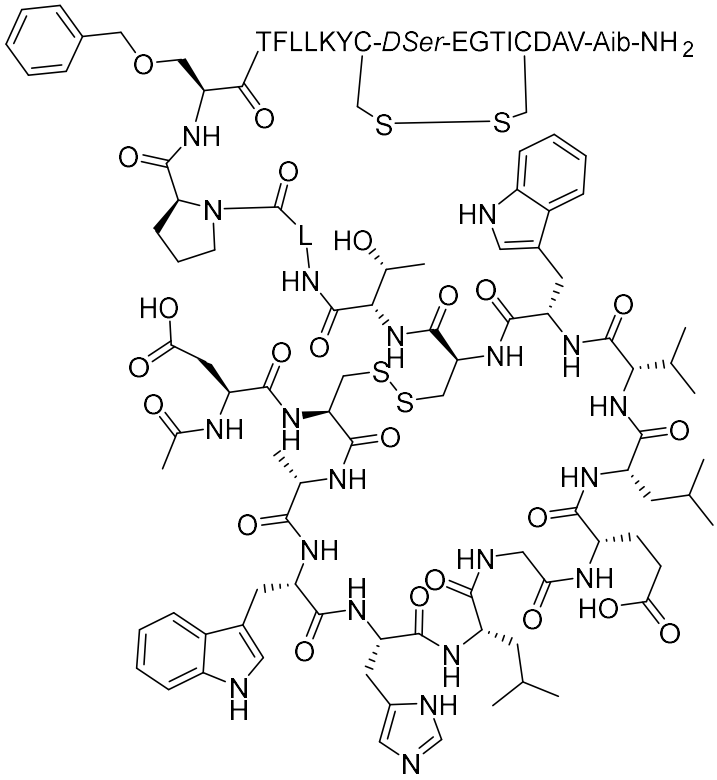
, or a salt thereof;



, or a salt thereof;

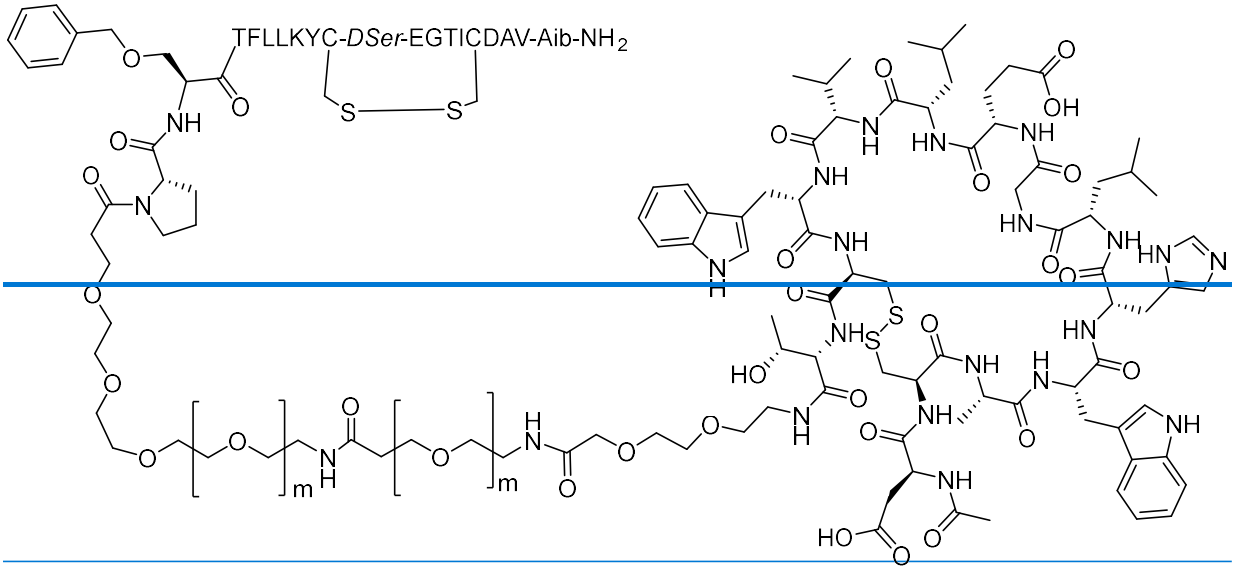


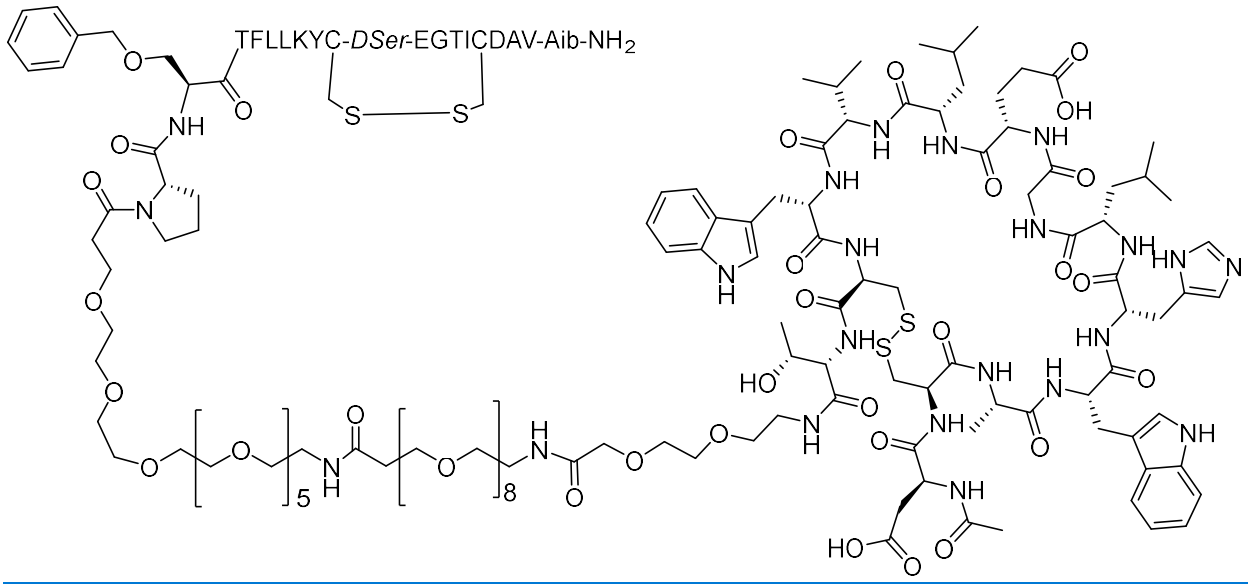
, or a salt thereof~~, wherein L is a linker moiety~~; or



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

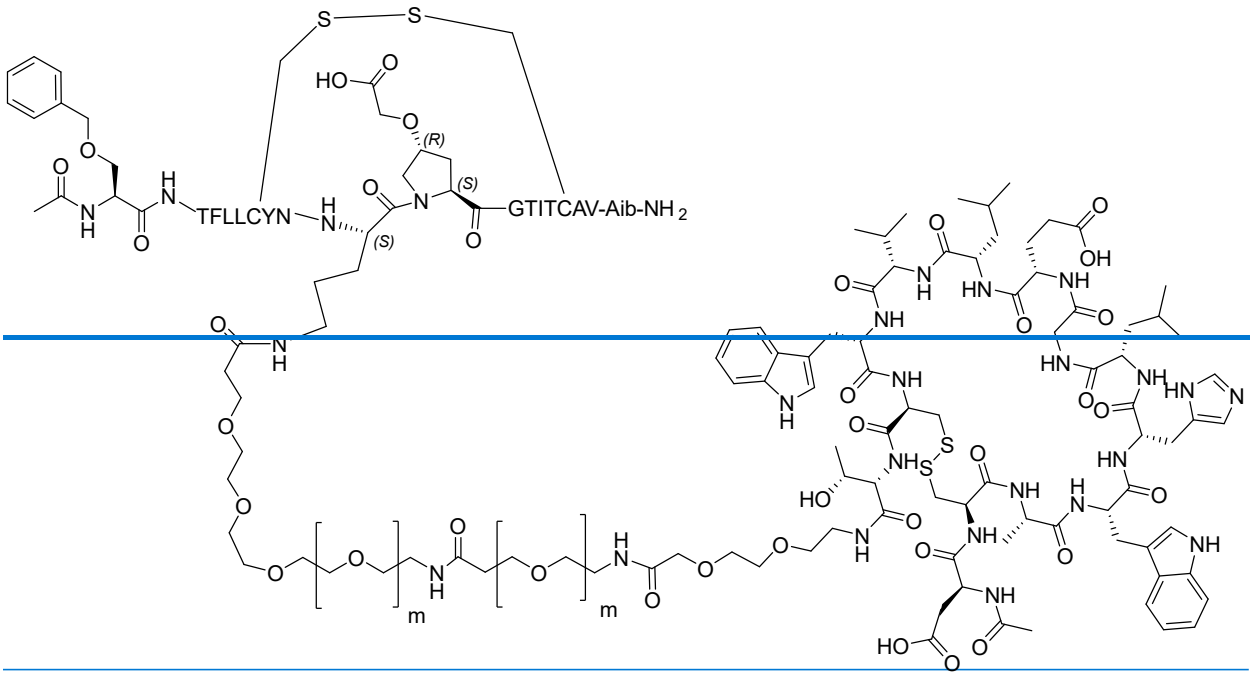
~~48.~~16. The agent of claim 1~~ or 2~~, wherein the agent has the structure of

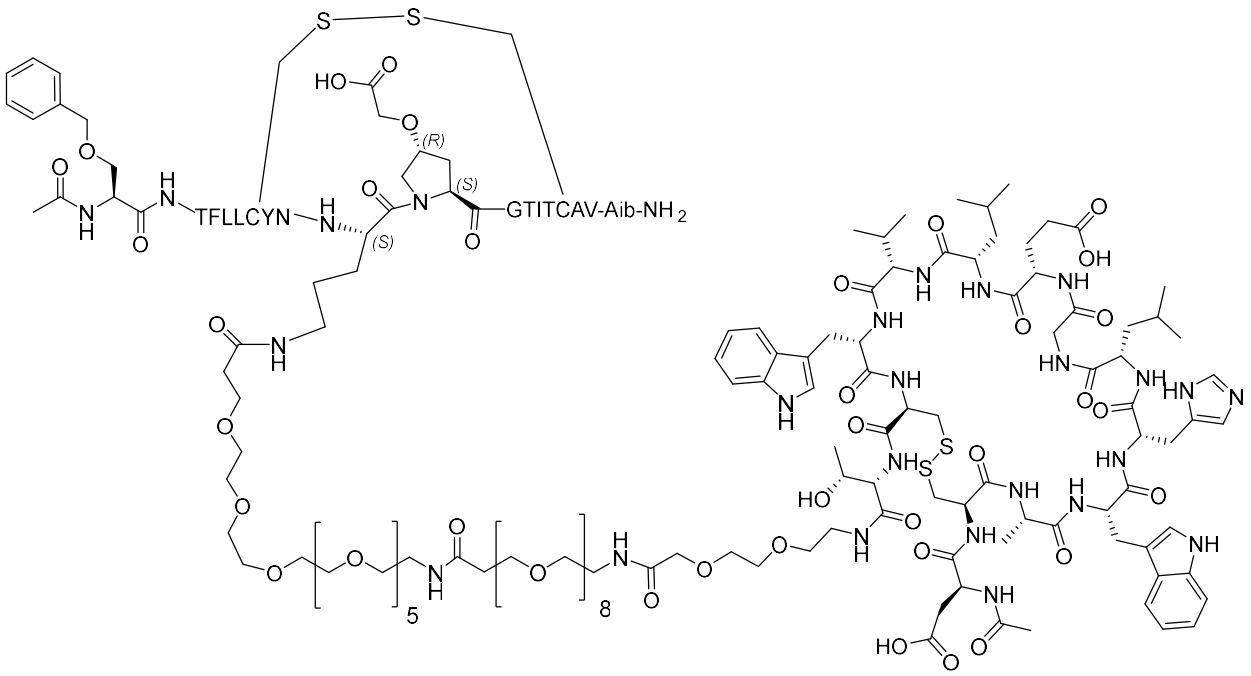




(I-1), or a salt thereof;

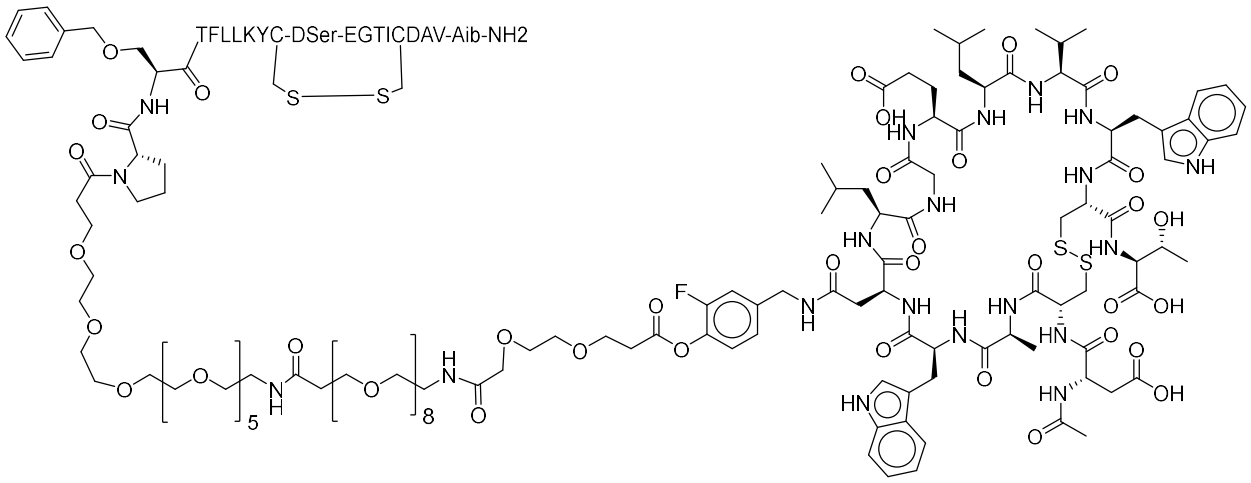
~~49. The agent of claim 1 or 2, wherein the agent has the structure of~~





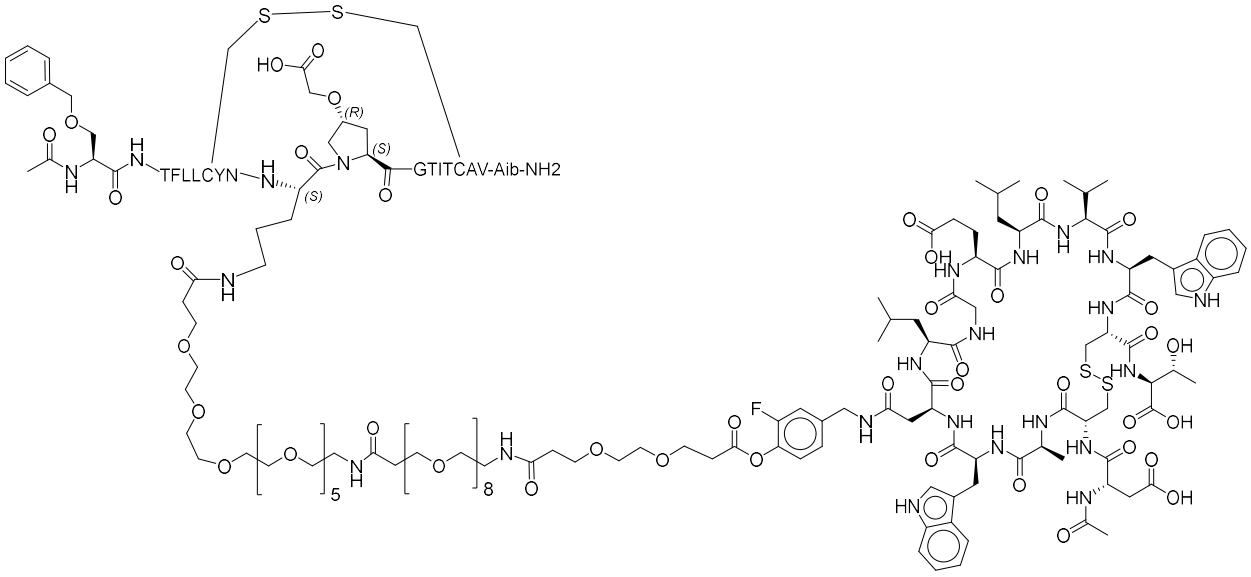
(I-2), or a salt thereof;.

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



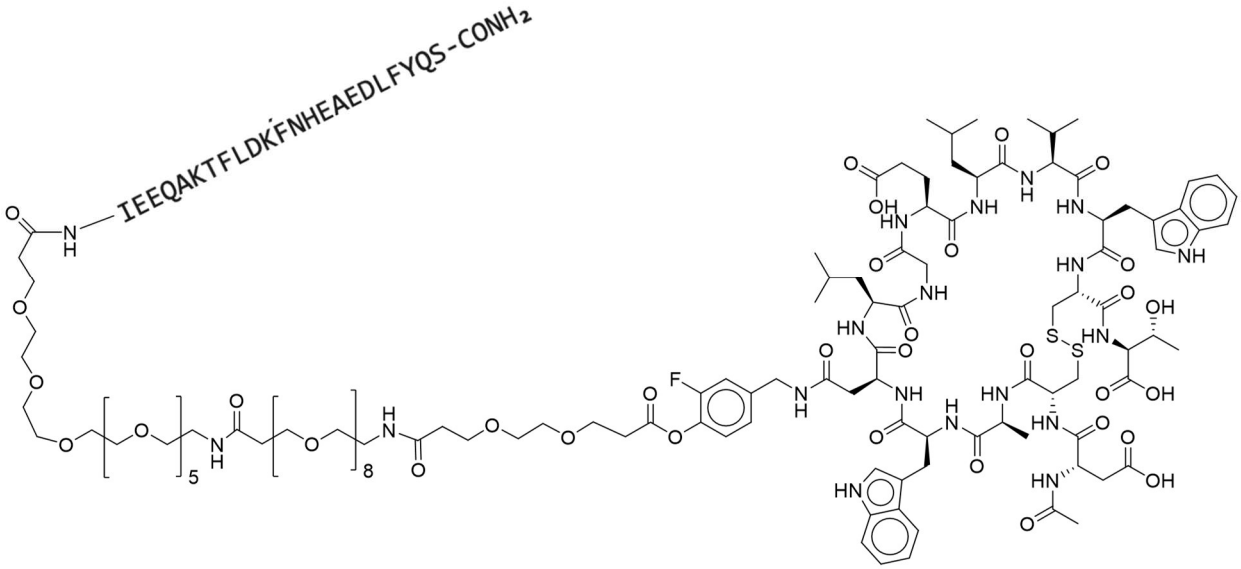
(I-3), or a salt thereof;.

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



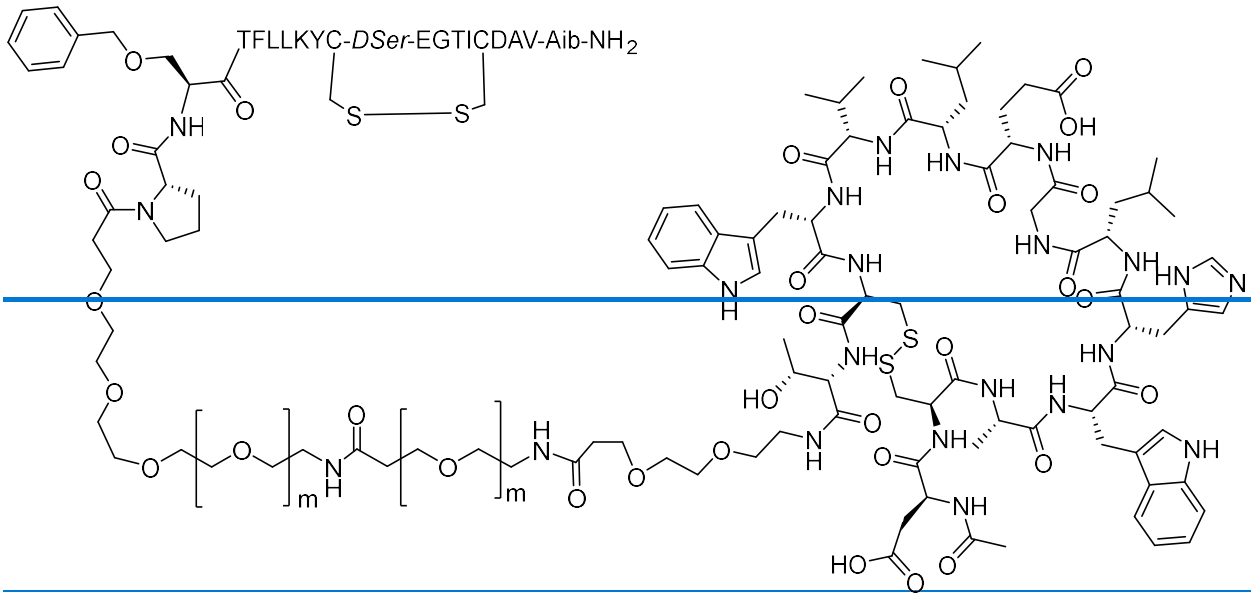
(I-4), or a salt thereof;.

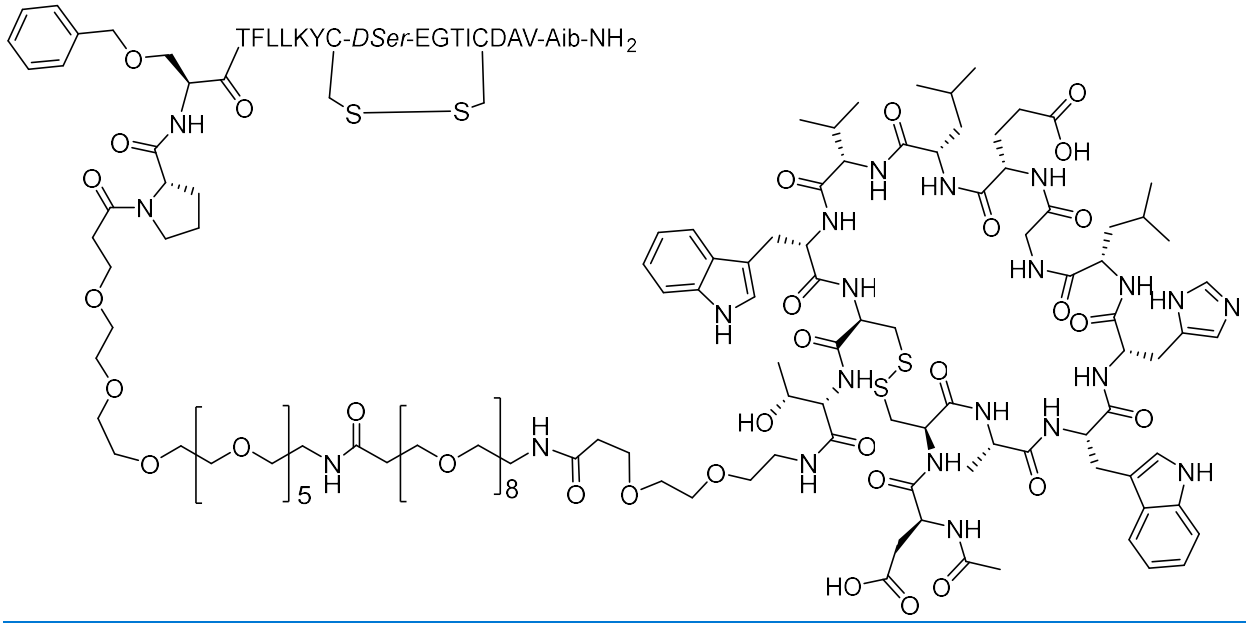
~~52. The agent of claim 1 or 2, wherein the agent has the structure of~~



(I-5), or a salt thereof;.

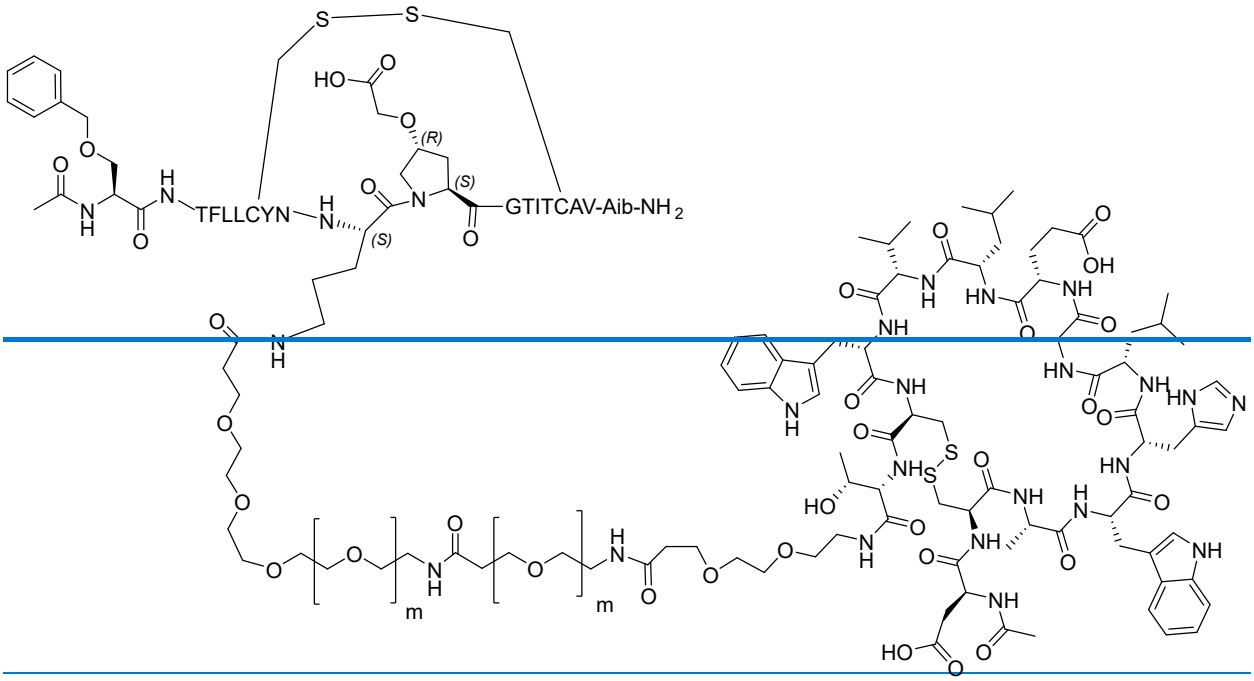
~~53. The agent of claim 1 or 2, wherein the agent has the structure of~~

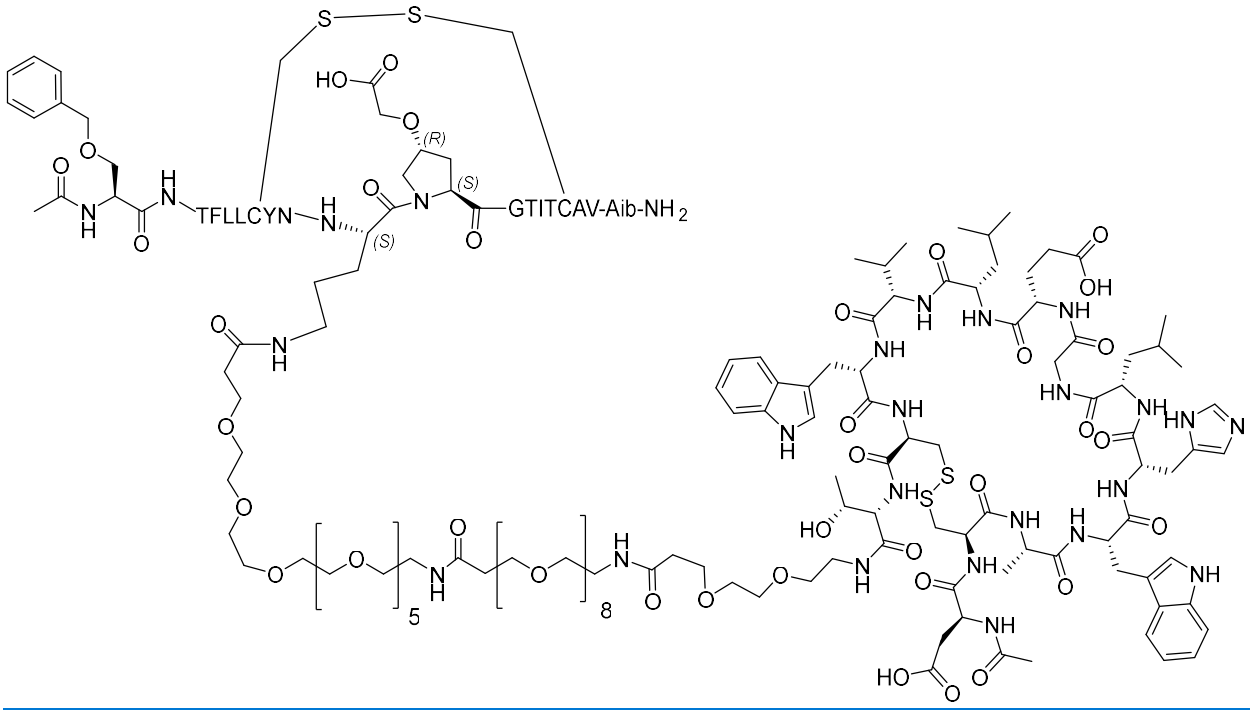




(I-9), or a salt thereof;

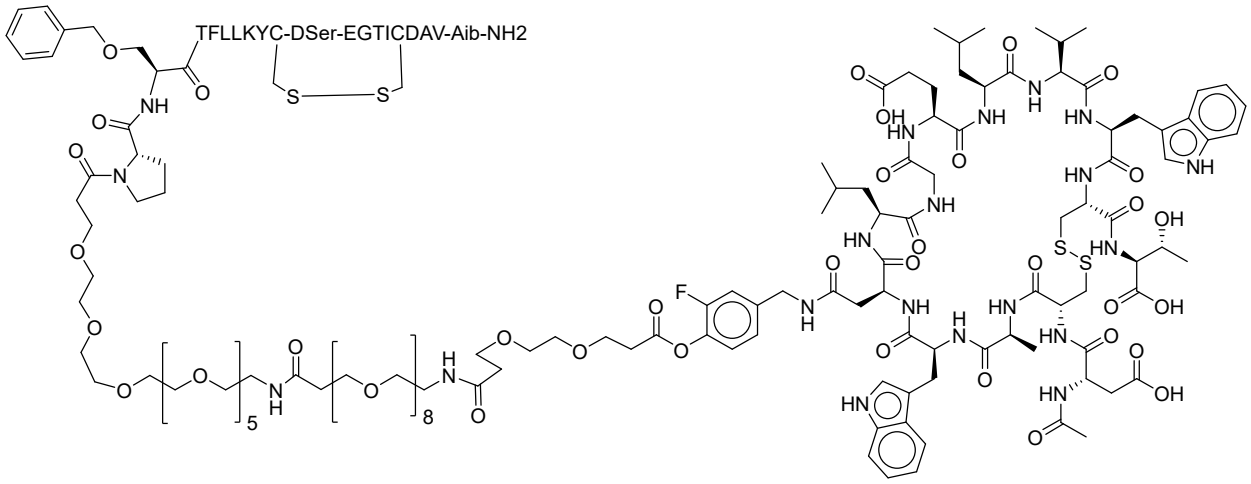
~~54. The agent of claim 1 or 2, wherein the agent has the structure of~~





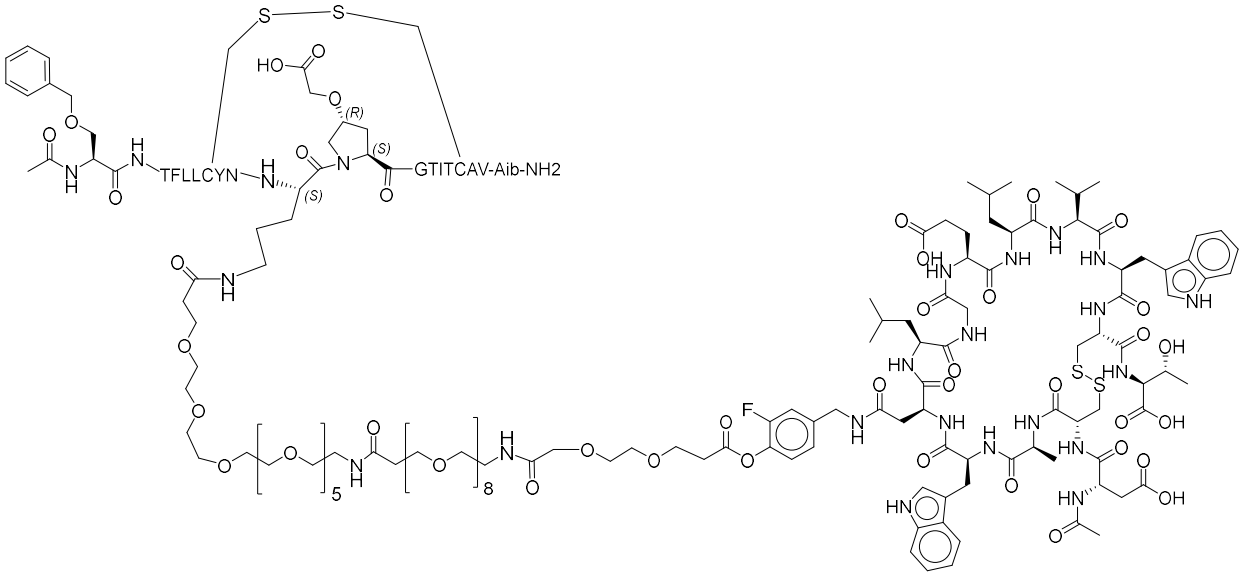
(I-10), or a salt thereof.

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



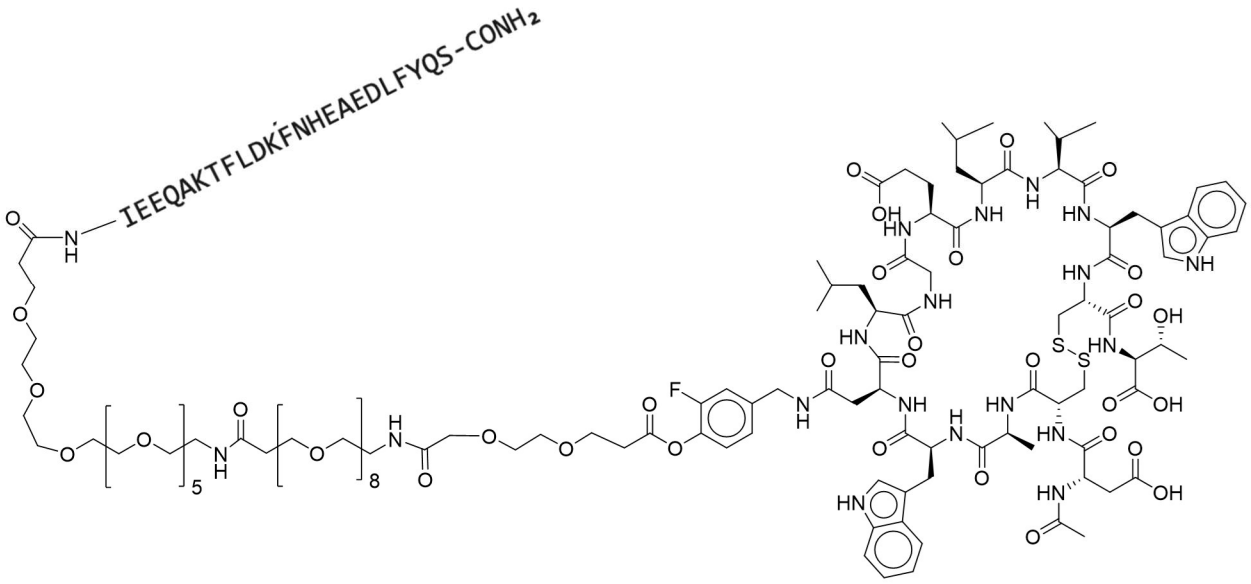
(I-11), or a salt thereof;.

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



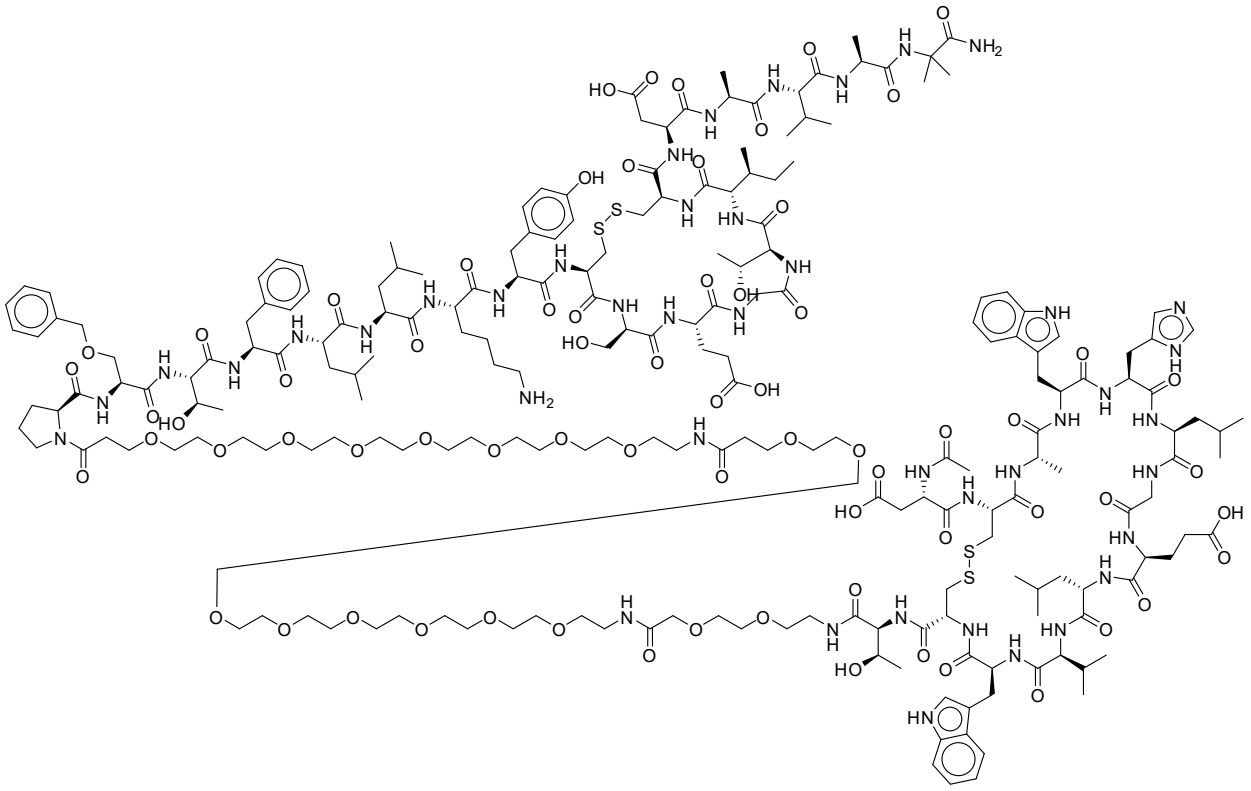
(I-12), or a salt thereof;.

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



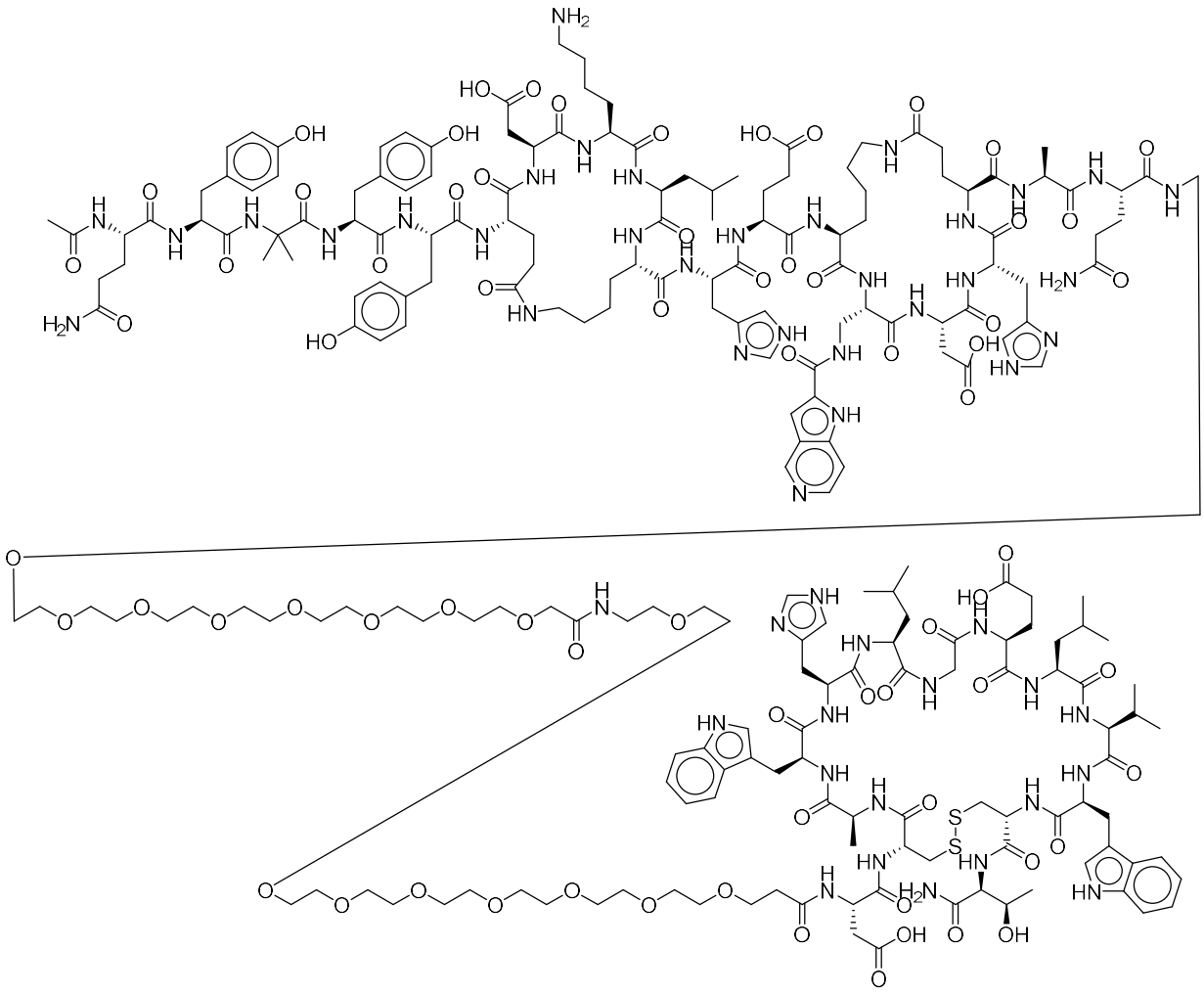
(I-13), or a salt thereof;.

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



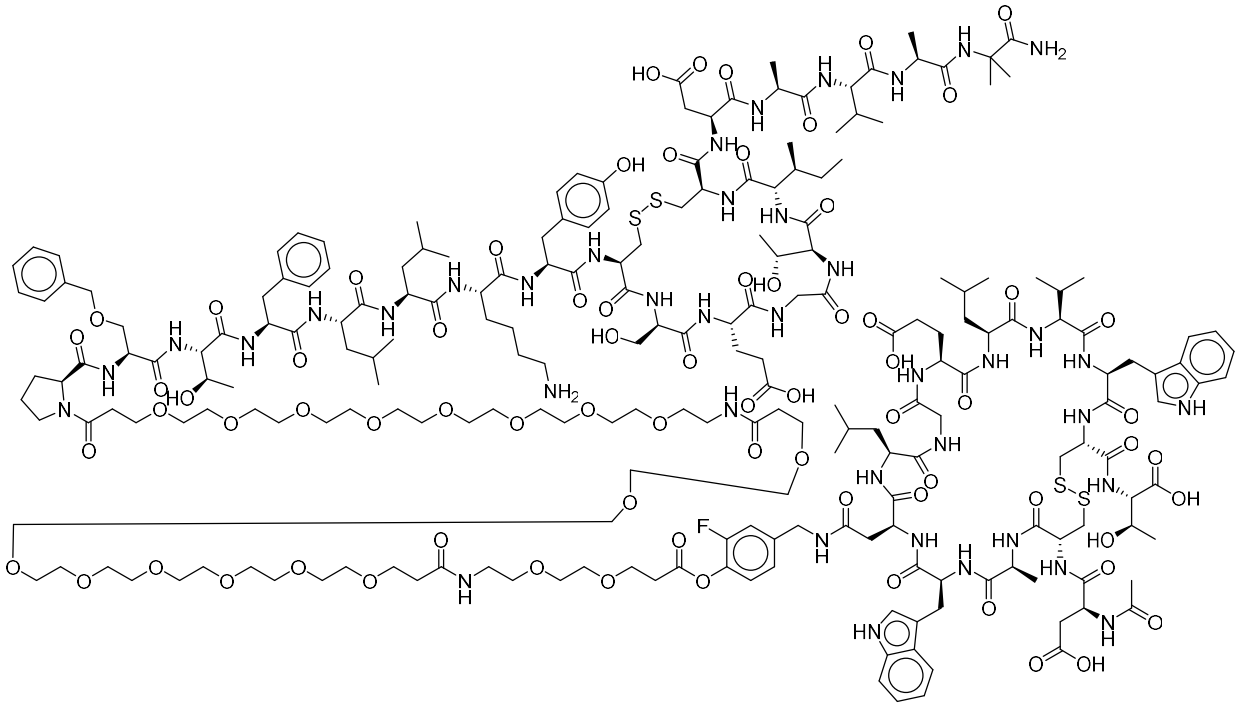
(I-17), or a salt thereof;.

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



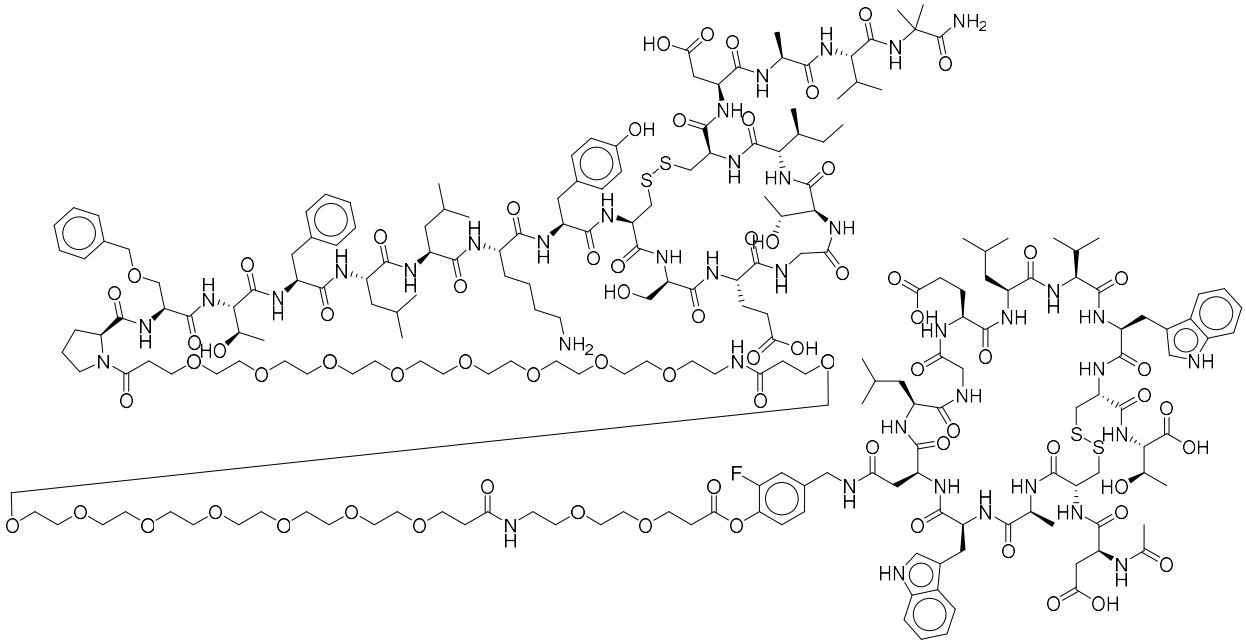
(I-18), or a salt thereof;.

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



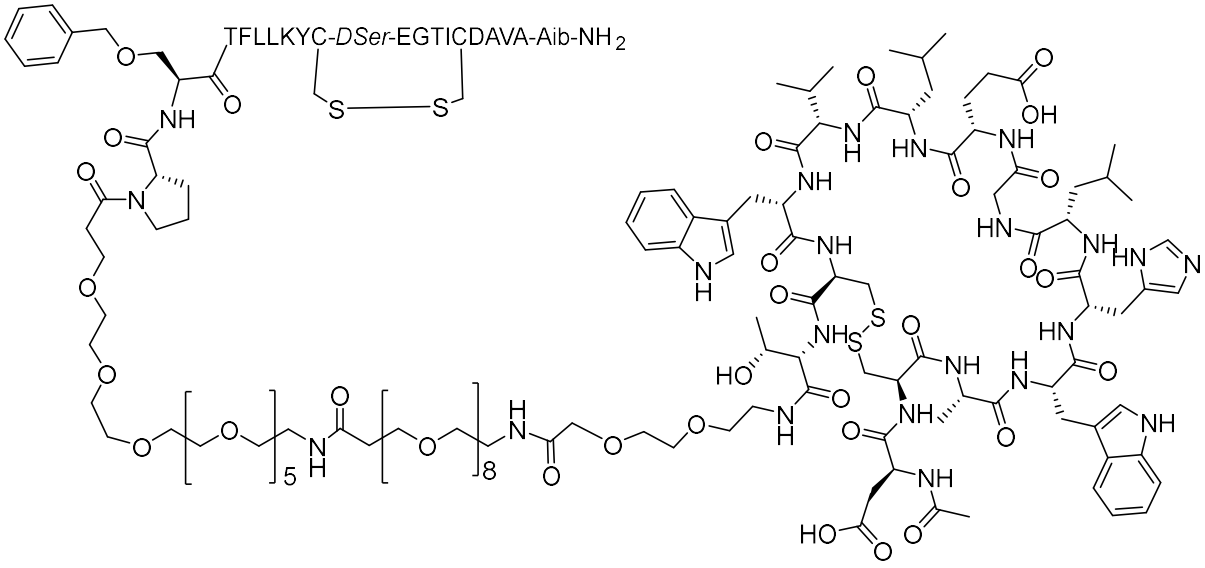
(I-19), or a salt thereof;.

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



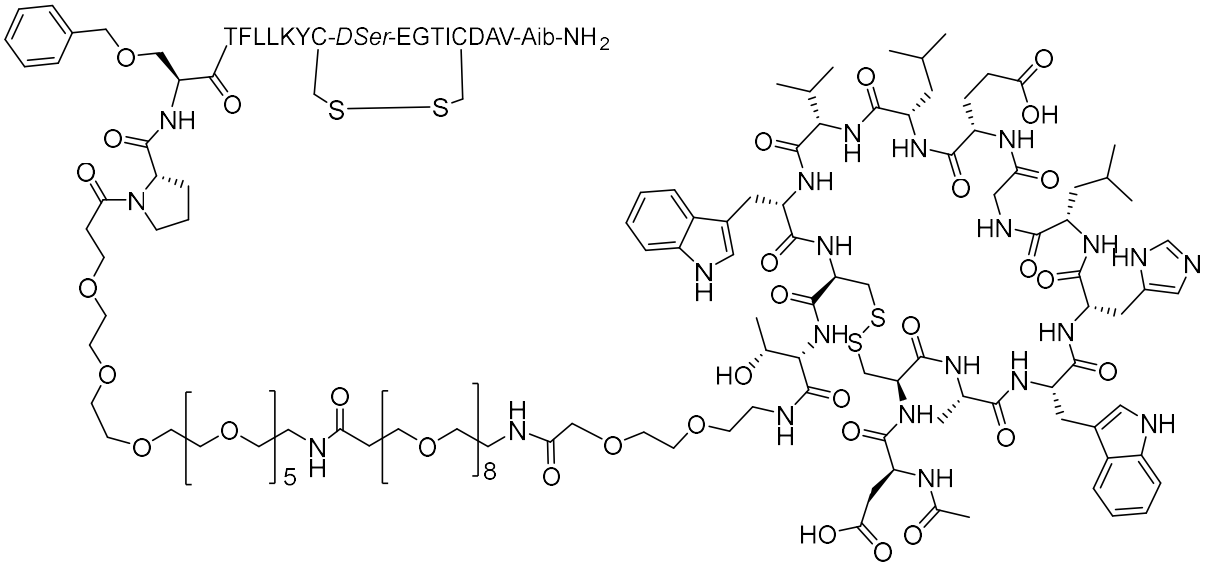
(I-20), or a salt thereof;.

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



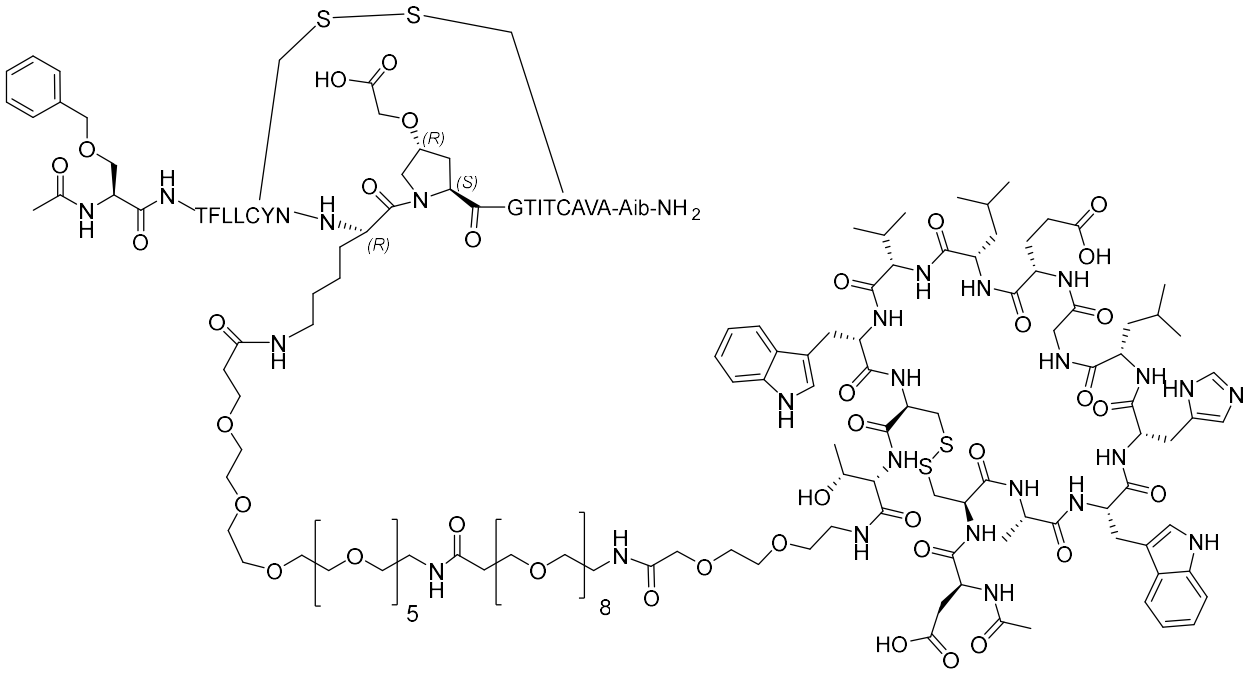
(I-23), or a salt thereof;.

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



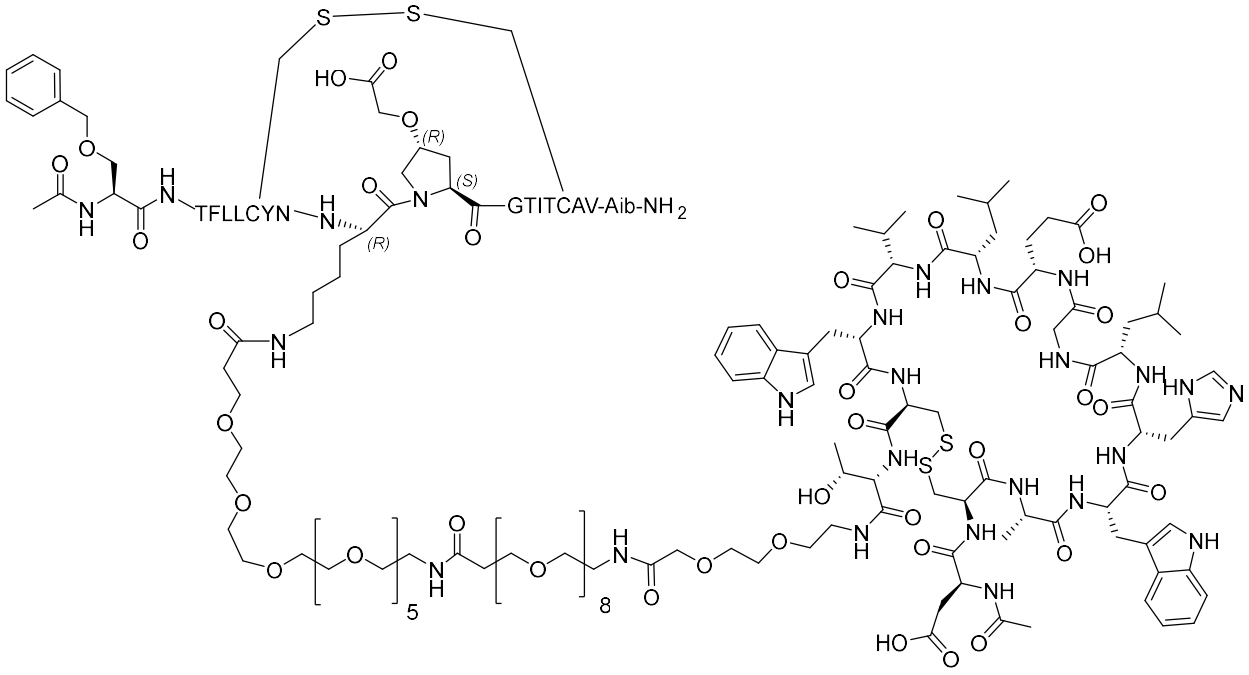
(I-24), or a salt thereof;.

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



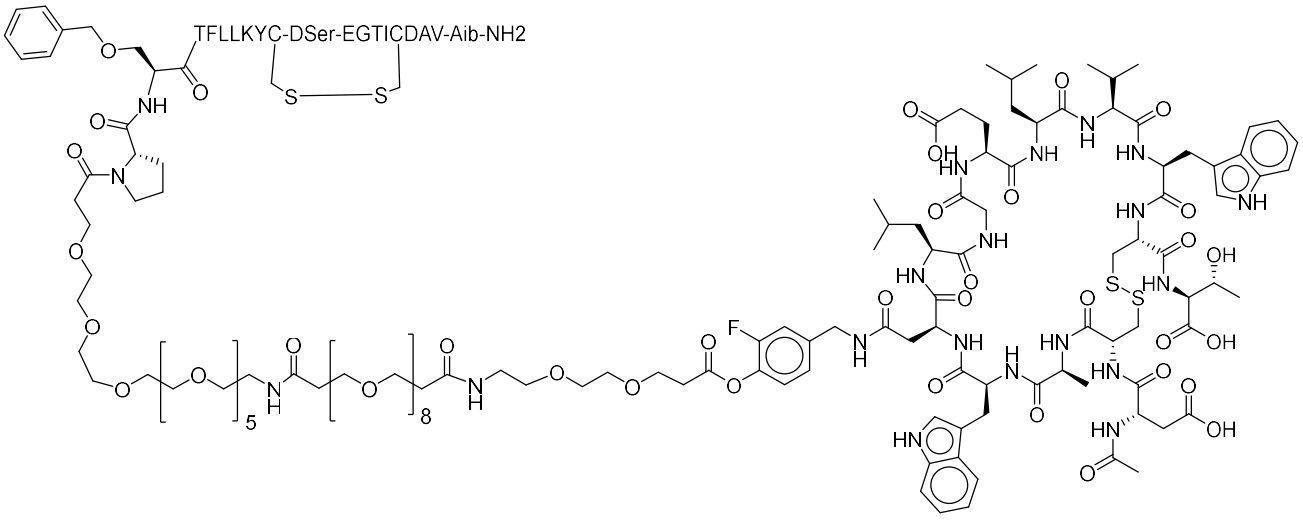
(I-25), or a salt thereof;.

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



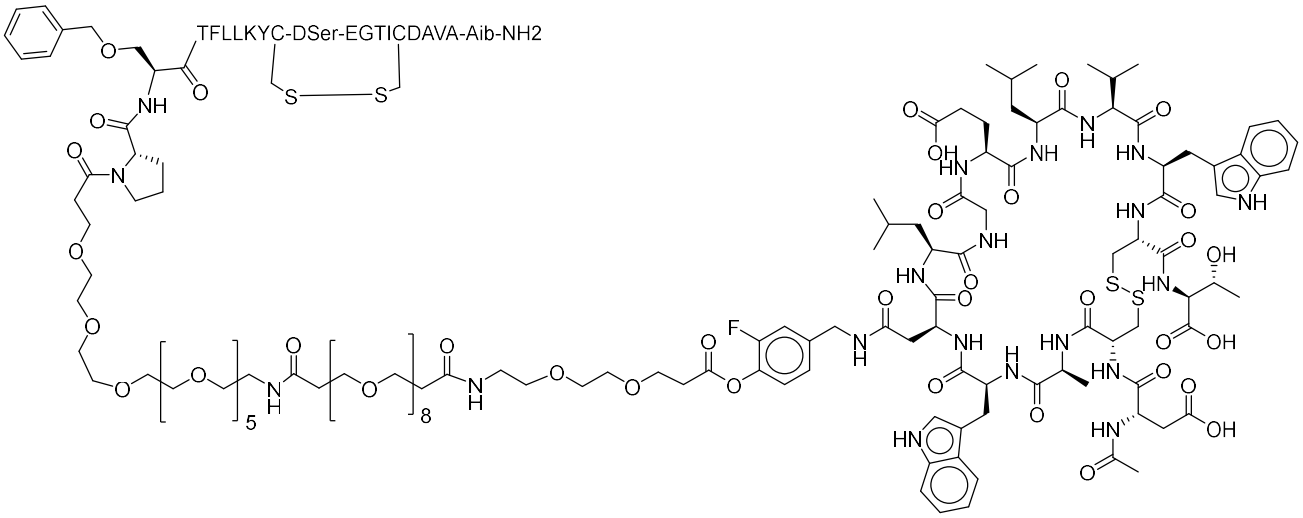
(I-26), or a salt thereof;.

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



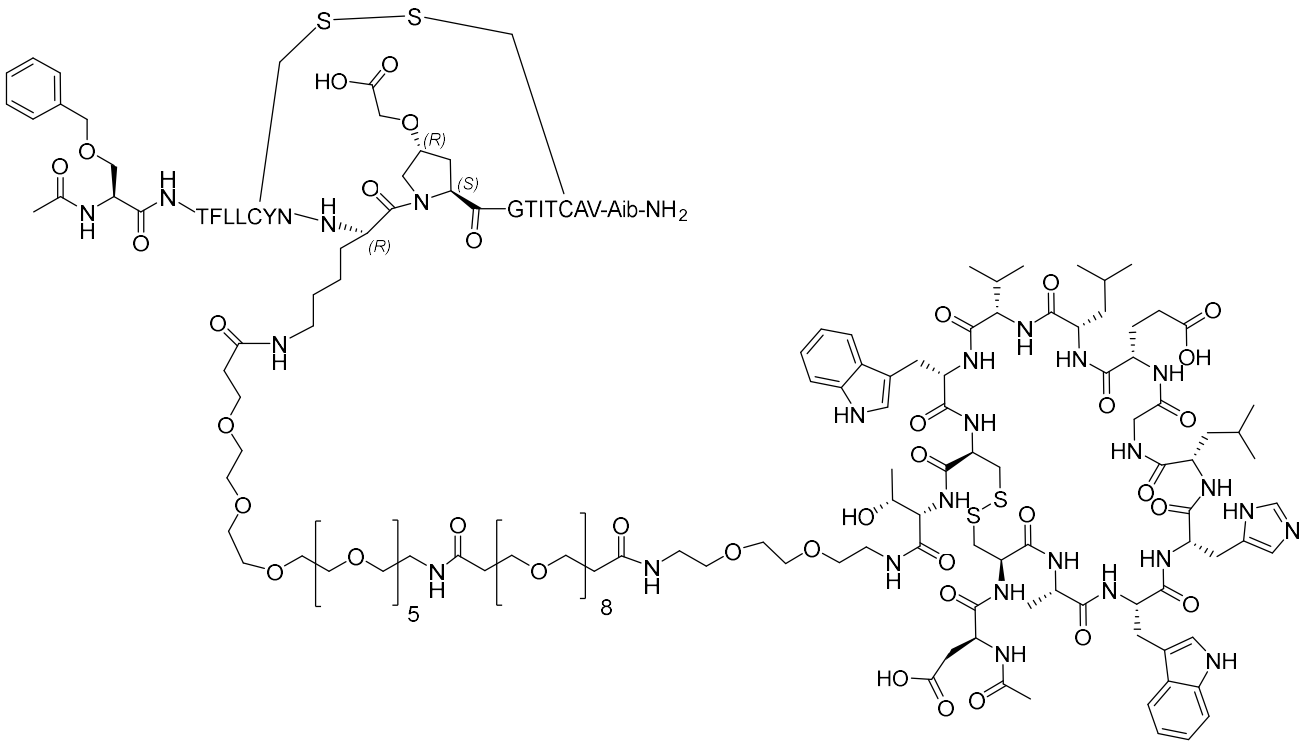
(I-27), or a salt thereof;.

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



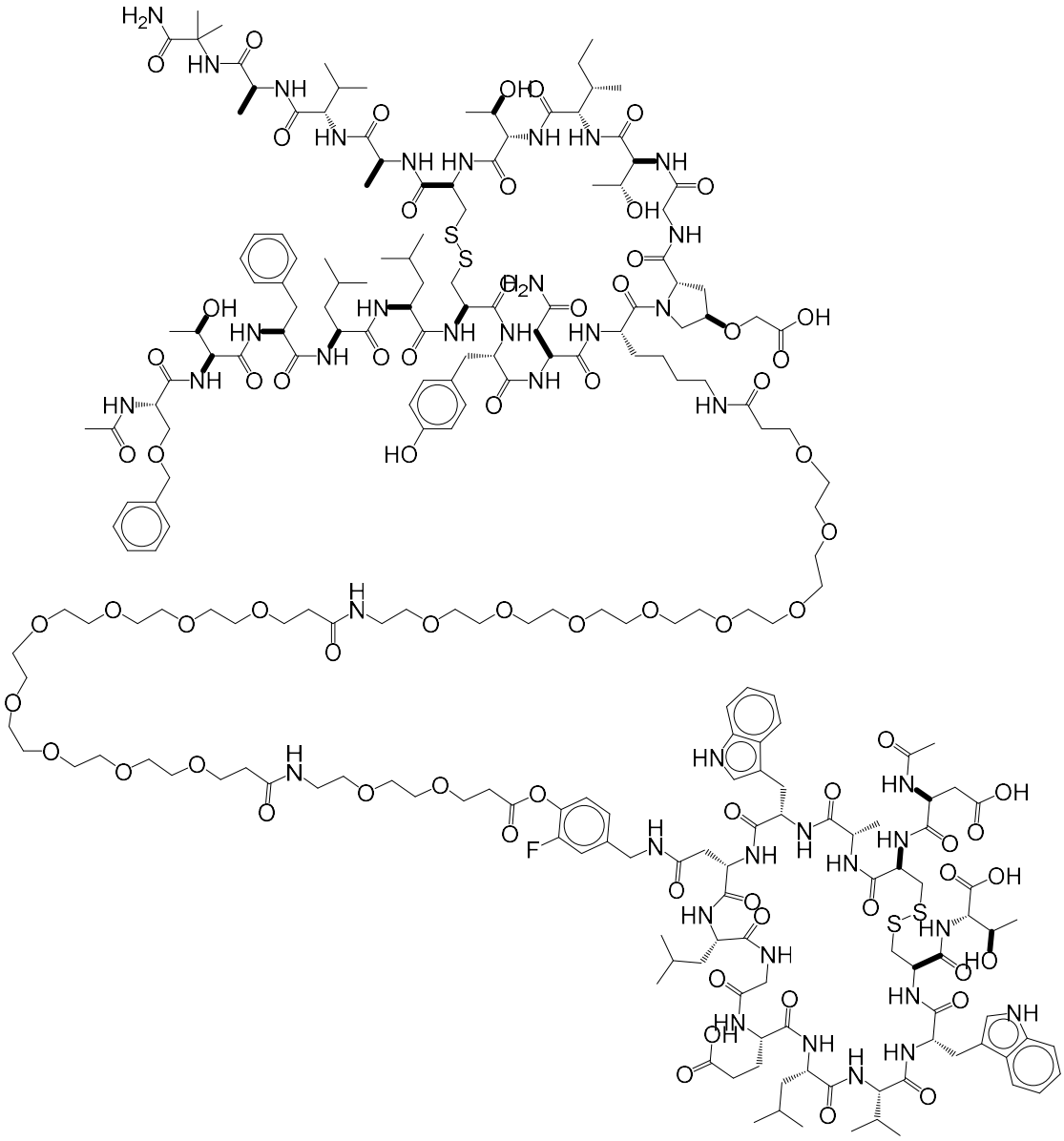
(I-28), or a salt thereof;.

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



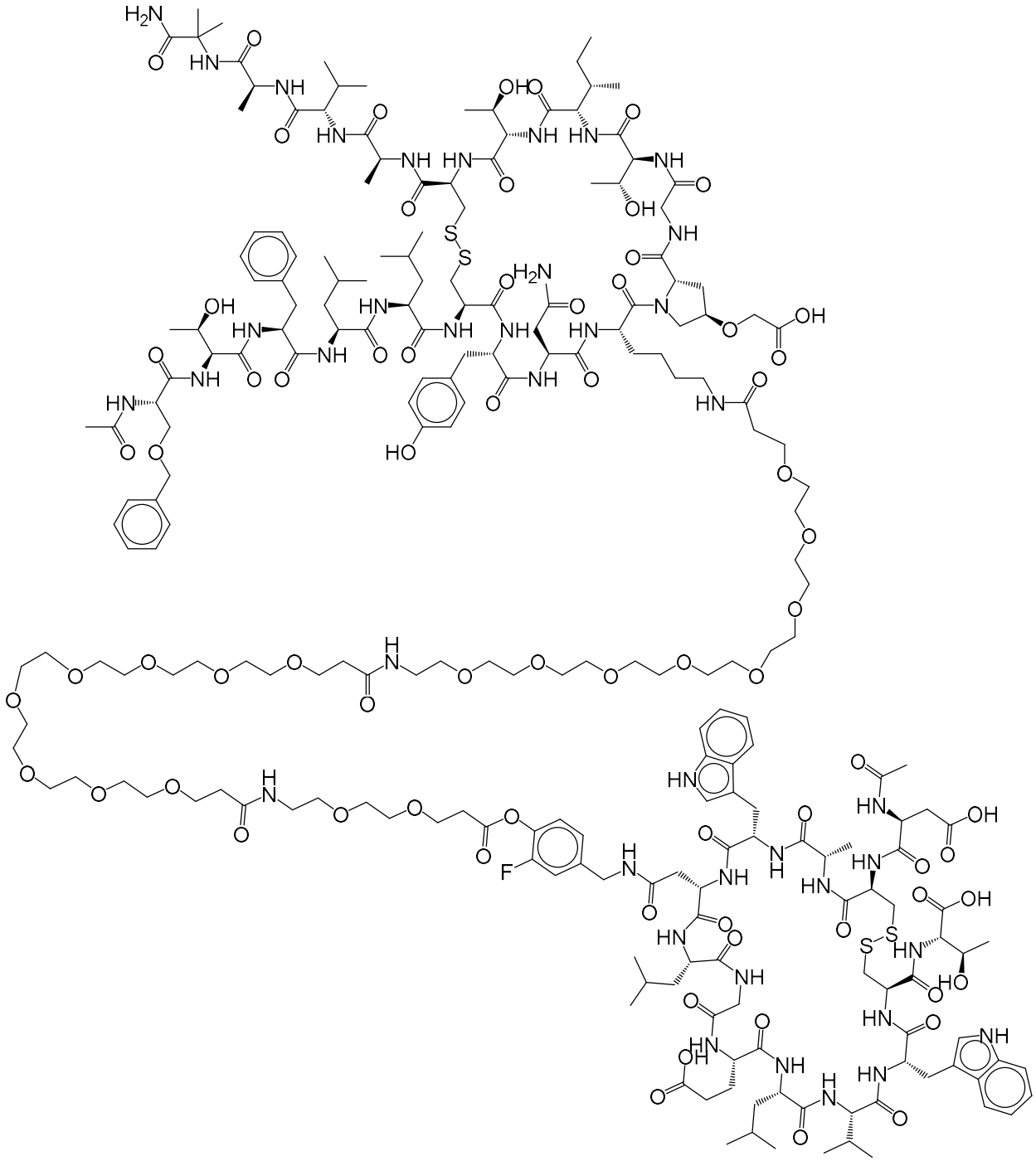
(I-29), or a salt thereof;.

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



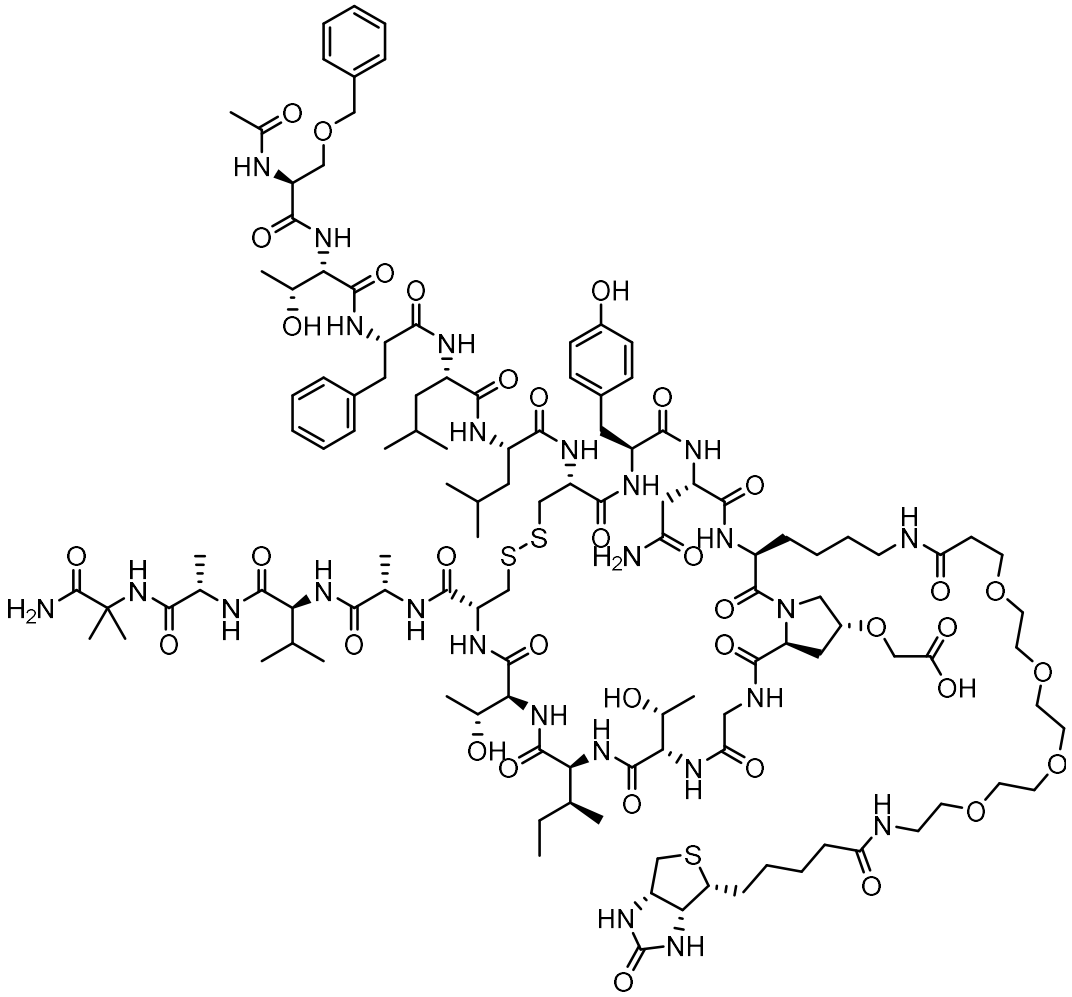
(I-30), or a salt thereof;.

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



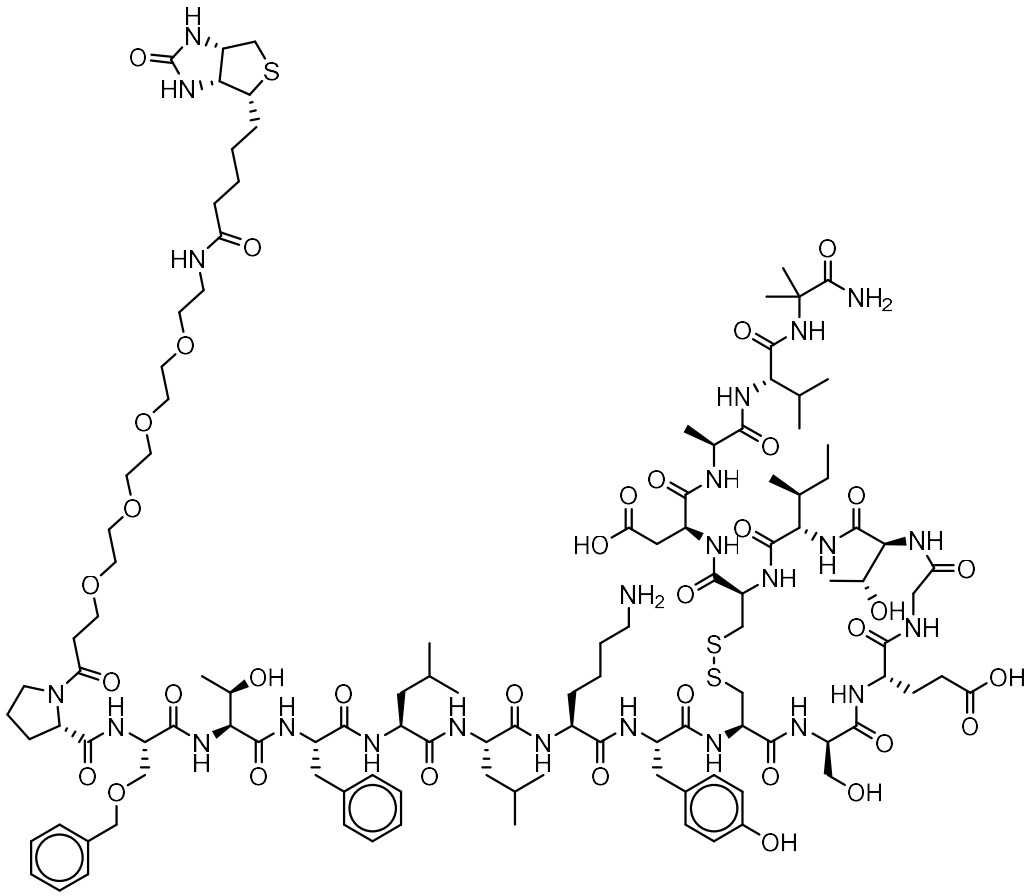
(I-31), or a salt thereof;.

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



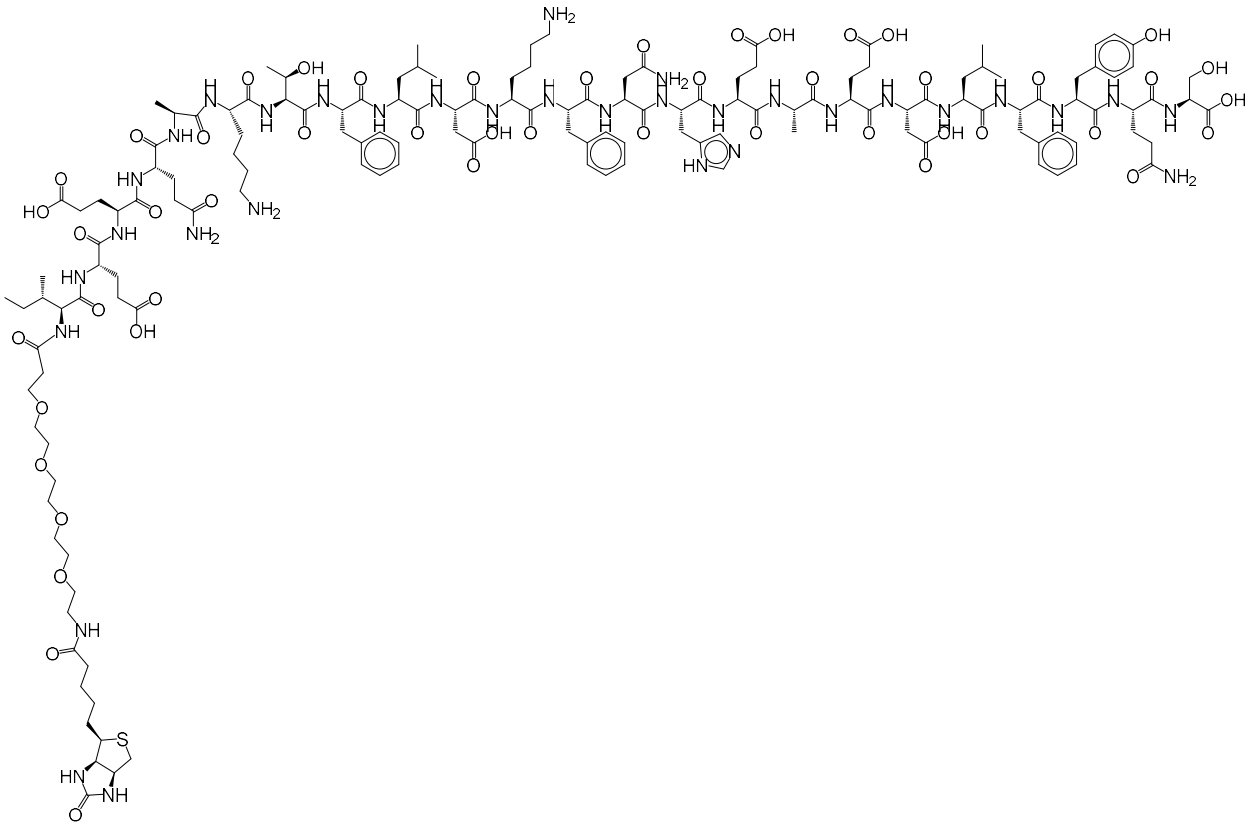
(I-32), or a salt thereof;.

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



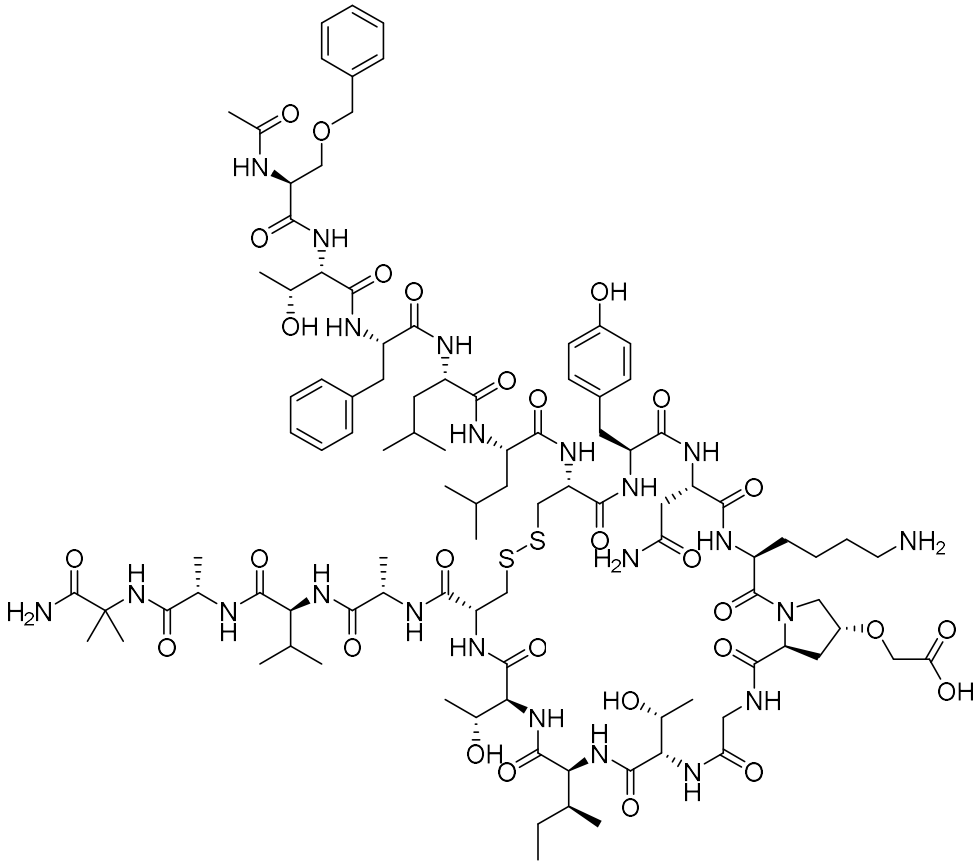
(I-33), orOr a salt thereof.; or

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

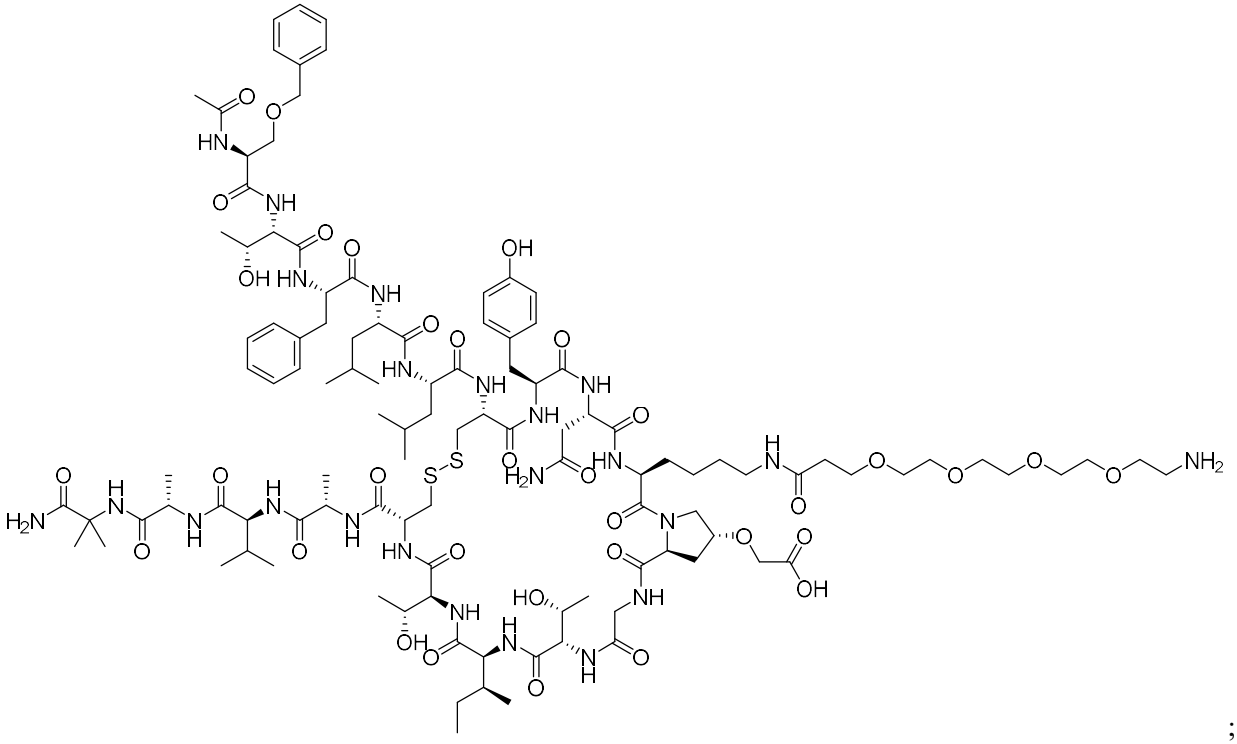


(I-34), or~~Or~~ a salt thereof.

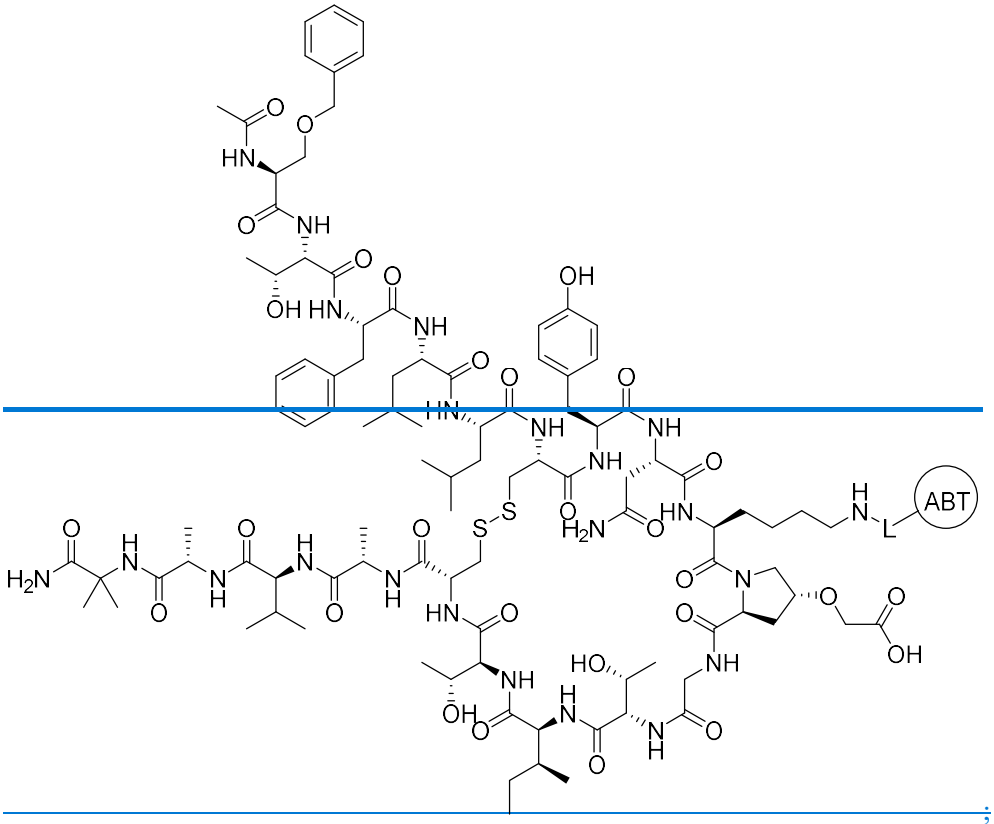
~~73.~~17. An agent~~, wherein the agent is~~ having any of the following structures or a salt thereof:~~, in the following list of agents L is a Linker, ABT is an antibody binding moiety, and AT is an antibody moiety,~~



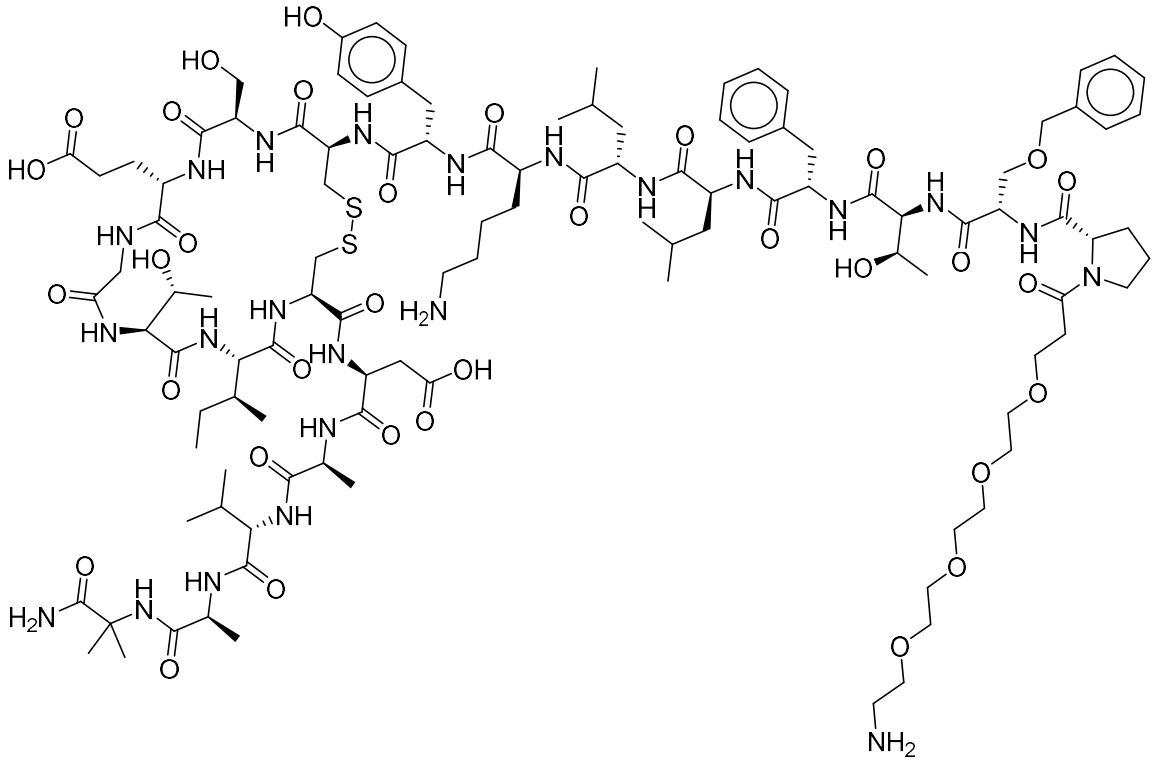
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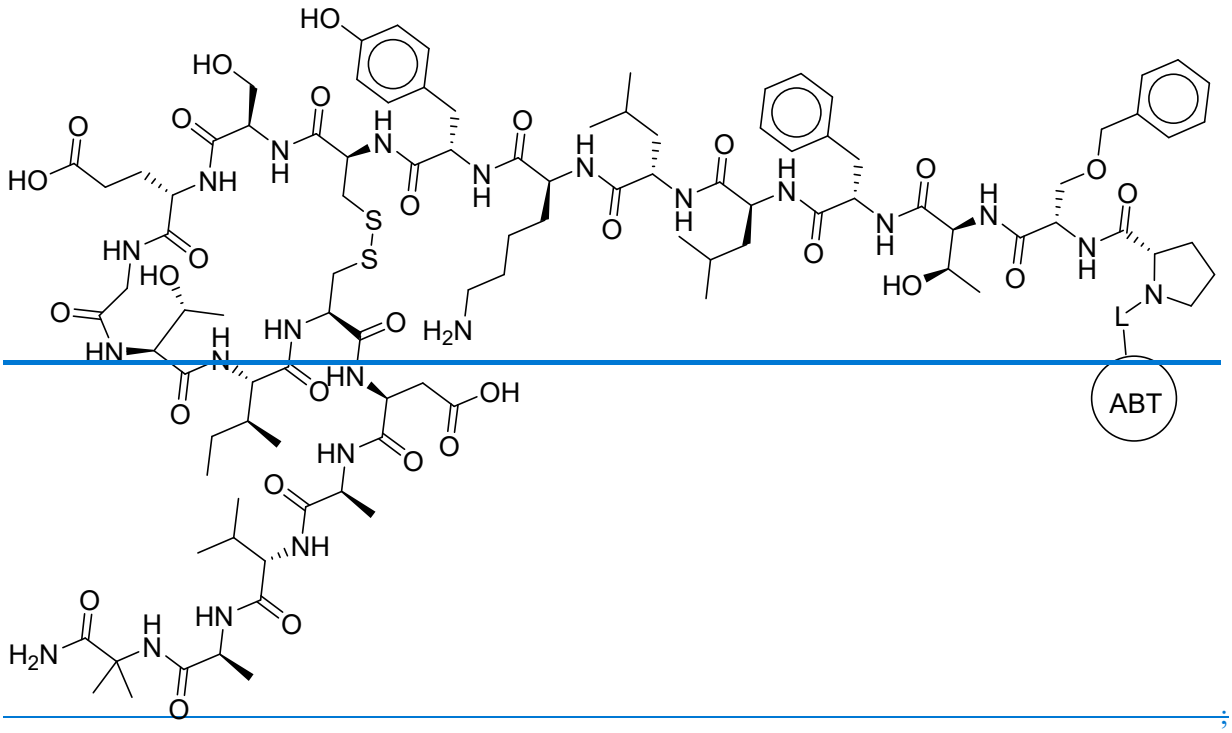
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ABT

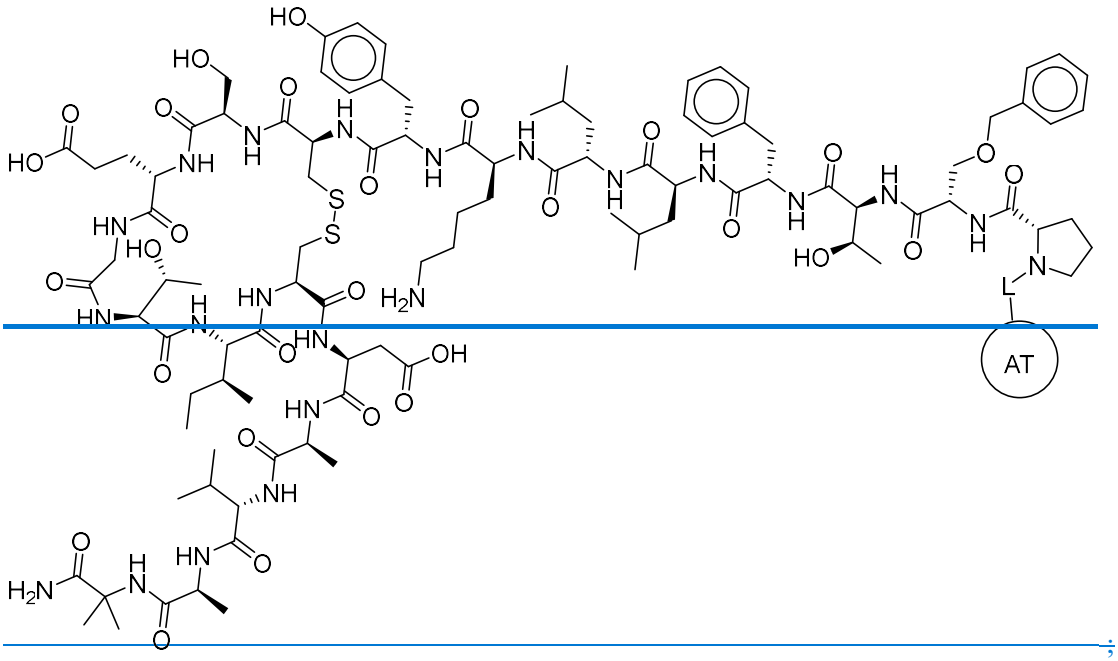
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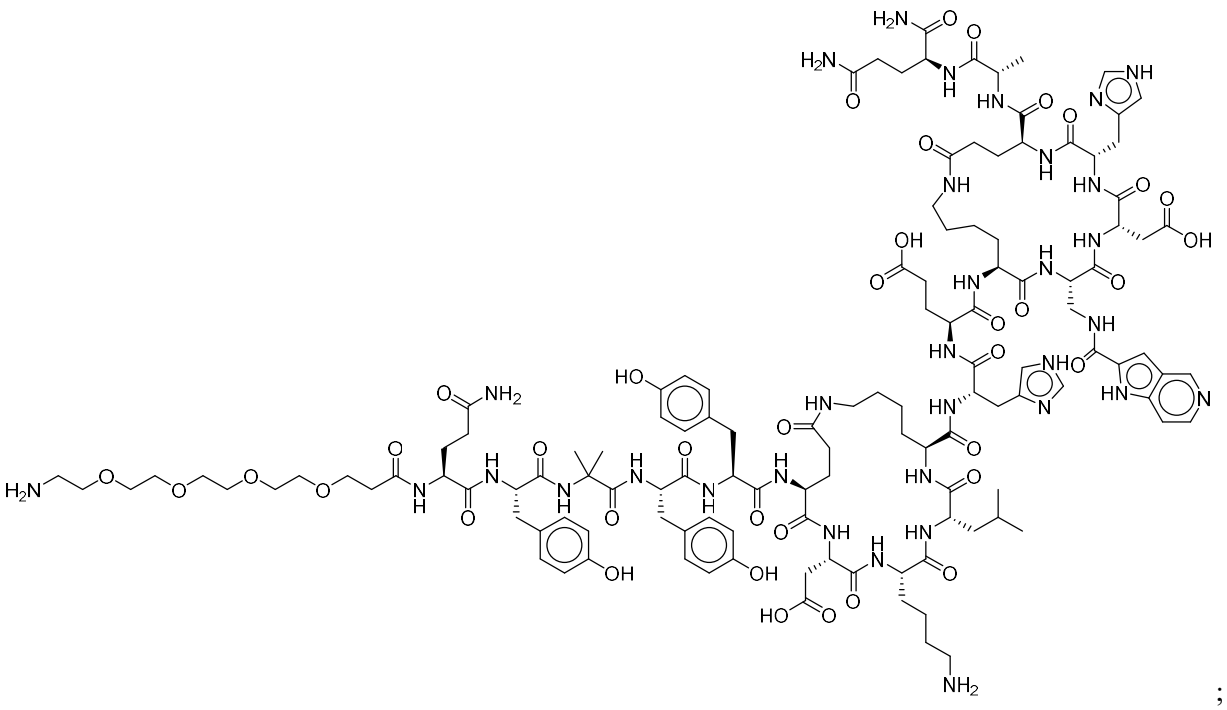
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ABT

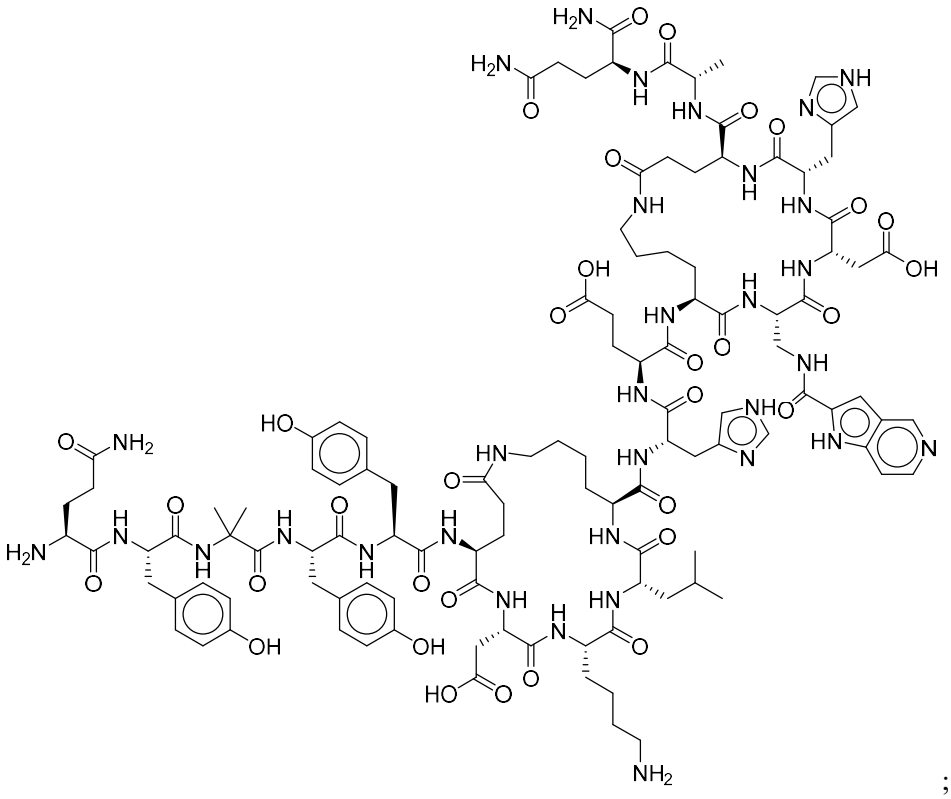
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AT

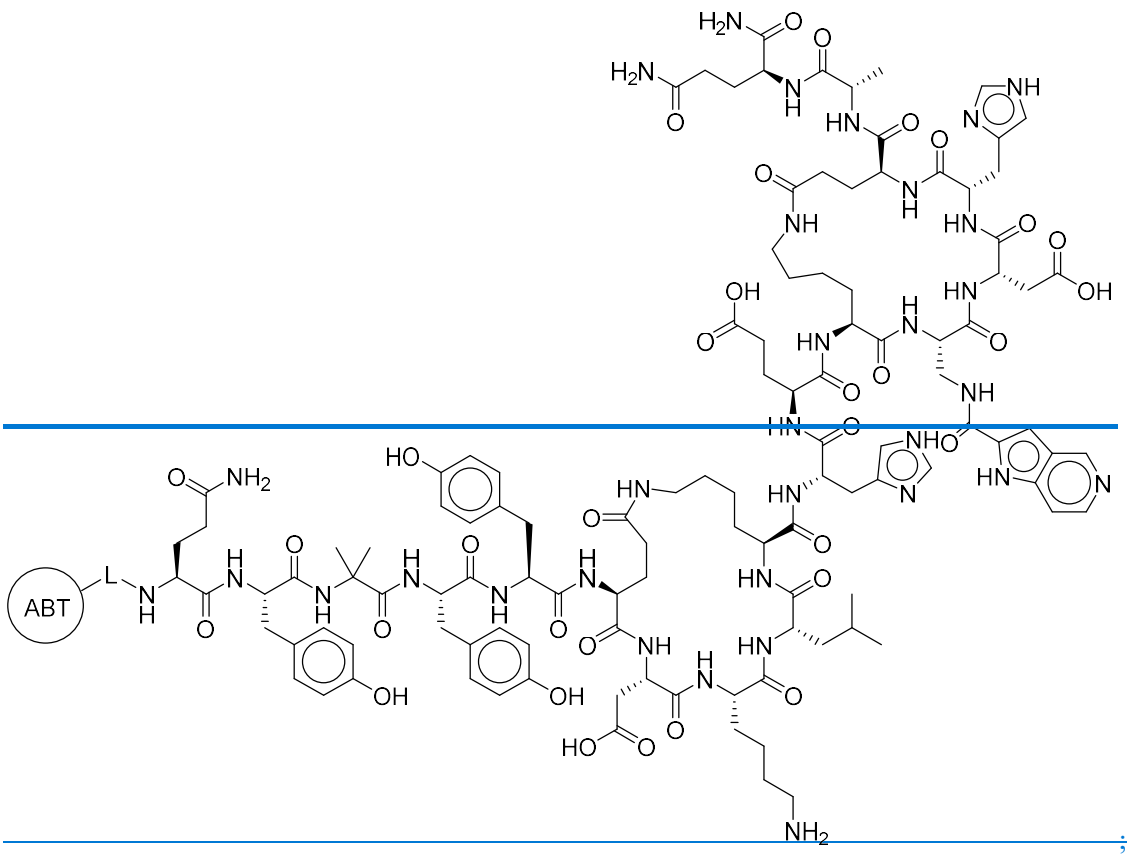
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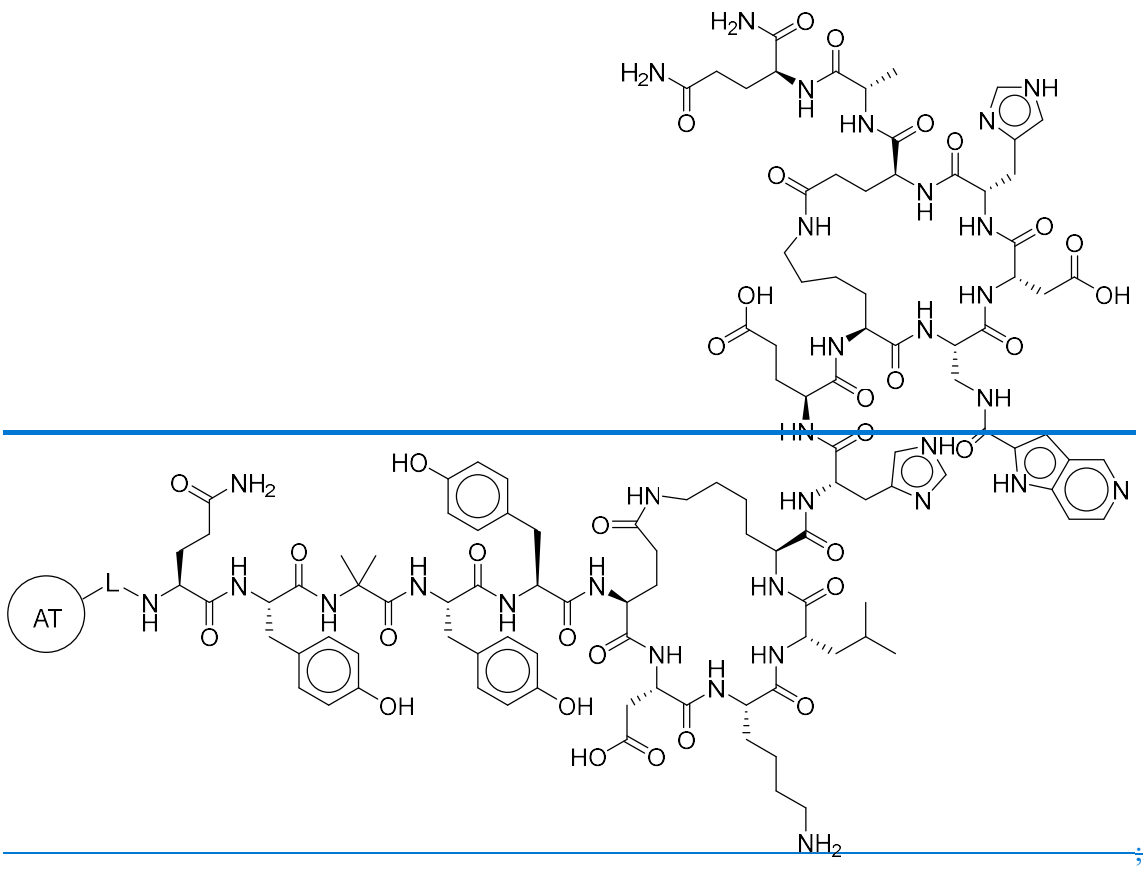
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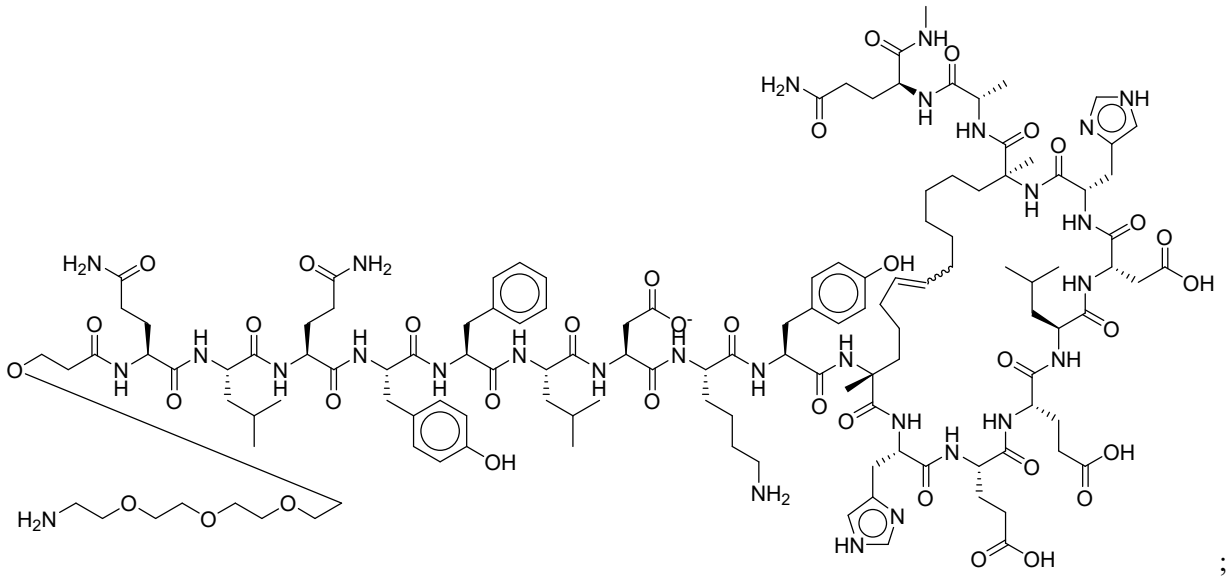


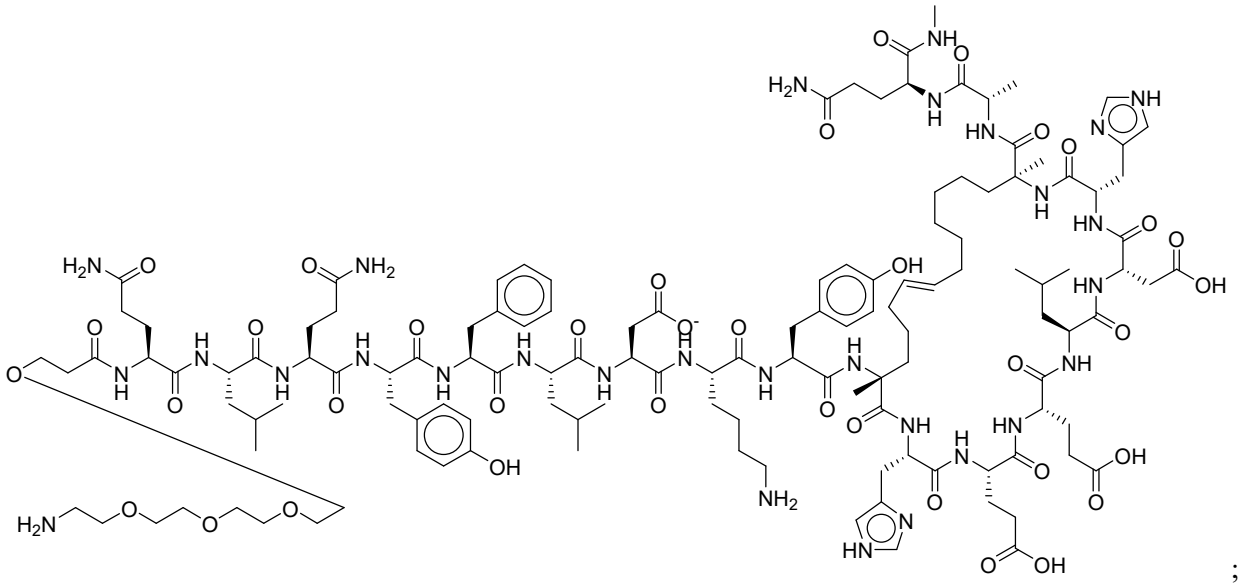
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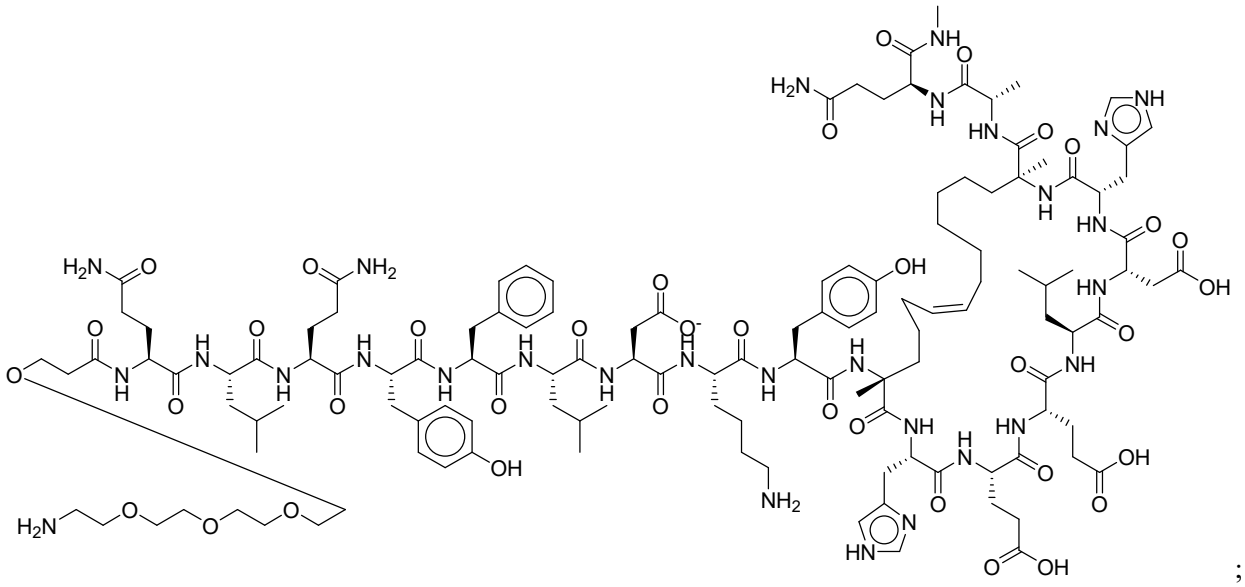

ABT
L

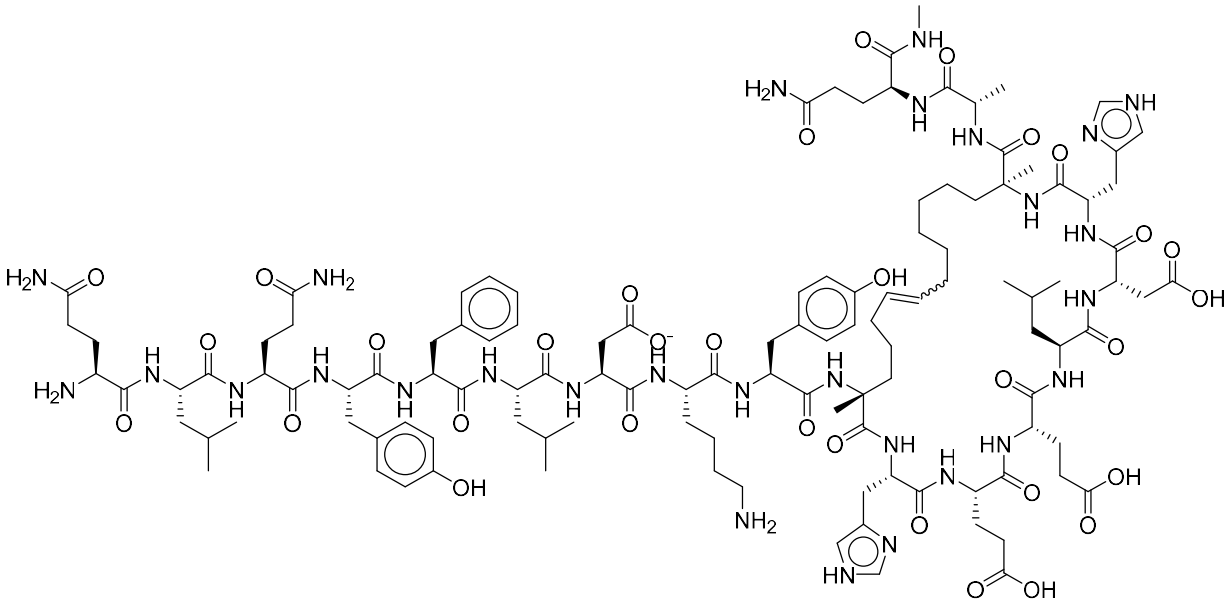
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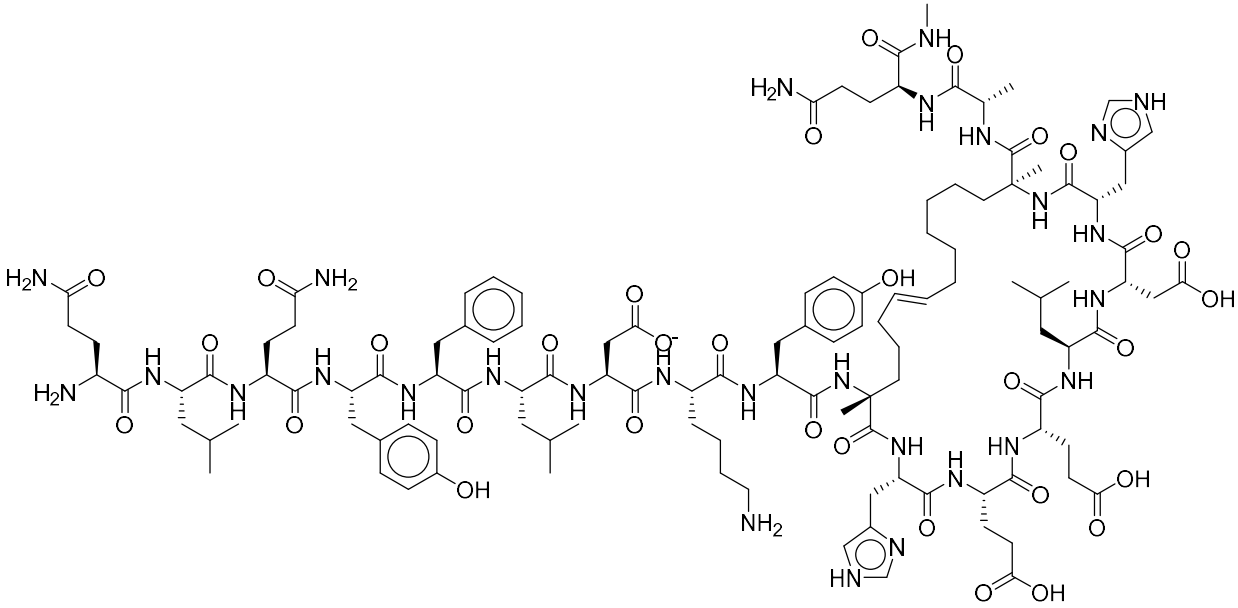

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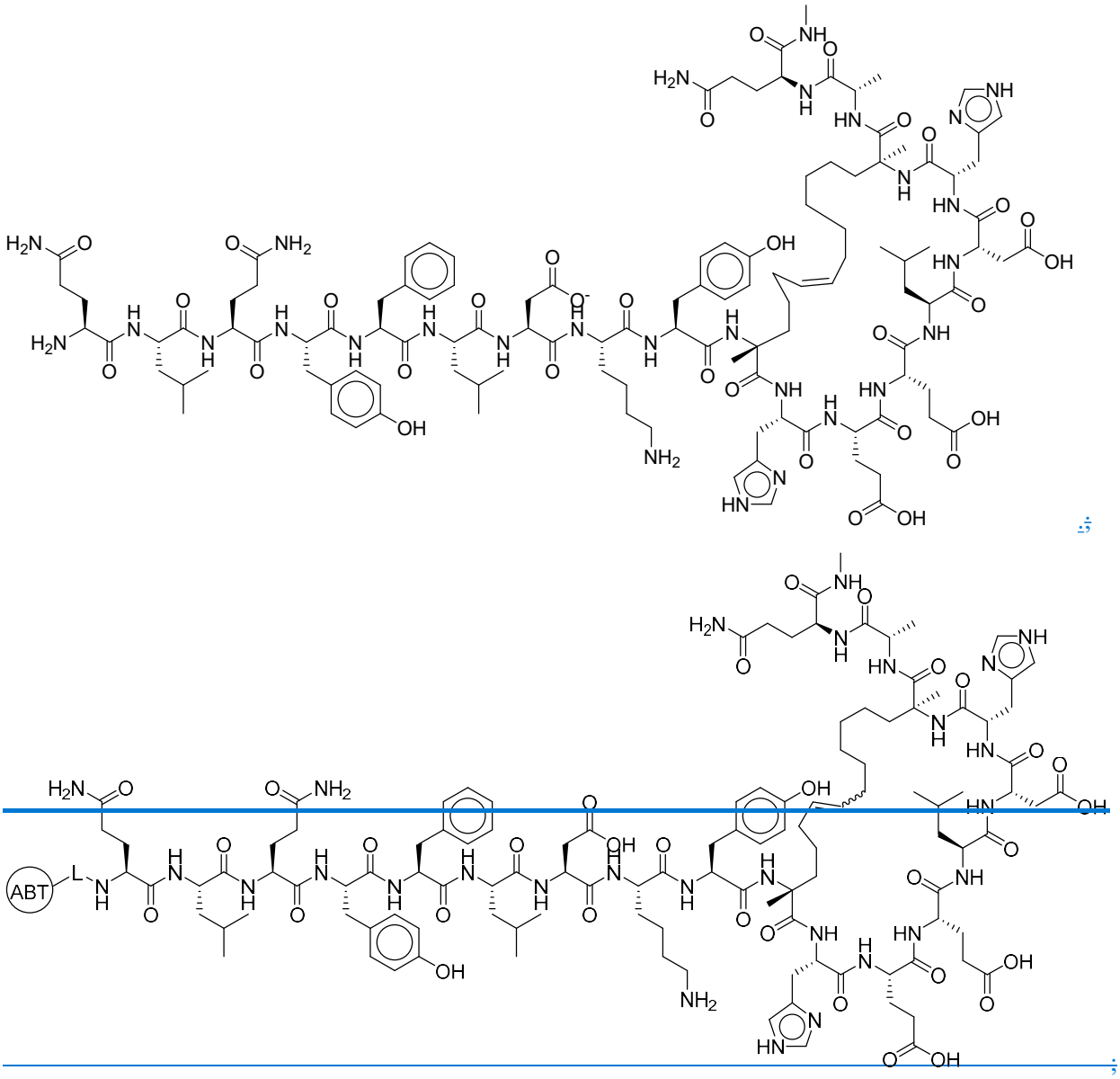


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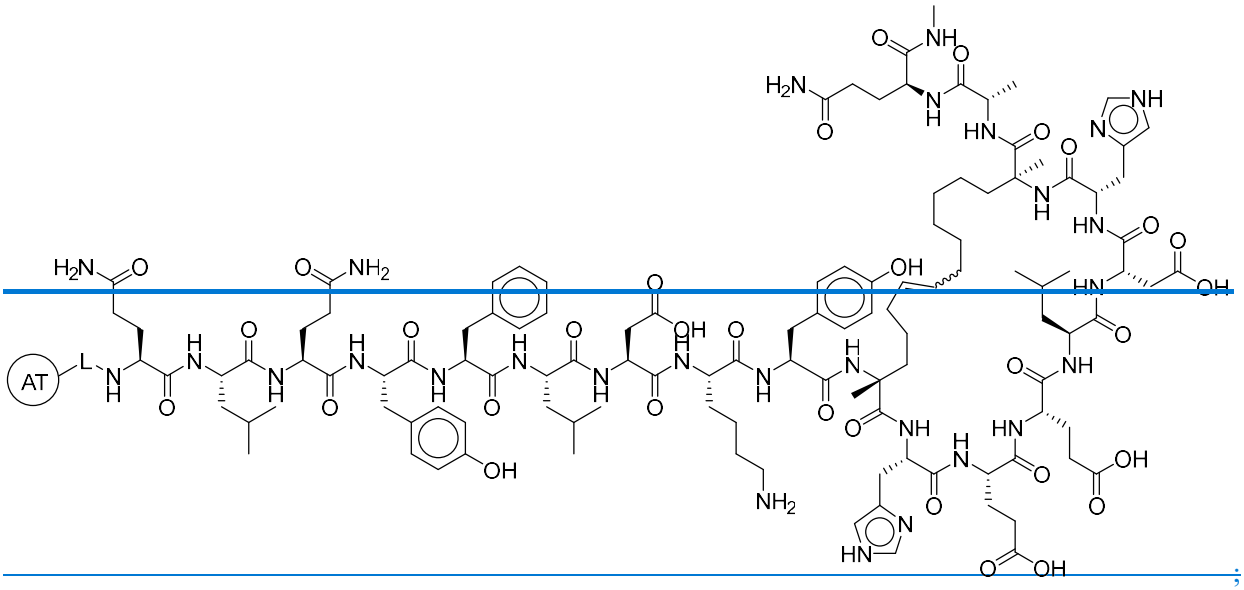


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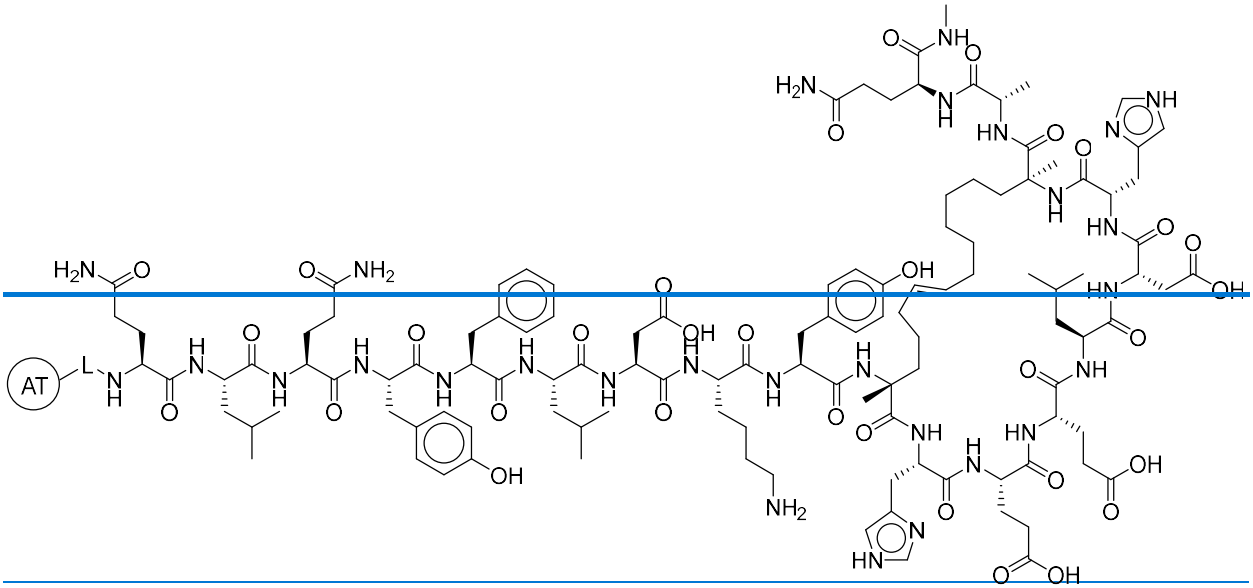
or

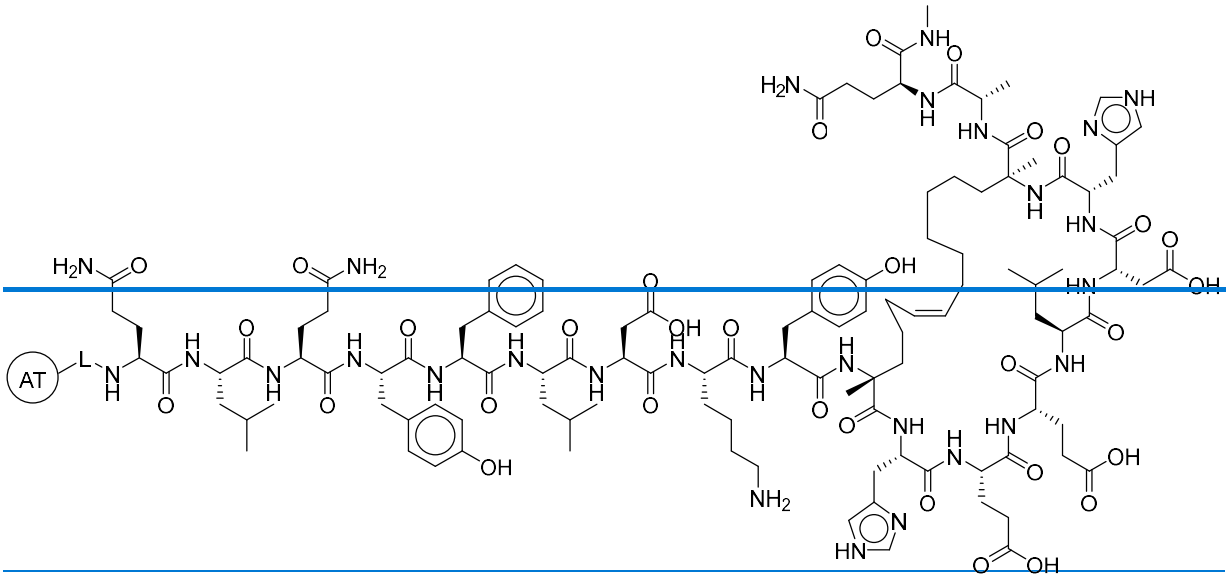


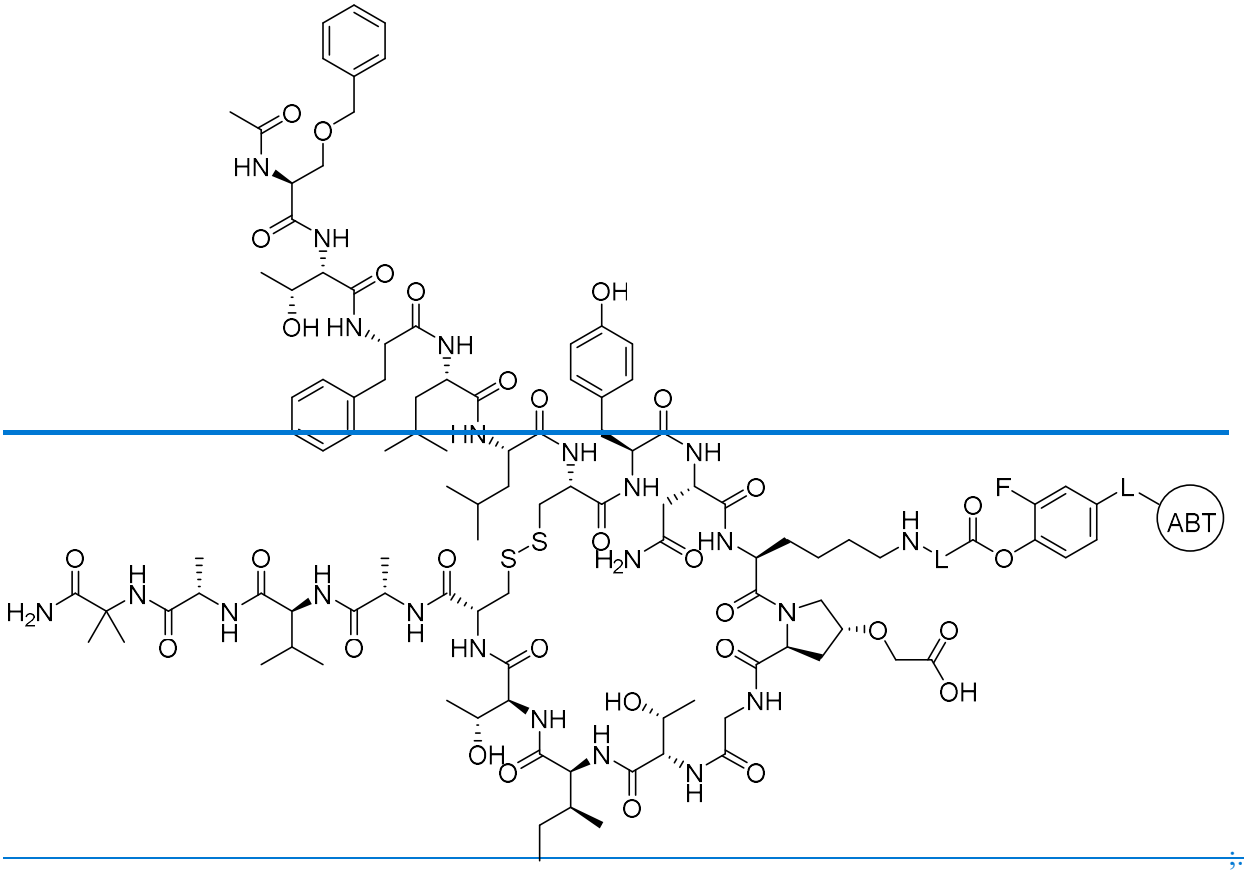



AT

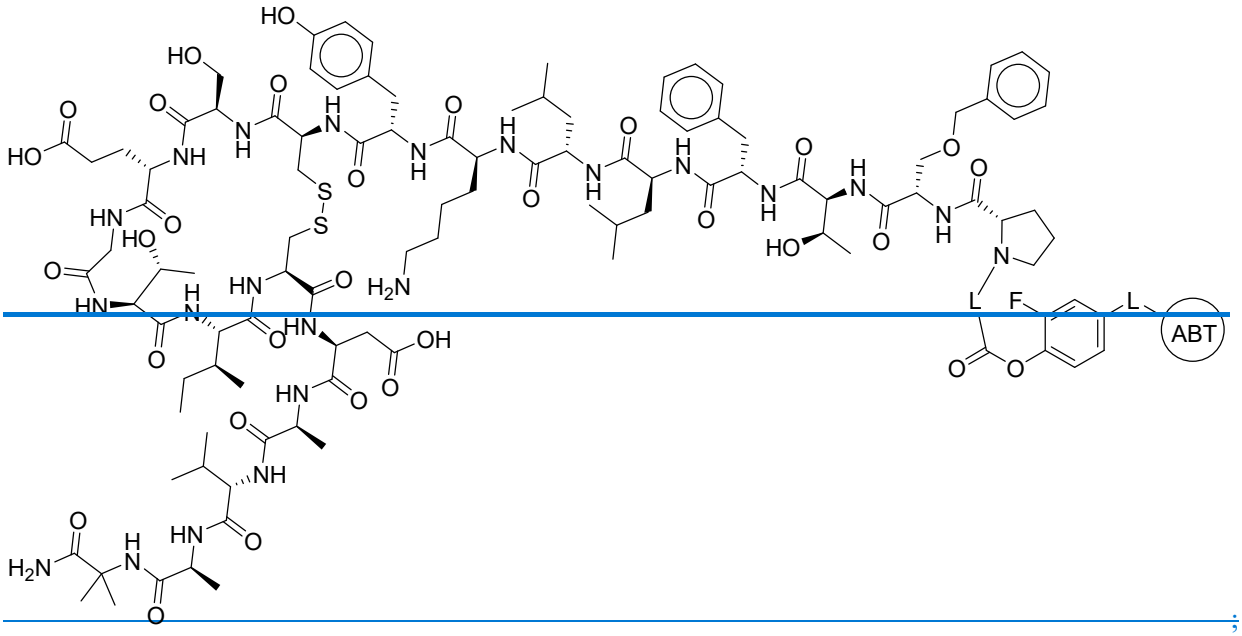
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AT

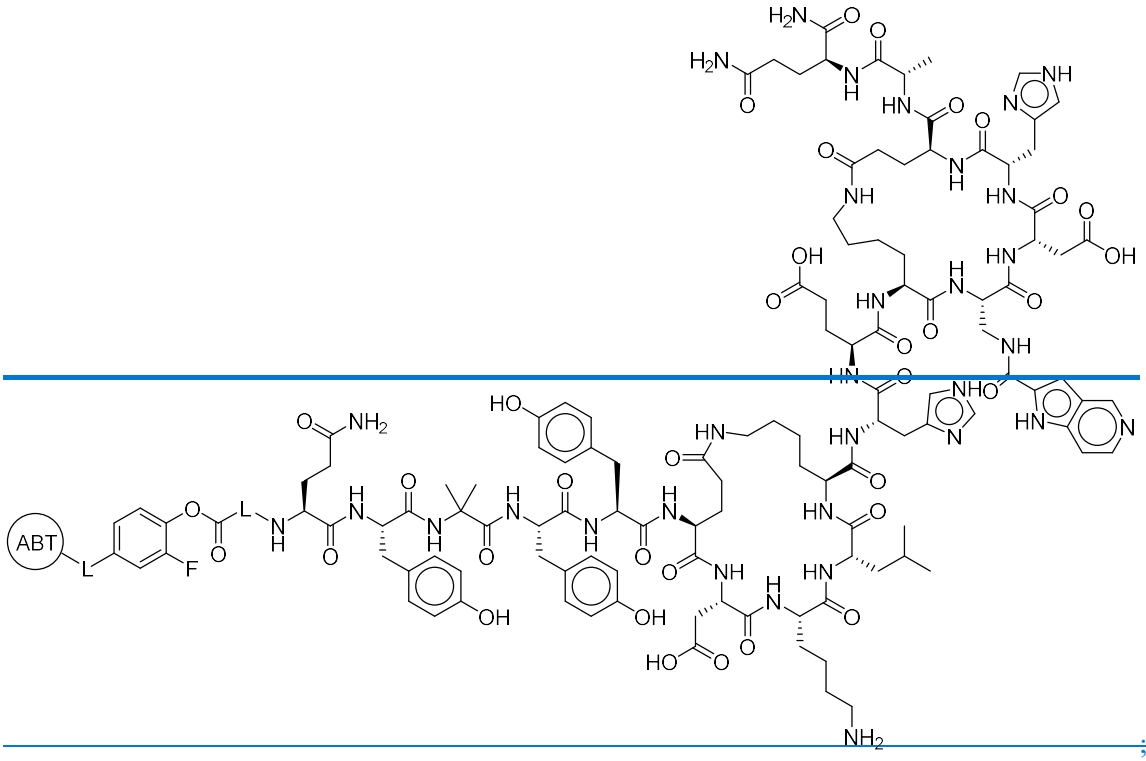

AT
L
NH2
OH
HN
O
NH
N


OH
NH
HN
O
S
S
F
L
ABT
N
H2N

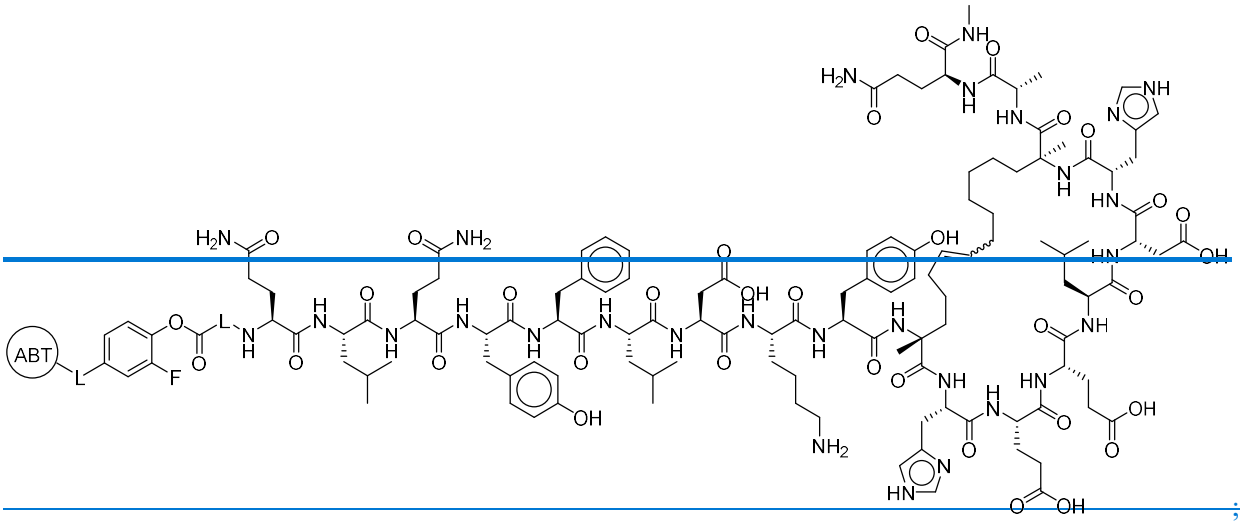
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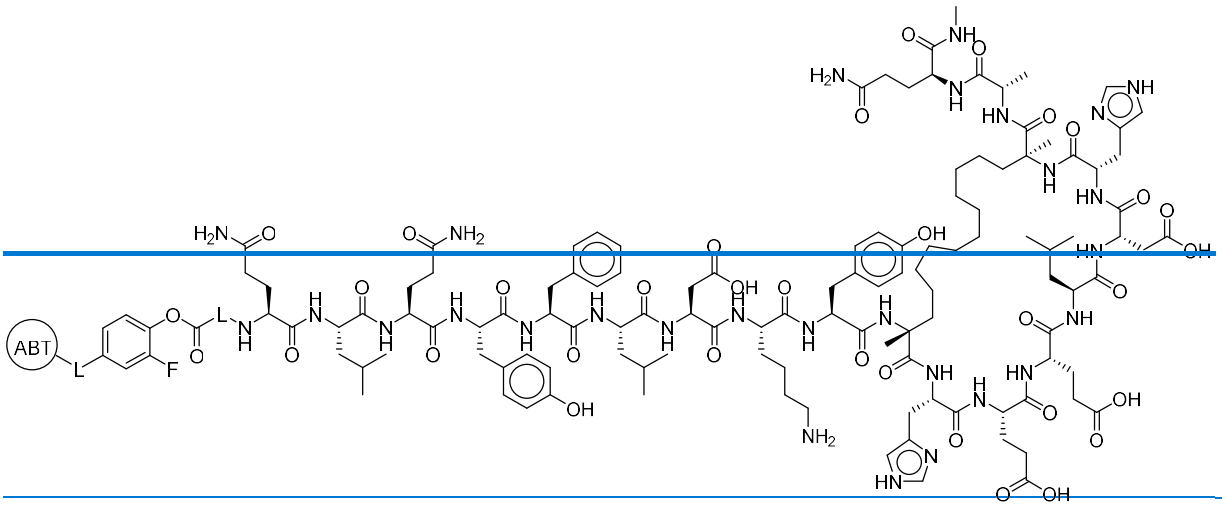


; ~~or~~

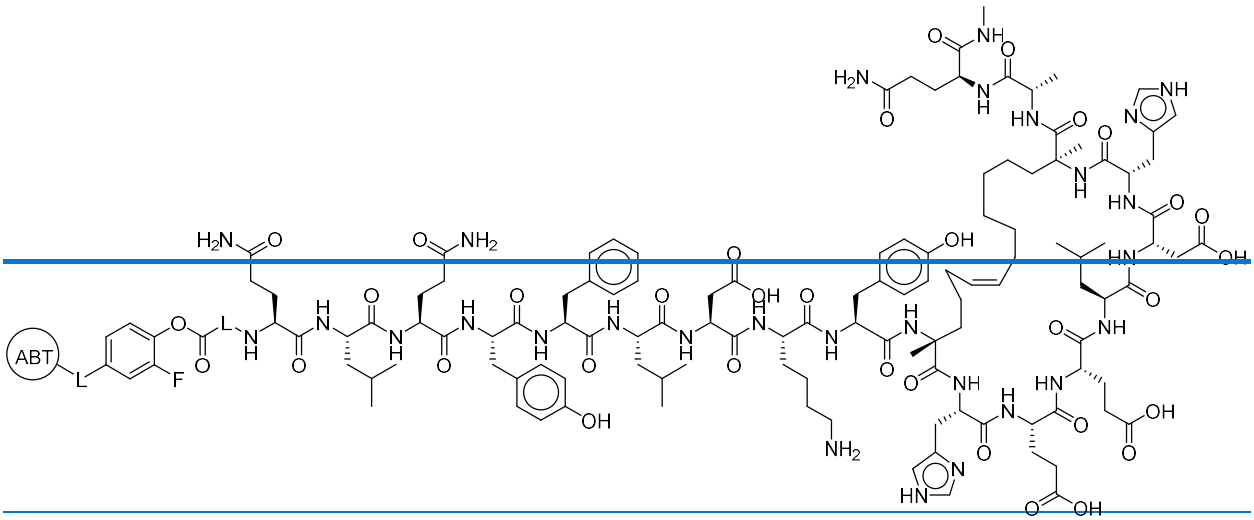


;

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~~18. A pharmaceutical composition, comprising an agent of ~~a preceding claims~~any one of claims 1-16, 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~~19. Use of an agent of any one of claims 1-16, or the pharmaceutical composition of claim 18, in the manufacture of a medicament for ~~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~~20. Use of an agent of any one of claims 1-16, or the pharmaceutical composition of claim 18, in the manufacture of a medicament ~~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~~21. The ~~method~~ use of claim ~~20~~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~~22. The ~~method~~ use of claim 20 or 21 ~~any one of claim 78-79~~, further comprising administering a population of immune cells (e.g., 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).

~~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.~~