CLAIMS

1. An amylin analogue which is a compound having the formula:

R^1-Z-R^2

wherein

R^1 is hydrogen, C_{1-4} acyl, benzoyl or C_{1-4} alkyl, or a half-life extending moiety M, wherein M is optionally linked to Z via a linker moiety L;

R^2 is OH or NHR^3, wherein R^3 is hydrogen or C_{1-3}-alkyl; and

Z is an amino acid sequence of formula I:

X1-X2-X3-X4-X5-X6-X7-Ala-Thr-X10-Arg-Leu-Ala-X14-Phe-Leu-X17-Arg-X19-X20-Phe-Gly(Me)-Ala-Ile(Me)-X27-Ser-Ser-Thr-Glu-X32-Gly-Ser-X35-Thr-X37 (I)

wherein

X1 is selected from the group consisting of Arg, Lys and Glu;

X3 is selected from the group consisting of Gly, Gln and Pro;

X4 is selected from the group consisting of Thr and Glu;

X5 is selected from the group consisting of Ala and Leu;

X6 is selected from the group consisting of Thr and Ser;

X10 is selected from the group consisting of Glu and Gln;

X14 is selected from the group consisting of Aad, His, Asp, Asn and Arg;

X17 is selected from the group consisting of Gln, His and Thr;

X19-X20 is selected from Ser-Ser, Thr-Thr, Ala-Thr, Ala-Ala, Gly-Thr, Gly-Gly and Ala-Asn or is absent;

X27 is selected from the group consisting of Leu and Pro;

X32 is selected from the group consisting of Val and Thr;

X35 is selected from the group consisting of Asn and Ser;

X37 is selected from the group consisting of Hyp and Pro; and

X2 and X7 are amino acid residues whose side chains together form a lactam bridge, wherein:

X2 is Asp and X7 is Lys;

X2 is Asp and X7 is Orn;

X2 is Asp and X7 is Dab;

X2 is Asp and X7 is hLys;

X2 is Dap and X7 is Aad;

X2 is Glu and X7 is Dab; or

X2 is Dab and X7 is Glu;

or a pharmaceutically acceptable salt or solvate thereof.

2. An amylin analogue or pharmaceutically acceptable salt according to claim 1 wherein:

(i) X1 is selected from Arg and Lys;

(ii) X3 is Gly, X4 is Thr, X5 is Ala and/or X6 is Thr;

(iii) X3 is Gly, X4 is Thr, X5 is Ala and X6 is Thr;

(iv) X14 is selected from His, Asp and Aad;

(v) X17 is Gln;

(vi) X19-X20 is selected from Ser-Ser and Thr-Thr, or is absent; and/or

(vii) X32 is Val, X35 is Asn and/or X37 is Hyp.

3. An amylin analogue or pharmaceutically acceptable salt according to claim 1 wherein Z is an amino acid sequence of formula II:

X1-X2-Gly-Thr-Ala-Thr-X7-Ala-Thr-X10-Arg-Leu-Ala-X14-Phe-Leu-Gln-Arg-X19-X20-Phe-Gly(Me)-Ala-Ile(Me)-X27-Ser-Ser-Thr-Glu-Val-Gly-Ser-Asn-Thr-Hyp (II)

wherein

X1 is selected from Arg and Lys;

X10 is selected from the group consisting of Glu and Gln;

X14 is selected from the group consisting of Aad, Asp and His;

X19-X20 is selected from Ser-Ser and Thr-Thr or is absent;

X27 is selected from the group consisting of Leu and Pro; and

X2 and X7 are amino acid residues whose side chains together form a lactam bridge, wherein:

X2 is Asp and X7 is Lys;

X2 is Asp and X7 is Orn;

X2 is Asp and X7 is Dab;

X2 is Asp and X7 is hLys;

X2 is Dap and X7 is Aad;

X2 is Glu and X7 is Dab; or

X2 is Dab and X7 is Glu.

4. An amylin analogue or pharmaceutically acceptable salt according to claim 3 wherein X14 is Aad, X19-X20 is Ser-Ser and X27 is Leu.

5. An amylin analogue or pharmaceutically acceptable salt according to claim 1 wherein Z is an amino acid sequence selected from the group consisting of:

RD()GTAT-Dab()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLAHFLQRF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLAHFLHRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNTP;

RD()GTAT-Orn()-ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLARFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

ED()GTATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GEATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTLTK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTASK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp;

RD()GTATK()ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp;

RD()GTATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-hLys()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLA-Aad-FLTRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSST-Hyp;

RD()GTAT-Orn()-ATERLA-Aad-FLQRTTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLA-Aad-FLQRTTF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLA-Aad-FLQRATF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLA-Aad-FLQRAAF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTAT-Orn()-ATERLA-Aad-FLQRGTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()QTAT-Orn()-ATERLA-Aad-FLQRGTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()PTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

ED()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp;

RD()GTATK()ATERLA-Aad-FLQRAAF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATERLA-Aad-FLQRGGF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATERLA-Aad-FLQRANF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp;

RD()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTETGSNT-Hyp;

ED()GTATK()ATERLA-Aad-FLQRSSFGly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATERLA-Aad-FLQRTTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

KD()GTATK()ATQRLA-Aad-FLQRSSF-Gly(Me)-AIle(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATQRLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATQRLADFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

RD()GTATK()ATQRLADFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTETGSNT-Hyp;

KD()GTATK()ATQRLANFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

KD()GTATK()ATQRLANFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTETGSNT-Hyp;

R-Dap()-GTAT-Aad()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

R-Dab()-GTATE()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp; and

RE()GTAT-Dab()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp;

wherein parentheses "()" indicate an intramolecular lactam bridge formed between the side chains of the residues at positions 2 and 7.

6. An amylin analogue or pharmaceutically acceptable salt according to any one of the preceding claims wherein R^1 is M or M-L-.

7. An amylin analogue or pharmaceutically acceptable salt according to claim 6 wherein M is a lipophilic substituent comprising a hydrocarbon chain having from 10 to 24 C atoms, e.g. from 14 to 22 C atoms, e.g. from 16 to 20 C atoms, wherein the lipophilic substituent optionally comprises a carboxylic acid group at the end of the hydrocarbon chain, and further optionally wherein the lipophilic substituent is a 15-carboxy-pentadecanoyl, 17-carboxy-heptadecanoyl or 19-carboxy-nonadecanoyl moiety.

8. An amylin analogue or pharmaceutically acceptable salt according to claim 6 or claim 7 wherein the linker L comprises a residue of Gly, Pro, Ala, Val, Leu, Ile, Met, Cys, Phe, Tyr, Trp, His, Lys, Arg, Gln, Asn, α-Glu, γ-Glu, ε-Lys, Asp, β-Asp, Ser, Thr, Gaba, Aib, β-Ala (i.e. 3-aminopropanoyl), 4-aminobutanoyl, 5-aminopentanoyl, 6-aminohexanoyl, 7-aminoheptanoyl, 8-aminooctanoyl, 9- aminononanoyl, 10-aminodecanoyl or 8Ado (i.e. 8-amino-3,6-dioxaoctanoyl), e.g. wherein L is a residue of Glu, γ-Glu, ε -Lys, β-Ala, 4-aminobutanoyl, 8-aminooctanoyl or 8Ado.

9. An amylin analogue or pharmaceutically acceptable salt according to claim 8 wherein R1 is a 19-carboxy-nonadecanoyl group covalently attached to the alpha amino group of an iso-glutamic acid linker ([19CD]-isoGlu).

10. An amylin analogue or pharmaceutically acceptable salt according to any one of the preceding claims wherein R^2 is NH_2.

11. An amylin analogue according to claim 1 which is:

[19CD]-isoGlu-RD()GTAT-Dab()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 2)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 3)

[19CD]-isoGlu-isoGlu-RD()GTAT-Orn()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 4)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2 (Compound 5)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLAHFLQRF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 6)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLAHFLHRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNTP-NH_2 (Compound 7)

[19CD]-isoGlu-RD()GTAT-Orn()-ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 8)

[19CD]-isoGlu-RD()GTAT-Orn()-ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2 (Compound 9)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLARFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 10)

[19CD]-isoGlu-ED()GTATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 11)

[19CD]-isoGlu-RD()GEATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 12)

[19CD]-isoGlu-RD()GTLTK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 13)

[19CD]-isoGlu-RD()GTASK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 14)

[19CD]-isoGlu-RD()GTATK()ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2 (Compound 15)

[19CD]-isoGlu-RD()GTATK()ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 16)

[19CD]-isoGlu-RD()GTATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2 (Compound 17)

[19CD]-isoGlu-RD()GTATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 18)

[19CD]-isoGlu-RD()GTAT-hLys()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 19)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 20)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2 (Compound 21)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLTRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSST-Hyp-NH_2 (Compound 22)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLQRTTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 23)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLQRTTF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2 (Compound 24)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLQRATF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 25)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLQRAAF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 26)

[19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLQRGTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH2 (Compound 27)

[19CD]-isoGlu-RD()QTAT-Orn()-ATERLA-Aad-FLQRGTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 28)

[19CD]-isoGlu-RD()PTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 29)

[19CD]-isoGlu-ED()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2 (Compound 30)

[19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRAAF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 31)

[19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRGGF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 32)

[19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRANF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 33)

[19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2 (Compound 34)

[19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 35)

[19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTETGSNT-Hyp-NH_2 (Compound 36)

[19CD]-isoGlu-ED()GTATK()ATERLA-Aad-FLQRSSFGly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 37)

[19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRTTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 38)

[19CD]-isoGlu-KD()GTATK()ATQRLA-Aad-FLQRSSF-Gly(Me)-AIle(Me)-LSSTEVGSNTHyp-NH_2 (Compound 39)

[19CD]-isoGlu-RD()GTATK()ATQRLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 40)

[19CD]-isoGlu-RD()GTATK()ATQRLADFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 41)

[19CD]-isoGlu-RD()GTATK()ATQRLADFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTETGSNT-Hyp-NH_2 (Compound 42)

[19CD]-isoGlu-KD()GTATK()ATQRLANFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 43)

[19CD]-isoGlu-KD()GTATK()ATQRLANFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTETGSNT-Hyp-NH_2 (Compound 44)

[19CD]-isoGlu-R-Dap()-GTAT-Aad()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 48)

[19CD]-isoGlu-R-Dab()-GTATE()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 49)

[19CD]-isoGlu-RE()GTAT-Dab()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2 (Compound 51)

or a pharmaceutically acceptable salt or solvate thereof; wherein parentheses "()" indicate an intramolecular lactam bridge formed between the side chains of the residues at positions 2 and 7.

12. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTATK()ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-PSSTEVGSNT-Hyp-NH_2.

13. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTATK()ATQRLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

14. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTATK()ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

15. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTAT-hLys()-ATERLAHFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

16. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTAT-Orn()-ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

17. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

18. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTETGSNT-Hyp-NH_2.

19. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTATK()ATERLA-Aad-FLQRTTF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

20. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-KD()GTATK()ATQRLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

21. An amylin analogue according to claim 1 which is: [19CD]-isoGlu-RD()GTATK()ATQRLA-Aad-FLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

22. An amylin analogue according to claim 1 which is:
[19CD]-isoGlu-RD()GTATK()ATQRLADFLQRSSF-Gly(Me)-A-Ile(Me)-LSSTEVGSNT-Hyp-NH_2.

23. A pharmaceutically acceptable salt of an amylin analogue according to any one of claims 12 to 22.

24. A pharmaceutical composition comprising an amylin analogue or pharmaceutically acceptable salt according to any one of the preceding claims in combination with a pharmaceutically acceptable carrier, excipient or vehicle.

25. A method for the synthesis of an amylin analogue or pharmaceutically acceptable salt according to any one of claims 1 to 22 comprising synthesising the analogue by solid-phase or liquid-phase peptide synthesis methodology, optionally isolating and/or purifying the final product, and optionally further comprising the step of forming an amide bond between the side chains at positions 2 and 7.

26. An amylin analogue or pharmaceutically acceptable salt according to any one of claims 1 to 23 for use in a method of medical treatment.

27. Use of an amylin analogue or pharmaceutically acceptable salt according to any one of claims 1 to 23 in the manufacture of a medicament for:
(i) a therapeutic method of treating, inhibiting or reducing weight gain, promoting weight loss and/or reducing excess body weight;
(ii) treating obesity, morbid obesity, obesity prior to surgery, obesity-linked inflammation, obesity-linked gallbladder disease and obesity-induced sleep apnea and respiratory problems, degeneration of cartilage, osteoarthritis, or reproductive health complications of obesity or overweight;
(iii) preventing or treating Alzheimer's disease, diabetes, type 1 diabetes, type 2 diabetes, pre-diabetes, insulin resistance syndrome, impaired glucose tolerance (IGT), disease states associated with elevated blood glucose levels, metabolic disease including metabolic syndrome, hyperglycemia, hypertension, atherogenic dyslipidemia, hepatic steatosis ("fatty liver"; including non-alcoholic fatty liver disease (NAFLD), which itself includes non-alcoholic steatohepatitis (NASH)), kidney failure, arteriosclerosis (e.g. atherosclerosis), macrovascular disease, microvascular disease, diabetic heart disease (including diabetic cardiomyopathy and heart failure

as a diabetic complication), coronary heart disease, peripheral artery disease or stroke, and combinations thereof; or

(iv) a therapeutic method of lowering circulating LDL levels and/or increasing HDL/LDL ratio.

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