CLAIMS

That which is claimed:

1. A polypeptide comprising the amino acid sequence:
ProLysProGluXaa$_1$ProGlyXaa$_2$AspAlaSerXaa$_3$GluGluXaa$_4$Xaa$_5$Xaa$_6$TyrTyrAla Xaa$_7$LeuArgXaa$_8$TyrXaa$_9$ AsnTrpXaa$_{10}$ThrArgGlnArgTyr (SEQ ID NO:1)
or a salt thereof, wherein:
Xaa$_1$ is Ala, His, or Ser;
Xaa$_2$ is Glu or Lys;
Xaa$_3$ is Pro or Ala;
Xaa$_4$ is Leu or Trp;
Xaa$_5$ is Asn, Ala, or Thr;
Xaa$_6$ is Arg or Lys;
Xaa$_7$ is Ser, Asp, or Ala;
Xaa$_8$ is His or Lys;
Xaa$_9$ is Leu or Ile; and
Xaa$_{10}$ is Val or Leu.

2. A polypeptide consisting of the amino acid sequence:
ProLysProGluXaa$_1$ProGlyXaa$_2$AspAlaSerXaa$_3$GluGlu Xaa$_4$Xaa$_5$ Xaa$_6$TyrTyrAlaXaa$_7$LeuArg Xaa$_8$Tyr Xaa$_9$ AsnTrp Xaa$_{10}$ThrArgGlnArgTyr –NH$_2$ (SEQ ID NO:2) or a salt thereof, wherein:
Xaa$_1$ is Ala, His, or Ser;
Xaa$_2$ is Glu or Lys;
Xaa$_3$ is Pro or Ala;
Xaa$_4$ is Leu or Trp;
Xaa$_5$ is Asn, Ala, or Thr;
Xaa$_6$ is Arg or Lys;
Xaa$_7$ is Ser, Asp, or Ala;
Xaa$_8$ is His or Lys;
Xaa$_9$ is Leu or Ile; and
Xaa$_{10}$ is Val or Leu.

3. The polypeptide of claim 2 which is selected from the group consisting of:
ProLysProGluAlaProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:3),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:4),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:5),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgLysTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:6),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:7),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ IDNO:8),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:9),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:10),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:11),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:12),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:13),
ProLysProGluAlaProGlyGluAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:14),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AlaLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:15),
ProLysProGluHisProGlyLysAspAlaSerProGluGluLeuAsnLysTyrTyrAla
AlaLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:16),
ProLysProGluHisProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:17),
ProLysProGluHisProGlyLysAspAlaSerProGluGluLeuAlaArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:18),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla

SerLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:19),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:20),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:21),
ProLysProGluSerProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:22),
ProLysProGluSerProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:23),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:24),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAlaLysTyrTyrAla
AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:25),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:26),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:27),
ProLysProGluHisProGlyLysAspAlaSerAlaGluGluTrpAlaLysTyrTyrAla
AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:28),
ProLysProGluAlaProGlyLysAspAlaSerAlaGluGluTrpAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:29),
ProLysProGluHisProGlyLysAspAlaSerAlaGluGluLeuAlaArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:30),
ProLysProGluAlaProGlyLysAspAlaSerAlaGluGluTrpAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:31),
ProLysProGluSerProGlyLysAspAlaSerAlaGluGluTrpThrLysTyrTyrAla
AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:32),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:33),
ProLysProGluHisProGlyGluAspAlaSerProGluGluTrpAlaLysTyrTyrAla
AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:34),
ProLysProGluAlaProGlyGluAspAlaSerAlaGluGluTrpAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:35),
ProLysProGluSerProGlyGluAspAlaSerProGluGluTrpThrLysTyrTyrAla

AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:36), and ProLysProGluAlaProGlyGluAspAlaSerProGluGluTrpAsnArgTyrTyrAla AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:37).

4. The polypeptide of claim 1 which comprises the amino acid sequence: ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr (SEQ IDNO:38).

5. The polypeptide of claim 1 which consists of the amino acid sequence: ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr (SEQ IDNO:38).

6. The polypeptide of claim 2 which consists of the amino acid sequence: ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:7).

7. A pharmaceutical combination comprising a polypeptide according to any one of claims 1-6 and exendin-4.

8. A pharmaceutical combination comprising a polypeptide according to any one of claims 1-6 and GLP-1.

9. A pharmaceutical composition comprising a polypeptide according to any one of claims 1-6 and a pharmaceutically acceptable carrier.

10. A method of treating a metabolic disorder in a human subject, said method comprising administering a polypeptide or pharmaceutical combination of any one of claims 1-8 to a subject in need thereof.

11. A method of treating obesity in a human subject, said method comprising administering a polypeptide or pharmaceutical combination of any one of claims 1-8 to a subject in need thereof.

12. Use of a polypeptide or pharmaceutical combination of any one of claims 1-8 in the preparation of a medicament for use in the treatment of a metabolic disorder.

13. Use of a polypeptide or pharmaceutical combination of any one of claims 1-8 in the preparation of a medicament for use in the treatment of obesity

14. A polypeptide or pharmaceutical combination according to any one of claims 1-8 for use in the treatment of a metabolic disorder.

15. A polypeptide or pharmaceutical combination according to any one of claims 1-8 for use in the treatment of obesity.

16. The method or use of any one of claims 10, 12, or 14 where the metabolic disorder is Type 2 Diabetes Mellitus.

17. A nucleic acid molecule encoding a polypeptide sequence according to any one of claims 1-6.

18. An expression vector comprising a nucleic acid molecule according to claim 17.

19. A host cell containing an expression vector according to claim 18.

CLAIMS

That which is claimed:

1. A polypeptide comprising the amino acid sequence:
ProLysProGluXaa$_1$ProGlyXaa$_2$AspAlaSerXaa$_3$GluGluXaa$_4$Xaa$_5$Xaa$_6$TyrTyrAla Xaa$_7$LeuArgXaa$_8$TyrXaa$_9$ AsnTrpXaa$_{10}$ThrArgGlnArgTyr (SEQ ID NO:1)
or a salt thereof, wherein:
Xaa$_1$ is Ala, His, or Ser;
Xaa$_2$ is Glu or Lys;
Xaa$_3$ is Pro or Ala;
Xaa$_4$ is Leu or Trp;
Xaa$_5$ is Asn, Ala, or Thr;
Xaa$_6$ is Arg or Lys;
Xaa$_7$ is Ser, Asp, or Ala;
Xaa$_8$ is His or Lys;
Xaa$_9$ is Leu or Ile; and
Xaa$_{10}$ is Val or Leu.

2. A polypeptide consisting of the amino acid sequence:
ProLysProGluXaa$_1$ProGlyXaa$_2$AspAlaSerXaa$_3$GluGlu Xaa$_4$Xaa$_5$ Xaa$_6$TyrTyrAlaXaa$_7$LeuArg Xaa$_8$Tyr Xaa$_9$ AsnTrp Xaa$_{10}$ThrArgGlnArgTyr –NH$_2$ (SEQ ID NO:2) or a salt thereof, wherein:
Xaa$_1$ is Ala, His, or Ser;
Xaa$_2$ is Glu or Lys;
Xaa$_3$ is Pro or Ala;
Xaa$_4$ is Leu or Trp;
Xaa$_5$ is Asn, Ala, or Thr;
Xaa$_6$ is Arg or Lys;
Xaa$_7$ is Ser, Asp, or Ala;
Xaa$_8$ is His or Lys;
Xaa$_9$ is Leu or Ile; and
Xaa$_{10}$ is Val or Leu.

3. The polypeptide of claim 2 which is selected from the group consisting of:
ProLysProGluAlaProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:3),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:4),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:5),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgLysTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:6),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:7),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ IDNO:8),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:9),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:10),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:11),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:12),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:13),
ProLysProGluAlaProGlyGluAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:14),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AlaLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:15),
ProLysProGluHisProGlyLysAspAlaSerProGluGluLeuAsnLysTyrTyrAla
AlaLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:16),
ProLysProGluHisProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:17),
ProLysProGluHisProGlyLysAspAlaSerProGluGluLeuAlaArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:18),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla

SerLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:19),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:20),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:21),
ProLysProGluSerProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:22),
ProLysProGluSerProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:23),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:24),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAlaLysTyrTyrAla
AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:25),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
AspLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:26),
ProLysProGluHisProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:27),
ProLysProGluHisProGlyLysAspAlaSerAlaGluGluTrpAlaLysTyrTyrAla
AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:28),
ProLysProGluAlaProGlyLysAspAlaSerAlaGluGluTrpAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:29),
ProLysProGluHisProGlyLysAspAlaSerAlaGluGluLeuAlaArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:30),
ProLysProGluAlaProGlyLysAspAlaSerAlaGluGluTrpAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:31),
ProLysProGluSerProGlyLysAspAlaSerAlaGluGluTrpThrLysTyrTyrAla
AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:32),
ProLysProGluAlaProGlyLysAspAlaSerProGluGluLeuAsnArgTyrTyrAla
SerLeuArgLysTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:33),
ProLysProGluHisProGlyGluAspAlaSerProGluGluTrpAlaLysTyrTyrAla
AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:34),
ProLysProGluAlaProGlyGluAspAlaSerAlaGluGluTrpAsnArgTyrTyrAla
SerLeuArgHisTyrLeuAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:35),
ProLysProGluSerProGlyGluAspAlaSerProGluGluTrpThrLysTyrTyrAla

AlaLeuArgHisTyrIleAsnTrpValThrArgGlnArgTyr–NH_2 (SEQ ID NO:36), and ProLysProGluAlaProGlyGluAspAlaSerProGluGluTrpAsnArgTyrTyrAla AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:37).

4. The polypeptide of claim 1 which comprises the amino acid sequence: ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr (SEQ IDNO:38).

5. The polypeptide of claim 1 which consists of the amino acid sequence: ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr (SEQ IDNO:38).

6. The polypeptide of claim 2 which consists of the amino acid sequence: ProLysProGluAlaProGlyLysAspAlaSerProGluGluTrpAsnArgTyrTyrAla AspLeuArgHisTyrLeuAsnTrpLeuThrArgGlnArgTyr–NH_2 (SEQ ID NO:7).

7. A salt form of the polypeptide of claim 6.

8. A salt form of the polypeptide according to claim 7, wherein said salt is the acetate salt.

9. A pharmaceutical combination comprising a polypeptide according to any one of claims 1-8 and an exendin-4 or GLP-1.

10. A pharmaceutical composition comprising a polypeptide according to any one of claims 1-8 and a pharmaceutically acceptable carrier.

11. Use of a polypeptide or pharmaceutical composition or combination of any one of claims 1-10 in the preparation of a medicament for use in the treatment of a metabolic disorder such as obesity or Type 2 diabetes mellitus.

12. A polypeptide or pharmaceutical composition or combination according to any one of claims 1-10 for use in the treatment of a metabolic disorder such as obesity or Type 2 diabetes mellitus.

13. A nucleic acid molecule encoding a polypeptide sequence according to any one of claims 1-6.

14. An expression vector comprising a nucleic acid molecule according to claim 13.

15. A host cell containing an expression vector according to claim 14.