65. Use as claimed in any one of claims 53 to 63 wherein the medicament is in the form of a sustained release or depot preparation.

66. Use as claimed in any one of claims 53 to 63 wherein the medicament is for administration orally, rectally, parenterally, intracisternally, intravaginally, intraperitonially, topically (as by powders, ointments, gels, drops or transdermal patch), buccally or as an oral or nasal spray.

67. Use as claimed in any one of claims 53 to 63 wherein the medicament is in the form of a controlled release preparation.

68. Use as claimed in any one of claims 53 to 63 wherein the medicament is in the form of a pump or implantable drug infusion device.

SEQUENCE LISTING

<110> Cowley, Michael
Cone, Roger
Low, Malcolm
Bulter, Andrew

<120> Stimulation of Neurons in the Arcuate Nucleus to Modify Feeding Behavio
r

<130> 0899-63727

<150> 60/324,406
<151> 2001-09-24

<150> 60/392,109
<151> 2002-06-28

<160> 335

<170> PatentIn version 3.1

<210> 1
<211> 36
<212> PRT
<213> Homo sapiens

<400> 1

Tyr Pro Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 2
<211> 36
<212> PRT
<213> Homo sapiens

<400> 2

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 3
<211> 36
<212> PRT
<213> Homo sapiens

<400> 3

Ala Ser Leu Glu Pro Glu Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 4
<211> 3
<212> PRT
<213> Homo sapiens

<400> 4

000
1

<210> 5
<211> 36
<212> PRT
<213> Rattus sp.

<400> 5

Tyr Pro Ala Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 6
<211> 36
<212> PRT
<213> Sus sp.

<400> 6

Tyr Pro Ala Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 7
<211> 36
<212> PRT
<213> Cavia porcellus

<400> 7

Tyr Pro Ser Lys Pro Glu Ala Pro Gly Ser Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ala Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 8
<211> 36
<212> PRT
<213> Rana sp.

<400> 8

Tyr Pro Pro Lys Pro Glu Asn Pro Gly Glu Asp Ala Ser Pro Glu Glu
1 5 10 15

Met Thr Lys Tyr Leu Thr Ala Leu Arg His Tyr Ile Asn Leu Val Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 9
<211> 36
<212> PRT
<213> Raja sp.

<400> 9

Tyr Pro Pro Lys Pro Glu Asn Pro Gly Asp Asp Ala Ala Pro Glu Glu
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 10
<211> 36
<212> PRT
<213> Dogfish sp.

<400> 10

Tyr Pro Pro Lys Pro Glu Asn Pro Gly Glu Asp Ala Pro Pro Glu Glu
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 11
<211> 36
<212> PRT
<213> Lampetra sp.

<400> 11

Phe Pro Pro Lys Pro Asp Asn Pro Gly Asp Asn Ala Ser Pro Glu Gln
1 5 10 15

Met Ala Arg Tyr Lys Ala Ala Val Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 12
<211> 36
<212> PRT
<213> Petromyzontidae gen. sp.

<400> 12

Met Pro Pro Lys Pro Asp Asn Pro Ser Pro Asp Ala Ser Pro Glu Glu
1 5 10 15

Leu Ser Lys Tyr Met Leu Ala Val Arg Asn Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 13
<211> 36
<212> PRT
<213> Rattus sp.

<400> 13

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 14
<211> 36
<212> PRT
<213> Oryctolagus cuniculus

<400> 14

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 15
<211> 36
<212> PRT
<213> Canis familiaris

<400> 15

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 16
<211> 36
<212> PRT
<213> Sus sp.

<400> 16

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 17
<211> 36
<212> PRT
<213> Bos taurus

<400> 17

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 18
<211> 36
<212> PRT
<213> Ovis aries

<400> 18

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Asp Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 19
<211> 36
<212> PRT
<213> Cavia porcellus

<400> 19

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 20
<211> 36
<212> PRT
<213> Avian

<400> 20

Tyr Pro Ser Lys Pro Asp Ser Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 21
<211> 36
<212> PRT
<213> Rana sp.

<400> 21

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Met Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 22
<211> 36
<212> PRT
<213> Carassius auratus

<400> 22

Tyr Pro Thr Lys Pro Asp Asn Pro Gly Glu Gly Ala Pro Ala Glu Glu
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 23
<211> 36
<212> PRT
<213> Dogfish sp.

<400> 23

Tyr Pro Ser Lys Pro Asp Asn Pro Gly Glu Gly Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Lys Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 24
<211> 36
<212> PRT
<213> Lampetra sp.

<400> 24

Pro Pro Asn Lys Pro Asp Ser Pro Gly Glu Asp Ala Pro Ala Glu Asp
1 5 10 15

Leu Ala Arg Tyr Leu Ser Ala Val Arg His Tyr Ile Asn Leu Ile Thr
20 25 30

Arg Gln Arg Tyr
35

<210> 25
<211> 36
<212> PRT
<213> Ovis aries

<400> 25

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Asp Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 26
<211> 36
<212> PRT
<213> Sus sp.

<400> 26

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asp Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 27
<211> 36
<212> PRT
<213> Canis familiaris

<400> 27

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asp Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 28
<211> 36
<212> PRT
<213> Felis catus

<400> 28

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 29
<211> 36
<212> PRT
<213> Bos taurus

<400> 29

Ala Pro Leu Glu Pro Glu Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Ala Ala Glu Leu Arg Arg Tyr Ile Asn Met Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 30
<211> 36
<212> PRT
<213> Rattus sp.

<400> 30

Ala Pro Leu Glu Pro Met Tyr Pro Gly Asp Tyr Ala Thr His Glu Gln
1 5 10 15

Arg Ala Gln Tyr Glu Thr Gln Leu Arg Arg Tyr Ile Asn Thr Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 31
<211> 36
<212> PRT
<213> Mus musculus

<400> 31

Ala Pro Leu Glu Pro Met Tyr Pro Gly Asp Tyr Ala Thr Pro Glu Gln
1 5 10 15

Met Ala Gln Tyr Glu Thr Gln Leu Arg Arg Tyr Ile Asn Thr Leu Thr
20 25 30

Arg Pro Arg Tyr
35

<210> 32
<211> 37
<212> PRT
<213> Cavia porcellus

<400> 32

Ala Pro Leu Glu Pro Val Tyr Pro Gly Asp Asn Ala Thr Pro Glu Gln
1 5 10 15

Gln Met Ala Gln Tyr Ala Ala Glu Met Arg Arg Tyr Ile Asn Met Leu
20 25 30

Thr Arg Pro Arg Tyr
35

<210> 33
<211> 36
<212> PRT
<213> Gallus gallus

<400> 33

Gly Pro Ser Gln Pro Thr Tyr Pro Gly Asp Asp Ala Pro Val Glu Asp
1 5 10 15

Leu Ile Arg Phe Tyr Asn Asp Leu Gln Gln Tyr Leu Asn Val Val Thr
20 25 30

Arg His Arg Tyr
35

<210> 34
<211> 36
<212> PRT
<213> Alligator sp.

<400> 34

Thr Pro Leu Gln Pro Lys Tyr Pro Gly Asp Gly Ala Pro Val Glu Asp
1 5 10 15

Leu Ile Gln Phe Tyr Asn Asp Leu Gln Gln Tyr Leu Asn Val Val Thr
20 25 30

Arg Pro Arg Phe
35

<210> 35
<211> 36
<212> PRT
<213> Rana catesbeiana

<400> 35

Ala Pro Ser Glu Pro His His Pro Gly Asp Gln Ala Thr Pro Asp Gln
1 5 10 15

Leu Ala Gln Tyr Tyr Ser Asp Leu Tyr Gln Tyr Ile Thr Phe Ile Thr
20 25 30

Arg Pro Arg Phe
35

<210> 36
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 36

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 37
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 37

Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 38
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 38

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 39
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 39

Arg His Tyr Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 40
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 40

Arg His Tyr Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 41
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 41
Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 42

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 43
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 43

Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 44
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 44

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 45
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 45

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr

1 5 10

<210> 46
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 46

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 47
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 47

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 48
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 48

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 49
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 49

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 50
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 50

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 51
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 51

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 52
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 52

Lys His Thr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 53
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 53

Lys His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 54
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 54

Lys His Tyr Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 55
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 55

Lys His Tyr Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 56
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 56

Lys His Tyr Leu Gln Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 57
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 57

Lys His Tyr Leu Asn Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 58
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 58

Lys His Tyr Leu Asn Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 59
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 59

Lys His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 60
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 60

Lys His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 61
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 61

Lys His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 62
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 62

Lys His Tyr Leu Asn Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 63
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 63

Lys His Tyr Leu Asn Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 64
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 64

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 65
<211> 12
<212> PRT

<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 65

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 66
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 66

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 67
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 67

Arg His Thr Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 68
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 68

Arg His Thr Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 69
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 69

Arg His Thr Leu Gln Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 70

<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 70

Arg His Thr Leu Asn Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 71
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 71

Arg His Thr Leu Asn Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 72
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 72

Arg His Thr Leu Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 73
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 73

Arg His Thr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 74
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 74

Arg His Thr Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 75
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 75

Arg His Thr Leu Asn Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 76
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 76

Arg His Thr Leu Asn Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 77
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 77

Arg His Thr Leu Asn Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 78
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 78

Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 79
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 79

Arg His Thr Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 80
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 80

Arg His Phe Ile Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 81
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 81

Arg His Phe Val Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 82
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 82

Arg His Phe Leu Gln Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 83
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 83

Arg His Phe Leu Asn Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 84
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 84

Arg His Phe Leu Asn Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 85
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 85

Arg His Phe Leu Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 86
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 86

Arg His Phe Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 87
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 87

Arg His Phe Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 88
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 88

Arg His Phe Leu Asn Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 89
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 89

Arg His Phe Leu Asn Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 90
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 90

Arg His Phe Leu Asn Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 91
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 91

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 92
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 92

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 93
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 93

Arg His Tyr Leu Gln Ile Val Thr Arg Gln Arg Tyr
1 5 10

<210> 94
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<400> 94

Arg His Tyr Leu Gln Val Val Thr Arg Gln Arg Tyr
1 5 10

<210> 95
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 95

Arg His Tyr Leu Gln Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 96
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 96

Arg His Tyr Leu Gln Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 97
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 97

Arg His Tyr Leu Gln Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 98
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 98

Arg His Tyr Leu Gln Leu Val Thr Lys Gln Arg Tyr
1 5 10

<210> 99
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 99

Arg His Tyr Leu Gln Leu Val Thr Arg Asn Arg Tyr
1 5 10

<210> 100
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 100

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Lys Tyr
1 5 10

<210> 101
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 101

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Thr
1 5 10

<210> 102
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 102

Arg His Tyr Leu Gln Leu Val Thr Arg Gln Arg Phe
1 5 10

<210> 103
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 103

Arg His Tyr Leu Asn Ile Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 104
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 104

Arg His Tyr Leu Asn Ile Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 105
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 105

Arg His Tyr Leu Asn Ile Val Ser Arg Gln Arg Tyr
1 5 10

<210> 106
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 106

Arg His Tyr Leu Asn Ile Val Thr Lys Gln Arg Tyr
1 5 10

<210> 107
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 107

Arg His Tyr Leu Asn Ile Val Thr Arg Asn Arg Tyr
1 5 10

<210> 108
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 108

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Lys Tyr
1 5 10

<210> 109

<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 109

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Thr
1 5 10

<210> 110
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 110

Arg His Tyr Leu Asn Ile Val Thr Arg Gln Arg Phe
1 5 10

<210> 111
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 111
Arg His Tyr Leu Asn Val Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 112
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 112

Arg His Tyr Leu Asn Val Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 113
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 113

Arg His Tyr Leu Asn Val Val Ser Arg Gln Arg Tyr
1 5 10

<210> 114
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 114

Arg His Tyr Leu Asn Val Val Thr Lys Gln Arg Tyr
1 5 10

<210> 115
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 115

Arg His Tyr Leu Asn Val Val Thr Arg Asn Arg Tyr
1 5 10

<210> 116
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 116

Arg His Tyr Leu Asn Val Val Thr Arg Gln Lys Tyr
1 5 10

<210> 117
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 117

Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Thr
1 5 10

<210> 118
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 118

Arg His Tyr Leu Asn Val Val Thr Arg Gln Arg Phe
1 5 10

<210> 119
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 119

Arg His Tyr Leu Asn Leu Ile Ser Arg Gln Arg Tyr
1 5 10

<210> 120
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 120

Arg His Tyr Leu Asn Leu Ile Thr Lys Gln Arg Tyr
1 5 10

<210> 121
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 121

Arg His Tyr Leu Asn Leu Ile Thr Arg Asn Arg Tyr
1 5 10

<210> 122
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 122

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Lys Tyr
1 5 10

<210> 123
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 123

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Thr
1 5 10

<210> 124
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 124

Arg His Tyr Leu Asn Leu Ile Thr Arg Gln Arg Phe
1 5 10

<210> 125
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 125

Arg His Tyr Leu Asn Leu Leu Ser Arg Gln Arg Tyr
1 5 10

<210> 126
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 126

Arg His Tyr Leu Asn Leu Leu Thr Lys Gln Arg Tyr
1 5 10

<210> 127
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 127

Arg His Tyr Leu Asn Leu Leu Thr Arg Asn Arg Tyr
1 5 10

<210> 128
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 128

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Lys Tyr
1 5 10

<210> 129
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 129

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Thr
1 5 10

<210> 130
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 130

Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Phe
1 5 10

<210> 131
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 131

Arg His Tyr Leu Asn Leu Val Ser Lys Gln Arg Tyr
1 5 10

<210> 132
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 132

Arg His Tyr Leu Asn Leu Val Ser Arg Asn Arg Tyr
1 5 10

<210> 133
<211> 12
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<400> 133

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Lys Tyr
1 5 10

<210> 134
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 134

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Thr
1 5 10

<210> 135
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 135

Arg His Tyr Leu Asn Leu Val Ser Arg Gln Arg Tyr
1 5 10

<210> 136
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 136

Arg His Tyr Leu Asn Leu Val Thr Lys Asn Arg Tyr
1 5 10

<210> 137
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 137

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Lys Tyr
1 5 10

<210> 138
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 138

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Thr
1 5 10

<210> 139
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 139

Arg His Tyr Leu Asn Leu Val Thr Lys Gln Arg Phe
1 5 10

<210> 140
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 140

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Lys Tyr
1 5 10

<210> 141
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 141

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Thr
1 5 10

<210> 142
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 142

Arg His Tyr Leu Asn Leu Val Thr Arg Asn Arg Phe
1 5 10

<210> 143
<211> 12

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 143

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Thr
1 5 10

<210> 144
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 144

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Lys Phe
1 5 10

<210> 145
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 145

Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 146
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 146
Ile Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 147
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 147

Val Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 148

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 148

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 149
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 149

Thr Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 150
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 150

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 151
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 151

Ser Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 152
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 152

Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 153
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 153

Thr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 154
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 154

Phe Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 155
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 155

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 156
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 156

Thr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 157
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 157

Phe Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 158
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 158

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 159
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 159

Lys Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 160
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 160

Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 161
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 161

Gln Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg

1 5 10 15

Gln Arg Tyr

<210> 162
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 162

Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 163
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 163

Ile Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 164
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 164

Val Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 165
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 165

Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 166
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 166

Asp Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 167
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 167

Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 168
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 168

Asp Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 169
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 169

Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr
20

<210> 170
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 170

Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 171
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 171

Thr Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 172
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 172

Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 173
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 173

Ser Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 174
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 174

Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 175
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 175

Glu Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 176
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 176

Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg
1 5 10 15

His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 177
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 177

Asp Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Arg
1 5 10 15

His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 178
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 178

Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu
1 5 10 15

Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 179
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 179

Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser
1 5 10 15

Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 180
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 180

Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala
1 5 10 15

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 181
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 181

Ser Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala
1 5 10 15

Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 182
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 182

Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr
1 5 10 15

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 183
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 183

Asp Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr
1 5 10 15

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 184
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 184

Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr
1 5 10 15

Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 185
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 185

Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 186
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 186

Arg Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 187
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 187

Gln Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 188
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 188

Asn Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 189
<211> 34

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 189

Leu Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
20 25 30

Arg Tyr

<210> 190
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 190

Val Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn
1 5 10 15

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
20 25 30

Arg Tyr

<210> 191
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 191

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 192
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 192

Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 193
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 193

Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 194
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 194

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 195
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 195

Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg
1 5 10 15

Tyr

<210> 196
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 196

Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 197
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 197

Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 198
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 198

Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 199
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 199

Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val
1 5 10 15

Thr Arg Gln Arg Tyr
20

<210> 200
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 200

Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu
1 5 10 15

Val Thr Arg Gln Arg Tyr
20

<210> 201
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 201

Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr
20

<210> 202
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 202

Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn
1 5 10 15

Leu Val Thr Arg Gln Arg Tyr
20

<210> 203
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 203

Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr Leu
1 5 10 15

Asn Leu Val Thr Arg Gln Arg Tyr
20

<210> 204
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 204

Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His Tyr
1 5 10 15

Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 205
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 205

Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu Lys His
1 5 10 15

Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 206
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 206

Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser Leu
1 5 10 15

Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 207
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 207

Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr Tyr Ala Ser
1 5 10 15

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 208
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 208

Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala Ser
1 5 10 15

Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25

<210> 209
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 209

Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr Tyr Ala
1 5 10 15

Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 210
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 210

Pro Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu Asn Arg Tyr
1 5 10 15

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 211
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 211

Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg Tyr
1 5 10 15

Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
20 25 30

<210> 212
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 212

Ile Lys Pro Glu Ala Pro Gly Glu Asp Ala Ser Glu Glu Leu Asn Arg
1 5 10 15

Tyr Tyr Ala Ser Leu Lys His Tyr Leu Asn Leu Val Thr Arg Gln Arg
20 25 30

Tyr

<210> 213
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)

<223> ACETYLATION

<400> 213

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 214
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<400> 214

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 215
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 215

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 216
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 216

Pro Ala Glu Asp Leu Ala Gln Tyr Ala Ala Glu Leu Arg His Tyr Leu
1 5 10 15

Asn Leu Leu Thr Arg Gln Arg Tyr
20

<210> 217
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE

<222> (1)..(1)
<223> H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 217

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 218
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 218

Met Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 219
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 219

Ala Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 220
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ala

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 220

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 221
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (18)..(18)
<223> AMIDATION

<400> 221

Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 222
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Nle

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 222

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 223
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ser

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 223

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 224
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 224

Ala Ala Arg Tyr Ser His Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 225
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ile

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 225

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 226
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<400> 226

Arg Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 227
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (18)..(18)
<223> AMIDATION

<400> 227

Gln Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
1 5 10 15

Arg Tyr

<210> 228
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 228

Ala Arg Phe Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 229
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)

<223> MeLeu

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 229

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 230
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> METHYLATION

<400> 230

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 231
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> desamino

<220>
<221> MOD_RES

<222> (19)..(19)
<223> AMIDATION

<400> 231

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 232
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> FORMYLATION

<400> 232

Ala Arg Tyr Tyr Ser Glu Leu Arg Arg Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 233
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Nva

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 233

Xaa Ala Arg Tyr Ala Ser Ala Leu Arg His Tyr Leu Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 234
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 234

Ala Arg Tyr Tyr Thr Gln Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 235
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> desamino

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 235

Leu Ala Arg Tyr Tyr Ser Asn Leu Arg His Tyr Ile Asn Val Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 236
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 236

Ala Arg Tyr Tyr Asp Ser Leu Arg His Tyr Ile Asn Thr Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 237
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 237

Ala Arg Tyr Tyr Ser Ala Leu Gln His Tyr Ile Asn Leu Leu Thr Arg
1 5 10 15

Pro Arg Tyr

<210> 238
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 238

Leu Ala Arg Tyr Tyr Ser Ala Leu Arg Gln Tyr Arg Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Phe

<210> 239
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (18)..(18)
<223> AMIDATION

<400> 239

Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln
1 5 10 15

Arg Phe

<210> 240
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 240

Ser Arg Tyr Tyr Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 241
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 241

Ser Arg Tyr Tyr Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 242
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> Nle

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 242

Xaa Ala Arg Tyr Tyr Asn Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 243
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D isomer of Ala

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 243

Xaa Arg Tyr Glu Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

His Arg Tyr

<210> 244
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (21)..(21)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Bz

<400> 244

Xaa Leu Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile
1 5 10 15

Thr Arg Pro Arg Phe
20

<210> 245
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 245

Ala Leu Tyr Tyr Ser Ala Leu Arg His Phe Val Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 246
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ala

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 246

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Val Asn Leu Ile Phe Arg
1 5 10 15

Gln Arg Tyr

<210> 247
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> MeSer

<220>
<221> MOD_RES
<222> (18)..(18)
<223> AMIDATION

<400> 247

Xaa Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Met Ile Thr Arg Gln
1 5 10 15

Arg Phe

<210> 248
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 248

Arg Ile Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Phe
20

<210> 249
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminal is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 249

Leu Ser Arg Tyr Tyr Ser Ala Leu Arg His Phe Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 250
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is MeIle

<400> 250

Xaa Arg Tyr Tyr Ser Ala Leu Gln His Phe Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 251
<211> 19
<212> PRT
<213> Artificial Sequence

<220>

<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ser

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)
<223> AMIDATION

<400> 251

Xaa Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr Arg
1 5 10 15

Gln Arg Phe

<210> 252
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 252

Met Ala Arg Tyr Tyr Ser Asp Leu Arg Arg Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 253
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MOD_RES
<222> (19)..(19)

<223> AMIDATION

<400> 253

Ala Arg Tyr Tyr Ser Glu Leu Arg His Tyr Ile Ile Leu Ile Thr Arg
1 5 10 15

Gln Arg Tyr

<210> 254
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> D Ala

<220>
<221> MOD_RES
<222> (20)..(20)
<223> AMIDATION

<400> 254

Xaa Ala Arg Tyr Tyr Ser Ala Leu Arg His Tyr Ile Asn Leu Ile Thr
1 5 10 15

Arg Gln Arg Tyr
20

<210> 255
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 255

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 256
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (25)..(25)
<223> im DNP HIS; 2,2 diphenylalanine Hisitidine

<220>
<221> MOD_RES
<222> (35)..(35)
<223> AMIDATION

<400> 256

Tyr Pro Ala Lys Glu Ala Pro Gly Glu Asp Ala Ser Pro Glu Glu Leu
1 5 10 15

Ser Thr Tyr Tyr Ala Ser Leu Arg Xaa Tyr Leu Asn Leu Val Thr Arg
20 25 30

Glx Arg Tyr
35

<210> 257
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 257

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 258
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 258

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Ala Arg Gln Arg Tyr
1 5 10 15

<210> 259
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation
<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 259

Ala Ala Leu Arg His Tyr Leu Asn Leu Val Ala Arg Gln Arg Tyr
1 5 10 15

<210> 260
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 260

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 261
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ornithine

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 261

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Xaa Arg Tyr
1 5 10 15

<210> 262
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is p.Cl.Pro; 4 chlorophenylalanine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>

<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 262

Ala Ser Leu Arg Xaa Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 263
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 263

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 264
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<400> 264

Ala Ser Leu Arg His Phe Glu Asn Leu Val Thr Arg Gln Arg Xaa
1 5 10 15

<210> 265
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ornithine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<400> 265

Ala Ser Leu Arg His Tyr Glu Asn Leu Val Thr Arg Xaa Arg Xaa
1 5 10 15

<210> 266
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> LIPID
<222> (1)..(1)
<223> N alpha myristoyl

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 266

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 267
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N alpha naphthateneacetyl

<220>
<221> MOD_RES

<222> (15)..(15)
<223> AMIDATION

<400> 267

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 268
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is N Me Tyr

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is Ornithine

<400> 268

Ala Ser Leu Arg His Phe Glu Asn Leu Val Thr Arg Xaa Arg Xaa
1 5 10 15

<210> 269
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 269

Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 270

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<220>
<221> MOD_RES
<222> (7)..(7)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<400> 270

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 271
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> Xaa is 4,4' biphenylalanine

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<400> 271

Xaa Ala Ser Leu Arg His Tyr Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 272
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)

<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<400> 272

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 273
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 3 benzothienyalanine

<400> 273

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 274
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 274

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr

1 5 10 15

<210> 275
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 275

Ala Ser Leu Arg His Trp Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 276
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 2 thienylalanine

<400> 276

Ala Ser Leu Arg Asn Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 277
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)

<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is tetrahydroisoquinoline

<400> 277

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 278
<211> 3
<212> PRT
<213> Homo sapiens

<400> 278

000
1

<210> 279
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> AMIDATION

<400> 279

His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 280
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MOD_RES

<222> (1)..(1)
<223> ACETYLATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is 2 thienylalanine

<400> 280

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Xaa
1 5 10 15

<210> 281
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 4 Thiazolylalanine

<400> 281

Ala Ser Leu Arg His Xaa Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 282
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (16)..(16)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 4 Thiazolylalanine

<400> 282

Ala Ser Leu Arg His Xaa Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 283
<211> 3
<212> PRT
<213> Homo sapiens

<400> 283

000
1

<210> 284
<211> 3
<212> PRT
<213> Homo sapiens

<400> 284

000
1

<210> 285
<211> 3
<212> PRT
<213> Homo sapiens

<400> 285

000
1

<210> 286
<211> 3
<212> PRT
<213> Homo sapiens

<400> 286

000
1

<210> 287
<211> 3
<212> PRT
<213> Homo sapiens

<400> 287

000
1

<210> 288
<211> 3
<212> PRT
<213> Homo sapiens

<400> 288

000

1

<210> 289
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 289

Phe Ser Leu Arg Asn Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 290
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 290

Tyr Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 291
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 291

Ala Ser Leu Arg His Tyr Trp Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 292
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 292

Ala Ser Leu Arg His Tyr Leu Asn Trp Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 293
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 293

Ala Ser Leu Arg Ala Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 294
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (14)..(14)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is 3' benzothienyalanine

<400> 294

Ala Ser Leu Arg Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 295
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 295

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 296
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 296

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Phe
1 5 10 15

<210> 297
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is D form of Trp

<220>
<221> MOD_RES
<222> (11)..(11)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (11)..(11)
<223> N alpha ACETYLATION

<400> 297

Ala Ser Leu Arg His Phe Leu Asn Leu Val Xaa Arg Gln Arg Tyr
1 5 10 15

<210> 298
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to CH3CO

<400> 298

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 299
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to CH3CO

<400> 299

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 300
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<400> 300

Leu Arg His Tyr Leu Asn Leu Leu Thr Arg Gln Arg Tyr
1 5 10

<210> 301
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (13)..(13)
<223> AMIDATION

<400> 301

Leu Arg His Tyr Ile Asn Leu Ile Thr Arg Gln Arg Tyr
1 5 10

<210> 302
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES

<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Norleucine

<400> 302

Ala Ser Xaa Arg His Trp Xaa Asn Xaa Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 303
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>

<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 303

Ala Ser Xaa Arg His Trp Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 304
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 304

Ala Ser Xaa Arg His Phe Xaa Asn Xaa Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 305
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 305

Ala Ser Xaa Arg His Phe Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 306
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (12)..(12)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<220>
<221> MISC_FEATURE
<222> (11)..(11)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH

<400> 306

Arg His Tyr Leu Asn Trp Val Thr Arg Gln Xaa Xaa
1 5 10

<210> 307
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<400> 307

Arg His Tyr Leu Asn Trp Val Thr Arg Gln Arg Tyr
1 5 10

<210> 308
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a psuedopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a psuedopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 308

Ala Ser Leu Arg His Tyr Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 309
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<220>
<221> MISC_FEATURE
<222> (15)..(15)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Xaa is a pseudopeptide bond consisting of CH2 NH2

<220>
<221> MISC_FEATURE
<222> (3)..(3)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa is Norleucine

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Norvaline

<400> 309

Ala Ser Xaa Arg His Tyr Xaa Asn Trp Xaa Thr Arg Gln Xaa Xaa
1 5 10 15

<210> 310
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> bonded to OCH3

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<400> 310

Ile Asn Pro Ile Tyr Arg Leu Arg Tyr
1 5

<210> 311
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> DISULFID
<222> (4)..(4)
<223> Sequence is linked to identical sequence by a disulfide bond

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> C terminus is bonded to NH2

<400> 311

Ile Asn Pro Cys Tyr Arg Leu Arg Tyr
1 5

<210> 312
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> C terminus is bonded to OCH3

<220>
<221> DISULFID
<222> (1)..(1)
<223> sequence is linked to an identical sequence

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<400> 312

Cys Tyr Arg Leu Arg Tyr
1 5

<210> 313
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> Connected by NH CH CO

<220>
<221> MISC_FEATURE
<222> (3)..(4)
<223> Identical peptide chains are connected by (CH2)4 at the CH o
f NH CH CO

<400> 313

Ile Asn Pro Tyr Arg Leu Arg Tyr
1 5

<210> 314
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminus is bonded to H

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> C terminus is bonded to OCH3

<400> 314

Tyr Arg Leu Arg Tyr Tyr Arg Leu Arg Tyr
1 5 10

<210> 315
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> DISULFID
<222> (18)..(22)
<223>

<400> 315

Ser Lys Pro Asp Asn Pro Gly Glu Asp Ala Pro Ala Glu Asp Met Ala
1 5 10 15

Arg Cys Tyr Ser Ala Cys Arg His Tyr Ile Asn Leu Ile Thr Arg Gln
20 25 30

Arg Tyr

<210> 316
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 316

Arg His Tyr Leu Asn Leu Ile Gly Arg Gln Arg Tyr
1 5 10

<210> 317
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (3)..(7)
<223> ACETYLATION

<400> 317

Arg His Gly Leu Asn Leu Leu Gly Arg Gln Arg Tyr
1 5 10

<210> 318
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 318

Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 319
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 319

His Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 320
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 320

Arg His Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10

<210> 321
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 321

Tyr Ile Asn Leu Leu Tyr Arg Gln Arg Tyr
1 5 10

<210> 322
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa is 6 amino hexanoic acid

<400> 322

Tyr Pro Ser Leu Xaa Tyr Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5 10 15

<210> 323
<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 323

Ile Asn Leu Ile Tyr Arg Leu Arg Tyr
1 5

<210> 324
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (12)..(12)
<223> AMIDATION

<400> 324

Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10

<210> 325
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 325

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 326
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MISC_FEATURE
<222> (1)..(1)
<223> N terminal is bonded to H

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 326

Ala Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 327
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (9)..(9)
<223> AMIDATION

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<400> 327

Ala Ser Leu Arg Thr Arg Gln Arg Tyr
1 5

<210> 328
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 2 thienylalanine

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 328

Ala Ser Leu Arg His Xaa Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 329
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<220>
<221> MOD_RES
<222> (1)..(1)
<223> N alpha ACETYLATION

<220>
<221> MOD_RES
<222> (15)..(15)
<223> AMIDATION

<400> 329

Tyr Ser Leu Arg His Phe Leu Asn Leu Val Thr Arg Gln Arg Tyr
1 5 10 15

<210> 330
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 330

Asp Asp Asp Asp Tyr
1 5

<210> 331
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 331

Gly Pro Arg
1

<210> 332
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Polypeptide variation

<400> 332

Ala Gly Gly
1

<210> 333