SEQUENCE LISTING

<110> DiMarchi, et al.

<120> GLUCAGON ANALOGS EXHIBITING GIP RECEPTOR ACTIVITY

<130> 31135/45700A

<160> 262

<170> PatentIn version 3.5

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Lys Asn Asp Trp Lys His Asn Ile Thr Gln
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Ser Gly Ala Pro Pro Pro Ser Lys
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Ser Gly Ala Pro Pro Pro Ser
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            20                  25                  30

Ser Gly Ala Pro Pro Pro Ser
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Lys Asn Trp Leu Lys His Asn Ile Thr Gln
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Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Glu
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Gln Ala Ala Lys Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser Lys
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Lys Asn Trp Leu Lys His Asn Ile Thr Gln
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Ser Gly Ala Pro Pro Pro Ser Lys
35 40

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Lys Asn Trp Leu Lys His Asn Ile Thr Gln
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Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Met Asp Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Lys Asp Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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20 25 30

Ser Gly Ala Pro Pro Pro Ser
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Arg Arg Ala Xaa Glu Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
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Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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20 25 30

Ser Gly Ala Pro Pro Pro Ser
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<400> 42

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Xaa
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Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
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<400> 43

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Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
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<400> 44

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Xaa
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Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
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Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
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Arg Arg Ala Lys Asp Phe Val Gln Trp Leu Met Asn Thr
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<400> 48

His Ser Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
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Ser Gly Ala Pro Pro Pro Ser Cys
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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser Cys
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<400> 51

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<400> 52

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Ser Gly Ala Pro Pro Pro Ser Cys
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20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
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Gln Ala Ala Xaa Glu Phe Val Xaa Trp Leu Leu Ala Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser Cys
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Ser Gly Ala Pro Pro Pro Ser Cys
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Glu Ala Ala Xaa Lys Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
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Ser Gly Ala Pro Pro Pro Ser Cys
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Ser Gly Ala Pro Pro Pro Ser Cys
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Ser Gly Ala Pro Pro Pro Ser Cys
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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
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Ser Gly Ala Pro Pro Pro Ser Lys
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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser Cys
35 40

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<400> 73

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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
35 40

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<400> 74

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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
35 40

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<400> 75

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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
35 40

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Arg Arg Ala Xaa Glu Phe Val Gln Trp Leu Leu Asp Gly Arg Gly
20 25 30

<210> 77
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20 25 30

<210> 78
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Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser Lys
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Ser Gly Ala Pro Pro Pro Ser Lys
35 40

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Ser Gly Ala Pro Pro Pro Ser Lys
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Ser Gly Ala Pro Pro Pro Ser Lys Gly
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Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Arg Arg Ala Xaa Glu Phe Val Gln Trp Leu Leu Asp Thr
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Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Thr
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Ser Gly Ala Pro Pro Pro Ser
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Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Val Lys Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Lys Asp Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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<400> 106

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20 25 30

Ser Gly Ala Pro Pro Pro Ser
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Ser Gly Ala Pro Pro Pro Ser
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Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
20 25

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<400> 111

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Xaa
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Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
20 25

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<400> 112

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Lys
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Arg Arg Ala Gln Asp Phe Val Gln Trp Leu Met Asn Thr
20 25

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<400> 113

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1 5 10 15

Arg Arg Ala Lys Asp Phe Val Gln Trp Leu Met Asn Thr
20 25

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<400> 114

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

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<220>
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<223> C-terminal amidation

<400> 115

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

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<223> C-terminal amidation

<400> 116

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys

1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 117
<211> 41
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<400> 117

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Cys
35 40

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<400> 118

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
35 40

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<223> Covalently bound to PEG

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<400> 119

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
35 40

<210> 120
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<400> 120

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Arg Ala Xaa Glu Phe Val Gln Trp Leu Leu Asp Gly Arg Gly
20 25 30

<210> 121
<211> 31
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<400> 121

His Ser Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Arg Ala Xaa Glu Phe Val Gln Trp Leu Leu Asp Gly Arg Gly
20 25 30

<210> 122
<211> 39
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<400> 122

His Ser Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Arg Ala Xaa Glu Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 123
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<400> 123

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Arg Ala Xaa Glu Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

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<400> 124

His Xaa Glu Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 125
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<400> 125

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

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<400> 126

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

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<400> 127

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Arg Ala Xaa Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 128
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<400> 128

His Xaa Glu Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Arg Ala Xaa Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 129
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<400> 129

His Xaa Glu Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Arg Ala Xaa Glu Phe Val Gln Trp Leu Leu Asp Thr
20 25

<210> 130
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<212> PRT
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<220>
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<223> C-terminal amidation

<400> 130

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

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<220>
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<223> C-terminal amidation

<400> 131

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 132
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<400> 132

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Asp Gly Gly Pro Ser

20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 133
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<220>
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<223> C-terminal amidation

<220>
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<222> (29)..(29)
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<400> 133

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Asp Thr
20 25

<210> 134
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<220>
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<223> C-terminal amidation

<400> 134

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 135
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<220>
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<223> C-terminal amidation

<400> 135

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 136
<211> 39
<212> PRT
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<220>
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<400> 136

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 137
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<212> PRT
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<220>
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<220>
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<400> 137

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 138
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<212> PRT
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<220>
<221> MISC_FEATURE
<222> (40)..(40)
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<400> 138

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 139
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<220>
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<400> 139

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

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<400> 140

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
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Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 141
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<222> (2)..(2)
<223> Xaa is AIB

<220>
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<222> (20)..(20)
<223> Xaa is AIB

<220>
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<222> (40)..(40)
<223> Covalently bound to a C16 succinoyl via a beta-Ala spacer

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 141

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 142

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

<220>
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<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C18 succinoyl

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 142

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 143
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> 4-amino-Phe covalently bound a C16 fatty acyl group via gamma-Glu-gamma-Glu spacer

<220>

<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 143

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Xaa Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 144
<211> 39
<212> PRT
<213> Artificial Sequence

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> 4-amino-Phe is covalently bound to a C16 succinoyl

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 144

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Xaa Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser

35

<210> 145
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> 4-amino-Phe covalently bound to a C16 fatty acyl group via gamma-Glu-gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 145

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Xaa Gly
35 40

<210> 146
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Xaa is AIB

<220>
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<222> (40)..(40)
<223> Xaa is 4-amino Phe

<220>
<221> MOD_RES

<222> (40)..(40)
<223> 4-amino Phe covalently bound to C16 succinoyl

<220>
<221> MOD_RES
<222> (41)..(41)
<223> C-terminal amidation

<400> 146

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Xaa Gly
35 40

<210> 147
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
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<222> (2)..(2)
<223> Xaa is AIB

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<222> (6)..(6)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> 4-amino-Phe covalently bound to C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 147

His Xaa Gln Gly Thr Xaa Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 148
<211> 39

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> 4-amino-Phe covalently bound to C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 148

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His Xaa Gln Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Glu
1               5                  10                  15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
            20                  25                  30

Ser Gly Ala Pro Pro Pro Ser
        35
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<210> 149
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is AIB

<220>
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<222> (13)..(13)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> 4-amino-Phe covalently bound to C16 fatty acyl group via gamma-Glu spacer

<220>

<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 149

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Xaa Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 150
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> 4-amino-Phe covalently bound to C16 succinoyl

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 150

His Xaa Gln Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 151
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Xaa is AIB

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<221> MOD_RES
<222> (13)..(13)
<223> Covalently bound to a C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MOD_RES
<222> (39)..(39)
<223> C-terminal amidation

<400> 151

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Lys Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 152
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Covalently bound to a C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 152

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Lys Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 153
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
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<222> (16)..(16)
<223> Covalently bound to C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 153

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Lys
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 154
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Covalently bound to C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 154

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Lys Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 155
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 155

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 156
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to C16 succinoyl

<220>
<221> MISC_FEATURE

<222> (41)..(41)
<223> C-terminal amidation

<400> 156

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 157
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to C16 fatty acyl group via a spacer comprising an amido miniPEG acid and a gamma-Glu, wherein the amido miniPEG acid has a structure {-N- CH2- CH2-[-O-CH2-CH2-]n-COO-}, wherein n is 2

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 157

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 158
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>

<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C16 fatty acyl group via spacer comprising an amido miniPEG acid and a gamma-Glu, wherein the amido miniPEG acid has a structure {-N- CH2- CH2-[-O-CH2-CH2-]n-COO-}, wherein n is 4

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 158

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 159
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C16 fatty acyl group via spacer comprising an amido miniPEG acid and a gamma-Glu, wherein the amido miniPEG acid has a structure {-N- CH2- CH2-[-O-CH2-CH2-]n-COO-}, wherein n is 8

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 159

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 160
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Covalently bound to a Lys spacer, wherein the Lys spacer is attached to two C16 fatty acyl groups, wherein each C16 fatty acyl group is attached to the Lys spacer via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 160

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 161
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a Lys spacer, wherein the Lys spacer is attached to two C16 fatty acyl groups, wherein each C16 fatty acyl group is attached to the Lys spacer via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (40)..(40)

<223> C-terminal amidation

<400> 161

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 162
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Covalently bound to a C12 fatty acyl group, which is covalently bound to a gamma-Glu spacer, which is covalently bound to a C16 fatty acyl group

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 162

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 163
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<222> (2)..(2)

<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Covalently bound to a C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C16 fatty acyl group via gamma-Glu spacer

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> C-terminal amidation

<400> 163

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 164
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Sulfur of Cys is S-alkylated with -C(COO)H(CH2)13CH3

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 164

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys Gly
35 40

<210> 165
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Lys covalently bound to Cys, the sulfur of which is S-alkylated with -C(COO)H(CH2)13CH3

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 165

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 166
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to gamma-Glu, which is bound to Cys, the sulfur of which is S-alkylated with -C(COO)H(CH2)13CH3

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 166

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu

1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 167
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to Cys, which is covalently bound to gamma-Glu, which is covalently bound to C16 fatty acyl group

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 167

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 168
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to Cys spacer, which is bound to gamma-Glu,

which is bound to C16 fatty acyl group

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to SEQ ID NO 167 via Cys spacer which is disulfide bonded to a 2nd Cys, which the 2nd Cys is bound to Lys at position 40 of SEQ ID NO 167 and is bound to gamma-Glu, which, in turn is bound to C16 fatty acyl group

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 168

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 169
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to Cys, which is bound to gamma-Glu, which is bound to C16 fatty acyl group and the sulfer of the Cys is thioether linked to a peptide of SEQ ID NO: 231 via Lys at position 40

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 169

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 170
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to Cys, which is bound to gamma-Glu, which is bound to C16 fatty acyl group, and the sulfur of the Cys is disulfide bonded to a 2nd Cys, which the 2nd Cys is bound to a peptide of SEQ ID NO: 231 via Lys at position 40

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 170

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 171
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to C16 fatty acyl group via gamma-Glu-gamma-Glu spacer

<220>
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<223> C-terminal amidation

<400> 171

His Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 172
<211> 40
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<220>
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<223> Covalently bound to PEG

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<223> Covalently bound to C8 fatty acyl group

<220>
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<223> C-terminal amidation

<400> 172

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Cys Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 173
<211> 40
<212> PRT
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<223> Covalently bound to PEG

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<223> Covalently bound to C12 fatty acyl group

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<400> 173

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Cys Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 174
<211> 40
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<223> Covalently bound to PEG

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<223> Covalently bound to C14 fatty acyl group

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<223> C-terminal amidation

<400> 174

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Cys Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 175
<211> 40
<212> PRT
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<220>
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<400> 175

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Cys
35 40

<210> 176
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<400> 176

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

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<220>
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<400> 177

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 178
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<223> Xaa is Tyr or an amino acid covalently bound to a C10 to C26 acyl or alkyl group

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<223> Xaa is Arg or Ala

<220>
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<223> Xaa is AIB or Gln

<220>
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<223> Xaa is Asp or Glu

<220>
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<223> Xaa is Asp of Glu

<220>
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<223> Xaa is Ala, Arg or Lys

<220>
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<222> (40)..(40)
<223> Xaa is absent or is Gly (e.g. when position 10 is not Tyr) or is an amino acid covalently bound to a C10-C26 acyl or alkyl group

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> Optionally present, when residue at position 40 is an amino acid covalently bound to C10-C26 acyl or alkyl group, Xaa is Gly

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 178

His Xaa Gln Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Leu Xaa Gly Gly Pro Ser
20 25 30

Ser Gly Xaa Pro Pro Pro Ser Xaa Xaa
35 40

<210> 179
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is Tyr or an amino acid covalently bound to a C10 to C26 acyl or alkyl group

<220>
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<223> Xaa is Arg or Ala

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa is AIB or Gln

<220>
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<222> (21)..(21)
<223> Xaa is Asp or Glu

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Xaa is absent or is Gly (e.g. when position 10 is not Tyr) or is an amino acid covalently bound to a C10-C26 acyl or alkyl group

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> Optionally present, when residue at position 40 is an amino acid covalently bound to C10-C26 acyl or alkyl group then Xaa is Gly

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 179

His Xaa Gln Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Glu

1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Xaa Xaa
35 40

<210> 180
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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<223> Xaa is AIB

<220>
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<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 180

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 181
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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<223> At least one amino acid is an amino acid covalently bound to a C10 to C26 acyl or alkyl group

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<223> Xaa is AIB

<220>
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<223> Xaa is Gln or Gln analog

<220>
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<222> (10)..(10)
<223> Xaa is Lys or Tyr

<220>
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<222> (18)..(18)
<223> Xaa is Arg or Ala

<220>
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<223> Xaa is AIB or Gln

<220>
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<223> Xaa is Asp or Glu

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> Xaa is Thr or Gly

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> C-terminal amidation

<400> 181

His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Leu Asp Xaa
20 25

<210> 182
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> Xaa is Gln or Gln analog

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<222> (10)..(10)
<223> Xaa is Lys covalently bound to a C10-C26 acyl or alkyl group

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<223> Xaa is Arg or Ala

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa is AIB or Gln

<220>
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<222> (21)..(21)
<223> Xaa is Asp or Glu

<220>
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<223> Xaa is Gly or Thr

<220>
<221> MISC_FEATURE
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<223> C-terminal amidation

<400> 182

His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Leu Asp Xaa
20 25

<210> 183
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<400> 183

Gly Pro Ser Ser Gly Arg Pro Pro Pro Ser
1 5 10

<210> 184
<211> 39
<212> PRT
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<220>
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<220>
<221> MISC_FEATURE

<222> (3)..(3)
<223> Xaa is Gln or Gln analog

<220>
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<222> (16)..(16)
<223> Xaa is any amino acid, optionally, any amino acid other than Gly, Pro, and Ser

<220>
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<222> (18)..(18)
<223> Xaa is Arg or Ala

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa is a negative charged amino acid or a charge-neutral amino acid, optionally, AIB or Gln

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> Xaa is is an acidic amino acid, optionally, Asp or Glu

<220>
<221> MISC_FEATURE
<222> (27)..(27)
<223> Xaa is Leu, Ala, Nle, or Met

<220>
<221> MISC_FEATURE
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<223> Xaa is Ala or an acidic amino acid, optionally, Asp or Glu

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> Xaa is Ala or Gly

<220>
<221> MISC_FEATURE
<222> (35)..(35)
<223> Xaa is Ala or a basic amino acid, optionally, Arg or Lys

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 184

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His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1               5                  10                  15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa Gly Pro Ser
            20                  25                  30

Ser Gly Xaa Pro Pro Pro Ser
        35
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<210> 185
<211> 39
<212> PRT
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<220>
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<221> MISC_FEATURE
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<223> Xaa is Tyr or an amino acid covalently attached to a C12 to C18 acyl or alkyl group

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa is Glu, an alpha, alpha disubstituted amino acid or Lys

<220>
<221> MISC_FEATURE
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<223> Xaa is Arg or Ala

<220>
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<223> Xaa is AIB or Gln

<220>
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<223> Xaa is Asp or Glu

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<221> MISC_FEATURE
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<223> Xaa is Leu, Nle, or Met

<220>
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<223> Xaa is Ala, Asp or Glu

<220>
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<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 185

His Xaa Gln Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 186
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<220>
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<223> Xaa is Gln or Gln analog

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<223> Xaa is Tyr or an amino acid covalently attached to a C10 to C26 acyl or alkyl group

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<222> (16)..(16)
<223> Xaa is any amino acid, optionally, any amino acid other than Gly, Pro, and Ser

<220>
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<222> (18)..(18)
<223> Xaa is Arg or Ala

<220>
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<222> (20)..(20)
<223> Xaa is a negative charged amino acid or a charge-neutral amino acid, optionally, AIB or Gln

<220>
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<223> Xaa is Leu, Ala, Nle, or Met

<220>
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<220>
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<223> Xaa is Ala, Gly or Thr

<220>
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<223> C-terminal amidation

<400> 186

His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa
20 25

<210> 187
<211> 29
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<223> Xaa is Tyr or an amino acid covalently bound to a C10 to C26 acyl or alkyl group

<220>
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<223> Xaa is Glu, alpha, alpha-disubstituted amino acid, or Lys

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<221> MISC_FEATURE
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<223> Xaa is Ala, Asp or Glu

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> Xaa is Gly or Thr

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> C-terminal amidation

<400> 187

His Xaa Gln Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa
20 25

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

<220>
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<220>
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<223> Xaa can be any amino acid, optionally any amino acid other than Gly, Pro or Ser

<220>
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<223> Xaa is Arg or Ala

<220>
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<223> Xaa is a negative charged amino acid or a charge-neutral amino acid, optionally, AIB or Gln

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<223> Xaa is an acidic amino acid, optionally, Asp or Glu

<220>
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<223> Xaa is Leu, Ala, Nle, or Met

<220>
<221> MISC_FEATURE
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<220>
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<223> Xaa is Ala or Gly

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<223> Xaa is Ala or a basic amino acid, optionally, Arg or Lys

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 188

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1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa Gly Pro Ser
20 25 30

Ser Gly Xaa Pro Pro Pro Ser
35

<210> 189
<211> 39
<212> PRT
<213> Artificial Sequence

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<220>
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<223> Xaa is Glu, an alpha, alpha disubstituted amino acid or Lys

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<222> (27)..(27)
<223> Xaa is Leu, Nle, or Met

<220>
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<223> Xaa is Ala, Asp or Glu

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<400> 189

His Xaa Glu Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 190
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<212> PRT
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<220>
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<223> Xaa is Tyr or an amino acid covalently bound to a C10 to C26 acyl or alkyl group

<220>
<221> MISC_FEATURE
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<223> Xaa is any amino acid, optionally, any amino acid other than Gly, Pro, and Ser

<220>
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<223> Xaa is Arg or Ala

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa is a negative charged amino acid or a charge-neutral amino acid, optionally, AIB or Gln

<220>
<221> MISC_FEATURE
<222> (21)..(21)
<223> Xaa is an acidic amino acid, optionally, Asp or Glu

<220>
<221> MISC_FEATURE
<222> (27)..(27)
<223> Xaa is Leu, Ala, Nle, or Met

<220>
<221> MISC_FEATURE
<222> (28)..(28)
<223> Xaa is Ala or an acidic amino acid, optionally, Asp or Glu

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> Xaa is Ala, Gly or Thr

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> C-terminal amidation

<400> 190

His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa
20 25

<210> 191
<211> 29
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<213> Artificial Sequence

<220>
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<223> Xaa is AIB

<220>
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<223> Xaa is Tyr or an amino acid covalently bound to a C10 to C26 acyl or alkyl group

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<220>
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<220>
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<223> Xaa is a negative charged amino acid or a charge-neutral amino acid, optionally, AIB or Gln

<220>
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<222> (21)..(21)
<223> Xaa is Asp or Glu

<220>
<221> MISC_FEATURE
<222> (27)..(27)
<223> Xaa is Leu, Ala, Nle, or Met

<220>
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<222> (28)..(28)
<223> Xaa is Ala, Asp or Glu

<220>
<221> MISC_FEATURE
<222> (29)..(29)
<223> Xaa is Gly or Thr

<220>
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<400> 191

His Xaa Glu Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa
20 25

<210> 192
<211> 39
<212> PRT
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<220>
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<220>

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<223> Xaa is AIB

<220>
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<222> (3)..(3)
<223> Xaa is Gln or Gln analog or acidic, basic or hydrophobic amino acid, optionally, is Glu or Gln

<220>
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<222> (10)..(10)
<223> Xaa is Tyr or an amino acid covalently bound to a C12 to C18 acyl or alkyl group

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Xaa is any amino acid, optionally, any amino acid other than Gly, Pro, and Ser

<220>
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<223> Xaa is Arg or Ala

<220>
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<223> Xaa is a negative charged amino acid or a charge-neutral amino acid, optionally, AIB or Gln

<220>
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<223> Xaa is an acidic amino acid, optionally, Asp or Glu

<220>
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<223> Xaa is Leu, Ala, Nle, or Met

<220>
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<223> Xaa is Ala or an acidic amino acid, optionally, Asp or Glu

<220>
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<223> Xaa is Ala or Gly

<220>
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<223> Xaa is Ala or a basic amino acid, optionally, Arg or Lys

<220>
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<222> (39)..(39)
<223> C-terminal amidation

<400> 192

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His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1               5                  10                  15
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Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa Gly Pro Ser
20 25 30

Ser Gly Xaa Pro Pro Pro Ser
35

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<223> Xaa is Gln or Gln analog or acidic, basic or hydrophobic amino acid, optionally, is Glu or Gln

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<220>
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<223> Xaa is Asp or Glu

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<223> Xaa is Leu, Nle, or Met

<220>
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<223> Xaa is Ala, Asp or Glu

<220>
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<222> (29)..(29)

<223> Xaa is Gly or Thr

<220>
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<223> C-terminal amidation

<400> 193

His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

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<223> Xaa is Tyr or an amino acid covalently bound to a C10 to C26 acyl or alkyl group

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<223> Xaa is any amino acid, optionally, any amino acid other than Gly, Pro, and Ser

<220>
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<223> Xaa is Ala or an acidic amino acid, optionally, Asp or Glu

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<220>
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<400> 194

His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
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Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa
20 25

<210> 195
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<400> 195

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Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa
20 25

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His Xaa Xaa Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Xaa
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Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa Gly Pro Ser
20 25 30

Ser Gly Xaa Pro Pro Pro Ser
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Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 198
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Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa
20 25

<210> 199
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<400> 199

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Arg Xaa Ala Xaa Xaa Phe Val Gln Trp Leu Xaa Xaa Xaa
20 25

<210> 200
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<220>
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<400> 200

Glu Arg Ala Ala Gln
1 5

<210> 201
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<400> 201

Glu Arg Ala Ala Gln Asp
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<210> 202

<400> 202
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<210> 203
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<222> (40)..(40)
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<400> 203

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 204
<211> 41
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<220>
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<400> 204

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Ala Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 205
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<220>
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1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Gly
35 40

<210> 206
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<220>
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<400> 206

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Glu Gly Gly Pro Ser
20 25 30

Ser Gly Arg Pro Pro Pro Ser
35

<210> 207
<211> 40
<212> PRT
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<220>
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<400> 207

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Gly
35 40

<210> 208
<211> 41
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<220>
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<223> Xaa is AIB

<220>
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<222> (40)..(40)
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<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 208

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 209

<400> 209
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<210> 210
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<220>
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<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (40)..(40)
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<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 210

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 211
<211> 41
<212> PRT
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<222> (2)..(2)
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<220>
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<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 211

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

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

<220>
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<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
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<220>
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<400> 212

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Tyr Gly
35 40

<210> 213

<400> 213
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<210> 214

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<220>
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<400> 219

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Cys Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 220
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<400> 220

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Cys Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 221
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<400> 221

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Xaa
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Gln Ala Ala Lys Glu Phe Ile Cys Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 222
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<220>
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<400> 222

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1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Cys Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 223
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<220>
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<222> (24)..(24)
<223> Covalently bound to 40kDa PEG via thioether made by reaction of peptide with haloacetyl-activated PEG

<220>
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<400> 223

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
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Gln Ala Ala Lys Glu Phe Ile Cys Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 224
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<223> MT-350

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (24)..(24)
<223> Covalently bound to 40kDa PEG via thioether made by reaction of peptide with haloacetyl-activated PEG

<220>
<221> MOD_RES
<222> (40)..(40)
<223> C-terminal amidation

<400> 224

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Cys Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 225
<211> 40
<212> PRT

<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<223> MT-351

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (24)..(24)
<223> Covalently bound to 40kDa PEG via thioether made by reaction of peptide with haloacetyl-activated PEG

<220>
<221> MOD_RES
<222> (40)..(40)
<223> Acylated with a C14 fatty acyl group

<220>
<221> MOD_RES
<222> (40)..(40)
<223> C-terminal amidation

<400> 225

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Cys Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 226
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<223> MT-352

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (24)..(24)
<223> Covalently bound to 40kDa PEG via thioether made by reaction of peptide with haloacetyl-activated PEG

<220>
<221> MOD_RES
<222> (40)..(40)
<223> C-terminal amidation

<400> 226

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Xaa
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Cys Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 227

<400> 227
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<210> 228
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<223> MT-361

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (16)..(16)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (40)..(40)
<223> C-terminal amidation

<400> 228

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Xaa
1 5 10 15

Gln Ala Ala Lys Glu Phe Val Asn Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 229
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<223> MT-364

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (40)..(40)
<223> Acylated with a C16 fatty acyl group

<220>
<221> MOD_RES
<222> (40)..(40)
<223> C-terminal amidation

<400> 229

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Met Asn Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 230
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)

<223> C-terminal amidation

<400> 230

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Ile Tyr Leu Asp Glu
1 5 10 15

Lys Arg Ala Lys Glu Phe Val Cys Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 231
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 231

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 232

<400> 232
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<210> 233
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> 4-amino-Phe covalently bound a C16 fatty acyl group via spacer comprising two acidic residues

<220>
<221> MISC_FEATURE
<222> (20)..(20)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 233

Tyr Xaa Glu Gly Thr Phe Thr Ser Asp Xaa Ser Ile Tyr Leu Asp Lys
1 5 10 15

Gln Ala Ala Xaa Glu Phe Val Asn Trp Leu Leu Ala Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 234
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> 4-amino-Phe covalently bound to a C16 fatty acyl group via spacer comprising two acidic residues

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 234

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu

1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Xaa Gly
35 40

<210> 235
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> 4-amino-Phe covalently bound to C16 fatty acyl group via spacer comprising acidic residue

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 235

His Xaa Gln Gly Thr Xaa Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 236
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> 4-amino-Phe covalently bound to C16 fatty acyl group via spacer comprising acidic residue

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 236

His Xaa Gln Gly Thr Phe Thr Ser Asp Xaa Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 237
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Xaa is 4-amino-Phe

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> 4-amino-Phe covalently bound to C16 fatty acyl group via spacer comprising acidic residue

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 237

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Xaa Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser

20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 238
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MOD_RES
<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MOD_RES
<222> (13)..(13)
<223> Covalently bound to a C16 fatty acyl group via spacer comprising acidic residue

<220>
<221> MOD_RES
<222> (39)..(39)
<223> C-terminal amidation

<400> 238

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Lys Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 239
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> Covalently bound to a C16 fatty acyl group via spacer comprising acidic residue

<220>
<221> MISC_FEATURE

<222> (39)..(39)
<223> C-terminal amidation

<400> 239

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Lys Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 240
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (16)..(16)
<223> Covalently bound to C16 fatty acyl group via spacer comprising acidic residue

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 240

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Lys
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 241
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
<221> MISC_FEATURE
<222> (2)..(2)

<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (17)..(17)
<223> Covalently bound to C16 fatty acyl group via spacer comprising acidic residue

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 241

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Lys Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 242
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C16 fatty acyl group via spacer comprising acidic residue

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 242

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 243
<211> 41

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to C16 fatty acyl group via a spacer comprising an amido miniPEG acid and an acidic amino acid, wherein the amido miniPEG acid has a structure {-N- CH2- CH2-[-O-CH2-CH2-]n-COO-}, wherein n is 2

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 243

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 244
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C16 fatty acyl group via spacer comprising an amido miniPEG acid and an acidic amino acid, wherein the amido miniPEG acid has a structure {-N- CH2- CH2-[-O-CH2-CH2-]n-COO-}, wherein n is 4

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 244

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 245
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C16 fatty acyl group via spacer comprising an amido miniPEG acid and an acidic amino acid, wherein the amido miniPEG acid has a structure {-N- CH2- CH2-[-O-CH2-CH2-]n-COO-}, wherein n is 8

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 245

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 246
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>

<221> MISC_FEATURE
<222> (10)..(10)
<223> Covalently bound to a Lys spacer, wherein the Lys spacer is attached to two C16 fatty acyl groups, wherein each C16 fatty acyl group is attached to the Lys spacer via spacer comprising an acidic residue

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 246

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 247
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a Lys spacer, wherein the Lys spacer is attached to two C16 fatty acyl groups, wherein each C16 fatty acyl group is attached to the Lys spacer via spacer comprising an acidic residue

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> C-terminal amidation

<400> 247

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 248

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

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Covalently bound to a C12 fatty acyl group, which is covalently bound to a spacer comprising an acidic residue, which is covalently bound to a C16 fatty acyl group

<220>
<221> MISC_FEATURE
<222> (39)..(39)
<223> C-terminal amidation

<400> 248

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser
35

<210> 249
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> Covalently bound to a C16 fatty acyl group via acidic amino acid spacer

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to a C16 fatty acyl group via spacer comprising an acidic residue

<220>
<221> MISC_FEATURE
<222> (40)..(40)

<223> C-terminal amidation

<400> 249

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys
35 40

<210> 250
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to an acidic residue, which is bound to Cys, the sulfur of which is S-alkylated with -C(COO)H(CH2)13CH3

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 250

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 251
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to Cys, which is covalently bound to an acidic residue, which is covalently bound to C16 fatty acyl group

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 251

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 252
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to Cys spacer, which is bound to an acidic residue, which is bound to C16 fatty acyl group

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to SEQ ID 251 via Cys spacer which is disulfide bonded to a 2nd Cys, which the 2nd Cys is bound to Lys at position 40 of SEQ ID 251 and is bound to an acidic residue, which, in turn is bound to C16 fatty acyl group

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 252

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 253
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to Cys, which is bound to an acidic residue, which is bound to C16 fatty acyl group and the sulfer of the Cys is thioether linked to a peptide of SEQ ID NO: 231 via Lys at position 40

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 253

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 254
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to Cys, which is bound to an acidic residue, which is bound to C16 fatty acyl group, and the sulfur of the Cys is disulfide bonded to a 2nd Cys, which the 2nd Cys is bound to a peptide of SEQ ID NO: 231 via Lys at position 40

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 254

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 255
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

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

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to C16 fatty acyl group via spacer comprising two acidic residues

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 255

His Xaa Glu Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

<210> 256
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>

<221> MISC_FEATURE
<222> (2)..(2)
<223> Xaa is AIB

<220>
<221> MISC_FEATURE
<222> (40)..(40)
<223> Covalently bound to C16 fatty acyl group via spacer comprising two acidic residues

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 256

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

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<223> Covalently bound to C16 fatty acyl group via spacer comprising two acidic residues

<220>
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<400> 257

His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Ala Gly Gly Pro Ser
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Ser Gly Ala Pro Pro Pro Ser Lys Gly
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His Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Ala Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40

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His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Gly
35 40

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<223> Xaa is AIB

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<223> Covalently bound to C16 fatty acyl group via spacer comprising an acidic residue

<220>
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<222> (39)..(39)
<223> C-terminal amidation

<400> 260

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Glu Gly Gly Pro Ser
20 25 30

Ser Gly Arg Pro Pro Pro Ser
35

<210> 261
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<223> Xaa is AIB

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<223> Covalently bound to C16 fatty acyl group via spacer comprising two acidic residues

<220>
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<223> C-terminal amidation

<400> 261

His Xaa Gln Gly Thr Phe Thr Ser Asp Lys Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Gly
35 40

<210> 262
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic peptide

<220>
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<222> (2)..(2)
<223> Xaa is AIB

<220>
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<222> (40)..(40)
<223> Covalently bound to Lys spacer, wherein Lys spacer is bound via the alpha amine to an acidic residue spacer, which is bound to a C16 fatty acyl group and Lys spacer is bound via the epsilon amine to an acidic residue which is bound to a C16 fatty acyl

<220>
<221> MISC_FEATURE
<222> (41)..(41)
<223> C-terminal amidation

<400> 262

Tyr Xaa Gln Gly Thr Phe Thr Ser Asp Tyr Ser Lys Tyr Leu Asp Glu
1 5 10 15

Arg Ala Ala Gln Asp Phe Val Gln Trp Leu Leu Asp Gly Gly Pro Ser
20 25 30

Ser Gly Ala Pro Pro Pro Ser Lys Gly
35 40