

0100-0013w01_SL
SEQUENCE LISTING

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<120> LIGAND INDUCIBLE POLYPEPTIDE COUPLER SYSTEM

<130> 0100-0013w01

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<150> 62/140,380

<151> 2015-03-30

<160> 94

<170> PatentIn version 3.5

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<211> 1054

<212> DNA

<213> Choristoneura fumiferana

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 <213> Choristoneura fumiferana

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Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Ser Asp Lys 50 55 60

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Leu Leu Glu Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu Thr Ala Asn
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 Gln Gln Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp Gly Tyr Glu
 85 90 95
 Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr Trp Gln Gln
 100 105 110
 Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg Gln Ile Thr
 115 120 125
 Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly
 130 135 140
 Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln Ile Thr Leu Leu
 145 150 155 160
 Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr
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 Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Gln Ala Tyr Thr
 180 185 190
 Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile Glu Asp Leu
 195 200 205
 Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp Asn Ile His
 210 215 220
 Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg Pro Gly Leu
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 260 265 270
 Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu Arg Thr Leu
 275 280 285
 Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg
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<211> 549

<212> PRT

<213> Drosophila melanogaster

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50 55 60

His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln
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Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr
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Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
100 105 110

Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp
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Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu
130 135 140

Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln
145 150 155 160

Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met
165 170 175

Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe
180 185 190

Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met
195 200 205

Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser
210 215 220

Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile
225 230 235 240

Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile

Gln Ser Tyr Tyr₂₆₀ Ile Asp Thr Leu Arg₂₆₅ Ile Tyr Ile Leu Asn₂₇₀ Arg His
 Cys Gly Asp₂₇₅ Ser Met Ser Leu Val₂₈₀ Phe Tyr Ala Lys Leu₂₈₅ Leu Ser Ile
 Leu Thr₂₉₀ Glu Leu Arg Thr Leu₂₉₅ Gly Asn Gln Asn Ala₃₀₀ Glu Met Cys Phe
 Ser₃₀₅ Leu Lys Leu Lys Asn₃₁₀ Arg Lys Leu Pro Lys₃₁₅ Phe Leu Glu Glu Ile₃₂₀
 Trp Asp Val His Ala₃₂₅ Ile Pro Pro Ser Val₃₃₀ Gln Ser His Leu Gln₃₃₅ Ile
 Thr Gln Glu Glu₃₄₀ Asn Glu Arg Leu Glu₃₄₅ Arg Ala Glu Arg Met₃₅₀ Arg Ala
 Ser Val Gly₃₅₅ Gly Ala Ile Thr Ala₃₆₀ Gly Ile Asp Cys Asp₃₆₅ Ser Ala Ser
 Thr Ser₃₇₀ Ala Ala Ala Ala Ala₃₇₅ Ala Gln His Gln Pro₃₈₀ Gln Pro Gln Pro
 Gln₃₈₅ Pro Gln Pro Ser Ser₃₉₀ Leu Thr Gln Asn Asp₃₉₅ Ser Gln His Gln Thr₄₀₀
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 Val Thr₄₅₀ Ala Pro Gly Ser Leu₄₅₅ Ser Ala Val Ser Thr₄₆₀ Ser Ser Glu Tyr
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 Ser Ile Thr Ala Ala₄₈₅ Val Thr Ala Ser Ser₄₉₀ Thr Thr Ser Ala Val₄₉₅ Pro
 Met Gly Asn Gly₅₀₀ Val Gly Val Gly Val₅₀₅ Gly Val Gly Gly Asn₅₁₀ Val Ser
 Met Tyr Ala Asn Ala Gln Thr Ala Met Ala Leu Met Gly Val Ala Leu

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525

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His Ser Thr Thr Ala
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<213> Choristoneura fumiferana

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 20 25 30

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 35 40 45

Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val
 50 55 60

Gly Met Arg Pro Glu Cys Val Val Pro Glu Thr Gln Cys Ala Met Lys
 65 70 75 80

Arg Lys Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Leu Pro Val Ser
 85 90 95

Thr Thr Thr Val Asp Asp His Met Pro Pro Ile Met Gln Cys Glu Pro
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Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu
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Ser Asp Lys Leu Leu Glu Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu
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Thr Ala Asn Gln Gln Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp
 145 150 155 160

Gly Tyr Glu Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr
 165 170 175

Trp Gln Gln Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg
 180 185 190

Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe
 195 200 205

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Arg Arg Tyr Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Gln
 245 250 255

Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile
 260 265 270

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 275 280 285

Asn Ile His Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg
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Leu Asn Thr Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser Ala
 325 330 335

Arg Ser Ser Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu
 340 345 350

Arg Thr Leu Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu
 355 360 365

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Leu

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 <213> Tenebrio molitor

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Gly Ser Pro Asp Val Ile Lys Ile Glu Pro Glu Leu Ser Asp Ser Glu
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35

40

45

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 Ser Glu Val Met Met Phe Arg Met Ala Arg Arg Tyr Asp Val Gln Ser
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 Val Asp Asn Arg Arg Ser Pro Ser Arg Gly Thr Ile Phe Ala Lys Leu
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<211> 316

<212> PRT

<213> Amblyomma americanum

<400> 10

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Glu Phe Glu Ser Pro Ser Glu Glu Asp Met Lys Lys Thr Thr Pro Phe
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Tyr Asp Val Lys Thr Asp Ser Ile Val Phe Ala Asn Asn Gln Pro Tyr
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Leu Phe Arg Phe Cys Arg Lys Met Cys Gln Leu Arg Val Asp Asn Ala
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Leu Val Asp Pro His Lys Val Glu Arg Ile Gln Glu Tyr Tyr Ile Glu
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Thr Leu Arg Met Tyr Ser Glu Asn His Arg Pro Pro Gly Lys Asn Tyr
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Phe Ala Arg Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly Asn
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290 295 300

Pro Pro Phe Leu Ala Glu Ile Trp Asp Ile Gln Glu
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<213> Artificial Sequence

<220>
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Chimeric RXR ligand binding domain

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<211> 720
<212> DNA
<213> Homo sapiens

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<210> 13
<211> 635
<212> DNA
<213> Locusta migratoria

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tgatggagat gcttgaatca ctttctgatt cataa 635

<210> 14
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Chimeric RXR ligand binding domain

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Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30
Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
35 40 45
Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
50 55 60

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Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
65 70 75 80

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
100 105 110

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
115 120 125

Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
130 135 140

Leu Arg Ser Val Ile Leu Phe Asn Pro Glu Val Arg Gly Leu Lys Ser
145 150 155 160

Ala Gln Glu Val Glu Leu Leu Arg Glu Lys Val Tyr Ala Ala Leu Glu
165 170 175

Glu Tyr Thr Arg Thr Thr His Pro Asp Glu Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ser Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

Glu His Leu Phe Phe Phe Arg Leu Ile Gly Asp Val Pro Ile Asp Thr
210 215 220

Phe Leu Met Glu Met Leu Glu Ser Pro Ser Asp Ser
225 230 235

<210> 15
<211> 239
<212> PRT
<213> Homo sapiens

<400> 15
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Val Glu Gln Lys Ser Asp Gln Gly Val Glu Gly Pro Gly Gly Thr Gly
20 25 30

Gly Ser Gly Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala
35 40 45

Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro
50 55 60

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His Phe Ser Ser Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala
65 70 75 80

Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Asp
85 90 95

Val Arg Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn
100 105 110

Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr
115 120 125

Glu Leu Val Ser Lys Met Arg Asp Met Arg Met Asp Lys Thr Glu Leu
130 135 140

Gly Cys Leu Arg Ala Ile Ile Leu Phe Asn Pro Asp Ala Lys Gly Leu
145 150 155 160

Ser Asn Pro Ser Glu Val Glu Val Leu Arg Glu Lys Val Tyr Ala Ser
165 170 175

Leu Glu Thr Tyr Cys Lys Gln Lys Tyr Pro Glu Gln Gln Gly Arg Phe
180 185 190

Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys
195 200 205

Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile
210 215 220

Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Leu Ala
225 230 235

<210> 16

<211> 210

<212> PRT

<213> Locusta migratoria

<400> 16

His Thr Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Lys Arg Val
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Lys His Ile Pro His Phe Thr Ser Leu Pro Leu Glu Asp Gln Val Leu
35 40 45

Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ala Phe Ser His
50 55 60

Arg Ser Val Asp Val Lys Asp Gly Ile Val Leu Ala Thr Gly Leu Thr
65 70 75 80

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Val His Arg Asn Ser Ala His Gln Ala Gly Val Gly Thr Ile Phe Asp
85 90 95

Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Glu Met Lys Met Asp
100 105 110

Lys Thr Glu Leu Gly Cys Leu Arg Ser Val Ile Leu Phe Asn Pro Glu
115 120 125

Val Arg Gly Leu Lys Ser Ala Gln Glu Val Glu Leu Leu Arg Glu Lys
130 135 140

Val Tyr Ala Ala Leu Glu Glu Tyr Thr Arg Thr Thr His Pro Asp Glu
145 150 155 160

Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu Arg Ser
165 170 175

Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Arg Leu Ile Gly
180 185 190

Asp Val Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ser Pro Ser
195 200 205

Asp Ser
210

<210> 17
<211> 240
<212> PRT
<213> Choristoneura fumiferana

<400> 17
Leu Thr Ala Asn Gln Gln Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln
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Asp Gly Tyr Glu Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln
20 25 30

Thr Trp Gln Gln Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe
35 40 45

Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu
50 55 60

Phe Ala Lys Gly Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln
65 70 75 80

Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val
85 90 95

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Ala Arg Arg Tyr Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn
100 105 110

Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val
115 120 125

Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu
130 135 140

Asp Asn Ile His Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp
145 150 155 160

Arg Pro Gly Leu Glu Gln Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr
165 170 175

Tyr Leu Asn Thr Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser
180 185 190

Ala Arg Ser Ser Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu
195 200 205

Leu Arg Thr Leu Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys
210 215 220

Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp Val
225 230 235 240

<210> 18

<211> 237

<212> PRT

<213> Drosophila melanogaster

<400> 18

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20 25 30

Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile
35 40 45

Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys
50 55 60

Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu
65 70 75 80

Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg
85 90 95

Tyr Asp His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr
100 105 110

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Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp
 115 120 125
 Leu Leu His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp Asn Val
 130 135 140
 Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly
 145 150 155 160
 Leu Glu Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp
 165 170 175
 Thr Leu Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser
 180 185 190
 Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr
 195 200 205
 Leu Gly Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn
 210 215 220
 Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val
 225 230 235
 <210> 19
 <211> 240
 <212> PRT
 <213> Amblyomma americanum
 <400> 19
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 20 25 30
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 35 40 45
 Arg Arg Phe Gln His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu
 50 55 60
 Ile Val Glu Phe Ser Lys Arg Val Pro Gly Phe Asp Thr Leu Ala Arg
 65 70 75 80
 Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met
 85 90 95
 Leu Arg Gly Ala Arg Lys Tyr Asp Val Lys Thr Asp Ser Ile Val Phe
 100 105 110

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Ala Asn Asn Gln Pro Tyr Thr Arg Asp Asn Tyr Arg Ser Ala Ser Val
 115 120 125

Gly Asp Ser Ala Asp Ala Leu Phe Arg Phe Cys Arg Lys Met Cys Gln
 130 135 140

Leu Arg Val Asp Asn Ala Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile
 145 150 155 160

Phe Ser Glu Arg Pro Ser Leu Val Asp Pro His Lys Val Glu Arg Ile
 165 170 175

Gln Glu Tyr Tyr Ile Glu Thr Leu Arg Met Tyr Ser Glu Asn His Arg
 180 185 190

Pro Pro Gly Lys Asn Tyr Phe Ala Arg Leu Leu Ser Ile Leu Thr Glu
 195 200 205

Leu Arg Thr Leu Gly Asn Met Asn Ala Glu Met Cys Phe Ser Leu Lys
 210 215 220

Val Gln Asn Lys Lys Leu Pro Pro Phe Leu Ala Glu Ile Trp Asp Ile
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<210> 20

<211> 1586

<212> DNA

<213> Bamecia argentifoli

<400> 20

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acccttatag tcccaccaat ggaagaatag ggaaagaaga gctttcgccg gcgaatagtc	180
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accagtgtaa atatggaaat aattgtgaaa ttgacatgta catgaggcga aaatgccaag	420
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<210> 21

<211> 1109

<212> DNA

<213> *Nephotetix cincticeps*

<400> 21

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<210> 22
 <211> 735
 <212> DNA
 <213> *Choristoneura fumiferana*

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 cgggtactacc tgaatacgtc ccgcatctat atcctgaacc agctgagcgg gtcggcgcggt 540
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<210> 23
 <211> 1338
 <212> DNA
 <213> *Drosophila melanogaster*

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<210> 24
 <211> 960
 <212> DNA
 <213> Choristoneura fumiferana

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ctctccgaca agctgttgga gacaaaccgg cagaaaaaca tccccagtt gacagccaac	240
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<210> 25
 <211> 969
 <212> DNA
 <213> Drosophila melanogaster

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caaatgttct cgatgaaggt ggacaacgtc gaatacgcg ttctcactgc cattgtgatc	720
ttctcggacc ggccgggcct ggagaaggcc caactagtcg aagcgatcca gagctactac	780
atcgacacgc tacgcattta tatactcaac cgccactgcg gcgactcaat gagcctcgtc	840
ttctacgcaa agctgctctc gatcctcacc gagctgcgta cgctgggcaa ccagaacgcc	900
gagatgtgtt tctcactaaa gctcaaaaac cgcaaactgc ccaagttcct cgaggagatc	960
tgggacggt	969

<210> 26

<211> 244

<212> PRT

<213> *Choristoneura fumiferana*

<400> 26

Tyr	Gln	Asp	Gly	Tyr	Glu	Gln	Pro	Ser	Asp	Glu	Asp	Leu	Lys	Arg	Ile
1				5					10					15	

Thr	Gln	Thr	Trp	Gln	Gln	Ala	Asp	Asp	Glu	Asn	Glu	Glu	Ser	Asp	Thr
			20					25					30		

Pro	Phe	Arg	Gln	Ile	Thr	Glu	Met	Thr	Ile	Leu	Thr	Val	Gln	Leu	Ile
		35					40					45			

Val	Glu	Phe	Ala	Lys	Gly	Leu	Pro	Gly	Phe	Ala	Lys	Ile	Ser	Gln	Pro
	50					55					60				

Asp	Gln	Ile	Thr	Leu	Leu	Lys	Ala	Cys	Ser	Ser	Glu	Val	Met	Met	Leu
65					70					75					80

Arg	Val	Ala	Arg	Arg	Tyr	Asp	Ala	Ala	Ser	Asp	Ser	Val	Leu	Phe	Ala
			85						90					95	

Asn	Asn	Gln	Ala	Tyr	Thr	Arg	Asp	Asn	Tyr	Arg	Lys	Ala	Gly	Met	Ala
			100					105					110		

Tyr	Val	Ile	Glu	Asp	Leu	Leu	His	Phe	Cys	Arg	Cys	Met	Tyr	Ser	Met
		115					120					125			

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Ala Leu Asp Asn Ile His Tyr Ala Leu Leu Thr Ala Val Val Ile Phe
130 135 140

Ser Asp Arg Pro Gly Leu Glu Gln Pro Gln Leu Val Glu Glu Ile Gln
145 150 155 160

Arg Tyr Tyr Leu Asn Thr Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser
165 170 175

Gly Ser Ala Arg Ser Ser Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu
180 185 190

Ser Glu Leu Arg Thr Leu Gly Met Gln Asn Ser Asn Met Cys Ile Ser
195 200 205

Leu Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp
210 215 220

Asp Val Ala Asp Met Ser His Thr Gln Pro Pro Pro Ile Leu Glu Ser
225 230 235 240

Pro Thr Asn Leu

<210> 27
<211> 445
<212> PRT
<213> Drosophila melanogaster

<400> 27
Tyr Glu Gln Pro Ser Glu Glu Asp Leu Arg Arg Ile Met Ser Gln Pro
1 5 10 15

Asp Glu Asn Glu Ser Gln Thr Asp Val Ser Phe Arg His Ile Thr Glu
20 25 30

Ile Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly Leu
35 40 45

Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp Gln Ile Thr Leu Leu Lys
50 55 60

Ala Cys Ser Ser Glu Val Met Met Leu Arg Met Ala Arg Arg Tyr Asp
65 70 75 80

His Ser Ser Asp Ser Ile Phe Phe Ala Asn Asn Arg Ser Tyr Thr Arg
85 90 95

Asp Ser Tyr Lys Met Ala Gly Met Ala Asp Asn Ile Glu Asp Leu Leu
100 105 110

His Phe Cys Arg Gln Met Phe Ser Met Lys Val Asp Asn Val Glu Tyr
 115 120 125
 Ala Leu Leu Thr Ala Ile Val Ile Phe Ser Asp Arg Pro Gly Leu Glu
 130 135 140
 Lys Ala Gln Leu Val Glu Ala Ile Gln Ser Tyr Tyr Ile Asp Thr Leu
 145 150 155 160
 Arg Ile Tyr Ile Leu Asn Arg His Cys Gly Asp Ser Met Ser Leu Val
 165 170 175
 Phe Tyr Ala Lys Leu Leu Ser Ile Leu Thr Glu Leu Arg Thr Leu Gly
 180 185 190
 Asn Gln Asn Ala Glu Met Cys Phe Ser Leu Lys Leu Lys Asn Arg Lys
 195 200 205
 Leu Pro Lys Phe Leu Glu Glu Ile Trp Asp Val His Ala Ile Pro Pro
 210 215 220
 Ser Val Gln Ser His Leu Gln Ile Thr Gln Glu Glu Asn Glu Arg Leu
 225 230 235 240
 Glu Arg Ala Glu Arg Met Arg Ala Ser Val Gly Gly Ala Ile Thr Ala
 245 250 255
 Gly Ile Asp Cys Asp Ser Ala Ser Thr Ser Ala Ala Ala Ala Ala Ala
 260 265 270
 Gln His Gln Pro Gln Pro Gln Pro Gln Pro Gln Pro Ser Ser Leu Thr
 275 280 285
 Gln Asn Asp Ser Gln His Gln Thr Gln Pro Gln Leu Gln Pro Gln Leu
 290 295 300
 Pro Pro Gln Leu Gln Gly Gln Leu Gln Pro Gln Leu Gln Pro Gln Leu
 305 310 315 320
 Gln Thr Gln Leu Gln Pro Gln Ile Gln Pro Gln Pro Gln Leu Leu Pro
 325 330 335
 Val Ser Ala Pro Val Pro Ala Ser Val Thr Ala Pro Gly Ser Leu Ser
 340 345 350
 Ala Val Ser Thr Ser Ser Glu Tyr Met Gly Gly Ser Ala Ala Ile Gly
 355 360 365
 Pro Ile Thr Pro Ala Thr Thr Ser Ser Ile Thr Ala Ala Val Thr Ala
 370 375 380

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Ser Ser Thr Thr Ser Ala Val Pro Met Gly Asn Gly Val Gly Val Gly
385 390 395 400

Val Gly Val Gly Gly Asn Val Ser Met Tyr Ala Asn Ala Gln Thr Ala
405 410 415

Met Ala Leu Met Gly Val Ala Leu His Ser His Gln Glu Gln Leu Ile
420 425 430

Gly Gly Val Ala Val Lys Ser Glu His Ser Thr Thr Ala
435 440 445

<210> 28

<211> 320

<212> PRT

<213> Choristoneura fumiferana

<400> 28

Pro Glu Cys Val Val Pro Glu Thr Gln Cys Ala Met Lys Arg Lys Glu
1 5 10 15

Lys Lys Ala Gln Lys Glu Lys Asp Lys Leu Pro Val Ser Thr Thr Thr
20 25 30

Val Asp Asp His Met Pro Pro Ile Met Gln Cys Glu Pro Pro Pro Pro
35 40 45

Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Ser Asp Lys
50 55 60

Leu Leu Glu Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu Thr Ala Asn
65 70 75 80

Gln Gln Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp Gly Tyr Glu
85 90 95

Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr Trp Gln Gln
100 105 110

Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg Gln Ile Thr
115 120 125

Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys Gly
130 135 140

Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln Ile Thr Leu Leu
145 150 155 160

Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg Tyr
165 170 175

Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn Gln Ala Tyr Thr
180 185 190

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Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val Ile Glu Asp Leu
195 200 205

Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp Asn Ile His
210 215 220

Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg Pro Gly Leu
225 230 235 240

Glu Gln Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu Asn Thr
245 250 255

Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser Ala Arg Ser Ser
260 265 270

Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu Arg Thr Leu
275 280 285

Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn Arg
290 295 300

Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp Val Ala Asp Met Ser
305 310 315 320

<210> 29
<211> 323
<212> PRT
<213> Drosophila melanogaster

<400> 29
Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Arg
1 5 10 15

Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Met Thr Thr Ser Pro Ser
20 25 30

Ser Gln His Gly Gly Asn Gly Ser Leu Ala Ser Gly Gly Gly Gln Asp
35 40 45

Phe Val Lys Lys Glu Ile Leu Asp Leu Met Thr Cys Glu Pro Pro Gln
50 55 60

His Ala Thr Ile Pro Leu Leu Pro Asp Glu Ile Leu Ala Lys Cys Gln
65 70 75 80

Ala Arg Asn Ile Pro Ser Leu Thr Tyr Asn Gln Leu Ala Val Ile Tyr
85 90 95

Lys Leu Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
100 105 110

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Leu Arg Arg Ile Met Ser Gln Pro Asp Glu Asn Glu Ser Gln Thr Asp
115 120 125

Val Ser Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu
130 135 140

Ile Val Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln
145 150 155 160

Glu Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met
165 170 175

Leu Arg Met Ala Arg Arg Tyr Asp His Ser Ser Asp Ser Ile Phe Phe
180 185 190

Ala Asn Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met
195 200 205

Ala Asp Asn Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Phe Ser
210 215 220

Met Lys Val Asp Asn Val Glu Tyr Ala Leu Leu Thr Ala Ile Val Ile
225 230 235 240

Phe Ser Asp Arg Pro Gly Leu Glu Lys Ala Gln Leu Val Glu Ala Ile
245 250 255

Gln Ser Tyr Tyr Ile Asp Thr Leu Arg Ile Tyr Ile Leu Asn Arg His
260 265 270

Cys Gly Asp Ser Met Ser Leu Val Phe Tyr Ala Lys Leu Leu Ser Ile
275 280 285

Leu Thr Glu Leu Arg Thr Leu Gly Asn Gln Asn Ala Glu Met Cys Phe
290 295 300

Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Lys Phe Leu Glu Glu Ile
305 310 315 320

Trp Asp Val

<210> 30
<211> 987
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 30
tgtgctatct gtggggaccg ctcctcaggc aaacactatg gggtatacag ttgtgagggc

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tgcaagggct tcttcaagag gacagtacgc aaagacctga cctacacctg ccgagacaac	120
aaggactgcc tgatcgacaa gagacagcgg aaccggtgtc agtactgccg ctaccagaag	180
tgcctggcca tgggcatgaa gcgggaagct gtgcaggagg agcggcagcg gggcaaggac	240
cggaatgaga acgaggtgga gtccaccagc agtgccaacg aggacatgcc tgtagagaag	300
attctggaag ccgagcttgc tgtcgagccc aagactgaga catacgtgga ggcaaacatg	360
gggctgaacc ccagctcacc aaatgaccct gttaccaaca tctgtcaagc agcagacaag	420
cagctcttca ctcttgtgga gtgggccaag aggatccac acttttctga gctgccccta	480
gacgaccagg tcatcctgct acgggcaggc tggaacgagc tgctgatcgc ctccttctcc	540
caccgctcca tagctgtgaa agatgggatt ctcttgcca ccggcctgca cgtacaccgg	600
aacagcgctc acagtgtggt ggtgggcgcc atctttgaca gggtgctaac agagctggtg	660
tctaagatgc gtgacatgca gatggacaag acggagctgg gctgcctgcg agccattgtc	720
ctgttcaacc ctgactctaa ggggctctca aaccctgtg aggtggaggc gttgaggag	780
aaggtgtatg cgtcactaga agcgtactgc aaacacaagt accctgagca gccgggcagg	840
tttgccaagc tgctgctccg cctgcctgca ctgcgttcca tcgggctcaa gtgcctggag	900
cacctgttct tcttcaagct catcggggac acgcccacg acaccttct catggagatg	960
ctggaggcac cacatcaagc cacctag	987

<210> 31

<211> 789

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 31

aagcgggaag ctgtgcagga ggagcggcag cggggcaagg accggaatga gaacgaggtg	60
gagtccacca gcagtgccaa cgaggacatg cctgtagaga agattctgga agccgagctt	120
gctgtcgagc ccaagactga gacatacgtg gaggcaaaca tggggctgaa cccagctca	180
ccaaatgacc ctgtttacca catctgtcaa gcagcagaca agcagctctt cactcttgtg	240
gagtgggcca agaggatccc acacttttct gagctgcccc tagacgacca ggtcatcctg	300
ctacgggcag gctggaacga gctgctgac gcctccttct cccaccgctc catagctgtg	360
aaagatggga ttctcctggc caccggcctg cacgtacacc ggaacagcgc tcacagtgtc	420
ggggtgggcg ccatctttga cagggtgcta acagagctgg tgtctaagat gcgtgacatg	480
cagatggaca agacggagct gggctgcctg cgagccattg tcctgttcaa ccctgactct	540
aaggggctct caaacctgc tgaggtggag gcgttgaggg agaaggtgta tgcgtcacta	600
gaagcgtact gcaaacacaa gtaccctgag cagccgggca ggtttgccaa gctgctgctc	660
cgcctgcctg cactgcgttc catcgggctc aagtgccctg agcacctgtt cttcttcaag	720
ctcatcgggg acacgcccac cgacaccttc ctcatggaga tgctggaggc accacatcaa	780

gccacctag

789

<210> 32
 <211> 714
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 32
 gccaacgagg acatgcctgt agagaagatt ctggaagccg agcttgctgt cgagcccaag 60
 actgagacat acgtggaggc aaacatgggg ctgaaccca gtcaccaa tgaccctgtt 120
 accaacaatct gtcaagcagc agacaagcag ctcttcactc ttgtggagtg ggccaagagg 180
 atccacact tttctgagct gcccctagac gaccaggtca tcctgctacg ggagggcttg 240
 aacgagctgc tgatgcctc cttctccac cgctccatag ctgtgaaaga tgggattctc 300
 ctggccaccg gcctgcacgt acaccggaac agcgctcaca gtgctggggg gggcgccatc 360
 ttgacaggg tgctaacaga gctgggtgtc aagatgcgtg acatgcagat ggacaagacg 420
 gagctgggct gcctgcgagc cattgtcctg ttcaaccctg actctaagg gctctcaaac 480
 cctgctgagg tggaggcgtt gagggagaag gtgtatgcgt cactagaagc gtactgcaaa 540
 cacaagtacc ctgagcagcc gggcagggtt gccaaagctg tgctccgcct gcctgcactg 600
 cgttccatcg ggctcaagt cctggagcac ctgttcttct tcaagctcat cggggacacg 660
 cccatcgaca ctttctcat ggagatgctg gaggcaccac atcaagccac ctag 714

<210> 33
 <211> 536
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 33
 ggatcccaca cttttctgag ctgcccctag acgaccaggt catcctgcta cgggcaggct 60
 ggaacgagct gctgatcgcc tccttctccc accgctccat agctgtgaaa gatgggattc 120
 tcctggccac cggcctgcac gtacaccgga acagcgctca cagtgtggg gtgggcgcca 180
 tctttgacag ggtgctaaca gagctgggtg ctaagatgcg tgacatgcag atggacaaga 240
 cggagctggg ctgcctgcga gccattgtcc tgttcaacc tgactctaag gggctctcaa 300
 accctgctga ggtggaggcg ttgagggaga aggtgtatgc gtcactagaa gcgtactgca 360
 aacacaagta ccctgagcag ccgggcagggt ttgccaagct gctgctccgc ctgcctgcac 420
 tgcgttccat cgggctcaag tgcctggagc acctgttctt cttcaagctc atcggggaca 480
 cgcccatcga caccttctc atggagatgc tggaggcacc acatcaagcc acctag 536

<210> 34
 <211> 672
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 34
 gccaacgagg acatgcctgt agagaagatt ctggaagccg agcttgctgt cgagcccaag 60
 actgagacat acgtggaggc aaacatgggg ctgaaccca gctcaccaa tgacctgtt 120
 accaacatct gtcaagcagc agacaagcag ctcttcactc ttgtggagt ggccaagagg 180
 atcccacact tttctgagct gcccctagac gaccaggtca tcctgctacg ggcaggctgg 240
 aacgagctgc tgatgcctc cttctccac cgctccatag ctgtgaaaga tgggattctc 300
 ctggccaccg gcctgcacgt acaccggaac agcgctcaca gtgctggggg gggcgccatc 360
 ttgacaggg tgctaacaga gctggtgtct aagatgcgtg acatgcagat ggacaagacg 420
 gagctgggct gcctgcgagc cattgtcctg ttcaaccctg actctaagg gctctcaaac 480
 cctgctgagg tggaggcggt gagggagaag gtgtatgcgt cactagaagc gtactgcaaa 540
 cacaagtacc ctgagcagcc gggcagggtt gccaaagctgc tgctccgcct gcctgcactg 600
 cgttccatcg ggctcaagt cctggagcac ctgttcttct tcaagctcat cggggacacg 660
 cccatcgaca cc 672

<210> 35
 <211> 1123
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic Novel polynucleotide sequence

<400> 35
 tgcgccatct gcggggaccg ctcctcaggc aagcactatg gagtgtacag ctgcgagggg 60
 tgcaagggct tcttcaagcg gacggtgcgc aaggacctga cctacacctg ccgcgacaac 120
 aaggactgcc tgattgacaa gcggcagcgg aaccggtgcc agtactgccg ctaccagaag 180
 tgcctggcca tgggcatgaa gcgggaagcc gtgcaggagg agcggcagcg tggcaaggac 240
 cggaacgaga atgaggtgga gtcgaccagc agcgccaacg aggacatgcc ggtggagagg 300
 atcctggagg ctgagctggc cgtggagccc aagaccgaga cctacgtgga ggcaaacatg 360
 gggctgaacc ccagctcgcc gaacgaccct gtcaccaaca ttgccaagc agccgacaaa 420
 cagcttttca ccctggtgga gtgggccaag cggatccac acttctcaga gctgcccctg 480
 gacgaccagg tcatcctgct gcgggcaggc tggaatgagc tgctcatcgc ctccttctcc 540
 caccgctcca tcgccgtgaa ggacgggatc ctcctggcca ccgggctgca cgtccaccgg 600
 aacagcggc acagcgcagg ggtgggcgcc atctttgaca gggctgctgac ggagcttggtg 660
 tccaagatgc gggacatgca gatggacaag acggagctgg gctgcctgcg cgccatcgtc 720

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ctctttaacc ctgactccaa ggggctctcg aacccggccg aggtggaggc gctgagggag	780
aaggtctatg cgtccttgga ggcctactgc aagcacaagt acccagagca gccgggaagg	840
ttcgctaagc tcttgctccg cctgccggct ctgcgctcca tcgggctcaa atgcctggaa	900
catctcttct tcttcaagct catcggggac acaccattg acaccttcct tatggagatg	960
ctggaggcgc cgcaccaa at gacttaggcc tgcggggcca tcctttgtgc ccaccgttc	1020
tggccaccct gcctggacgc cagctgttct tctcagcctg agccctgtcc ctgcccttct	1080
ctgcctggcc tgtttgact ttggggcaca gcctgtcact gct	1123

<210> 36

<211> 925

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Novel polynucleotide sequence

<400> 36

aagcgggaag ccgtgcagga ggagcggcag cgtggcaagg accggaacga gaatgaggtg	60
gagtcgacca gcagcgccaa cgaggacatg ccggtggaga ggatcctgga ggctgagctg	120
gccgtggagc ccaagaccga gacctacgtg gaggcaaaca tggggctgaa cccagctcg	180
ccgaacgacc ctgtcaccaa catttgccaa gcagccgaca aacagctttt caccctggtg	240
gagtgggcca agcggatccc acacttctca gagctgcccc tggacgacca ggtcatcctg	300
ctgcgggcag gctggaatga gctgctcatc gcctccttct cccaccgctc catcgccgtg	360
aaggacggga tcctcctggc caccgggctg cacgtccacc ggaacagcgc ccacagcgca	420
gggggtgggcg ccatctttga cagggtgctg acggagcttg tgtccaagat gcgggacatg	480
cagatggaca agacggagct gggctgcctg cgcgccatcg tcctctttaa ccctgactcc	540
aaggggctct cgaaccggc cgaggtggag gcgctgaggg agaaggtcta tgcgtccttg	600
gaggcctact gcaagcacia gtaccagag cagccgggaa ggttcgctaa gctcttgctc	660
cgcctgccgg ctctgcgctc catcgggctc aaatgcctgg aacatctctt cttcttcaag	720
ctcatcgggg acacacccat tgacaccttc cttatggaga tgctggaggc gccgcaccaa	780
atgacttagg cctgcggggc catcctttgt gccacccgt tctggccacc ctgcctggac	840
gccagctgtt cttctcagcc tgagccctgt ccctgccctt ctctgcctgg cctgtttgga	900
ctttggggca cagcctgtca ctgct	925

<210> 37

<211> 850

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Novel polynucleotide sequence

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<400> 37
gccaacgagg acatgccggt ggagaggatc ctggaggctg agctggccgt ggagcccaag 60
accgagacct acgtggaggc aaacatgggg ctgaaccca gctcgccgaa cgacctgtc 120
accaacattt gccaagcagc cgacaaacag cttttcaccc tgggtggagt ggccaagcgg 180
atcccacact tctcagagct gcccctggac gaccaggctca tcctgctgcg ggcaggctgg 240
aatgagctgc tcatgcctc cttctcccac cgctccatcg ccgtgaagga cgggatcctc 300
ctggccaccg ggctgcacgt ccaccggaac agcgcccaca gcgcaggggt gggcgccatc 360
tttgacaggg tgctgacgga gcttgtgtcc aagatgcggg acatgcagat ggacaagacg 420
gagctgggct gcctgcgcgc catcgtcctc ttttaaccctg actccaaggg gctctcgaac 480
ccggccgagg tggaggcgct gagggagaag gtctatgctg ccttggaggc ctactgcaag 540
cacaagtacc cagagcagcc ggggaagggtc gctaagctct tgctccgcct gccggctctg 600
cgctccatcg ggctcaaagt cctggaacat ctcttcttct tcaagctcat cggggacaca 660
cccattgaca ctttccttat ggagatgctg gaggcgccgc accaaatgac ttaggcctgc 720
gggcccaccc tttgtgccc cccgttcttg ccaccctgcc tggacgccag ctgttcttct 780
cagcctgagc cctgtccctg cccttctctg cctggcctgt ttggactttg gggcacagcc 840
tgtcactgct 850

<210> 38
<211> 670
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 38
atcccacact tctcagagct gcccctggac gaccaggctca tcctgctgcg ggcaggctgg 60
aatgagctgc tcatgcctc cttctcccac cgctccatcg ccgtgaagga cgggatcctc 120
ctggccaccg ggctgcacgt ccaccggaac agcgcccaca gcgcaggggt gggcgccatc 180
tttgacaggg tgctgacgga gcttgtgtcc aagatgcggg acatgcagat ggacaagacg 240
gagctgggct gcctgcgcgc catcgtcctc ttttaaccctg actccaaggg gctctcgaac 300
ccggccgagg tggaggcgct gagggagaag gtctatgctg ccttggaggc ctactgcaag 360
cacaagtacc cagagcagcc ggggaagggtc gctaagctct tgctccgcct gccggctctg 420
cgctccatcg ggctcaaagt cctggaacat ctcttcttct tcaagctcat cggggacaca 480
cccattgaca ctttccttat ggagatgctg gaggcgccgc accaaatgac ttaggcctgc 540
gggcccaccc tttgtgccc cccgttcttg ccaccctgcc tggacgccag ctgttcttct 600
cagcctgagc cctgtccctg cccttctctg cctggcctgt ttggactttg gggcacagcc 660
tgtcactgct 670

<210> 39

<211> 672
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polynucleotide

<400> 39
 gccaacgagg acatgccggt ggagaggatc ctggaggctg agctggccgt ggagcccaag 60
 accgagacct acgtggaggc aaacatgggg ctgaaccca gctcgccgaa cgaccctgtc 120
 accaacattt gccaaacagc cgacaaacag cttttcacc tggtggagt ggccaagcgg 180
 atcccacact tctcagagct gcccctggac gaccaggctca tcctgctgcg ggcaggctgg 240
 aatgagctgc tcatcgcttc cttctccac cgctccatcg ccgtgaagga cgggatcctc 300
 ctggccaccg ggctgcacgt ccaccggaac agcgcccaca gcgcaggggt gggcgccatc 360
 ttgacaggg tgctgacgga gcttggtgcc aagatgcggg acatgcagat ggacaagacg 420
 gagctgggct gcctgcgcgc catcgctcctc tttaaccctg actccaagg gctctcgaac 480
 ccggccgagg tggaggcgct gagggagaag gtctatgcgt ccttgaggc ctactgcaag 540
 cacaagtacc cagagcagcc gggaagggtc gctaagctct tgctccgcct gccggctctg 600
 cgctccatcg ggctcaaagt cctggaacat ctcttcttct tcaagctcat cggggacaca 660
 cccattgaca cc 672

<210> 40
 <211> 328
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 40
 Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His Tyr Gly Val Tyr
 1 5 10 15
 Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp
 20 25 30
 Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp Cys Leu Ile Asp Lys Arg
 35 40 45
 Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Met
 50 55 60
 Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp
 65 70 75 80
 Arg Asn Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met
 85 90 95

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Pro Val Glu Lys Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr
100 105 110

Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn
115 120 125

Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr
130 135 140

Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu
145 150 155 160

Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile
165 170 175

Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu
180 185 190

Ala Thr Gly Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val
195 200 205

Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg
210 215 220

Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val
225 230 235 240

Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu
245 250 255

Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His
260 265 270

Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu
275 280 285

Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe
290 295 300

Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met
305 310 315 320

Leu Glu Ala Pro His Gln Ala Thr
325

<210> 41

<211> 262

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

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<400> 41

Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn
1 5 10 15

Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met Pro Val
20 25 30

Glu Lys Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr
35 40 45

Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro
50 55 60

Val Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val
65 70 75 80

Glu Trp Ala Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp
85 90 95

Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser
100 105 110

Phe Ser His Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr
115 120 125

Gly Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala
130 135 140

Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met
145 150 155 160

Gln Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe
165 170 175

Asn Pro Asp Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu
180 185 190

Arg Glu Lys Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr
195 200 205

Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala
210 215 220

Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys
225 230 235 240

Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu
245 250 255

Ala Pro His Gln Ala Thr
260

<210> 42
 <211> 237
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 42
 Ala Asn Glu Asp Met Pro Val Glu Lys Ile Leu Glu Ala Glu Leu Ala
 1 5 10 15
 Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
 20 25 30
 Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
 35 40 45
 Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
 50 55 60
 Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
 65 70 75 80
 Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
 85 90 95
 Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
 100 105 110
 His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
 115 120 125
 Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
 130 135 140
 Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
 145 150 155 160
 Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
 165 170 175
 Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
 180 185 190
 Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
 195 200 205
 Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
 210 215 220

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Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Ala Thr
225 230 235

<210> 43
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 43
Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu
1 5 10 15

Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser
20 25 30

Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His
35 40 45

Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val
50 55 60

Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr
65 70 75 80

Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys
85 90 95

Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr
100 105 110

Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly
115 120 125

Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly
130 135 140

Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr
145 150 155 160

Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Ala
165 170 175

Thr

<210> 44
<211> 224
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 44

Ala Asn Glu Asp Met Pro Val Glu Lys Ile Leu Glu Ala Glu Leu Ala
1 5 10 15

Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30

Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
35 40 45

Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
50 55 60

Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
65 70 75 80

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
100 105 110

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
115 120 125

Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
130 135 140

Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
145 150 155 160

Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
210 215 220

<210> 45

<211> 328

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

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<400> 45

Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His Tyr Gly Val Tyr
1 5 10 15

Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp
20 25 30

Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp Cys Leu Ile Asp Lys Arg
35 40 45

Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Met
50 55 60

Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp
65 70 75 80

Arg Asn Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met
85 90 95

Pro Val Glu Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr
100 105 110

Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn
115 120 125

Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr
130 135 140

Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu
145 150 155 160

Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile
165 170 175

Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu
180 185 190

Ala Thr Gly Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val
195 200 205

Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg
210 215 220

Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val
225 230 235 240

Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu
245 250 255

Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His
260 265 270

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Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu
275 280 285

Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe
290 295 300

Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met
305 310 315 320

Leu Glu Ala Pro His Gln Met Thr
325

<210> 46

<211> 262

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 46

Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn
1 5 10 15

Glu Asn Glu Val Glu Ser Thr Ser Ser Ala Asn Glu Asp Met Pro Val
20 25 30

Glu Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Thr
35 40 45

Tyr Val Glu Ala Asn Met Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro
50 55 60

Val Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val
65 70 75 80

Glu Trp Ala Lys Arg Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp
85 90 95

Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser
100 105 110

Phe Ser His Arg Ser Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr
115 120 125

Gly Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala
130 135 140

Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met
145 150 155 160

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Gln Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe
165 170 175

Asn Pro Asp Ser Lys Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu
180 185 190

Arg Glu Lys Val Tyr Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr
195 200 205

Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala
210 215 220

Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys
225 230 235 240

Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu
245 250 255

Ala Pro His Gln Met Thr
260

<210> 47

<211> 237

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 47

Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu Ala
1 5 10 15

Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30

Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
35 40 45

Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
50 55 60

Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
65 70 75 80

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
100 105 110

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
115 120 125

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Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
130 135 140

Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
145 150 155 160

Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
210 215 220

Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr
225 230 235

<210> 48
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 48
Ile Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu
1 5 10 15

Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser
20 25 30

Ile Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His
35 40 45

Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val
50 55 60

Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr
65 70 75 80

Glu Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys
85 90 95

Gly Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr
100 105 110

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Ala Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly
 115 120 125
 Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly
 130 135 140
 Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr
 145 150 155 160
 Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met
 165 170 175

Thr

<210> 49
 <211> 224
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 49
 Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu Ala
 1 5 10 15
 Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
 20 25 30
 Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
 35 40 45
 Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
 50 55 60
 Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
 65 70 75 80
 Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
 85 90 95
 Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
 100 105 110
 His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
 115 120 125
 Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
 130 135 140
 Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
 145 150 155 160

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Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
210 215 220

<210> 50
<211> 635
<212> DNA
<213> Locusta migratoria

<400> 50
tgcatacaga catgcctggt gaacgcatac ttgaagctga aaaacgagtg gagtgcaaag 60
cagaaaacca agtgggaatat gagctggtgg agtgggctaa acacatcccg cacttcacat 120
ccctacctct ggaggaccag gttctcctcc tcagagcagg ttggaatgaa ctgctaattg 180
cagcattttc acatcgatct gtagatgtta aagatggcat agtacttgcc actggtctca 240
cagtgcacg aaattctgcc catcaagctg gagtcggcac aatatttgac agagtgttga 300
cagaactggt agcaaagatg agagaaatga aaatggataa aactgaactt ggctgcttgc 360
gatctgttat tcttttcaat ccagagggtga ggggtttgaa atccgcccag gaagttgaac 420
ttctacgtga aaaagtatat gccgctttgg aagaatatac tagaacaaca catcccgatg 480
aaccaggaag atttgcaaaa cttttgcttc gtctgccttc tttacgttcc ataggcctta 540
agtgtttgga gcatttgttt ttctttcgcc ttattggaga tgttccaatt gatacgttcc 600
tgatggagat gcttgaatca ccttctgatt cataa 635

<210> 51
<211> 687
<212> DNA
<213> Amblyomma americanum

<400> 51
cctcctgaga tgcctctgga gcgcatactg gaggcagagc tgcggggtga gtcacagacg 60
gggaccctct cggaagcgc acagcagcag gatccagtga gcagcatctg ccaagctgca 120
gaccgacagc tgcaccagct agttcaatgg gccaagcaca ttccacattt tgaagagctt 180
ccccttgagg accgcatggt gttgctcaag gctggctgga acgagctgct cattgctgct 240
ttctcccacc gttctgttga cgtgcgtgat ggcatgtgc tcgctacagg tcttgtggtg 300
cagcggcata gtgctcatgg ggctggcggt ggggccatat ttgatagggt tctcactgaa 360
ctggtagcaa agatgcgtga gatgaagatg gaccgcactg agcttgatg cctgcttgct 420
gtggtacttt ttaatcctga ggccaagggg ctgcggacct gcccaagtgg aggccctgag 480

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ggagaaagtg tatctgcctt ggaagagcac tgccggcagc agtaccaga ccagcctggg	540
cgctttgccca agctgctgct gcggttgcca gctctgcgca gtattggcct caagtgcctc	600
gaacatctct ttttcttcaa gctcatcggg gacacgcca tcgacaactt tcttctttcc	660
atgctggagg cccctctga cccctaa	687

<210> 52
 <211> 693
 <212> DNA
 <213> Amblyomma americanum

<400> 52 tctccggaca tgccactcga acgcattctc gaagccgaga tgcgcgtcga gcagccggca	60
ccgtccgttt tggcgcagac ggccgcatcg ggccgcgacc ccgtcaacag catgtgccag	120
gctgccccgc cacttcacga gctcgtacag tgggcccggc gaattccgca cttcgaagag	180
cttcccatcg aggatcgac cgcgctgctc aaagccggct ggaacgaact gcttattgcc	240
gccttttcgc accgttctgt ggcggtgcgc gacggcatcg ttctggccac cgggctggtg	300
gtgcagcggc acagcgcaca cggcgcaggc gttggcgaca tcttcgaccg cgtactagcc	360
gagctggtgg ccaagatgcg cgacatgaag atggacaaa cggagctcgg ctgcctgcgc	420
gccgtggtgc tcttcaatcc agacgccaag ggtctccgaa acgccaccag agtagaggcg	480
ctccgcgaga aggtgtatgc ggcgctggag gagcactgcc gtcggcacca cccggaccaa	540
ccgggtcgct tcggcaagct gctgctgcgg ctgcctgcct tgcgcagcat cgggctcaaa	600
tgcctcgagc atctgttctt cttcaagctc atcggagaca ctcccataga cagcttcctg	660
ctcaacatgc tggaggcacc ggcagacccc tag	693

<210> 53
 <211> 801
 <212> DNA
 <213> Celuca pugilator

<400> 53 tcagacatgc caattgccag catacgggag gcagagctca gcgtggatcc catagatgag	60
cagccgctgg accaaggggt gaggcttcag gttccactcg cacctcctga tagtgaaaag	120
tgtagcttta ctttaccttt tcatcccgtc agtgaagtat cctgtgctaa ccctctgcag	180
gatgtggtga gcaacatatg ccaggcagct gacagacatc tgggtgcagct ggtggagtgg	240
gccaagcaca tcccacactt cacagacctt cccatagagg accaagtggg attactcaaa	300
gccgggtgga acgagttgct tattgcctca ttctcacacc gtagcatggg cgtggaggat	360
ggcatcgtgc tggccacagg gctcgtgatc cacagaagta gtgctcacca ggctggagtg	420
ggtgccatat ttgatcgtgt cctctctgag ctggtggcca agatgaagga gatgaagatt	480
gacaagacag agctgggctg ccttcgctcc atcgtcctgt tcaaccaga tgccaaagga	540
ctaaactgcg tcaatgatgt ggagatcttg cgtgagaagg tgtatgctgc cctggaggag	600
tacacacgaa ccacttacct tgatgaacct ggacgctttg ccaagtgtgt tctgcgactt	660

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cctgcactca ggtctatagg cctgaagtgt cttgagtacc tcttcctggt taagctgatt	720
ggagacactc ccctggacag ctacttgatg aagatgctcg tagacaaccc aaatacaagc	780
gtcactcccc ccaccagcta g	801

<210> 54
 <211> 690
 <212> DNA
 <213> *Tenebrio molitor*

<400> 54	
gccgagatgc ccctcgacag gataatcgag gcggagaaac ggatagaatg cacacccgct	60
ggtggctctg gtggtgtcgg agagcaacac gacgggggtga acaacatctg tcaagccact	120
aacaagcagc tgttccaact ggtgcaatgg gctaagctca tacctcactt tacctcgttg	180
ccgatgtcgg accaggtgct tttattgagg gcaggatgga atgaattgct catcgccgca	240
ttctcgcaca gatctataca ggcgcaggat gccatcggtc tagccacggg gttgacagtt	300
aacaaaacgt cggcgcacgc cgtgggcgtg ggcaacatct acgaccgct cctctccgag	360
ctggtgaaca agatgaaaga gatgaagatg gacaagacgg agctgggctg cttgagagcc	420
atcatcctct acaacccac gtgtcgcggc atcaagtccg tgcaggaagt ggagatgctg	480
cgtgagaaaa tttacggcgt gctggaagag tacaccagga ccaccaccc gaacgagccc	540
ggcagggttcg ccaaactgct tctgcgcctc ccggccctca ggtccatcgg gttgaaatgt	600
tccgaacacc tctttttctt caagctgatc ggtgatgttc caatagacac gttcctgatg	660
gagatgctgg agtctccggc ggacgcttag	690

<210> 55
 <211> 681
 <212> DNA
 <213> *Apis mellifera*

<400> 55	
cattcggaca tgccgatcga gcgtatcctg gaggccgaga agagagtcga atgtaagatg	60
gagcaacagg gaaattacga gaatgcagtg tcgcacattt gcaacgccac gaacaaacag	120
ctgttccagc tggtagcatg ggcgaaacac atcccgcatt ttacctcgtt gccactggag	180
gatcaggtac ttctgctcag ggccgggttg aacgagttgc tgatagcctc cttttccac	240
cgttccatcg acgtgaagga cggatcgtg ctggcgacgg ggatcaccgt gcatcggaac	300
tcggcgcagc aggccggcgt gggcacgata ttcgaccgtg tcctctcgga gcttgtctcg	360
aaaatgcgtg aaatgaagat ggacaggaca gagcttggct gtctcagatc tataatactc	420
ttcaatcccg aggttcgagg actgaaatcc atccaggaag tgaccctgct ccgtgagaag	480
atctacggcg ccctggaggg ttattgccgc gtagcttggc ccgacgacgc tggaagattc	540
gcgaaattac ttctacgcct gcccgccatc cgctcgatcg gattaaagt cctcgagtac	600
ctgttcttct tcaaaatgat cggtgacgta ccgatcgacg attttctcgt ggagatgtta	660
gaatcgcgat cagatcctta g	681

<210> 56
 <211> 210
 <212> PRT
 <213> *Locusta migratoria*

<400> 56
 His Thr Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Lys Arg Val
 1 5 10 15
 Glu Cys Lys Ala Glu Asn Gln Val Glu Tyr Glu Leu Val Glu Trp Ala
 20 25 30
 Lys His Ile Pro His Phe Thr Ser Leu Pro Leu Glu Asp Gln Val Leu
 35 40 45
 Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ala Phe Ser His
 50 55 60
 Arg Ser Val Asp Val Lys Asp Gly Ile Val Leu Ala Thr Gly Leu Thr
 65 70 75 80
 Val His Arg Asn Ser Ala His Gln Ala Gly Val Gly Thr Ile Phe Asp
 85 90 95
 Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Glu Met Lys Met Asp
 100 105 110
 Lys Thr Glu Leu Gly Cys Leu Arg Ser Val Ile Leu Phe Asn Pro Glu
 115 120 125
 Val Arg Gly Leu Lys Ser Ala Gln Glu Val Glu Leu Leu Arg Glu Lys
 130 135 140
 Val Tyr Ala Ala Leu Glu Glu Tyr Thr Arg Thr Thr His Pro Asp Glu
 145 150 155 160
 Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu Arg Ser
 165 170 175
 Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Arg Leu Ile Gly
 180 185 190
 Asp Val Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ser Pro Ser
 195 200 205
 Asp Ser
 210

<210> 57
 <211> 228
 <212> PRT
 <213> *Amblyomma americanum*

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<400> 57

Pro Pro Glu Met Pro Leu Glu Arg Ile Leu Glu Ala Glu Leu Arg Val
1 5 10 15
Glu Ser Gln Thr Gly Thr Leu Ser Glu Ser Ala Gln Gln Gln Asp Pro
20 25 30
Val Ser Ser Ile Cys Gln Ala Ala Asp Arg Gln Leu His Gln Leu Val
35 40 45
Gln Trp Ala Lys His Ile Pro His Phe Glu Glu Leu Pro Leu Glu Asp
50 55 60
Arg Met Val Leu Leu Lys Ala Gly Trp Asn Glu Leu Leu Ile Ala Ala
65 70 75 80
Phe Ser His Arg Ser Val Asp Val Arg Asp Gly Ile Val Leu Ala Thr
85 90 95
Gly Leu Val Val Gln Arg His Ser Ala His Gly Ala Gly Val Gly Ala
100 105 110
Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ala Lys Met Arg Glu Met
115 120 125
Lys Met Asp Arg Thr Glu Leu Gly Cys Leu Leu Ala Val Val Leu Phe
130 135 140
Asn Pro Glu Ala Lys Gly Leu Arg Thr Cys Pro Ser Gly Gly Pro Glu
145 150 155 160
Gly Glu Ser Val Ser Ala Leu Glu Glu His Cys Arg Gln Gln Tyr Pro
165 170 175
Asp Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu
180 185 190
Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu
195 200 205
Ile Gly Asp Thr Pro Ile Asp Asn Phe Leu Leu Ser Met Leu Glu Ala
210 215 220
Pro Ser Asp Pro
225

<210> 58

<211> 230

<212> PRT

<213> Amblyomma americanum

<400> 58

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Ser Pro Asp Met Pro Leu Glu Arg Ile Leu Glu Ala Glu Met Arg Val
1 5 10 15

Glu Gln Pro Ala Pro Ser Val Leu Ala Gln Thr Ala Ala Ser Gly Arg
20 25 30

Asp Pro Val Asn Ser Met Cys Gln Ala Ala Pro Pro Leu His Glu Leu
35 40 45

Val Gln Trp Ala Arg Arg Ile Pro His Phe Glu Glu Leu Pro Ile Glu
50 55 60

Asp Arg Thr Ala Leu Leu Lys Ala Gly Trp Asn Glu Leu Leu Ile Ala
65 70 75 80

Ala Phe Ser His Arg Ser Val Ala Val Arg Asp Gly Ile Val Leu Ala
85 90 95

Thr Gly Leu Val Val Gln Arg His Ser Ala His Gly Ala Gly Val Gly
100 105 110

Asp Ile Phe Asp Arg Val Leu Ala Glu Leu Val Ala Lys Met Arg Asp
115 120 125

Met Lys Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Val Val Leu
130 135 140

Phe Asn Pro Asp Ala Lys Gly Leu Arg Asn Ala Thr Arg Val Glu Ala
145 150 155 160

Leu Arg Glu Lys Val Tyr Ala Ala Leu Glu Glu His Cys Arg Arg His
165 170 175

His Pro Asp Gln Pro Gly Arg Phe Gly Lys Leu Leu Leu Arg Leu Pro
180 185 190

Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe
195 200 205

Lys Leu Ile Gly Asp Thr Pro Ile Asp Ser Phe Leu Leu Asn Met Leu
210 215 220

Glu Ala Pro Ala Asp Pro
225 230

<210> 59
<211> 266
<212> PRT
<213> Celuca pugilator

<400> 59
Ser Asp Met Pro Ile Ala Ser Ile Arg Glu Ala Glu Leu Ser Val Asp
1 5 10 15

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Pro Ile Asp Glu Gln Pro Leu Asp Gln Gly Val Arg Leu Gln Val Pro
20 25 30

Leu Ala Pro Pro Asp Ser Glu Lys Cys Ser Phe Thr Leu Pro Phe His
35 40 45

Pro Val Ser Glu Val Ser Cys Ala Asn Pro Leu Gln Asp Val Val Ser
50 55 60

Asn Ile Cys Gln Ala Ala Asp Arg His Leu Val Gln Leu Val Glu Trp
65 70 75 80

Ala Lys His Ile Pro His Phe Thr Asp Leu Pro Ile Glu Asp Gln Val
85 90 95

Val Leu Leu Lys Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser
100 105 110

His Arg Ser Met Gly Val Glu Asp Gly Ile Val Leu Ala Thr Gly Leu
115 120 125

Val Ile His Arg Ser Ser Ala His Gln Ala Gly Val Gly Ala Ile Phe
130 135 140

Asp Arg Val Leu Ser Glu Leu Val Ala Lys Met Lys Glu Met Lys Ile
145 150 155 160

Asp Lys Thr Glu Leu Gly Cys Leu Arg Ser Ile Val Leu Phe Asn Pro
165 170 175

Asp Ala Lys Gly Leu Asn Cys Val Asn Asp Val Glu Ile Leu Arg Glu
180 185 190

Lys Val Tyr Ala Ala Leu Glu Glu Tyr Thr Arg Thr Thr Tyr Pro Asp
195 200 205

Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg
210 215 220

Ser Ile Gly Leu Lys Cys Leu Glu Tyr Leu Phe Leu Phe Lys Leu Ile
225 230 235 240

Gly Asp Thr Pro Leu Asp Ser Tyr Leu Met Lys Met Leu Val Asp Asn
245 250 255

Pro Asn Thr Ser Val Thr Pro Pro Thr Ser
260 265

<210> 60
<211> 229

<212> PRT

<213> *Tenebrio molitor*

<400> 60

Ala Glu Met Pro Leu Asp Arg Ile Ile Glu Ala Glu Lys Arg Ile Glu
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20 25 30Val Asn Asn Ile Cys Gln Ala Thr Asn Lys Gln Leu Phe Gln Leu Val
35 40 45Gln Trp Ala Lys Leu Ile Pro His Phe Thr Ser Leu Pro Met Ser Asp
50 55 60Gln Val Leu Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ala
65 70 75 80Phe Ser His Arg Ser Ile Gln Ala Gln Asp Ala Ile Val Leu Ala Thr
85 90 95Gly Leu Thr Val Asn Lys Thr Ser Ala His Ala Val Gly Val Gly Asn
100 105 110Ile Tyr Asp Arg Val Leu Ser Glu Leu Val Asn Lys Met Lys Glu Met
115 120 125Lys Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Ile Leu Tyr
130 135 140Asn Pro Thr Cys Arg Gly Ile Lys Ser Val Gln Glu Val Glu Met Leu
145 150 155 160Arg Glu Lys Ile Tyr Gly Val Leu Glu Glu Tyr Thr Arg Thr Thr His
165 170 175Pro Asn Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala
180 185 190Leu Arg Ser Ile Gly Leu Lys Cys Ser Glu His Leu Phe Phe Phe Lys
195 200 205Leu Ile Gly Asp Val Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu
210 215 220Ser Pro Ala Asp Ala
225

<210> 61

<211> 226

<212> PRT

<213> *Apis mellifera*

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<400> 61

His Ser Asp Met Pro Ile Glu Arg Ile Leu Glu Ala Glu Lys Arg Val
1 5 10 15

Glu Cys Lys Met Glu Gln Gln Gly Asn Tyr Glu Asn Ala Val Ser His
20 25 30

Ile Cys Asn Ala Thr Asn Lys Gln Leu Phe Gln Leu Val Ala Trp Ala
35 40 45

Lys His Ile Pro His Phe Thr Ser Leu Pro Leu Glu Asp Gln Val Leu
50 55 60

Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His
65 70 75 80

Arg Ser Ile Asp Val Lys Asp Gly Ile Val Leu Ala Thr Gly Ile Thr
85 90 95

Val His Arg Asn Ser Ala Gln Gln Ala Gly Val Gly Thr Ile Phe Asp
100 105 110

Arg Val Leu Ser Glu Leu Val Ser Lys Met Arg Glu Met Lys Met Asp
115 120 125

Arg Thr Glu Leu Gly Cys Leu Arg Ser Ile Ile Leu Phe Asn Pro Glu
130 135 140

Val Arg Gly Leu Lys Ser Ile Gln Glu Val Thr Leu Leu Arg Glu Lys
145 150 155 160

Ile Tyr Gly Ala Leu Glu Gly Tyr Cys Arg Val Ala Trp Pro Asp Asp
165 170 175

Ala Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Ile Arg Ser
180 185 190

Ile Gly Leu Lys Cys Leu Glu Tyr Leu Phe Phe Phe Lys Met Ile Gly
195 200 205

Asp Val Pro Ile Asp Asp Phe Leu Val Glu Met Leu Glu Ser Arg Ser
210 215 220

Asp Pro
225

<210> 62

<211> 714

<212> DNA

<213> Mus musculus

<400> 62

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accaacatct	gtcaagcagc	agacaagcag	ctcttcactc	ttgtggagtg	ggccaagagg	180
atcccacact	tttctgagct	gcccctagac	gaccagggtca	tcctgctacg	ggcaggctgg	240
aacgagctgc	tgatcgcctc	cttctcccac	cgctccatag	ctgtgaaaga	tgggattctc	300
ctggccaccg	gcctgcacgt	acaccggaac	agcgctcaca	gtgctggggg	gggcgccatc	360
tttgacaggg	tgctaacaga	gctgggtgtct	aagatgcgtg	acatgcagat	ggacaagacg	420
gagctgggct	gcctgcgagc	cattgtcctg	ttcaaccctg	actctaagg	gctctcaaac	480
cctgctgagg	tggaggcggt	gagggagaag	gtgtatgcgt	cactagaagc	gtactgcaaa	540
cacaagtacc	ctgagcagcc	gggcagggtt	gccaagctgc	tgctccgcct	gcctgcactg	600
cgttccatcg	ggctcaagt	cctggagcac	ctgttcttct	tcaagctcat	cggggacacg	660
cccatcgaca	ccttcctcat	ggagatgctg	gaggcaccac	atcaagccac	ctag	714

<210> 63
 <211> 720
 <212> DNA
 <213> Mus musculus

<400> 63	
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ccagtgacta	acatctgcca ggcagctgac aaacagctgt tcacactcgt tgagtgggca 180
aagaggatcc	cgcacttctc ctccctacct ctggacgatc aggtcatact gctgcgggca 240
ggctggaacg	agctcctcat tgcgtccttc tcccatcggt ccattgatgt ccgagatggc 300
atcctcctgg	ccacgggtct tcatgtgcac agaaactcag cccattccgc aggcgtggga 360
gccatctttg	atcgggtgct gacagagcta gtgtccaaaa tgcgtgacat gaggatggac 420
aagacagagc	ttggctgcct gcgggcaatc atcatgttta atccagacgc caagggcctc 480
tccaaccctg	gagagggtgga gatccttcgg gagaagggtg acgcctcact ggagacctat 540
tgcaagcaga	agtaccctga gcagcagggc cggtttgcca agctgctgtt acgtcttcct 600
gccctccgct	ccatcggcct caagtgtctg gagcacctgt tcttcttcaa gctcattggc 660
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<210> 64
 <211> 705
 <212> DNA
 <213> Mus musculus

<400> 64	
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tgccatgctg	cagataagca acttttcacc ctcgttgagt gggccaaacg catccccac 180

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gtccttacag	agttggtgtc	caagatgaaa	gacatgcaga	tgataaagtc	agagctgggg	420
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ggcttgaaat	gcctggaaca	cctcttcttc	ttcaagctca	ttggagacac	tcccatcgac	660
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<210> 65
 <211> 850
 <212> DNA
 <213> Homo sapiens

<400> 65						
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accaacattt	gccaagcagc	cgacaaacag	cttttcaccc	tggtggagtg	ggccaagcgg	180
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aatgagctgc	tcatgcctc	cttctccac	cgctccatcg	ccgtgaagga	cgggatcctc	300
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ccggccgagg	tgagggcgct	gagggagaag	gtctatgcgt	ccttggaggc	ctactgcaag	540
cacaagtacc	cagagcagcc	gggaagggtt	gctaagctct	tgctccgcct	gccggctctg	600
cgctccatcg	ggctcaaagt	cctggaacat	ctcttcttct	tcaagctcat	cggggacaca	660
cccattgaca	ccttccttat	ggagatgctg	gaggcgccgc	accaaagac	ttaggcctgc	720
gggcccattc	tttgtgcca	cccgttcttg	ccaccctgcc	tgagcgccag	ctgttcttct	780
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tgctactgct						850

<210> 66
 <211> 720
 <212> DNA
 <213> Homo sapiens

<400> 66						
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cctgtgacta	acatctgtca	ggcagctgac	aaacagctat	tcacgcttgt	tgagtgggcg	180

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atcctccttg	ccacaggtct	tcacgtgcac	cgcaactcag	cccattcagc	aggagtagga	360
gccatctttg	atcgggtgct	gacagagcta	gtgtccaaaa	tgcgtagacat	gaggatggac	420
aagacagagc	ttggctgcct	gagggcaatc	attctgttta	atccagatgc	caagggcctc	480
tccaacccta	gtgaggtgga	ggtcctgcgg	gagaaagtgt	atgcatcact	ggagacctac	540
tgcaaacaga	agtaccctga	gcagcagggg	cggtttgcca	agctgctgct	acgtcttcct	600
gccctccggt	ccattggcct	taagtgtcta	gagcatctgt	ttttcttcaa	gctcattggt	660
gacaccccca	tcgacacctt	cctcatggag	atgcttgagg	ctccccatca	actggcctga	720

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<210> 67
<211> 705
<212> DNA
<213> Homo sapiens
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<400> 67							
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tgtcatgctg	ctgacaagca	gcttttcacc	ctcgttgaat	gggccaaagc	tattccccac		180
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ctgattgcct	ctttctccca	ccgctcagtt	tccgtgcagg	atggcatcct	tctggccacg		300
ggttttacatg	tccaccggag	cagtgtcccac	agtgtctggg	tcggctccat	ctttgacaga		360
gttctaactg	agctggtttc	caaaatgaaa	gacatgcaga	tggacaagtc	ggaactggga		420
tgcttgcgag	ccattgtact	ctttaaccca	gatgccaaag	gcctgtccaa	cccccttgag		480
gtggagactc	tgcgagagaa	ggtttatgcc	acccttgagg	cctacaccaa	gcagaagtat		540
ccggaacagc	caggcagggt	tgccaagctg	ctgctgcgcc	tcccagctct	gcgttccatt		600
ggcttgaaat	gcctggagca	cctcttcttc	ttcaagctca	tcggggacac	ccccattgac		660
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<210> 68
<211> 237
<212> PRT
<213> Mus musculus

<400> 68
Ala Asn Glu Asp Met Pro Val Glu Lys Ile Leu Glu Ala Glu Leu Ala
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Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30

Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
35 40 45

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Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
50 55 60

Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
65 70 75 80

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
100 105 110

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
115 120 125

Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
130 135 140

Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
145 150 155 160

Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
210 215 220

Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Ala Thr
225 230 235

<210> 69
<211> 239
<212> PRT
<213> Mus musculus

<400> 69
Ala Pro Glu Glu Met Pro Val Asp Arg Ile Leu Glu Ala Glu Leu Ala
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Val Glu Gln Lys Ser Asp Gln Gly Val Glu Gly Pro Gly Ala Thr Gly
20 25 30

Gly Gly Gly Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala
35 40 45

Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro
50 55 60

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His Phe Ser Ser Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala
65 70 75 80

Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Asp
85 90 95

Val Arg Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn
100 105 110

Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr
115 120 125

Glu Leu Val Ser Lys Met Arg Asp Met Arg Met Asp Lys Thr Glu Leu
130 135 140

Gly Cys Leu Arg Ala Ile Ile Met Phe Asn Pro Asp Ala Lys Gly Leu
145 150 155 160

Ser Asn Pro Gly Glu Val Glu Ile Leu Arg Glu Lys Val Tyr Ala Ser
165 170 175

Leu Glu Thr Tyr Cys Lys Gln Lys Tyr Pro Glu Gln Gln Gly Arg Phe
180 185 190

Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys
195 200 205

Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile
210 215 220

Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Leu Ala
225 230 235

<210> 70
<211> 234
<212> PRT
<213> Mus musculus

<400> 70
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1 5 10 15

Val Glu Pro Lys Thr Glu Ser Tyr Gly Asp Met Asn Val Glu Asn Ser
20 25 30

Thr Asn Asp Pro Val Thr Asn Ile Cys His Ala Ala Asp Lys Gln Leu
35 40 45

Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe Ser Asp Leu
50 55 60

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Thr Leu Glu Asp Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu
65 70 75 80

Leu Ile Ala Ser Phe Ser His Arg Ser Val Ser Val Gln Asp Gly Ile
85 90 95

Leu Leu Ala Thr Gly Leu His Val His Arg Ser Ser Ala His Ser Arg
100 105 110

Gly Val Gly Ser Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys
115 120 125

Met Lys Asp Met Gln Met Asp Lys Ser Glu Leu Gly Cys Leu Arg Ala
130 135 140

Ile Val Leu Phe Asn Pro Asp Ala Lys Gly Leu Ser Asn Pro Ser Glu
145 150 155 160

Val Glu Thr Leu Arg Glu Lys Val Tyr Ala Thr Leu Glu Ala Tyr Thr
165 170 175

Lys Gln Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu
180 185 190

Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu
195 200 205

Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Ser Phe Leu Met
210 215 220

Glu Met Leu Glu Thr Pro Leu Gln Ile Thr
225 230

<210> 71
<211> 237
<212> PRT
<213> Homo sapiens

<400> 71
Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu Ala
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Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu Asn
20 25 30

Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
35 40 45

Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
50 55 60

Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
65 70 75 80

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Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val Lys
85 90 95

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
100 105 110

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
115 120 125

Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly Cys
130 135 140

Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser Asn
145 150 155 160

Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
165 170 175

Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys
180 185 190

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
195 200 205

Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
210 215 220

Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr
225 230 235

<210> 72
<211> 239
<212> PRT
<213> Homo sapiens

<400> 72
Ala Pro Glu Glu Met Pro Val Asp Arg Ile Leu Glu Ala Glu Leu Ala
1 5 10 15

Val Glu Gln Lys Ser Asp Gln Gly Val Glu Gly Pro Gly Gly Thr Gly
20 25 30

Gly Ser Gly Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala
35 40 45

Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro
50 55 60

His Phe Ser Ser Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala
65 70 75 80

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Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Asp
85 90 95

Val Arg Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn
100 105 110

Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr
115 120 125

Glu Leu Val Ser Lys Met Arg Asp Met Arg Met Asp Lys Thr Glu Leu
130 135 140

Gly Cys Leu Arg Ala Ile Ile Leu Phe Asn Pro Asp Ala Lys Gly Leu
145 150 155 160

Ser Asn Pro Ser Glu Val Glu Val Leu Arg Glu Lys Val Tyr Ala Ser
165 170 175

Leu Glu Thr Tyr Cys Lys Gln Lys Tyr Pro Glu Gln Gln Gly Arg Phe
180 185 190

Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys
195 200 205

Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile
210 215 220

Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Leu Ala
225 230 235

<210> 73
<211> 234
<212> PRT
<213> Homo sapiens

<400> 73
Gly His Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu Ala
1 5 10 15

Val Glu Pro Lys Thr Glu Ser Tyr Gly Asp Met Asn Met Glu Asn Ser
20 25 30

Thr Asn Asp Pro Val Thr Asn Ile Cys His Ala Ala Asp Lys Gln Leu
35 40 45

Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe Ser Asp Leu
50 55 60

Thr Leu Glu Asp Gln Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu
65 70 75 80

Leu Ile Ala Ser Phe Ser His Arg Ser Val Ser Val Gln Asp Gly Ile
85 90 95

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Leu Leu Ala Thr Gly Leu His Val His Arg Ser Ser Ala His Ser Ala
100 105 110

Gly Val Gly Ser Ile Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys
115 120 125

Met Lys Asp Met Gln Met Asp Lys Ser Glu Leu Gly Cys Leu Arg Ala
130 135 140

Ile Val Leu Phe Asn Pro Asp Ala Lys Gly Leu Ser Asn Pro Ser Glu
145 150 155 160

Val Glu Thr Leu Arg Glu Lys Val Tyr Ala Thr Leu Glu Ala Tyr Thr
165 170 175

Lys Gln Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala Lys Leu Leu Leu
180 185 190

Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu
195 200 205

Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr Phe Leu Met
210 215 220

Glu Met Leu Glu Thr Pro Leu Gln Ile Thr
225 230

<210> 74
<211> 516
<212> DNA
<213> Locusta migratoria

<400> 74
atccctacct ctggaggacc aggttctcct cctcagagca gggttggaatg aactgctaata 60
tgcagcattt tcacatcgat ctgtagatgt taaagatggc atagtacttg ccactgggtct 120
cacagtgcac cgaaattctg cccatcaagc tggagtcggc acaatatttg acagagtttt 180
gacagaactg gtagcaaaga tgagagaaat gaaaatggat aaaactgaac ttggctgctt 240
gcgatctgtt attcttttca atccagaggt gagggggttg aaatccgccc aggaagttga 300
acttctacgt gaaaaagtat atgccgcttt ggaagaatat actagaacaa cacatcccga 360
tgaaccagga agatttgcaa aacttttgct tcgtctgcct tctttacgtt ccataggcct 420
taagtgtttg gagcatttgt tttctttcgc cttattggag atgttccaat tgatacggtc 480
ctgatggaga tgcttgaatc accttctgat tcataa 516

<210> 75
<211> 528
<212> DNA
<213> Amblyomma americanum

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<400> 75
attccacatt ttgaagagct tccccttgag gaccgcatgg tgttgctcaa ggctggctgg 60
aacgagctgc tcattgctgc tttctccac cgttctgttg acgtgcgtga tggcattgtg 120
ctcgctacag gtcttggtgt gcagcggcat agtgctcatg gggctggcgt tggggccata 180
tttgataggg ttctcactga actggtagca aagatgcgtg agatgaagat ggaccgcact 240
gagcttggtg gcctgcttgc tgtggtactt ttaaatcctg aggccaaggg gctgcggacc 300
tgcccaagtg gaggccctga gggagaaaagt gtatctgcct tggaagagca ctgccggcag 360
cagtaccag accagcctgg gcgctttgcc aagctgctgc tgcggttgcc agctctgcgc 420
agtattggcc tcaagtgcct cgaacatctc tttttcttca agctcatcgg ggacacgccc 480
atcgacaact ttcttctttc catgctggag gccccctctg acccctaa 528

<210> 76
<211> 531
<212> DNA
<213> Amblyomma americanum

<400> 76
attccgcact tcgaagagct tcccatcgag gatcgcaccg cgctgctcaa agccggctgg 60
aacgaactgc ttattgccgc cttttcgcac cgttctgttg cggcgcgga cggcatcggt 120
ctggccaccg ggctggtggt gcagcggcac agcgcacacg gcgcaggcgt tggcgacatc 180
ttcgaccgcg tactagccga gctggtggcc aagatgcgcg acatgaagat ggacaaaacg 240
gagctcggct gcctgcgcgc cgtggtgctc ttcaatccag acgccaaggg tctccgaaac 300
gccaccagag tagaggcgct ccgcgagaag gtgtatgcgg cgctggagga gcactgccgt 360
cggcaccacc cggaccaacc gggctcgctt ggcaagctgc tgctgcggct gcctgccttg 420
cgcagcatcg ggctcaaatt cctcgagcat ctgttcttct tcaagctcat cggagacact 480
cccatagaca gcttcctgct caacatgctg gaggcaccgg cagacccta g 531

<210> 77
<211> 552
<212> DNA
<213> Celuca pugilator

<400> 77
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aacgagttgc ttattgcctc attctcacac cgtagcatgg gcgtggagga tggcatcgtg 120
ctggccacag ggctcgtgat ccacagaagt agtgctcacc aggctggagt ggggtgccata 180
tttgatcgtg tcctctctga gctggtggcc aagatgaagg agatgaagat tgacaagaca 240
gagctgggct gccttcgctc catcgtcctg ttcaaccag atgccaaagg actaaactgc 300
gtcaatgatg tggagatctt gcgtgagaag gtgtatgctg ccctggagga gtacacacga 360
accacttacc ctgatgaacc tggacgcttt gccaaagtgc ttctgcgact tcctgcactc 420
aggtctatag gcctgaagtg tcttgagtac ctcttcctgt ttaagctgat tggagacact 480
cccctggaca gctacttgat gaagatgctc gtagacaacc caaatacaag cgtcactccc 540

cccaccagct ag

552

<210> 78

<211> 531

<212> DNA

<213> *Tenebrio molitor*

<400> 78

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atacctcact ttacctcggt gccgatgtcg gaccaggtgc ttttattgag ggcaggatgg      60
aatgaattgc tcatcgccgc attctcgcac agatctatac aggcgcagga tgccatcggt      120
ctagccacgg gggtgacagt taacaaaacg tcggcgcacg ccgtgggcgt gggcaacatc      180
tacgaccgcg tcctctccga gctggtgaac aagatgaaag agatgaagat ggacaagacg      240
gagctgggct gcttgagagc catcatcctc tacaaccca cgtgtcgcgg catcaagtcc      300
gtgcaggaag tggagatgct gcgtgagaaa atttacggcg tgctggaaga gtacaccagg      360
accaccacc cgaacgagcc cggcagggtt gccaaactgc ttctgcgcct cccggccctc      420
aggtccatcg gggtgaaatg ttccgaacac ctcttttct tcaagctgat cggatgatgtt      480
ccaatagaca cgttcctgat ggagatgctg gagtctccgg cggacgctta g              531

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<210> 79

<211> 531

<212> DNA

<213> *Apis mellifera*

<400> 79

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atcccgcat ttacctcggt gccactggag gatcaggtac ttctgctcag ggccgggttg      60
aacgagttgc tgatagcctc cttttccac cgttccatcg acgtgaagga cggatcctgt      120
ctggcgacgg ggatcaccgt gcatcggaac tcggcgcagc aggccggcgt gggcacgata      180
ttcgaccgtg tcctctcgga gcttgtctcg aaaatgcgtg aaatgaagat ggacaggaca      240
gagcttggct gtctcagatc tataatactc ttcaatcccg aggttcgagg actgaaatcc      300
atccaggaag tgaccctgct ccgtgagaag atctacggcg ccctggaggg ttattgccgc      360
gtagcttggc ccgacgacgc tggaagattc gcgaaattac ttctacgcct gcccgccatc      420
cgctcgatcg gattaaagtg cctcgagtac ctgttcttct tcaaaatgat cggatgacgta      480
ccgatcgacg attttctcgt ggagatgtta gaatcgcgat cagatcctta g              531

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<210> 80

<211> 176

<212> PRT

<213> *Locusta migratoria*

<400> 80

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Ile Pro His Phe Thr Ser Leu Pro Leu Glu Asp Gln Val Leu Leu Leu
1          5          10          15

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Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ala Phe Ser His Arg Ser
          20          25          30

```

Val Asp Val Lys Asp Gly Ile Val Leu Ala Thr Gly Leu Thr Val His
35 40 45

Arg Asn Ser Ala His Gln Ala Gly Val Gly Thr Ile Phe Asp Arg Val
50 55 60

Leu Thr Glu Leu Val Ala Lys Met Arg Glu Met Lys Met Asp Lys Thr
65 70 75 80

Glu Leu Gly Cys Leu Arg Ser Val Ile Leu Phe Asn Pro Glu Val Arg
85 90 95

Gly Leu Lys Ser Ala Gln Glu Val Glu Leu Leu Arg Glu Lys Val Tyr
100 105 110

Ala Ala Leu Glu Glu Tyr Thr Arg Thr Thr His Pro Asp Glu Pro Gly
115 120 125

Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu Arg Ser Ile Gly
130 135 140

Leu Lys Cys Leu Glu His Leu Phe Phe Phe Arg Leu Ile Gly Asp Val
145 150 155 160

Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ser Pro Ser Asp Ser
165 170 175

<210> 81

<211> 175

<212> PRT

<213> Amblyomma americanum

<400> 81

Ile Pro His Phe Glu Glu Leu Pro Leu Glu Asp Arg Met Val Leu Leu
1 5 10 15

Lys Ala Gly Trp Asn Glu Leu Leu Ile Ala Ala Phe Ser His Arg Ser
20 25 30

Val Asp Val Arg Asp Gly Ile Val Leu Ala Thr Gly Leu Val Val Gln
35 40 45

Arg His Ser Ala His Gly Ala Gly Val Gly Ala Ile Phe Asp Arg Val
50 55 60

Leu Thr Glu Leu Val Ala Lys Met Arg Glu Met Lys Met Asp Arg Thr
65 70 75 80

Glu Leu Gly Cys Leu Leu Ala Val Val Leu Phe Asn Pro Glu Ala Lys
85 90 95

Gly Leu Arg Thr Cys Pro Ser Gly Gly Pro Glu Gly Glu Ser Val Ser
100 105 110

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Ala Leu Glu Glu His Cys Arg Gln Gln Tyr Pro Asp Gln Pro Gly Arg
115 120 125

Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu
130 135 140

Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro
145 150 155 160

Ile Asp Asn Phe Leu Leu Ser Met Leu Glu Ala Pro Ser Asp Pro
165 170 175

<210> 82

<211> 176

<212> PRT

<213> Amblyomma americanum

<400> 82

Ile Pro His Phe Glu Glu Leu Pro Ile Glu Asp Arg Thr Ala Leu Leu
1 5 10 15

Lys Ala Gly Trp Asn Glu Leu Leu Ile Ala Ala Phe Ser His Arg Ser
20 25 30

Val Ala Val Arg Asp Gly Ile Val Leu Ala Thr Gly Leu Val Val Gln
35 40 45

Arg His Ser Ala His Gly Ala Gly Val Gly Asp Ile Phe Asp Arg Val
50 55 60

Leu Ala Glu Leu Val Ala Lys Met Arg Asp Met Lys Met Asp Lys Thr
65 70 75 80

Glu Leu Gly Cys Leu Arg Ala Val Val Leu Phe Asn Pro Asp Ala Lys
85 90 95

Gly Leu Arg Asn Ala Thr Arg Val Glu Ala Leu Arg Glu Lys Val Tyr
100 105 110

Ala Ala Leu Glu Glu His Cys Arg Arg His His Pro Asp Gln Pro Gly
115 120 125

Arg Phe Gly Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly
130 135 140

Leu Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr
145 150 155 160

Pro Ile Asp Ser Phe Leu Leu Asn Met Leu Glu Ala Pro Ala Asp Pro
165 170 175

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<210> 83

<211> 183

<212> PRT

<213> Celuca pugilator

<400> 83

Ile Pro His Phe Thr Asp Leu Pro Ile Glu Asp Gln Val Val Leu Leu
1 5 10 15

Lys Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser
20 25 30

Met Gly Val Glu Asp Gly Ile Val Leu Ala Thr Gly Leu Val Ile His
35 40 45

Arg Ser Ser Ala His Gln Ala Gly Val Gly Ala Ile Phe Asp Arg Val
50 55 60

Leu Ser Glu Leu Val Ala Lys Met Lys Glu Met Lys Ile Asp Lys Thr
65 70 75 80

Glu Leu Gly Cys Leu Arg Ser Ile Val Leu Phe Asn Pro Asp Ala Lys
85 90 95

Gly Leu Asn Cys Val Asn Asp Val Glu Ile Leu Arg Glu Lys Val Tyr
100 105 110

Ala Ala Leu Glu Glu Tyr Thr Arg Thr Thr Tyr Pro Asp Glu Pro Gly
115 120 125

Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly
130 135 140

Leu Lys Cys Leu Glu Tyr Leu Phe Leu Phe Lys Leu Ile Gly Asp Thr
145 150 155 160

Pro Leu Asp Ser Tyr Leu Met Lys Met Leu Val Asp Asn Pro Asn Thr
165 170 175

Ser Val Thr Pro Pro Thr Ser
180

<210> 84

<211> 176

<212> PRT

<213> Tenebrio molitor

<400> 84

Ile Pro His Phe Thr Ser Leu Pro Met Ser Asp Gln Val Leu Leu Leu
1 5 10 15

Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ala Phe Ser His Arg Ser
20 25 30

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Ile Gln Ala Gln Asp Ala Ile Val Leu Ala Thr Gly Leu Thr Val Asn
35 40 45

Lys Thr Ser Ala His Ala Val Gly Val Gly Asn Ile Tyr Asp Arg Val
50 55 60

Leu Ser Glu Leu Val Asn Lys Met Lys Glu Met Lys Met Asp Lys Thr
65 70 75 80

Glu Leu Gly Cys Leu Arg Ala Ile Ile Leu Tyr Asn Pro Thr Cys Arg
85 90 95

Gly Ile Lys Ser Val Gln Glu Val Glu Met Leu Arg Glu Lys Ile Tyr
100 105 110

Gly Val Leu Glu Glu Tyr Thr Arg Thr Thr His Pro Asn Glu Pro Gly
115 120 125

Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly
130 135 140

Leu Lys Cys Ser Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Val
145 150 155 160

Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ser Pro Ala Asp Ala
165 170 175

<210> 85

<211> 176

<212> PRT

<213> Apis mellifera

<400> 85

Ile Pro His Phe Thr Ser Leu Pro Leu Glu Asp Gln Val Leu Leu Leu
1 5 10 15

Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser
20 25 30

Ile Asp Val Lys Asp Gly Ile Val Leu Ala Thr Gly Ile Thr Val His
35 40 45

Arg Asn Ser Ala Gln Gln Ala Gly Val Gly Thr Ile Phe Asp Arg Val
50 55 60

Leu Ser Glu Leu Val Ser Lys Met Arg Glu Met Lys Met Asp Arg Thr
65 70 75 80

Glu Leu Gly Cys Leu Arg Ser Ile Ile Leu Phe Asn Pro Glu Val Arg
85 90 95

Gly Leu Lys Ser Ile Gln Glu Val Thr Leu Leu Arg Glu Lys Ile Tyr
100 105 110

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Gly Ala Leu Glu Gly Tyr Cys Arg Val Ala Trp Pro Asp Asp Ala Gly
115 120 125

Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Ile Arg Ser Ile Gly
130 135 140

Leu Lys Cys Leu Glu Tyr Leu Phe Phe Phe Lys Met Ile Gly Asp Val
145 150 155 160

Pro Ile Asp Asp Phe Leu Val Glu Met Leu Glu Ser Arg Ser Asp Pro
165 170 175

<210> 86

<211> 259

<212> PRT

<213> Choristoneura fumiferana

<400> 86

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

Asp Gly Tyr Glu Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln
20 25 30

Thr Trp Gln Gln Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe
35 40 45

Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu
50 55 60

Phe Ala Lys Gly Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln
65 70 75 80

Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val
85 90 95

Ala Arg Arg Tyr Asp Ala Ala Ser Asp Ser Val Leu Phe Ala Asn Asn
100 105 110

Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Tyr Val
115 120 125

Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu
130 135 140

Asp Asn Ile His Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp
145 150 155 160

Arg Pro Gly Leu Glu Gln Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr
165 170 175

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Tyr Leu Asn Thr Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser
180 185 190

Ala Arg Ser Ser Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu
195 200 205

Leu Arg Thr Leu Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys
210 215 220

Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp Val
225 230 235 240

Ala Asp Met Ser His Thr Gln Pro Pro Pro Ile Leu Glu Ser Pro Thr
245 250 255

Asn Leu Gly

<210> 87

<211> 674

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87

Met Asp Tyr Lys Asp Asp Asp Asp Lys Glu Met Pro Val Asp Arg Ile
1 5 10 15

Leu Glu Ala Glu Leu Ala Val Glu Gln Lys Ser Asp Gln Gly Val Glu
20 25 30

Gly Pro Gly Gly Thr Gly Gly Ser Gly Ser Ser Pro Asn Asp Pro Val
35 40 45

Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val Glu
50 55 60

Trp Ala Lys Arg Ile Pro His Phe Ser Ser Leu Pro Leu Asp Asp Gln
65 70 75 80

Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe
85 90 95

Ser His Arg Ser Ile Asp Val Arg Asp Gly Ile Leu Leu Ala Thr Gly
100 105 110

Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile
115 120 125

Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Arg
130 135 140

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Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Ile Leu Phe Asn
145 150 155 160

Pro Glu Val Arg Gly Leu Lys Ser Ala Gln Glu Val Glu Leu Leu Arg
165 170 175

Glu Lys Val Tyr Ala Ala Leu Glu Glu Tyr Thr Arg Thr Thr His Pro
180 185 190

Asp Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu
195 200 205

Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Arg Leu
210 215 220

Ile Gly Asp Val Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ser
225 230 235 240

Pro Ser Asp Ser Gln Ile Ser Tyr Ala Ser Arg Gly Gly Gly Ser Ser
245 250 255

Gly Gly Gly Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe
260 265 270

Tyr Pro Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met
275 280 285

Lys Arg Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His
290 295 300

Ile Glu Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg
305 310 315 320

Leu Ala Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile
325 330 335

Val Val Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly
340 345 350

Ala Leu Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn
355 360 365

Glu Arg Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val
370 375 380

Phe Val Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys
385 390 395 400

Leu Pro Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr
405 410 415

Gln Gly Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro
 420 425 430
 Gly Phe Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys
 435 440 445
 Thr Ile Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
 450 455 460
 Gly Val Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala
 465 470 475 480
 Arg Asp Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu
 485 490 495
 Ser Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
 500 505 510
 Tyr Leu Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu
 515 520 525
 Glu Leu Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu
 530 535 540
 Leu Val Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp
 545 550 555 560
 Lys Tyr Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro
 565 570 575
 Leu Ser Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro
 580 585 590
 Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu
 595 600 605
 Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val
 610 615 620
 Pro Phe Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu
 625 630 635 640
 Gly Val Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met
 645 650 655
 Ser Gly Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys
 660 665 670
 Asp Gly

<210> 88
 <211> 463
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 88
 Gln Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn
 1 5 10 15
 Ile Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu
 20 25 30
 Leu Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu
 35 40 45
 Lys Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys
 50 55 60
 Leu Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr
 65 70 75 80
 Gly Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys
 85 90 95
 Lys Gly Gly Lys Ser Lys Leu Gly Gly Gly Ser Ser Gly Gly Gly Gln
 100 105 110
 Ile Ser Tyr Ala Ser Arg Gly Arg Pro Glu Cys Val Val Pro Glu Thr
 115 120 125
 Gln Cys Ala Met Lys Arg Lys Glu Lys Lys Ala Gln Lys Glu Lys Asp
 130 135 140
 Lys Leu Pro Val Ser Thr Thr Thr Val Asp Asp His Met Pro Pro Ile
 145 150 155 160
 Met Gln Cys Glu Pro Pro Pro Pro Glu Ala Ala Arg Ile His Glu Val
 165 170 175
 Val Pro Arg Phe Leu Ser Asp Lys Leu Leu Val Thr Asn Arg Gln Lys
 180 185 190
 Asn Ile Pro Gln Leu Thr Ala Asn Gln Gln Phe Leu Ile Ala Arg Leu
 195 200 205
 Ile Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Asp Glu Asp Leu Lys
 210 215 220

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Arg Ile Thr Gln Thr Trp Gln Gln Ala Asp Asp Glu Asn Glu Glu Ser
225 230 235 240

Asp Thr Pro Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln
245 250 255

Leu Ile Val Glu Phe Ala Lys Gly Leu Pro Gly Phe Ala Lys Ile Ser
260 265 270

Gln Pro Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met
275 280 285

Met Leu Arg Val Ala Arg Arg Tyr Asp Ala Ala Ser Asp Ser Ile Leu
290 295 300

Phe Ala Asn Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly
305 310 315 320

Met Ala Glu Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr
325 330 335

Ser Met Ala Leu Asp Asn Ile His Tyr Ala Leu Leu Thr Ala Val Val
340 345 350

Ile Phe Ser Asp Arg Pro Gly Leu Glu Gln Pro Gln Leu Val Glu Glu
355 360 365

Ile Gln Arg Tyr Tyr Leu Asn Thr Leu Arg Ile Tyr Ile Leu Asn Gln
370 375 380

Leu Ser Gly Ser Ala Arg Ser Ser Val Ile Tyr Gly Lys Ile Leu Ser
385 390 395 400

Ile Leu Ser Glu Leu Arg Thr Leu Gly Met Gln Asn Ser Asn Met Cys
405 410 415

Ile Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu
420 425 430

Ile Trp Asp Val Ala Asp Met Ser His Thr Gln Pro Pro Pro Ile Leu
435 440 445

Glu Ser Pro Thr Asn Leu Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
450 455 460

<210> 89
<211> 675
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 89

Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Asp Glu Asp Leu Lys Arg
 1 5 10 15
 Ile Thr Gln Thr Trp Gln Gln Ala Asp Asp Glu Asn Glu Glu Ser Asp
 20 25 30
 Thr Pro Phe Arg Gln Ile Thr Glu Met Thr Ile Leu Thr Val Gln Leu
 35 40 45
 Ile Val Glu Phe Ala Lys Gly Leu Pro Gly Phe Ala Lys Ile Ser Gln
 50 55 60
 Pro Asp Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met
 65 70 75 80
 Leu Arg Val Ala Arg Arg Tyr Asp Ala Ala Ser Asp Ser Ile Leu Phe
 85 90 95
 Ala Asn Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met
 100 105 110
 Ala Glu Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser
 115 120 125
 Met Ala Leu Asp Asn Ile His Tyr Ala Leu Leu Thr Ala Val Val Ile
 130 135 140
 Phe Ser Asp Arg Pro Gly Leu Glu Gln Pro Gln Leu Val Glu Glu Ile
 145 150 155 160
 Gln Arg Tyr Tyr Leu Asn Thr Leu Arg Ile Tyr Ile Leu Asn Gln Leu
 165 170 175
 Ser Gly Ser Ala Arg Ser Ser Val Ile Tyr Gly Lys Ile Leu Ser Ile
 180 185 190
 Leu Ser Glu Leu Arg Thr Leu Gly Met Gln Asn Ser Asn Met Cys Ile
 195 200 205
 Ser Leu Lys Leu Lys Asn Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile
 210 215 220
 Trp Asp Val Ala Asp Met Ser His Thr Gln Pro Pro Pro Ile Leu Glu
 225 230 235 240
 Ser Pro Thr Asn Leu Gln Ile Ser Tyr Ala Ser Arg Gly Gly Gly Ser
 245 250 255
 Ser Gly Gly Gly Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro
 260 265 270

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Phe Tyr Pro Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala
 275 280 285
 Met Lys Arg Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala
 290 295 300
 His Ile Glu Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val
 305 310 315 320
 Arg Leu Ala Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg
 325 330 335
 Ile Val Val Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu
 340 345 350
 Gly Ala Leu Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr
 355 360 365
 Asn Glu Arg Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val
 370 375 380
 Val Phe Val Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys
 385 390 395 400
 Lys Leu Pro Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp
 405 410 415
 Tyr Gln Gly Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro
 420 425 430
 Pro Gly Phe Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp
 435 440 445
 Lys Thr Ile Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro
 450 455 460
 Lys Gly Val Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His
 465 470 475 480
 Ala Arg Asp Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile
 485 490 495
 Leu Ser Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu
 500 505 510
 Gly Tyr Leu Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu
 515 520 525
 Glu Glu Leu Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala
 530 535 540

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Leu Leu Val Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile
545 550 555 560

Asp Lys Tyr Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala
565 570 575

Pro Leu Ser Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu
580 585 590

Pro Gly Ile Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile
595 600 605

Leu Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val
610 615 620

Val Pro Phe Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr
625 630 635 640

Leu Gly Val Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile
645 650 655

Met Ser Gly Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp
660 665 670

Lys Asp Gly
675

<210> 90
<211> 412
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 90
Met Ser Gly Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp
1 5 10 15

Lys Asp Gly Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp
20 25 30

Glu His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys
35 40 45

Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His
50 55 60

Pro Asn Ile Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala
65 70 75 80

Gly Glu Leu Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met
 85 90 95
 Thr Glu Lys Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala
 100 105 110
 Lys Lys Leu Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly
 115 120 125
 Leu Thr Gly Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys
 130 135 140
 Ala Lys Lys Gly Gly Lys Ser Lys Leu Gly Gly Gly Ser Ser Gly Gly
 145 150 155 160
 Gly Gln Ile Ser Tyr Ala Ser Arg Gly Glu Met Pro Val Asp Arg Ile
 165 170 175
 Leu Glu Ala Glu Leu Ala Val Glu Gln Lys Ser Asp Gln Gly Val Glu
 180 185 190
 Gly Pro Gly Gly Thr Gly Gly Ser Gly Ser Ser Pro Asn Asp Pro Val
 195 200 205
 Thr Asn Ile Cys Gln Ala Ala Asp Lys Gln Leu Phe Thr Leu Val Glu
 210 215 220
 Trp Ala Lys Arg Ile Pro His Phe Ser Ser Leu Pro Leu Asp Asp Gln
 225 230 235 240
 Val Ile Leu Leu Arg Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe
 245 250 255
 Ser His Arg Ser Ile Asp Val Arg Asp Gly Ile Leu Leu Ala Thr Gly
 260 265 270
 Leu His Val His Arg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile
 275 280 285
 Phe Asp Arg Val Leu Thr Glu Leu Val Ser Lys Met Arg Asp Met Arg
 290 295 300
 Met Asp Lys Thr Glu Leu Gly Cys Leu Arg Ala Ile Ile Leu Phe Asn
 305 310 315 320
 Pro Glu Val Arg Gly Leu Lys Ser Ala Gln Glu Val Glu Leu Leu Arg
 325 330 335
 Glu Lys Val Tyr Ala Ala Leu Glu Glu Tyr Thr Arg Thr Thr His Pro
 340 345 350

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Asp Glu Pro Gly Arg Phe Ala Lys Leu Leu Leu Arg Leu Pro Ser Leu
355 360 365

Arg Ser Ile Gly Leu Lys Cys Leu Glu His Leu Phe Phe Phe Arg Leu
370 375 380

Ile Gly Asp Val Pro Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ser
385 390 395 400

Pro Ser Asp Ser Asp Tyr Lys Asp Asp Asp Asp Lys
405 410

<210> 91

<211> 1189

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 91

Met Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Gln Trp Tyr Glu Leu
1 5 10 15

Gln Gln Leu Asp Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp
20 25 30

Asp Ser Phe Pro Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu
35 40 45

Lys Gln Asp Trp Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile
50 55 60

Arg Phe His Asp Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe
65 70 75 80

Ser Leu Glu Asn Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys
85 90 95

Arg Asn Leu Gln Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met
100 105 110

Ile Ile Tyr Ser Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala
115 120 125

Gln Arg Phe Asn Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met
130 135 140

Leu Asp Lys Gln Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp
145 150 155 160

Lys Val Met Cys Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln
165 170 175

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Asp Glu Tyr Asp Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu
 180 185 190
 Thr Asn Gly Val Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Leu
 195 200 205
 Lys Lys Met Tyr Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His
 210 215 220
 Lys Ile Ile Glu Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu
 225 230 235 240
 Ile Asn Asp Glu Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys
 245 250 255
 Ile Gly Gly Pro Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe
 260 265 270
 Thr Ile Val Ala Glu Ser Leu Gln Gln Val Arg Gln Gln Leu Lys Lys
 275 280 285
 Leu Glu Glu Leu Glu Gln Lys Tyr Thr Tyr Glu His Asp Pro Ile Thr
 290 295 300
 Lys Asn Lys Gln Val Leu Trp Asp Arg Thr Phe Ser Leu Phe Gln Gln
 305 310 315 320
 Leu Ile Gln Ser Ser Phe Val Val Glu Arg Gln Pro Cys Met Pro Thr
 325 330 335
 His Pro Gln Arg Pro Leu Val Leu Lys Thr Gly Val Gln Phe Thr Val
 340 345 350
 Lys Leu Arg Leu Leu Val Lys Leu Gln Glu Leu Asn Tyr Asn Leu Lys
 355 360 365
 Val Lys Val Leu Phe Asp Lys Asp Val Asn Glu Arg Asn Thr Val Lys
 370 375 380
 Gly Phe Arg Lys Phe Asn Ile Leu Gly Thr His Thr Lys Val Met Asn
 385 390 395 400
 Met Glu Glu Ser Thr Asn Gly Ser Leu Ala Ala Glu Phe Arg His Leu
 405 410 415
 Gln Leu Lys Glu Gln Lys Asn Ala Gly Thr Arg Thr Asn Glu Gly Pro
 420 425 430
 Leu Ile Val Thr Glu Glu Leu His Ser Leu Ser Phe Glu Thr Gln Leu
 435 440 445

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Cys Gln Pro Gly Leu Val Ile Asp Leu Glu Thr Thr Ser Leu Pro Val
 450 455 460
 Val Val Ile Ser Asn Val Ser Gln Leu Pro Ser Gly Trp Ala Ser Ile
 465 470 475 480
 Leu Trp Tyr Asn Met Leu Val Ala Glu Pro Arg Asn Leu Ser Phe Phe
 485 490 495
 Leu Thr Pro Pro Cys Ala Arg Trp Ala Gln Leu Ser Glu Val Leu Ser
 500 505 510
 Trp Gln Phe Ser Ser Val Thr Lys Arg Gly Leu Asn Val Asp Gln Leu
 515 520 525
 Asn Met Leu Gly Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp Gly
 530 535 540
 Leu Ile Pro Trp Thr Arg Phe Cys Lys Glu Asn Ile Asn Asp Lys Asn
 545 550 555 560
 Phe Pro Phe Trp Leu Trp Ile Glu Ser Ile Leu Glu Leu Ile Lys Lys
 565 570 575
 His Leu Leu Pro Leu Trp Asn Asp Gly Cys Ile Met Gly Phe Ile Ser
 580 585 590
 Lys Glu Arg Glu Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe
 595 600 605
 Leu Leu Arg Phe Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr
 610 615 620
 Trp Val Glu Arg Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val
 625 630 635 640
 Glu Pro Tyr Thr Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile
 645 650 655
 Ile Arg Asn Tyr Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro
 660 665 670
 Leu Lys Tyr Leu Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys
 675 680 685
 Tyr Tyr Ser Arg Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly
 690 695 700
 Pro Lys Gly Thr Gly Tyr Ile Lys Thr Glu Leu Ile Ser Val ser Glu
 705 710 715 720

Val His Pro Ser Arg 725 Leu Gln Thr Thr Asp 730 Asn Leu Leu Pro Met 735 Ser
 Pro Glu Glu Phe 740 Asp Glu Val Ser Arg 745 Ile Val Gly Ser Val 750 Glu Phe
 Asp Ser Met 755 Met Asn Thr Val Gln 760 Ile Ser Tyr Ala Ser 765 Arg Gly Gly
 Gly Ser 770 Ser Gly Gly Gly Glu 775 Asp Ala Lys Asn Ile 780 Lys Lys Gly Pro
 Ala 785 Pro Phe Tyr Pro Leu 790 Glu Asp Gly Thr Ala 795 Gly Glu Gln Leu His 800
 Lys Ala Met Lys Arg 805 Tyr Ala Leu Val Pro 810 Gly Thr Ile Ala Phe 815 Thr
 Asp Ala His Ile 820 Glu Val Asn Ile Thr 825 Tyr Ala Glu Tyr Phe 830 Glu Met
 Ser Val Arg 835 Leu Ala Glu Ala Met 840 Lys Arg Tyr Gly Leu 845 Asn Thr Asn
 His Arg 850 Ile Val Val Cys Ser 855 Glu Asn Ser Leu Gln 860 Phe Phe Met Pro
 Val 865 Leu Gly Ala Leu Phe 870 Ile Gly Val Ala Val 875 Ala Pro Ala Asn Asp 880
 Ile Tyr Asn Glu Arg 885 Glu Leu Leu Asn Ser 890 Met Asn Ile Ser Gln 895 Pro
 Thr Val Val Phe 900 Val Ser Lys Lys Gly 905 Leu Gln Lys Ile Leu 910 Asn Val
 Gln Lys Lys 915 Leu Pro Ile Ile Gln 920 Lys Ile Ile Ile Met 925 Asp Ser Lys
 Thr Asp 930 Tyr Gln Gly Phe Gln 935 Ser Met Tyr Thr Phe 940 Val Thr Ser His
 Leu 945 Pro Pro Gly Phe Asn 950 Glu Tyr Asp Phe Val 955 Pro Glu Ser Phe Asp 960
 Arg Asp Lys Thr Ile 965 Ala Leu Ile Met Asn 970 Ser Ser Gly Ser Thr 975 Gly
 Leu Pro Lys Gly 980 Val Ala Leu Pro His 985 Arg Thr Ala Cys Val 990 Arg Phe

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Ser His Ala Arg Asp Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr
995 1000 1005

Ala Ile Leu Ser Val Val Pro Phe His His Gly Phe Gly Met Phe
1010 1015 1020

Thr Thr Leu Gly Tyr Leu Ile Cys Gly Phe Arg Val Val Leu Met
1025 1030 1035

Tyr Arg Phe Glu Glu Glu Leu Phe Leu Arg Ser Leu Gln Asp Tyr
1040 1045 1050

Lys Ile Gln Ser Ala Leu Leu Val Pro Thr Leu Phe Ser Phe Phe
1055 1060 1065

Ala Lys Ser Thr Leu Ile Asp Lys Tyr Asp Leu Ser Asn Leu His
1070 1075 1080

Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser Lys Glu Val Gly Glu
1085 1090 1095

Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile Arg Gln Gly Tyr
1100 1105 1110

Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr Pro Glu Gly
1115 1120 1125

Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe Phe Glu
1130 1135 1140

Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val Asn
1145 1150 1155

Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
1160 1165 1170

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp
1175 1180 1185

Gly

<210> 92

<211> 926

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 92

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Met Ser Gly Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp
1 5 10 15

Lys Asp Gly Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp
20 25 30

Glu His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys
35 40 45

Gly Tyr Gln Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His
50 55 60

Pro Asn Ile Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala
65 70 75 80

Gly Glu Leu Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met
85 90 95

Thr Glu Lys Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala
100 105 110

Lys Lys Leu Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly
115 120 125

Leu Thr Gly Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys
130 135 140

Ala Lys Lys Gly Gly Lys Ser Lys Leu Gly Gly Gly Ser Ser Gly Gly
145 150 155 160

Gly Gln Ile Ser Tyr Ala Ser Arg Gly Ser Gln Trp Tyr Glu Leu Gln
165 170 175

Gln Leu Asp Ser Lys Phe Leu Glu Gln Val His Gln Leu Tyr Asp Asp
180 185 190

Ser Phe Pro Met Glu Ile Arg Gln Tyr Leu Ala Gln Trp Leu Glu Lys
195 200 205

Gln Asp Trp Glu His Ala Ala Asn Asp Val Ser Phe Ala Thr Ile Arg
210 215 220

Phe His Asp Leu Leu Ser Gln Leu Asp Asp Gln Tyr Ser Arg Phe Ser
225 230 235 240

Leu Glu Asn Asn Phe Leu Leu Gln His Asn Ile Arg Lys Ser Lys Arg
245 250 255

Asn Leu Gln Asp Asn Phe Gln Glu Asp Pro Ile Gln Met Ser Met Ile
260 265 270

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Ile Tyr Ser Cys Leu Lys Glu Glu Arg Lys Ile Leu Glu Asn Ala Gln
275 285

Arg Phe Asn Gln Ala Gln Ser Gly Asn Ile Gln Ser Thr Val Met Leu
290 295 300

Asp Lys Gln Lys Glu Leu Asp Ser Lys Val Arg Asn Val Lys Asp Lys
305 310 315 320

Val Met Cys Ile Glu His Glu Ile Lys Ser Leu Glu Asp Leu Gln Asp
325 330 335

Glu Tyr Asp Phe Lys Cys Lys Thr Leu Gln Asn Arg Glu His Glu Thr
340 345 350

Asn Gly Val Ala Lys Ser Asp Gln Lys Gln Glu Gln Leu Leu Leu Lys
355 360 365

Lys Met Tyr Leu Met Leu Asp Asn Lys Arg Lys Glu Val Val His Lys
370 375 380

Ile Ile Glu Leu Leu Asn Val Thr Glu Leu Thr Gln Asn Ala Leu Ile
385 390 395 400

Asn Asp Glu Leu Val Glu Trp Lys Arg Arg Gln Gln Ser Ala Cys Ile
405 410 415

Gly Gly Pro Pro Asn Ala Cys Leu Asp Gln Leu Gln Asn Trp Phe Thr
420 425 430

Ile Val Ala Glu Ser Leu Gln Gln Val Arg Gln Gln Leu Lys Lys Leu
435 440 445

Glu Glu Leu Glu Gln Lys Tyr Thr Tyr Glu His Asp Pro Ile Thr Lys
450 455 460

Asn Lys Gln Val Leu Trp Asp Arg Thr Phe Ser Leu Phe Gln Gln Leu
465 470 475 480

Ile Gln Ser Ser Phe Val Val Glu Arg Gln Pro Cys Met Pro Thr His
485 490 495

Pro Gln Arg Pro Leu Val Leu Lys Thr Gly Val Gln Phe Thr Val Lys
500 505 510

Leu Arg Leu Leu Val Lys Leu Gln Glu Leu Asn Tyr Asn Leu Lys Val
515 520 525

Lys Val Leu Phe Asp Lys Asp Val Asn Glu Arg Asn Thr Val Lys Gly
530 535 540

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Phe Arg Lys Phe Asn Ile Leu Gly Thr His Thr Lys Val Met Asn Met
 545 550 555 560
 Glu Glu Ser Thr Asn Gly Ser Leu Ala Ala Glu Phe Arg His Leu Gln
 565 570 575
 Leu Lys Glu Gln Lys Asn Ala Gly Thr Arg Thr Asn Glu Gly Pro Leu
 580 585 590
 Ile Val Thr Glu Glu Leu His Ser Leu Ser Phe Glu Thr Gln Leu Cys
 595 600 605
 Gln Pro Gly Leu Val Ile Asp Leu Glu Thr Thr Ser Leu Pro Val Val
 610 615 620
 Val Ile Ser Asn Val Ser Gln Leu Pro Ser Gly Trp Ala Ser Ile Leu
 625 630 635 640
 Trp Tyr Asn Met Leu Val Ala Glu Pro Arg Asn Leu Ser Phe Phe Leu
 645 650 655
 Thr Pro Pro Cys Ala Arg Trp Ala Gln Leu Ser Glu Val Leu Ser Trp
 660 665 670
 Gln Phe Ser Ser Val Thr Lys Arg Gly Leu Asn Val Asp Gln Leu Asn
 675 680 685
 Met Leu Gly Glu Lys Leu Leu Gly Pro Asn Ala Ser Pro Asp Gly Leu
 690 695 700
 Ile Pro Trp Thr Arg Phe Cys Lys Glu Asn Ile Asn Asp Lys Asn Phe
 705 710 715 720
 Pro Phe Trp Leu Trp Ile Glu Ser Ile Leu Glu Leu Ile Lys Lys His
 725 730 735
 Leu Leu Pro Leu Trp Asn Asp Gly Cys Ile Met Gly Phe Ile Ser Lys
 740 745 750
 Glu Arg Glu Arg Ala Leu Leu Lys Asp Gln Gln Pro Gly Thr Phe Leu
 755 760 765
 Leu Arg Phe Ser Glu Ser Ser Arg Glu Gly Ala Ile Thr Phe Thr Trp
 770 775 780
 Val Glu Arg Ser Gln Asn Gly Gly Glu Pro Asp Phe His Ala Val Glu
 785 790 795 800
 Pro Tyr Thr Lys Lys Glu Leu Ser Ala Val Thr Phe Pro Asp Ile Ile
 805 810 815

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Arg Asn Tyr Lys Val Met Ala Ala Glu Asn Ile Pro Glu Asn Pro Leu
820 825 830

Lys Tyr Leu Tyr Pro Asn Ile Asp Lys Asp His Ala Phe Gly Lys Tyr
835 840 845

Tyr Ser Arg Pro Lys Glu Ala Pro Glu Pro Met Glu Leu Asp Gly Pro
850 855 860

Lys Gly Thr Gly Tyr Ile Lys Thr Glu Leu Ile Ser Val Ser Glu Val
865 870 875 880

His Pro Ser Arg Leu Gln Thr Thr Asp Asn Leu Leu Pro Met Ser Pro
885 890 895

Glu Glu Phe Asp Glu Val Ser Arg Ile Val Gly Ser Val Glu Phe Asp
900 905 910

Ser Met Met Asn Thr Val Asp Tyr Lys Asp Asp Asp Asp Lys
915 920 925

<210> 93

<211> 335

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 93

Arg Pro Glu Cys Val Val Pro Glu Thr Gln Cys Ala Met Lys Arg Lys
1 5 10 15

Glu Lys Lys Ala Gln Lys Glu Lys Asp Lys Leu Pro Val Ser Thr Thr
20 25 30

Thr Val Asp Asp His Met Pro Pro Ile Met Gln Cys Glu Pro Pro Pro
35 40 45

Pro Glu Ala Ala Arg Ile His Glu Val Val Pro Arg Phe Leu Ser Asp
50 55 60

Lys Leu Leu Val Thr Asn Arg Gln Lys Asn Ile Pro Gln Leu Thr Ala
65 70 75 80

Asn Gln Gln Phe Leu Ile Ala Arg Leu Ile Trp Tyr Gln Asp Gly Tyr
85 90 95

Glu Gln Pro Ser Asp Glu Asp Leu Lys Arg Ile Thr Gln Thr Trp Gln
100 105 110

Gln Ala Asp Asp Glu Asn Glu Glu Ser Asp Thr Pro Phe Arg Gln Ile
115 120 125

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Thr Glu Met Thr Ile Leu Thr Val Gln Leu Ile Val Glu Phe Ala Lys
 130 135 140
 Gly Leu Pro Gly Phe Ala Lys Ile Ser Gln Pro Asp Gln Ile Thr Leu
 145 150 155 160
 Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg Val Ala Arg Arg
 165 170 175
 Tyr Asp Ala Ala Ser Asp Ser Ile Leu Phe Ala Asn Asn Gln Ala Tyr
 180 185 190
 Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ala Glu Val Ile Glu Asp
 195 200 205
 Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ala Leu Asp Asn Ile
 210 215 220
 His Tyr Ala Leu Leu Thr Ala Val Val Ile Phe Ser Asp Arg Pro Gly
 225 230 235 240
 Leu Glu Gln Pro Gln Leu Val Glu Glu Ile Gln Arg Tyr Tyr Leu Asn
 245 250 255
 Thr Leu Arg Ile Tyr Ile Leu Asn Gln Leu Ser Gly Ser Ala Arg Ser
 260 265 270
 Ser Val Ile Tyr Gly Lys Ile Leu Ser Ile Leu Ser Glu Leu Arg Thr
 275 280 285
 Leu Gly Met Gln Asn Ser Asn Met Cys Ile Ser Leu Lys Leu Lys Asn
 290 295 300
 Arg Lys Leu Pro Pro Phe Leu Glu Glu Ile Trp Asp Val Ala Asp Met
 305 310 315 320
 Ser His Thr Gln Pro Pro Pro Ile Leu Glu Ser Pro Thr Asn Leu
 325 330 335

<210> 94
 <211> 235
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 94
 Glu Met Pro Val Asp Arg Ile Leu Glu Ala Glu Leu Ala Val Glu Gln
 1 5 10 15

Lys Ser Asp Gln Gly Val Glu Gly Pro Gly Gly Thr Gly Gly Ser Gly
 20 25 30
 Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp Lys
 35 40 45
 Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe Ser
 50 55 60
 Ser Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp Asn
 65 70 75 80
 Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Asp Val Arg Asp
 85 90 95
 Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala His
 100 105 110
 Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu Val
 115 120 125
 Ser Lys Met Arg Asp Met Arg Met Asp Lys Thr Glu Leu Gly Cys Leu
 130 135 140
 Arg Ala Ile Ile Leu Phe Asn Pro Glu Val Arg Gly Leu Lys Ser Ala
 145 150 155 160
 Gln Glu Val Glu Leu Leu Arg Glu Lys Val Tyr Ala Ala Leu Glu Glu
 165 170 175
 Tyr Thr Arg Thr Thr His Pro Asp Glu Pro Gly Arg Phe Ala Lys Leu
 180 185 190
 Leu Leu Arg Leu Pro Ser Leu Arg Ser Ile Gly Leu Lys Cys Leu Glu
 195 200 205
 His Leu Phe Phe Phe Arg Leu Ile Gly Asp Val Pro Ile Asp Thr Phe
 210 215 220
 Leu Met Glu Met Leu Glu Ser Pro Ser Asp Ser
 225 230 235