

SEQUENCE LISTING

<110> REGENXBIO INC.

<120> FULLY-HUMAN POST-TRANSLATIONALLY MODIFIED ANTIBODY THERAPEUTICS

<130> 38013.0001P1

<140>

<141>

<150> 62/967,472

<151> 2020-01-29

<150> 62/838,165

<151> 2019-04-24

<160> 454

<170> PatentIn version 3.5

<210> 1

<211> 237

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> SITE

<222> (217)..(237)

<223> /note="This region may be absent in its entirety"

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<222> (220)..(220)

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 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
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 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 1
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20 25 30

Ser Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Leu Val
 35 40 45

Ala Gln Ile Asn Ser Val Gly Asn Ser Thr Tyr Tyr Pro Asp Thr Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Ser Gly Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 100 105 110

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
 115 120 125

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 130 135 140

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 145 150 155 160

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser

165

170

175

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 180 185 190

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 195 200 205

Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 210 215 220

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235

<210> 2

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 2

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Leu Gly
 1 5 10 15

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Ile Tyr Ser
 20 25 30

Asp Gly Asn Ala Tyr Leu His Trp Phe Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Ser
 85 90 95

Thr His Val Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 3
<211> 240
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
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<220>
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 <222> (230)..(240)
 <223> /note="This region may be absent in its entirety"

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<220>
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 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 3
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Asn
 20 25 30

 Gly Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

 Ser Phe Ile Ser Asn Leu Ala Tyr Ser Ile Asp Tyr Ala Asp Thr Val
 50 55 60

 Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Val Ser Gly Thr Trp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110

Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
115 120 125

Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
130 135 140

Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
145 150 155 160

Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
165 170 175

Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly
180 185 190

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys
195 200 205

Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu
225 230 235 240

<210> 4
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 4
Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Val Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ser Gln Thr
85 90 95

Arg His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 5
<211> 254
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

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<222> (234)..(254)

<223> /note="This region may be absent in its entirety"

<220>

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<222> (237)..(237)

<223> /replace="Leu"

<220>

<221> SITE

<222> (238)..(254)

<223> /note="This region may be absent in its entirety"

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<222> (244)..(254)

<223> /note="This region may be absent in its entirety"

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<222> (1)..(254)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 5

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

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Lys	Tyr
			20				25						30		

Tyr	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
			35				40					45			

Gly Ile Ile Asn Pro Ile Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Pro Ser Gly Ile Ala Leu Ala Gly Pro Ala Ser Arg Gly
100 105 110

Tyr Gln Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
145 150 155 160

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
165 170 175

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
180 185 190

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
210 215 220

Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
245 250

<210> 6

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

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 6
Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ala Arg Leu Gly Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 7
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
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polypeptide"

<220>
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<223> /note="This region may be absent in its entirety"

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<220>
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<222> (227)..(237)
<223> /note="This region may be absent in its entirety"

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<222> (1)..(237)
<223> /note="Variant residues given in the sequence have no
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for variant positions"

<220>
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<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 7
Glu Val Lys Val Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235

<210> 8
 <211> 218
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 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 8
 Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
 1 5 10 15

Glu Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
 20 25 30

Arg Tyr Ser Tyr Ile His Trp Tyr Gln Gln Lys Pro Gly Gln Phe Pro
 35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ser
 50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
 65 70 75 80

Pro Leu Glu Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His His Ser Trp
 85 90 95

Glu Ile Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
 100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 9
 <211> 240
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 <213> Artificial Sequence

<220>
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 polypeptide"

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 <222> (61)..(61)
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 <222> (221)..(240)
 <223> /note="This region may be absent in its entirety"

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 <223> /replace="Ser"

<220>
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 <222> (230)..(240)
 <223> /note="This region may be absent in its entirety"

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<222> (1)..(240)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 9

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Asn
20 25 30

Asp Ile Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Thr Ile Trp Thr Asp Gly Ser Thr Asn Tyr Asn Ala Ala Val Gln
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg His Arg Leu Tyr Tyr Gly Ala Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
225 230 235 240

<210> 10

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 10

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Glu Tyr Ser
20 25 30

Asp Gly Tyr Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

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

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Ala
85 90 95

Thr His Asn Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 11
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<222> (229)..(249)
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<220>
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<222> (232)..(232)
<223> /replace="Leu"

<220>
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 <222> (233)..(249)
 <223> /note="This region may be absent in its entirety"

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 <222> (239)..(249)
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 <223> /note="Variant residues given in the sequence have no
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 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

 <400> 11
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

 Ser Leu Arg Val Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

 Asp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

 Ala Val Ile Trp Phe Asp Gly Ser Asn Glu Phe Tyr Ala Asp Ser Val
 50 55 60

 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 65 70 75 80

 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95

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

 His Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
 225 230 235 240

Leu Ala Gly Ala Pro Ser Val Phe Leu
 245

<210> 12
 <211> 213
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<220>
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 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 12
 Ser Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1 5 10 15

Thr Ala Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Lys Arg Tyr Val
 20 25 30

Tyr Trp Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Glu Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Thr Phe Ser Gly Ser
50 55 60

Ser Ser Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Thr Asp Ser Asn Gly His His
85 90 95

Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Cys Ser
210

<210> 13

<211> 245

<212> PRT

<213> Artificial Sequence

<220>
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 <223> /note="This region may be absent in its entirety"

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 <223> /replace="Ser"

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 <223> /note="This region may be absent in its entirety"

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 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
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 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 13
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser Asp Tyr
 20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gln Ile Asn Pro Thr Thr Gly Gly Ala Ser Tyr Asn Gln Lys Phe
 50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Tyr Gly Arg His Phe Asp Val Trp Gly Gln Gly Thr
100 105 110

Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Thr Val
165 170 175

Ser Ser Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
210 215 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu
245

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<400> 14

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Asn
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Phe
100 105 110

Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
115 120 125

Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp
130 135 140

Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr
145 150 155 160

Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr
165 170 175

Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val
180 185 190

Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
195 200 205

Glu Cys
210

<210> 15
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<222> (224)..(224)
<223> /replace="Leu"

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<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 15
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Gly Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Pro Asp Asn Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gly Ala Gly Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu

<210> 16
 <211> 220
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
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<400> 16
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
 20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
 35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
 50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln
 85 90 95

Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
 100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
 145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
 165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
 180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
 195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215 220

<210> 17
 <211> 249
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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 <223> /note="This region may be absent in its entirety"

<220>
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 <223> /replace="Leu"

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<220>
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 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

 <400> 17
 Glu Val Gln Leu Val Glu Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
 20 25 30

 Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met
 35 40 45

 Gly Trp Ile Asn Ala Gly Asn Gly Lys Arg Lys Tyr Ser Gln Lys Phe
 50 55 60

 Gln Asp Arg Val Thr Ile Asn Arg Asp Thr Ser Ala Ser Thr Ile Tyr
 65 70 75 80

 Met Glu Leu Ser Ser Leu Gly Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Arg Glu Glu Asp His Ala Gly Ser Gly Ser Tyr Leu Ser Met Asp
 100 105 110

 Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys
 115 120 125

 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 130 135 140

 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu
245

<210> 18
<211> 220
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 18
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ser Ile Gln Thr Leu Leu Tyr Ser
20 25 30

Ser Asn Gln Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Lys
35 40 45

Ala Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ile Arg Lys Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Pro Glu Asp Leu Ala Thr Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 19
<211> 247
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<220>
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        for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
        substitutions and preferred embodiments"

<400> 19
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20          25          30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35          40          45

Ser Ser Ile Ser His Leu Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50          55          60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65          70          75          80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95

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Ala Gly Gly Ala Asn His Gly Lys Tyr Tyr Tyr Gly Met Asp Lys Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu
 225 230 235 240

Gly Gly Pro Ser Val Phe Leu
 245

<210> 20

<211> 221

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 20

Gln Ala Val Leu Thr Gln Pro Ala Ser Leu Ser Ala Ser Pro Gly Ala
 1 5 10 15

Ser Ala Ser Leu Thr Cys Thr Leu Arg Ser Gly Ala Pro Leu Pro Lys
20 25 30

Tyr Arg Ile Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Pro Pro Gln Tyr
35 40 45

Leu Leu Arg Tyr Lys Ser Asp Ala Asp Lys His Gln Gly Ser Gly Val
50 55 60

Pro Ser Arg Phe Ser Gly Ser Lys Asp Ala Ser Ala Asn Ala Gly Ile
65 70 75 80

Leu Leu Ile Ser Gly Leu Gln Ser Glu Asp Glu Ala Asp Tyr Tyr Cys
85 90 95

Met Val Trp Asp His Gly Val Trp Tyr Phe Gly Gly Gly Thr Lys Leu
100 105 110

Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro
115 120 125

Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu
130 135 140

Ile Ser Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp
145 150 155 160

Ser Ser Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln
165 170 175

Ser Asn Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu
180 185 190

Gln Trp Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly
195 200 205

Ser Thr Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
210 215 220

<210> 21
 <211> 251
 <212> PRT
 <213> Artificial Sequence

<220>
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 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<220>
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<220>
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 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 21
 Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Arg Pro Gly Gly
 1 5 10 15

 Ser Leu Arg Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Asn Tyr
 20 25 30

Trp Met His Trp Val Arg Gln Ala Pro Gly Gln Arg Pro Val Trp Val
35 40 45

Ser Arg Thr Asn Thr Asp Gly Arg Asn Thr Ala Tyr Ala Asp Tyr Ala
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr Leu Tyr
65 70 75 80

Leu Gln Leu Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys
85 90 95

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

Met Asp Val Trp Gly Lys Gly Thr Leu Val Thr Val Ser Ser Ala Ser
115 120 125

Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr
130 135 140

Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro
145 150 155 160

Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
165 170 175

His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser
180 185 190

Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile
195 200 205

Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val
210 215 220

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
225 230 235 240

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu

<210> 22

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 22

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ala Cys Arg Ala Ser Gln Ser Val Gly Thr Tyr Leu
20 25 30

Asn Trp Tyr Gln Gln Lys Arg Gly Lys Ala Pro Lys Leu Leu Ile Phe
35 40 45

Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

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

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Pro Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 23
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

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<223> /note="This region may be absent in its entirety"

<220>
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<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations"

for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 23

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

Ser Val Thr Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Arg Glu Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Ser Thr Gly Thr Thr Phe Tyr Ala Gln Asn Phe
50 55 60

Pro Asp Arg Val Ser Val Thr Arg Asp Thr Ser Thr Ser Thr Val Phe
65 70 75 80

Met Glu Leu His Asn Leu Lys Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Ile Ser Glu His Gly Ser Gly Ser Tyr Ser Pro Tyr Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val

180

185

190

Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val
 195 200 205

Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 210 215 220

Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala
 225 230 235 240

Ala Gly Gly Pro Ser Val Phe Leu
 245

<210> 24

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 24

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

Met Ala Ala Ile Thr Cys Ser Gly Glu Ala Leu Pro Lys Lys Tyr Gly
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Val Leu Leu Ile Tyr
 35 40 45

Arg Asp Val Glu Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 50 55 60

Ser Ser Gly Thr Met Val Thr Leu Thr Ile Ser Gly Val Gln Ala Glu
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Leu Ser Ala Asp Ser Ser Gly Thr Trp
 85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
100 105 110

Asn Pro Thr Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
115 120 125

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
130 135 140

Val Thr Val Ala Trp Lys Ala Asp Gly Ser Pro Val Lys Ala Gly Val
145 150 155 160

Glu Thr Thr Lys Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
165 170 175

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
180 185 190

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
195 200 205

Pro Thr Glu Cys Ser
210

<210> 25
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (216)..(236)
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<220>
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 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 25
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Ile Asp Leu Ser Gly Tyr
 20 25 30

Tyr Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Gly Val Ile Gly Ile Asn Gly Ala Thr Tyr Tyr Ala Ser Trp Ala Lys
 50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Thr Thr Val Tyr Leu
 65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys Ala
 85 90 95

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

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser

115

120

125

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
 130 135 140

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
 145 150 155 160

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
 165 170 175

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr
 180 185 190

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Ala Arg
 195 200 205

Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 210 215 220

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Thr Leu
 225 230 235

<210> 26

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 26

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

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

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Val Pro Lys Gln Leu
 35 40 45

Ile Tyr Asp Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65 70 75 80

Pro Glu Asp Val Ala Thr Tyr Tyr Cys Leu Gly Ser Tyr Asp Cys Thr
85 90 95

Asn Gly Asp Cys Phe Val Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 27

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>

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<222> (228)..(238)

<223> /note="This region may be absent in its entirety"

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<222> (234)..(238)

<223> /note="This region may be absent in its entirety"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 27

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Trp Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Glu Ile Arg Ser Glu Ser Asp Ala Ser Ala Thr His Tyr Ala Glu
50 55 60

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

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

Tyr Cys Leu Ala Tyr Phe Asp Tyr Gly Leu Ala Ile Gln Asn Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 180 185 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
 195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
 210 215 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
 225 230 235

<210> 28
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
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<400> 28
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Lys Arg Val Thr Thr Tyr
 20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Gly Ala Ser Asn Arg Tyr Leu Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Ser Gln Ser Tyr Asn Tyr Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 29

<211> 241

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>

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<222> (222)..(241)
 <223> /note="This region may be absent in its entirety"

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 <222> (231)..(241)
 <223> /note="This region may be absent in its entirety"

 <220>
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 <222> (1)..(241)
 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

 <400> 29
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Gly Asn Tyr
 20 25 30

 Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

 Gly Ala Ile Tyr Glu Gly Thr Gly Lys Thr Val Tyr Ile Gln Lys Phe
 50 55 60

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

 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Arg Leu Ser Asp Tyr Val Ser Gly Phe Gly Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225 230 235 240

Leu

<210> 30

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 30

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Asp Ile Ser Lys Tyr

20

25

30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Gly Tyr His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Ala Leu Pro Pro
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 31
 <211> 247

<212> PRT
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

 <220>
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 <223> /note="This region may be absent in its entirety"

 <220>
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 <222> (230)..(230)
 <223> /replace="Leu"

 <220>
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 <222> (231)..(247)
 <223> /note="This region may be absent in its entirety"

 <220>
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 <222> (237)..(247)
 <223> /note="This region may be absent in its entirety"

 <220>
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 <222> (1)..(247)
 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

 <400> 31
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
 1 5 10 15

 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Asn Asn
 20 25 30

 Asp Val Met Cys Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 35 40 45

Ile Gly Cys Ile Met Thr Thr Asp Val Val Thr Glu Tyr Ala Asn Trp
50 55 60

Ala Lys Ser Arg Phe Thr Val Ser Arg Asp Ser Ala Lys Asn Ser Val
65 70 75 80

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe
85 90 95

Cys Ala Arg Asp Ser Val Gly Ser Pro Leu Met Ser Phe Asp Leu Trp
100 105 110

Gly Pro Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240

Gly Gly Pro Ser Val Phe Leu
245

<210> 32
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 32
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Asn Cys Gln Ala Ser Gln Ser Ile Tyr Asn Asn
 20 25 30

Asn Glu Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Pro Pro Lys Leu
 35 40 45

Leu Ile Tyr Arg Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe
 50 55 60

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
 65 70 75 80

Gln Pro Glu Asp Val Ala Thr Tyr Tyr Cys Gly Gly Tyr Lys Ser Tyr
 85 90 95

Ser Asn Asp Gly Asn Gly Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 33
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> SITE
<222> (222)..(242)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (225)..(225)
<223> /replace="Leu"

<220>
<221> SITE
<222> (232)..(242)
<223> /note="This region may be absent in its entirety"

<220>
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<222> (1)..(242)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 33

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
 20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
 35 40 45

Gly Trp Ile Asp Pro Tyr Arg Ser Glu Ile Arg Tyr Ser Pro Ser Phe
 50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg Val Ser Ser Glu Pro Phe Asp Ser Trp Gly Gln Gly Thr Leu
 100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
 195 200 205

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His

210

215

220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
 225 230 235 240

Phe Leu

<210> 34

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 34

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

Thr Ala Arg Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp His Tyr Ala
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Asp Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Ala Thr Trp Thr Phe Glu Gly Asp Tyr
 85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
 100 105 110

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
 115 120 125

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
 130 135 140

Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
 145 150 155 160

Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
 165 170 175

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
 180 185 190

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
 195 200 205

Pro Thr Glu Cys Ser
 210

<210> 35
 <211> 252
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<220>
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 <222> (232)..(252)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> VARIANT
 <222> (235)..(235)
 <223> /replace="Leu"

<220>
 <221> SITE
 <222> (236)..(252)
 <223> /note="This region may be absent in its entirety"

<220>
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<222> (242)..(252)
<223> /note="This region may be absent in its entirety"

<220>
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<222> (1)..(252)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 35
Gln Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30

Thr Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Ser Arg Gly Leu Glu
35 40 45

Trp Leu Gly Val Ile Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

Gln Phe Ser Leu Gln Leu Asn Ser Val Thr Pro Glu Asp Thr Ala Val
85 90 95

Tyr Tyr Cys Ala Arg Ser Val Pro Gly Gly Asp Pro Gly Leu Glu His
100 105 110

Ala Phe Ala Tyr Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser
130 135 140

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Phe Ala Ser Trp Ser Asp Ser
85 90 95

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala
100 105 110

Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala
115 120 125

Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala
130 135 140

Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val
145 150 155 160

Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser
165 170 175

Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser Tyr
180 185 190

Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala
195 200 205

Pro Thr Glu Cys Ser
210

<210> 37

<211> 234

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>

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<222> (224)..(234)
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<220>
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<223> /note="This region may be absent in its entirety"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 37
Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly
20 25 30

Glu Tyr Tyr Trp Asn Trp Ile Arg Gln His Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Glu Ser Val Ala Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys
210 215 220

Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
225 230

<210> 38
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 38
Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35 40 45

Ile Tyr Gly Thr Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85 90 95

Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala
100 105 110

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
115 120 125

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
130 135 140

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser
145 150 155 160

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu
165 170 175

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val
180 185 190

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
195 200 205

Ser Phe Asn Arg Gly Glu Cys
210 215

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

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<222> (221)..(241)
<223> /note="This region may be absent in its entirety"

<220>

<221> VARIANT
 <222> (224)..(224)
 <223> /replace="Leu"

 <220>
 <221> SITE
 <222> (225)..(241)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> SITE
 <222> (231)..(241)
 <223> /note="This region may be absent in its entirety"

 <220>
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 <222> (1)..(241)
 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 39
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Gly Pro Phe Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Thr Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225 230 235 240

Leu

<210> 40

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 40

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

Thr Ala Arg Ile Thr Cys Ser Gly Asp Ser Ile Pro Asn Tyr Tyr Val
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Ala Gln Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Phe Asp Ser Ser Leu Asn Ala
85 90 95

Glu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 41

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> SITE
<222> (223)..(243)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (226)..(226)
<223> /replace="Leu"

<220>
<221> SITE
<222> (227)..(243)
<223> /note="This region may be absent in its entirety"

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<222> (233)..(243)
<223> /note="This region may be absent in its entirety"

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<222> (1)..(243)
<223> /note="Variant residues given in the sequence have no
      preference with respect to those in the annotations
      for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
      substitutions and preferred embodiments"

<400> 41
Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15

Ser Met Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ala
          20          25          30

Trp Met Asp Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
          35          40          45

```

Ala Glu Ile Arg Ser Lys Ala Ser Asn His Ala Thr Tyr Tyr Ala Glu
50 55 60

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

Val Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Gly Ile Tyr
85 90 95

Tyr Cys Thr Arg Trp Arg Arg Phe Phe Asp Ser Trp Gly Gln Gly Thr
100 105 110

Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
210 215 220

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
225 230 235 240

Val Phe Leu

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 42
Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser

165

170

175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
 195 200 205

Asn Arg Gly Glu Cys
 210

<210> 43

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> SITE

<222> (226)..(246)

<223> /note="This region may be absent in its entirety"

<220>

<221> VARIANT

<222> (229)..(229)

<223> /replace="Leu"

<220>

<221> SITE

<222> (230)..(246)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (236)..(246)

<223> /note="This region may be absent in its entirety"

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<221> SITE

<222> (1)..(246)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 43

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

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr His Phe Thr Ser Tyr
20 25 30

Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Val Ile His Pro Asn Ser Gly Ser Ile Asn Tyr Asn Glu Lys Phe
50 55 60

Glu Ser Arg Val Thr Ile Thr Val Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gly Glu Arg Asp Ser Thr Glu Val Leu Pro Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu
245

<210> 44

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 44

Asp Val Gln Ile Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Lys Ser Ile Asn Lys Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ser Gly Ser Thr Leu Gln Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Met Tyr Tyr Cys Gln Gln His Asn Glu Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala

100

105

110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 45

<211> 246

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> SITE

<222> (226)..(246)

<223> /note="This region may be absent in its entirety"

<220>

<221> VARIANT

<222> (229)..(229)

<223> /replace="Leu"

<220>

<221> SITE
 <222> (230)..(246)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (236)..(246)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (1)..(246)
 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 45
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
 20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Glu Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Lys Val Ser Tyr Leu Ser Thr Ala Ser Ser Leu Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
 115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
 130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
 165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
 180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
 195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
 210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
 225 230 235 240

Gly Pro Ser Val Phe Leu
 245

<210> 46
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 46
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

35

40

45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Arg Tyr Asn Arg Ala Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 47

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> SITE
 <222> (225)..(245)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> VARIANT
 <222> (228)..(228)
 <223> /replace="Leu"

<220>
 <221> SITE
 <222> (229)..(245)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (235)..(245)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (1)..(245)
 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 47
 Glu Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

 Ser Met Lys Leu Ser Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His
 20 25 30

 Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val
 35 40 45

 Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
 50 55 60

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

Val Tyr Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr
85 90 95

Tyr Cys Ser Arg Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu
245

<210> 48

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 48

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Val Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser
20 25 30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65 70 75 80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95

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

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 49
<211> 254
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> SITE
<222> (234)..(254)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (237)..(237)
<223> /replace="Leu"

<220>
<221> SITE
<222> (238)..(254)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (244)..(254)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (1)..(254)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 49

Ser Lys Leu Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1 5 10 15

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe
20 25 30

Ser Ser Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu
35 40 45

Glu Trp Val Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala
50 55 60

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65 70 75 80

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

Tyr Tyr Cys Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
145 150 155 160

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
165 170 175

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
180 185 190

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 210 215 220

Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
 245 250

<210> 50
 <211> 218
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 50
 Ala Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu
 1 5 10 15

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

Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
 35 40 45

Leu Leu Ile Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg
 50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
 65 70 75 80

Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn
 85 90 95

Trp Pro Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
 100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
 130 135 140

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
 180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 51
 <211> 245
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> SITE
 <222> (225)..(245)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> VARIANT
 <222> (228)..(228)
 <223> /replace="Leu"

<220>
 <221> SITE
 <222> (229)..(245)
 <223> /note="This region may be absent in its entirety"

<220>

<221> SITE
 <222> (235)..(245)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> SITE
 <222> (1)..(245)
 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

 <400> 51
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser His
 20 25 30

 Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Asp Trp Met
 35 40 45

 Gly Trp Ile Ser Pro Tyr Ser Gly Asn Thr Asn Tyr Ala Gln Lys Leu
 50 55 60

 Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
 65 70 75 80

 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Arg Val Gly Ser Gly Pro Tyr Tyr Tyr Met Asp Val Trp Gly Gln
 100 105 110

 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
 195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp
 210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
 225 230 235 240

Pro Ser Val Phe Leu
 245

<210> 52
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 52
 Gln Ser Ala Leu Thr Gln Pro Arg Ser Val Ser Gly Ser Pro Gly Gln
 1 5 10 15

Ser Val Thr Ile Ser Cys Thr Gly Thr Ser Ser Ser Val Gly Asp Ser
 20 25 30

Ile Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
 35 40 45

Met Leu Tyr Asp Val Thr Lys Arg Pro Ser Gly Val Pro Asp Arg Phe
 50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Tyr Ala Gly Thr
85 90 95

Asp Thr Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu Gly Gln Pro
100 105 110

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125

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

Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
145 150 155 160

Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175

Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205

Val Ala Pro Thr Glu Cys Ser
210 215

<210> 53

<211> 245

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
 <221> SITE
 <222> (225)..(245)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> VARIANT
 <222> (228)..(228)
 <223> /replace="Leu"

<220>
 <221> SITE
 <222> (229)..(245)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (235)..(245)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (1)..(245)
 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 53
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile Ile Ser Arg
 20 25 30

Ser Ser Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
 35 40 45

Trp Ile Gly Gly Ile Tyr His Ser Gly Asn Thr Tyr Asp Asn Pro Ser
 50 55 60

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

Ser Leu Asn Leu Arg Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Ile Val Pro Gly Gly Asp Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu
245

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 54

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ala Cys Arg Ala Ser Gln Ser Val Gly Thr Tyr Leu
20 25 30

Asn Trp Tyr Gln Gln Lys Arg Gly Lys Ala Pro Lys Leu Leu Ile Phe
35 40 45

Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
50 55 60

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

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Pro Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 55
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> SITE
<222> (222)..(242)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (225)..(225)
<223> /replace="Leu"

<220>
<221> SITE
<222> (226)..(242)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (232)..(242)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (1)..(242)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 55
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Ile Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ser Ile Ser Ser Gly Gly Ser Thr Tyr Tyr Pro Asp Ser Val Lys
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Tyr Tyr Tyr Gly Gln Tyr Phe Asp Phe Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val

225 230 235 240

Phe Leu

<210> 56
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 56
 Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Thr
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ala Ser Tyr Arg Ser Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln His Tyr Ser Thr Pro Leu
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 57
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> SITE
<222> (221)..(241)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (224)..(224)
<223> /replace="Leu"

<220>
<221> SITE
<222> (225)..(241)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (231)..(241)
<223> /note="This region may be absent in its entirety"

<220>

<221> SITE
 <222> (1)..(241)
 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 57
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Gly Pro Phe Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Asp Thr Pro Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
 130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser

165

170

175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
 195 200 205

Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
 210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
 225 230 235 240

Leu

<210> 58

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 58

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

Thr Ala Arg Ile Thr Cys Ser Gly Asp Ser Ile Pro Asn Tyr Tyr Val
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
 35 40 45

Asp Asp Ser Asn Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Ala Gln Ala Gly
 65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Phe Asp Ser Ser Leu Asn Ala
85 90 95

Glu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 59
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> SITE
<222> (225)..(235)
<223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (231)..(235)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 59
 Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu
 1 5 10 15

Thr Leu Ser Leu Thr Cys Ala Val Ser Gly His Ser Ile Ser His Asp
 20 25 30

His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Glu Gly Leu Glu Trp
 35 40 45

Ile Gly Phe Ile Ser Tyr Ser Gly Ile Thr Asn Tyr Asn Pro Ser Leu
 50 55 60

Gln Gly Arg Val Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Glu Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Ser Cys Val Glu
210 215 220

Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
225 230 235

<210> 60

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 60

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Ser Val Thr Ile Thr Cys Gln Ala Ser Thr Asp Ile Ser Ser His
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Glu Leu Leu Ile
35 40 45

Tyr Tyr Gly Ser His Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Glu Ala
65 70 75 80

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Glu Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 61
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> SITE
<222> (221)..(241)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (224)..(224)
<223> /replace="Leu"

<220>
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 <222> (225)..(241)
 <223> /note="This region may be absent in its entirety"

 <220>
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 <222> (231)..(241)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> SITE
 <222> (1)..(241)
 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

 <400> 61
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Arg
 1 5 10 15

 Ser Leu Arg Leu Ser Cys Ala Ala Ser Arg Phe Thr Phe Asp Asp Tyr
 20 25 30

 Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

 Ser Gly Ile Ser Trp Asn Ser Gly Arg Ile Gly Tyr Ala Asp Ser Val
 50 55 60

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

 Leu Gln Met Asn Gly Leu Arg Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

 Ala Lys Gly Arg Asp Ser Phe Asp Ile Trp Gly Gln Gly Thr Met Val
 100 105 110

 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225 230 235 240

Leu

<210> 62
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 62
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Val Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Ser Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 63

<211> 246

<212> PRT

<213> Artificial Sequence

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<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> SITE
<222> (226)..(246)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (229)..(229)
<223> /replace="Leu"

<220>
<221> SITE
<222> (230)..(246)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (236)..(246)
<223> /note="This region may be absent in its entirety"

<220>
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<222> (1)..(246)
<223> /note="Variant residues given in the sequence have no
      preference with respect to those in the annotations
      for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
      substitutions and preferred embodiments"

<400> 63
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Ser
      20          25          30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
      35          40          45

Gly Arg Ile Tyr Pro Gly Asp Gly Asp Thr Asn Tyr Asn Val Lys Phe
      50          55          60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Gly Phe Ile Thr Thr Val Arg Asp Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu
245

<210> 64
<211> 218
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 64

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

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

Gly Ile Ser Phe Met Asn Trp Phe Gln Gln Lys Pro Asp Gln Ser Pro
35 40 45

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

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn
65 70 75 80

Ser Leu Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Lys
85 90 95

Glu Val Pro Phe Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys

180

185

190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 65

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> SITE

<222> (222)..(242)

<223> /note="This region may be absent in its entirety"

<220>

<221> VARIANT

<222> (225)..(225)

<223> /replace="Leu"

<220>

<221> SITE

<222> (226)..(242)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (232)..(242)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (1)..(242)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 65

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Phe Ile Thr Asn Asn
20 25 30

Tyr Trp Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Tyr Ile Ser Tyr Ser Gly Ser Thr Ser Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Asn Thr Phe Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Thr Gly Ser Ser Gly Tyr Phe Asp Phe Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu

<210> 66
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 66
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Ser Val Asp Asp Leu
20 25 30

Leu His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Lys Tyr Ala Ser Gln Ser Ile Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asn Ser Leu Pro Asn
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

115

120

125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 67

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> SITE

<222> (229)..(239)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (235)..(239)

<223> /note="This region may be absent in its entirety"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 67

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Glu Ile Asn Pro Asn Ser Gly Gly Ala Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Gly Tyr Asp Asp Ile Tyr Asp Asp Trp Tyr Phe Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys
210 215 220

Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
225 230 235

<210> 68

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 68

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu Leu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Asp Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 69
 <211> 247
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> SITE
 <222> (227)..(247)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> VARIANT
 <222> (230)..(230)
 <223> /replace="Leu"

<220>
 <221> SITE
 <222> (231)..(247)
 <223> /note="This region may be absent in its entirety"

<220>
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 <222> (237)..(247)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (1)..(247)
 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

 <400> 69
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser His Tyr
 20 25 30

 Ile Met Met Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

 Ser Gly Ile Tyr Ser Ser Gly Gly Ile Thr Val Tyr Ala Asp Ser Val
 50 55 60

 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Tyr Arg Arg Ile Gly Val Pro Arg Arg Asp Glu Phe Asp Ile Trp
 100 105 110

 Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 130 135 140

 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240

Gly Gly Pro Ser Val Phe Leu
245

<210> 70

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 70

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Thr Tyr Trp Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro
100 105 110

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe
195 200 205

Asn Arg Gly Glu Cys
210

<210> 71
<211> 711
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> misc_feature
<222> (649)..(711)
<223> /note="This region may be absent in its entirety"

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<220>
<221> variation
<222> (658)..(660)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (661)..(711)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (679)..(711)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(711)
<223> /note="Variant nucleotides given in the sequence have no
        preference with respect to those in the annotations
        for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
        substitutions and preferred embodiments"

<400> 71
gaggtgcagc tggtggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg      60
agctgcgccg ccagcggctt caccttcagc aggtacagca tgagctgggt gaggcaggcc      120
cccggcaagg gcctggagct ggtggcccag atcaacagcg tgggcaacag cacctactac      180
cccgacaccg tgaagggcag gttcaccatc agcagggaca acgccaagaa caccctgtac      240
ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc cagcggcgac      300
tactggggcc agggcacctt ggtgaccgtg agcagcgcca gcaccaaggg cccagcgtg      360
ttccccctgg cccccagcag caagagcacc agcggcggca ccgccgccct gggctgcctg      420
gtgaaggact acttccccga gcccgtgacc gtgagctgga acagcggcgc cctgaccagc      480
ggcgtgcaca ccttccccgc cgtgctgcag agcagcggcc tgtacagcct gagcagcgtg      540
gtgaccgtgc ccagcagcag cctgggcacc cagacctaca tctgcaacgt gaaccacaag      600
cccagcaaca ccaaggtgga caagaaggtg gagcccaaga gctgcgacaa gaccacacc      660
tgccccccct gccccgcccc cgagctgctg ggcggcccca gcgtgttcct g              711

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<210> 72
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 72
 gacgtggtga tgaccagag ccccctgagc ctgcccgtga ccctgggcca gcccgccagc 60
 atcagctgca ggagcagcca ggcctgatc tacagcgacg gcaacgccta cctgcactgg 120
 ttctctcaga agcccggcca gagccccagg ctgctgatct acaaggtgag caacaggttc 180
 agcggcgtgc ccgacagggt cagcggcagc ggcagcggca ccgacttcac cctgaagatc 240
 agcaggggtg aggccgagga cgtgggcgtg tactactgca gccagagcac ccacgtgccc 300
 tggaccttcg gccagggcac caaggtggag atcaagagga ccgtggccgc cccagcgtg 360
 ttcatcttcc ccccagcga cgagcagctg aagagcggca ccgccagcgt ggtgtgcctg 420
 ctgaacaact tctaccccag ggaggccaag gtgcagtgga aggtggacaa cgccctgcag 480
 agcggcaaca gccaggagag cgtgaccgag caggacagca aggacagcac ctacagcctg 540
 agcagcacc tgaccctgag caaggccgac tacgagaagc acaaggtgta cgcctgcgag 600
 gtgaccacc agggcctgag cagccccgtg accaagagct tcaacagggg cgagtgc 657

<210> 73
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> variation
 <222> (70)..(72)
 <223> /replace="gtg"

<220>
 <221> misc_feature

<222> (658)..(720)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> variation
 <222> (667)..(669)
 <223> /replace="ctg"

 <220>
 <221> misc_feature
 <222> (670)..(720)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> misc_feature
 <222> (688)..(720)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> misc_feature
 <222> (1)..(720)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 73
 gaggtgcagc tggtggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg 60
 agctgcgccg ccagcggcctt caccttcagc gacaacggca tggcctgggt gaggcaggcc 120
 cccggcaagg gcctggagtg ggtgagcttc atcagcaacc tggcctacag catcgactac 180
 gccgacaccg tgaccggcag gttcaccatc agcagggaca acgccaagaa cagcctgtac 240
 ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgt gagcggcacc 300
 tggttcgcct actgggggcca gggcaccctg gtgaccgtga gcagcgccag caccaagggc 360
 cccagcgtgt tccccctggc cccagcagc aagagcacca gcggcggcac cgccgccctg 420
 ggctgcctgg tgaaggacta cttccccgag cccgtgaccg tgagctggaa cagcggcgcc 480
 ctgaccagcg gcgtgcacac cttccccgcc gtgctgcaga gcagcggcct gtacagcctg 540
 agcagcgtgg tgaccgtgcc cagcagcagc ctgggcaccc agacctacat ctgcaacgtg 600
 aaccacaagc ccagcaacac caaggtggac aagaaggtgg agcccaagag ctgcgacaag 660

acccacacct gccccccctg ccccgcccc gagctggccg gcgccccag cgtgttcctg 720

<210> 74

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 74

gacatcgtga tgaccagag ccccctgagc ctgcccgtga ccccggcga gcccgccagc 60

atcagctgca gggtagcca gagcctgctg cacagcaacg gctacaccta cctgcactgg 120

tacctgcaga agcccgcca gagccccag ctgctgatct acaaggtgag caacaggttc 180

agcggcgtgc ccgacagggt cagcggcagc ggcagcggca ccgacttcac cctgaagatc 240

agcaggggtg aggccgagga cgtgggcgtg tactactgca gccagaccag gcacgtgccc 300

tacaccttcg gcggcggcac caaggtggag atcaagagga ccgtggccgc cccagcgtg 360

ttcatcttcc ccccgagca cgagcagctg aagagcggca ccgccagcgt ggtgtgcctg 420

ctgaacaact tctacccag ggaggccaag gtgcagtgga aggtggacaa cgccctgcag 480

agcggcaaca gccaggagag cgtgaccgag caggacagca aggacagcac ctacagcctg 540

agcagcacc tgaccctgag caaggccgac tacgagaagc acaaggtgta cgcctgcgag 600

gtgaccacc agggcctgag cagccccgtg accaagagct tcaacagggg cgagtgc 657

<210> 75

<211> 762

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (700)..(762)

<223> /note="This region may be absent in its entirety"

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<220>
<221> variation
<222> (709)..(711)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (712)..(762)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (730)..(762)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(762)
<223> /note="Variant nucleotides given in the sequence have no
        preference with respect to those in the annotations
        for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
        substitutions and preferred embodiments"

<400> 75
caggtgcagc tggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtgaaggtg      60
agctgcaagg ccagcggcta caccttcacc aagtactaca tgagctgggt gaggcaggcc      120
cccggccagg gcctggagtg gatgggcatc atcaacccca tcggcggcag caccagctac      180
gcccagaagt tccagggcag ggtgaccatg accagggaca ccagcaccag caccgtgtac      240
atggagctga gcagcctgag gagcgaggac accgccgtgt actactgcgc cagggacccc      300
agcggcatcg ccctggccgg ccccgccagc aggggctacc agggcatgga cgtgtggggc      360
cagggcacca ccgtgaccgt gagcagcgcc agcaccaagg gccccagcgt gttccccctg      420
gccccagca gcaagagcac cagcggcggc accgccgccc tgggctgcct ggtgaaggac      480
tacttccccg agcccgtgac cgtgagctgg aacagcggcg ccctgaccag cggcgtgcac      540
accttccccg ccgtgctgca gagcagcggc ctgtacagcc tgagcagcgt ggtgaccgtg      600
cccagcagca gcctgggcac ccagacctac atctgcaacg tgaaccacaa gcccagcaac      660
accaaggtgg acaagagggt ggagcccaag agctgcgaca agaccacac ctgccccccc      720
tgccccgccc ccgagctgct gggcgggccc agcgtgttcc tg                          762

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<210> 76
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 76
 gagatcgtga tgaccagag ccccgccacc ctgagcgtga gcccgcgga gagggccacc 60
 ctgagctgca gggccagcca gagcgtgagc agcaacctgg cctggtacca gcagaagccc 120
 ggccaggccc ccaggctgct gatctacggc gccagcacca gggccaccgg catccccgcc 180
 aggttcagcg gcagcggcag cggcaccgag ttcacctga ccatcagcag cctgcagagc 240
 gaggacttcg ccgtgtacta ctgccagcag gccaggctgg gcccctggac cttcggcggc 300
 ggcaccaagg tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc 360
 agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac 420
 cccagggagg ccaagggtgca gtggaagggtg gacaacgccc tgcaagcgg caacagccag 480
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 540
 ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600
 ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 77
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (652)..(711)
 <223> /note="This region may be absent in its entirety"

<220>

<221> variation
 <222> (667)..(668)
 <223> /replace="ag"

 <220>
 <221> misc_feature
 <222> (679)..(711)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> misc_feature
 <222> (1)..(711)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

 <400> 77
 gaggtgaagg tgggtggagag cggcggcggc ctggtgcagc ccggcggcag catgaagctg 60
 agctgcgtgg tgagcggctt caccttcagc aactactggg tgaactgggt gaggcaggcc 120
 cccggcaagg gcctggagtg ggtggcccag atcaggctga agagcgacaa ctacgccacc 180
 cactacgagg agagcgtgaa gggcaggttc accatcagca gggacgacag caagagcagc 240
 gtgtacctgc agatgaacaa cctgagggcc gaggacagcg gcatctacta ctgcaccaac 300
 tgggaggact actggggcca gggcaccacc gtgaccgtga gcagcgccag caccaagggc 360
 cccagcgtgt tccccctggc cccctgcagc aggagcacca gcgagagcac cgccgccctg 420
 ggctgcctgg tgaaggacta cttccccgag cccgtgaccg tgagctggaa cagcggcgcc 480
 ctgaccagcg gcgtgcacac cttccccgcc gtgctgcaga gcagcggcct gtacagcctg 540
 agcagcgtgg tgaccgtgcc cagcagcagc ctgggcacca agacctacac ctgcaacgtg 600
 gaccacaagc ccagcaacac caaggtggac aagagggtgg agagcaagta cggccccccc 660
 tgccccccct gccccgcccc cgagttcctg ggcggcccca gcgtgttcct g 711

 <210> 78
 <211> 654
 <212> DNA
 <213> Artificial Sequence

 <220>

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<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

<400> 78
gacatcgtgc tgaccagag ccccgacagc ctggccgtga gcctgggcga gagggccacc      60
atcagctgca gggccagcca gagcgtgagc accagcaggt acagctacat ccactggtac      120
cagcagaagc ccggccagtt cccaagctg ctgatcaagt acgccagcaa cctggagagc      180
ggcgtgcca gcaggttcag cggcagcggc agcggcaccg acttcaccct gaacatccac      240
cccctggagc ccgaggactt cgccacctac tactgccacc acagctggga gatccccctg      300
accttcggcc agggcaccaa gctggagatc aagaggaccg tggccgcccc cagcgtgttc      360
atcttcccc ccagcgacga gcagctgaag agcggcaccg ccagcgtggt gtgcctgctg      420
aacaacttct accccaggga ggccaaggtg cagtggaagg tggacaacgc cctgcagagc      480
ggcaacagcc aggagagcgt gaccgagcag gacagcaagg acagcaccta cagcctgagc      540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgagaggtg      600
acccaccagg gcctgagcag ccccgtagc aagagcttca acaggggcga gtgc          654

<210> 79
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

<220>
<221> variation
<222> (181)..(183)
<223> /replace="acc"

<220>
<221> misc_feature
<222> (661)..(720)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (676)..(677)
<223> /replace="ag"

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<220>
 <221> misc_feature
 <222> (688)..(720)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> misc_feature
 <222> (1)..(720)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 79
 gaggtgcagc tgcaggagag cggccccggc ctggtgaagc ccagcgagac cctgagcctg 60
 acctgcaccg tgagcggctt cagcctgacc agcaacgaca tcgcctggat caggcagccc 120
 cccggcaagg gcctggagtg gatgggcacc atctggaccg acggcagcac caactacaac 180
 gccgccgtgc agagcagggt gaccatcagc gtggacacca gcaagaacca gttcagcctg 240
 aagctgagca gcgtgaccgc cgccgacacc gccgtgtact actgcgccag gcacaggctg 300
 tactacggcg ccttcgacta ctggggccag ggcaccatgg tgaccgtgag cagcgccagc 360
 accaagggcc ccagcgtgtt ccccctggcc ccctgcagca ggagcaccag cgagagcacc 420
 gccgccctgg gctgcctggt gaaggactac ttccccgagc ccgtgaccgt gagctggaac 480
 agcggcgccc tgaccagcgg cgtgcacacc ttccccgccg tgctgcagag cagcggcctg 540
 tacagcctga gcagcgtggt gaccgtgccc agcagcagcc tgggcaccaa gacctacacc 600
 tgcaacgtgg accacaagcc cagcaacacc aaggtggaca agagggtgga gagcaagtac 660
 ggccccccct gccccccctg ccccgcccc gagttcctgg gcggccccag cgtgttcctg 720

<210> 80
 <211> 657
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 80
gacatcgtga tgaccagac ccccctgagc ctgagcgtga cccccggcca gcccgccagc 60
atcagctgca ggagcagcca gagcctggag tacagcgacg gctacaccta cctggagtgg 120
tacctgcaga agcccggcca gagccccag ctgctgatct acgaggtgag caacaggttc 180
agcggcgtgc ccgacaggtt cagcggcagc ggcagcggca ccgacttcac cctgaagatc 240
agcaggggtgg aggccgagga cgtgggcgtg tactactgct tccaggccac ccacaacccc 300
tacaccttcg gccagggcac caagctggag atcaagagga ccgtggccgc cccagcgtg 360
ttcatcttcc cccccagcga cgagcagctg aagagcggca ccgccagcgt ggtgtgcctg 420
ctgaacaact tctaccccag ggaggccaag gtgcagtgga aggtggacaa cgccctgcag 480
agcggcaaca gccaggagag cgtgaccgag caggacagca aggacagcac ctacagcctg 540
agcagcacc tgaccctgag caaggccgac tacgagaagc acaaggtgta cgcctgcgag 600
gtgaccacc agggcctgag cagccccgtg accaagagct tcaacagggg cgagtgc 657

<210> 81
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> misc_feature
<222> (685)..(747)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (694)..(696)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (697)..(747)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature

<222> (715)..(747)
 <223> /note="This region may be absent in its entirety"
 <220>
 <221> misc_feature
 <222> (1)..(747)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"
 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 81
 caggtgcagc tggtggagag cggcggcggc gtggtgcagc ccggcaggag cctgagggtg 60
 agctgcgccg ccagcggcctt caccttcagc agctacgaca tgcactgggt gaggcaggcc 120
 cccggcaagg gcctggagtg ggtggccgtg atctggttcg acggcagcaa cgagttctac 180
 gccgacagcg tgaagggcag gttcaccatc agcagggaca acagcaagaa caccctgttc 240
 cagatgaaca gcctgagggc cgaggacacc gccgtgtact actgcgccag ggacctgggc 300
 gccagcgtga ccaccagcaa cgccgagaac ttccaccact ggggccaggg caccctgggtg 360
 accgtgagca gcgccagcac caagggccccc agcgtgttcc ccctggcccc cagcagcaag 420
 agcaccagcg gcggcaccgc cgccctgggc tgcctggtga aggactactt ccccgagccc 480
 gtgaccgtga gctggaacag cggcgccctg accagcggcg tgcacacctt ccccgccgtg 540
 ctgcagagca gcggcctgta cagcctgagc agcgtggtga ccgtgcccag cagcagcctg 600
 ggcacccaga cctacatctg caacgtgaac cacaagccca gcaacaccaa ggtggacaag 660
 aaggtggagc ccaagagctg cgacaagacc cacacctgcc ccccctgccc cgcccccgag 720
 ctggccggcg ccccagcgt gttcctg 747

<210> 82
 <211> 639
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 82
 agctacgagc tgacccagcc ccccagcgtg agcgtgagcc ccggccagac cgccaggatc 60
 acctgcagcg gcgacgccct gcccaagagg tacgtgtact ggtaccagca gaagagcggc 120
 caggcccccg tgctgggtgat ctacaggagc agcaagaggc ccagcggcat ccccgagacc 180
 ttcagcggca gcagcagcgg caccatggcc accctgacca tcagcggcgc ccaggtggag 240
 gacgaggccg actactactg ctacagcacc gacagcaacg gccaccactg ggtgttcggc 300
 ggcggcacca agctgaccgt gctgggccag cccaaggccg ccccagcgt gaccctgttc 360
 cccccagca gcgaggagct gcaggccaac aaggccaccc tggtgtgcct gatcagcgac 420
 ttctaccccg gcgccgtgac cgtggcctgg aaggccgaca gcagccccgt gaaggccggc 480
 gtggagacca ccacccccag caagcagagc aacaacaagt acgccgccag cagctacctg 540
 agcctgaccc ccgagcagtg gaagagccac aggagctaca gctgccaggt gaccacagag 600
 ggagcaccg tggagaagac cgtggccccc acctgcagc 639

<210> 83
 <211> 735
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (676)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (691)..(692)
 <223> /replace="ag"

<220>
 <221> misc_feature
 <222> (703)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(735)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 83

caggtgcagc	tggtgcagag	cggcgccgag	gtgaagaagc	ccggcagcag	cgtgaagggtg	60
agctgcaagg	ccagcggcta	cagcttcagc	gactactaca	tgactgggt	gaggcaggcc	120
cccggccagg	gcctggagt	gatgggccag	atcaaccca	ccaccggcgg	cgccagctac	180
aaccagaagt	tcaagggcaa	ggccaccatc	accgtggaca	agagcaccag	caccgcctac	240
atggagctga	gcagcctgag	gagcgaggac	accgccgtgt	actactgcgc	caggtactac	300
tacggcaggc	acttcgacgt	gtggggccag	ggcaccaccg	tgaccgtgag	cagcgccagc	360
accaagggcc	ccagcgtgtt	ccccctggcc	ccctgcagca	ggagcaccag	cgagagcacc	420
gccgccctgg	gctgcctggt	gaaggactac	ttccccgagc	ccgtgaccgt	gagctggaac	480
agcggcgccc	tgaccagcgg	cgtgcacacc	ttccccgccg	tgaccgtgag	cagcgtgctg	540
cagagcagcg	gcctgtacag	cctgagcagc	gtggtgaccg	tgcccagcag	cagcctgggc	600
accaagacct	acacctgcaa	cgtggaccac	aagcccagca	acaccaaggt	ggacaagagg	660
gtggagagca	agtacggccc	cccctgcccc	ccctgccccg	cccccgagtt	cctgggcggc	720
cccagcgtgt	tcctg					735

<210> 84

<211> 630

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 84

gacatcgtga	tgaccagag	ccccgacagc	ctggccgtga	gcctgggcga	gagggccacc	60
atcaactgca	aggccagcca	gagcgtggac	tacgacggcg	acagctacat	gaactggtac	120
cagcagaagc	ccggccagcc	ccccaaagctg	ctgatctacg	ccgccagcaa	cctggagagc	180

ggcgtgccccg acaggttcag cggcagcggc agcggcaccg acttcaccct gaccatcagc	240
agcctgcagg ccgaggacgt ggccgtgtac tactgccagc agagcaacga ggacccctac	300
accttcggcc agggcaccaa gctggagatc aagttcatct tccccccag cgacgagcag	360
ctgaagagcg gcaccgccag cgtggtgtgc ctgctgaaca acttctaccc cagggaggcc	420
aaggtgcagt ggaaggtgga caacgccctg cagagcggca acagccagga gagcgtgacc	480
gagcaggaca gcaaggacag cacctacagc ctgagcagca ccctgaccct gagcaaggcc	540
gactacgaga agcacaaggt gtacgcctgc gaggtgaccc accagggcct gagcagcccc	600
gtgaccaaga gcttcaacag gggcgagtgc	630

<210> 85

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (661)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (670)..(672)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (673)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (691)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(723)

<223> /note="Variant nucleotides given in the sequence have no

preference with respect to those in the annotations
for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 85

gaggtgcagc tgggtggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg	60
agctgcgccg ccagcggcctt caccttcagc aactacggca tgagctgggt gaggcaggcc	120
cccggcaagg gcctggagtg ggtggccagc atcagcagcg gcggcggcag cacctactac	180
cccgacaacg tgaagggcag gttcaccatc agcagggacg acgccaagaa cagcctgtac	240
ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc caggggcggc	300
gccggcatcg actactgggg ccagggcacc ctggtgaccg tgagcagcgc cagcaccaag	360
ggccccagcg tgttccccct ggcccccagc agcaagagca ccagcggcgg caccgccgcc	420
ctgggctgcc tgggtgaagga ctacttcccc gagcccgtga ccgtgagctg gaacagcggc	480
gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc	540
ctgagcagcg tggtgaccgt gcccagcagc agcctgggca ccagacctt catctgcaac	600
gtgaaccaca agcccagcaa caccaaggtg gacaagaggg tggagcccaa gagctgcgac	660
aagaccaca cctgcccccc ctgccccgcc cccgagctgc tgggcggccc cagcgtgttc	720
ctg	723

<210> 86

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 86

gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagggtgacc	60
atcacctgca agagcatcca gaccctgctg tacagcagca accagaagaa ctacctggcc	120
tggttccagc agaagcccgg caaggcccc aagctgctga tctactgggc cagcatcagg	180

aagagcggcg tgcccagcag gttcagcggc agcggcagcg gcaccgactt caccctgacc	240
atcagcagcc tgcagcccga ggacctggcc acctactact gccagcagta ctacagctac	300
cccctgacct tcggcggcgg caccaagctg gagatcaaga ggaccgtggc cgcccccagc	360
gtgttcatct tcccccccag cgacgagcag ctgaagagcg gcaccgccag cgtggtgtgc	420
ctgctgaaca acttctaccc cagggaggcc aaggtgcagt ggaaggtgga caacgccctg	480
cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggacag cacctacagc	540
ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgc	600
gaggtgaccc accagggcct gagcagcccc gtgaccaaga gcttcaacag gggcgagtgc	660

<210> 87

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (685)..(747)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (694)..(696)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (697)..(747)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (715)..(747)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(747)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations"

for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 87

gaggtgcagc	tggtggagag	cggcgccgag	gtgaagaagc	ccggcgccag	cgtgaaggtg	60
agctgcaagg	ccagcggcta	caccttcacc	aactacgcca	tgactgggt	gaggcaggcc	120
cccgccaga	ggctggagt	gatgggctgg	atcaacgccg	gcaacggcaa	gaggaagtac	180
agccagaagt	tccaggacag	ggtgaccatc	aacagggaca	ccagcgccag	caccatctac	240
atggagctga	gcagcctggg	cagcaggagc	accgccgtgt	actactgcgc	cagggaggag	300
gaccacgccg	gcagcggcag	ctacctgagc	atggacgtgt	ggggccaggg	caccctggtg	360
accgtgagca	gcgccagcac	caagggcccc	agcgtgttcc	ccctggcccc	cagcagcaag	420
agcaccagcg	gcggcaccgc	cgccctgggc	tgcttggtga	aggactactt	ccccgagccc	480
gtgaccgtga	gctggaacag	cggcgccctg	accagcggcg	tgcacacctt	ccccgccgtg	540
ctgcagagca	gcggcctgta	cagcctgagc	agcgtgggtga	ccgtgcccag	cagcagcctg	600
ggcaccaga	cctacatctg	caacgtgaac	cacaagccca	gcaacaccaa	ggtggacaag	660
aggggtggagc	ccaagagctg	cgacaagacc	cacacctgcc	ccccctgccc	cgcccccgag	720
ctgctgggcg	gccccagcgt	gttcctg				747

<210> 88

<211> 660

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 88

gacatccaga	tgaccagag	ccccagcagc	ctgagcgcca	gcgtgggcga	cagggtgacc	60
atcacctgca	agagcatcca	gaccctgctg	tacagcagca	accagaagaa	ctacctggcc	120
tggttcagc	agaagcccgg	caaggccccc	aagctgctga	tctactgggc	cagcatcagg	180
aagagcggcg	tgcccagcag	gttcagcggc	agcggcagcg	gcaccgactt	caccctgacc	240

atcagcagcc tgcagcccga ggacctggcc acctactact gccagcagta ctacagctac	300
cccctgacct tcggcggcgg caccaagctg gagatcaaga ggaccgtggc cgcccccagc	360
gtgttcatct tccccccag cgacgagcag ctgaagagcg gcaccgccag cgtggtgtgc	420
ctgctgaaca acttctaccc caggaggaggcc aaggtgcagt ggaaggtgga caacgccctg	480
cagagcggca acagccagga gagcgtgacc gagcaggaca gcaaggacag cacctacagc	540
ctgagcagca ccctgaccct gagcaaggcc gactacgaga agcacaaggt gtacgcctgc	600
gaggtgaccc accagggcct gagcagcccc gtgaccaaga gcttcaacag gggcgagtgc	660

<210> 89

<211> 741

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (679)..(741)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (688)..(690)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (691)..(741)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (709)..(741)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(741)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 89

gaggtgcagc tgctggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg	60
agctgcgccg ccagcggctt caccttcagc agctacgcca tgagctgggt gaggcaggcc	120
cccggcaagg gcctggagtg ggtgagcagc atcagccacc tgggcggcag cacctactac	180
gccgacagcg tgaagggcag gttcaccatc agcagggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc cggcggcgcc	300
aaccacggca agtactacta cggcatggac aagtggggcc agggcaccac cgtgaccgtg	360
agcagcgcca gcaccaaggg cccagcgtg ttccccctgg cccccagcag caagagcacc	420
agcggcggca ccgccgccct gggctgcctg gtgaaggact acttccccga gcccgtagacc	480
gtgagctgga acagcggcgc cctgaccagc ggcgtgcaca ctttccccgc cgtgctgcag	540
agcagcggcc tgtacagcct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc	600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagagggtg	660
gagcccaaga gctgcgacaa gaccacacc tgccccccct gccccgcccc cgagttcgag	720
ggcggcccca gcgtgttcct g	741

<210> 90

<211> 663

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 90

caggccgtgc tgaccagcc cgccagcctg agcgccagcc ccggcgccag cgccagcctg	60
acctgcaccc tgaggagcgg cgccccctg cccaagtaca ggatctactg gtaccagcag	120
aagcccggca gccccccca gtacctgctg aggtacaaga gcgacgccga caagcaccag	180
ggcagcggcg tgcccagcag gttcagcggc agcaaggacg ccagcgccaa cgccggcatc	240

ctgctgatca gcggcctgca gagcgaggac gaggccgact actactgcat ggtgtgggac	300
cacggcgtgt ggtacttcgg cggcggcacc aagctgaccg tgctgggcca gccaaggcc	360
gccccagcg tgaccctgtt cccccccagc agcgaggagc tgcaggccaa caaggccacc	420
ctggtgtgcc tgatcagcga cttctacccc ggcgccgtga ccgtggcctg gaaggccgac	480
agcagccccg tgaaggccgg cgtggagacc accaccccc gcaagcagag caacaacaag	540
tacgccgcca gcagctacct gagcctgacc cccgagcagt ggaagagcca caggagctac	600
agctgccagg tgaccacga gggcagcacc gtggagaaga ccgtggcccc caccgagtg	660
agc	663

<210> 91
 <211> 753
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (691)..(753)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (700)..(702)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (703)..(753)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (721)..(753)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(753)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations"

for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 91

gaggtgcagc tgggtggagag cggcggcgac ctggtgaggc ccggcggcag cctgaggctg	60
agctgcgtgg ccagcggctt caccttcagc aactactgga tgcactgggt gaggcaggcc	120
cccggccaga ggcccgtgtg ggtgagcagg accaacaccg acggcaggaa caccgcctac	180
gccgactacg ccaagggcag gttcaccatc agcagggaca acgccaagag caccctgtac	240
ctgcagctga acagcctgag ggccgaggac accgccgtgt acttctgcgc caggctgagg	300
aggaacgtgg ccgaccagat caccacaac tactacatgg acgtgtgggg caagggcacc	360
ctggtgaccg ttagcagcgc cagcaccaag ggccccagcg tgttccccct ggcccccagc	420
agcaagagca ccagcggcgg caccgccgcc ctgggctgcc tgggtgaagga ctacttcccc	480
gagcccgtga ccgtgagctg gaacagcggc gccctgacca gcggcgtgca caccttcccc	540
gccgtgctgc agagcagcgg cctgtacagc ctgagcagcg tggtgaccgt gccagcagc	600
agcctgggca cccagaccta catctgcaac gtgaaccaca agcccagcaa caccaaggtg	660
gacaagaagg tggagcccaa gagctgcgac aagaccaca cctgcccccc ctgccccgcc	720
cccgaggccg ccggcggccc cagcgtgttc ctg	753

<210> 92

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 92

gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagggtgacc	60
gcctgcaggg ccagccagag cgtgggcacc tacctgaact ggtaccagca gaagaggggc	120
aaggcccca agctgctgat cttgccgcc agcagcctgc agagcggcgt gccagcagg	180
ttcagcggca gcggcagcgg caccgacttc accctgacca tcagcagcct gcagcccag	240

gacttcgcca cctactactg ccagcagagc tacagcagcc cccccacctt cggccagggc	300
accaaggtgg agatcaagag gaccgtggcc gccccagcg tgttcattctt cccccccagc	360
gacgagcagc tgaagagcgg caccgccagc gtggtgtgcc tgctgaacaa cttctacccc	420
agggaggcca aggtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggag	480
agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg	540
agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg	600
agcagccccg tgaccaagag cttcaacagg ggcgagtgc	639

<210> 93
 <211> 744
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (682)..(744)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (691)..(693)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (694)..(744)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (712)..(744)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(744)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 93

caggtgcagc tggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtgaccctg	60
agctgcaagg ccagcggcta caccttcacc gcctactaca tccactgggt gaggcaggcc	120
agggagcagg gcctggagtg gatgggcgtg atcaacccca gcaccggcac caccttctac	180
gcccagaact tccccgacag ggtgagcgtg accagggaca ccagcaccag caccgtgttc	240
atggagctgc acaacctgaa gagcgaggac accgccgtgt actactgcgc cagggccatc	300
agcgagcacg gcagcggcag ctacagcccc tactactggg gccagggcac cctggtgacc	360
gtgagcagcg ccagcaccaa gggccccagc gtgttcccc tggccccag cagcaagagc	420
accagcggcg gcaccgccgc cctgggctgc ctggtgaagg actacttccc cgagcccgtg	480
accgtgagct ggaacagcgg cgccctgacc agcggcgtgc acaccttccc cgccgtgctg	540
cagagcagcg gcctgtacag cctgagcagc gtggtgaccg tgcccagcag cagcctgggc	600
accagacct acatctgcaa cgtgaaccac aagcccagca acaccaaggt ggacaagaag	660
gtggagccca agagctgcga caagaccac acctgcccc cctgccccgc ccccgaggcc	720
gccggcggcc ccagcgtgtt cctg	744

<210> 94

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 94

agctacgagc tgaccagcc cccagcgtg agcgtgagcc tgggccagat ggccgccatc	60
acctgcagcg gcgaggccct gcccaagaag tacggctact ggtaccagca gaagcccggc	120
caggtgcccg tgctgctgat ctacaggac gtggagaggc ccagcggcgt gcccgacagg	180
ttcagcggca gcagcagcgg caccatggtg accctgacca tcagcggcgt gcaggccgag	240

gacgaggccg actactactg cctgagcgcc gacagcagcg gcacctgggt gttcggcggc 300
ggcaccaagc tgaccgtgct g 321

<210> 95
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature
<222> (646)..(708)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (655)..(657)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (658)..(708)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (676)..(708)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(708)
<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 95
gaggtgcagc tggtggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg 60
agctgcgccg tgagcggcat cgacctgagc ggctactaca tgaactgggt gaggcaggcc 120

cccggcaagg gcctggagtg ggtgggcgtg atcggcatca acggcgccac ctactacgcc	180
agctggggcca agggcagggtt caccatcagc agggacaaca gcaagaccac cgtgtacctg	240
cagatgaaca gcctgagggc cgaggacacc gccgtgtact tctgcgccag gggcgacatc	300
tggggccagg gcaccctggt gaccgtgagc agcgccagca ccaaggggccc cagcgtgttc	360
cccctggccc ccagcagcaa gagcaccagc ggcggcaccg ccgccctggg ctgcctggtg	420
aaggactact tccccgagcc cgtgaccgtg agctggaaca gcggcgccct gaccagcggc	480
gtgcacacct tccccgccgt gctgcagagc agcggcctgt acagcctgag cagcgtggtg	540
accgtgcca gcagcagcct gggcacccag acctacatct gcaacgtgaa ccacaagccc	600
agcaacacca aggtggacgc cagggtggag cccaagagct gcgacaagac ccacacctgc	660
ccccctgcc ccgccccga gctgctgggc ggccccagcg tgaccctg	708

<210> 96

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 96

caggtgctga cccagagccc cagcagcctg agcgccagcg tgggcgacag ggtgaccatc	60
aactgccagg ccagccagag cgtgtaccac aacacctacc tggcctggta ccagcagaag	120
cccggcaagg tgccaagca gctgatctac gacgccagca ccctggccag cggcgtgccc	180
agcaggttca gcggcagcgg cagcggcacc gacttcaccc tgaccatcag cagcctgcag	240
cccgaggacg tggccaccta ctactgcctg ggcagctacg actgcaccaa cggcgactgc	300
ttcgtgttcg gcggcggcac caaggtggag atcaagagga ccgtggccgc cccagcgtg	360
ttcatcttcc cccccagcga cgagcagctg aagagcggca ccgccagcgt ggtgtgcctg	420
ctgaacaact tctaccccag ggaggccaag gtgcagtgga aggtggacaa cgccctgcag	480
agcggcaaca gccaggagag cgtgaccgag caggacagca aggacagcac ctacagcctg	540
agcagcacc tgaccctgag caaggccgac tacgagaagc acaaggtgta cgcctgcgag	600
gtgaccacc agggcctgag cagccccgtg accaagagct tcaacagggg cgagtgc	657

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<210> 97
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

<220>
<221> misc_feature
<222> (682)..(714)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (700)..(714)
<223> /note="This region may be absent in its entirety"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
        substitutions and preferred embodiments"

<400> 97
gaggtgcagc tggtggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg      60
agctgcgccg ccagcggcctt caccttcagc aactactgga tcagctgggt gaggcaggcc      120
cccggcaagg gcctggagtg ggtggccgag atcaggagcg agagcgacgc cagcgccacc      180
cactacgccg aggccgtgaa gggcagggtt accatcagca gggacaacgc caagaacagc      240
ctgtacctgc agatgaacag cctgagggcc gaggacaccg ccgtgtacta ctgcctggcc      300
tacttcgact acggcctggc catccagaac tactggggcc agggcaccct ggtgaccgtg      360
agcagcgcca gcaccaaggg cccagcgtg ttccccctgg cccctgcag caggagcacc      420
agcgagagca ccgccgccct gggctgcctg gtgaaggact acttccccga gcccgtagacc      480
gtgagctgga acagcggcgc cctgaccagc ggcgtgcaca ctttccccgc cgtgctgcag      540
agcagcggcc tgtacagcct gagcagcgtg gtgaccgtgc ccagcagcaa cttcggcacc      600
cagacctaca cctgcaacgt ggaccacaag cccagcaaca ccaaggtgga caagaccgtg      660
gagaggaagt gctgcgtgga gtgccccccc tgccccgccc ccccctgggc cggc          714

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<210> 98
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 98
 gagatcgtgc tgaccagag ccccgccacc ctgagcctga gcccggcga gagggccacc 60
 ctgagctgca aggccagcaa gagggtgacc acctacgtga gctggtacca gcagaagccc 120
 ggccaggccc ccaggctgct gatctacggc gccagcaaca ggtacctggg catccccgcc 180
 aggttcagcg gcagcggcag cggcaccgac ttcacctga ccatcagcag cctggagccc 240
 gaggacttcg ccgtgtacta ctgcagccag agctacaact acccctacac cttcggccag 300
 ggaccaagc tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc 360
 agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac 420
 cccagggagg ccaagggtgca gtggaagggtg gacaacgccc tgagagcgg caacagccag 480
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 540
 ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600
 ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 99
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (664)..(723)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation

<222> (679)..(680)
 <223> /replace="ag"

<220>
 <221> misc_feature
 <222> (691)..(723)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(723)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 99
 caggtgcagc tggtgcagag cggcgccgag gtgaagaagc ccggcagcag cgtgaaggtg 60
 agctgcaagg ccagcggcta caccttcggc aactactgga tgcagtgggt gaggcaggcc 120
 cccggccagg gcctggagtg gatgggcgcc atctacgagg gcaccggcaa gaccgtgtac 180
 atccagaagt tcgccgacag ggtgaccatc accgccgaca agagcaccag caccgcctac 240
 atggagctga gcagcctgag gagcgaggac accgccgtgt actactgcgc caggctgagc 300
 gactacgtga gcggcttcgg ctactggggc cagggcacca ccgtgaccgt gagcagcgcc 360
 agcaccaagg gccccagcgt gttccccctg gccccctgca gcaggagcac cagcgagagc 420
 accgccgccc tgggctgcct ggtgaaggac tacttccccg agcccgtgac cgtgagctgg 480
 aacagcggcg ccctgaccag cggcgtgcac accttccccg ccgtgctgca gagcagcggc 540
 ctgtacagcc tgagcagcgt ggtgaccgtg cccagcagca gcctgggcac caagacctac 600
 acctgcaacg tggaccacaa gcccagcaac accaaggtgg acaagagggt ggagagcaag 660
 tacggcccc cctgcccccc ctgccccgcc cccgaggccg ccggcggccc cagcgtgttc 720
 ctg 723

<210> 100
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 100
 gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagggtgacc 60
 atcacctgca gggccagcaa ggacatcagc aagtaccta actggtacca gcagaagccc 120
 ggcaaggccc ccaagctgct gatctactac accagcggct accacagcgg cgtgcccagc 180
 aggttcagcg gcagcggcag cggcaccgac ttcacccta ccatcagcag cctgcagccc 240
 gaggacttcg ccacctacta ctgccagcag ggcgacgccc tgccccccac cttcggcggc 300
 ggaccaagg tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc 360
 agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac 420
 cccagggagg ccaaggtgca gtggaagggtg gacaacgccc tgcagagcgg caacagccag 480
 gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 540
 ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600
 ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 101
 <211> 741
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (679)..(741)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (688)..(690)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (691)..(741)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (709)..(741)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(741)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 101

gaggtgcagc tggtggagag cggcggcggc ctggtgaagc ccggcggcag cctgaggctg 60

agctgcgccg ccagcggctt cagcttcagc aacaacgacg tgatgtgctg ggtgaggcag 120

gccccggca agggcctgga gtggatcggc tgcacatga ccaccgacgt ggtgaccgag 180

tacgccaact gggccaagag caggttcacc gtgagcaggg acagcgccaa gaacagcgtg 240

tacctgcaga tgaacagcct gagggccgag gacaccgccg tgtacttctg cgccagggac 300

agcgtgggca gccccctgat gagcttcgac ctgtggggcc ccggcaccct ggtgaccgtg 360

agcagcgcca gcaccaaggg cccagcgtg ttccccctgg ccccgagcag caagagcacc 420

agcggcggca ccgccgccct gggctgcctg gtgaaggact acttccccga gcccgtagacc 480

gtgagctgga acagcggcgc cctgaccagc ggcgtgcaca ctttccccgc cgtgctgcag 540

agcagcggcc tgtacagcct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc 600

cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagaaggtg 660

gagcccaaga gctgcgacaa gaccacacc tgccccccct gccccgcccc cgagctgctg 720

ggcggcccca gcgtgttcct g 741

<210> 102

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 102
 gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagggtgacc 60
 atcaactgcc aggccagcca gagcatctac aacaacaacg agctgagctg gtaccagcag 120
 aagcccggca agcccccaa gctgctgata tacagggcca gcaccctggc cagcggcgtg 180
 cccagcaggt tcagcggcag cggcagcggc accgacttca ccctgaccat cagcagcctg 240
 cagcccaggg acgtggccac ctactactgc ggcggctaca agagctacag caacgacggc 300
 aacggcttcg gcggcggcac caaggtggag atcaagagga ccgtggccgc ccccagcgtg 360
 ttcatcttcc ccccagcga cgagcagctg aagagcggca ccgccagcgt ggtgtgcctg 420
 ctgaacaact tctacccag ggaggccaag gtgcagtgga aggtggacaa cgccctgcag 480
 agcggcaaca gccaggagag cgtgaccgag caggacagca aggacagcac ctacagcctg 540
 agcagcacc tgaccctgag caaggccgac tacgagaagc acaagtgta cgcctgcgag 600
 gtgaccacc agggcctgag cagccccgtg accaagagct tcaacagggg cgagtgc 657

<210> 103
 <211> 726
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (664)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (673)..(675)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (676)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (694)..(726)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> misc_feature
 <222> (1)..(726)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 103
 gaggtgcagc tgggtgcagag cggcgccgag gtgaagaagc ccggcgagag cctgaagatc 60
 agctgcaagg gcagcggcta cagcttcacc agctactgga tcggctgggt gaggcagatg 120
 cccggcaagg gcctggagtg gatgggctgg atcgaccctt acaggagcga gatcaggtac 180
 agccccagct tccagggcca ggtgaccatc agcgccgaca agagcatcag caccgcctac 240
 ctgcagtgga gcagcctgaa ggccagcgac accgccatgt actactgcgc cagggtgagc 300
 agcgagccct tcgacagctg gggccagggc accctgggtga ccgtgagcag cgccagcacc 360
 aagggcccca gcgtgttccc cctggccccc agcagcaaga gcaccagcgg cggcaccgcc 420
 gccctgggct gcctgggtgaa ggactacttc cccgagcccg tgaccgtgag ctggaacagc 480
 ggcgccctga ccagcggcgt gcacaccttc cccgccgtgc tgacagagcag cggcctgtac 540
 agcctgagca gcgtgggtgac cgtgcccagc agcagcctgg gcaccagac ctacatctgc 600
 aacgtgaacc acaagcccag caacaccaag gtggacaaga ggggtggagcc caagagctgc 660
 gacaagaccc acacctgccc cccctgcccc gccccgagc tgctgggcgg cccagcgtg 720
 ttcctg 726

<210> 104
 <211> 639
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 104

agctacgtgc tgaccagcc cccagcgtg agcgtggccc ccggcaagac cgccaggatc	60
acctgcagcg gcgacaagct gggcgaccac tacgcctact ggtaccagca gaagcccggc	120
caggcccccg tgctggtgat ctacgacgac agcaagaggc ccagcggcat ccccgagagg	180
ttcagcggca gcaacagcgg caacaccgcc accctgacca tcagcagggt ggaggccggc	240
gacgaggccg actactactg cgccacctgg accttcgagg gcgactacgt gttcggcggc	300
ggcaccaagc tgaccgtgct gggccagccc aaggccgccc ccagcgtgac cctgttcccc	360
cccagcagcg aggagctgca ggccaacaag gccaccctgg tgtgcctgat cagcgacttc	420
taccccggcg ccgtgaccgt ggcctggaag gccgacagca gccccgtgaa ggccggcgtg	480
gagaccacca ccccgagcaa gcagagcaac aacaagtacg ccgccagcag ctacctgagc	540
ctgacccccg agcagtggaa gagccacagg agctacagct gccaggtgac ccacgagggc	600
agcaccgtgg agaagaccgt ggccccacc gagtgcagc	639

<210> 105

<211> 756

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (694)..(756)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (703)..(705)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (706)..(756)

<223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (724)..(756)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> misc_feature
 <222> (1)..(756)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 105
 caggtgcagc tgcagcagag cggccccggc ctggtgaagc ccagccagac cctgagcctg 60
 acctgcgcca tcagcggcga cagcgtgagc agcaacaccg ccgcctggaa ctggatcagg 120
 cagagcccca gcaggggcct ggagtggctg ggcgtgatct actacaggag caagtgttac 180
 aacgactacg ccgtgagcgt gaagagcagg atcaccatca accccgacac cagcaagaac 240
 cagttcagcc tgcagctgaa cagcgtgacc cccgaggaca ccgccgtgta ctactgcgcc 300
 aggagcgtgc ccggcggcga ccccgccctg gagcacgcct tcgcctactg gggcaggggc 360
 accctgggtga ccgtgagcag cgccagcacc aaggggccca gcgtgttccc cctggcccc 420
 agcagcaaga gcaccagcgg cggcaccgcc gccctgggct gcctggtgaa ggactacttc 480
 cccgagcccc tgaccgtgag ctggaacagc ggcgccctga ccagcggcgt gcacaccttc 540
 cccgccgtgc tgcagagcag cggcctgtac agcctgagca gcgtggtgac cgtgcccagc 600
 agcagcctgg gcacccagac ctacatctgc aacgtgaacc acaagcccag caacaccaag 660
 gtggacaaga ggggtggagcc caagagctgc gacaagaccc acacctgccc cccctgcccc 720
 gcccccgagc tgctgggcgg cccagcgtg ttcctg 756

<210> 106
 <211> 639
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

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<400> 106
agctacgtgc tgaccagcc cccagcgtg agcgtggccc ccggcaagac cgccaggatc      60
acctgcagcg gcgacaacct gggcacctac tacgtggagt ggtaccagca gaagcccggc    120
caggcccccg tgctggtgat ctacgacgac agcgacaggc ccagcggcat ccccgagagg    180
ttcagcggca gcaacagcgg caacaccgcc accctgacca tcagcagggt ggaggccggc    240
gacgaggccg actactactg cgccagcttc gccagctgga gcgacagcgt gttcggcggc    300
ggcaccaagc tgaccgtgct gggccagccc aaggccgccc ccagcgtgac cctgttcccc    360
cccagcagcg aggagctgca ggccaacaag gccaccctgg tgtgcctgat cagcgacttc    420
taccggcg ccgtgaccgt ggcctggaag gccgacagca gcccgtgaa ggccggcgtg     480
gagaccacca cccagcaa gcagagcaac aacaagtacg ccgccagcag ctacctgagc     540
ctgacccccg agcagtggaa gagccacagg agctacagct gccaggtgac ccacgagggc    600
agcaccgtgg agaagaccgt ggccccacc gagtgcagc                             639
```

```
<210> 107
<211> 642
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"
```

```
<220>
<221> misc_feature
<222> (610)..(642)
<223> /note="This region may be absent in its entirety"
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```
<220>
<221> misc_feature
<222> (628)..(642)
<223> /note="This region may be absent in its entirety"
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```
<220>
<221> source
<223> /note="See specification as filed for detailed description of
      substitutions and preferred embodiments"
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```
<400> 107
```

acctgcaccg tgagcggcgg cagcatcagc agcggcgagt actactggaa ctggatcagg	60
cagcaccgcc gcaagggcct ggagtggatc ggctacatct actacagcgg cagcacctac	120
tacaacccca gcctgaagag caggggtgacc atcagcgtgg acaccagcaa gaaccagttc	180
agcctgaagc tgagcagcgt gaccgccgcc gacaccgccg tgtactactg cgccaggag	240
agcgtggccg gcttcgacta ctggggccag ggcaccctgg tgaccgtgag cagcgccagc	300
accaagggcc ccagcgtggt ccccctggcc ccctgcagca ggagcaccag cgagagcacc	360
gccgccctgg gctgcctggt gaaggactac ttccccgagc ccgtgaccgt gagctggaac	420
agcggcgccc tgaccagcgg cgtgcacacc ttccccgccg tgctgcagag cagcggcctg	480
tacagcctga gcagcgtggt gaccgtgccc agcagcaact tcggcaccca gacctacacc	540
tgcaacgtgg accacaagcc cagcaacacc aaggtggaca agaccgtgga gaggaagtgc	600
tgctgtggagt gccccccctg ccccgcccc cccgtggccg gc	642

<210> 108

<211> 645

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 108

gagatcgtgc tgaccagag ccccggcacc ctgagcctga gccccggcga gagggccacc	60
ctgagctgca gggccagcca gagcgtgagc agcagctacc tggcctggta ccagcagaag	120
cccggccagg cccccaggct gctgatctac ggcaccagca gcagggccac cggcatcccc	180
gacaggttca gcggcagcgg cagcggcacc gacttcaccc tgaccatcag caggctggag	240
cccgaggact tcgccgtgta ctactgccag cagtacggca gcagcccat caccttcggc	300
cagggcacca ggctggagat caagaggacc gtggccgccc ccagcgtggt catcttcccc	360
cccagcgacg agcagctgaa gagcggcacc gccagcgtgg tgtgcctgct gaacaacttc	420
taccccaggg aggccaaggt gcagtggaag gtggacaacg ccctgcagag cggcaacagc	480
caggagagcg tgaccagca ggacagcaag gacagcacct acagcctgag cagcaccttg	540
accctgagca aggccgacta cgagaagcac aaggtgtacg cctgcgaggt gaccaccag	600

ggcctgagca gccccgtgac caagagcttc aacaggggagc agtgc

645

<210> 109

<211> 723

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (661)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (670)..(672)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (673)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (691)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(723)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 109

gaggtgcagc tggtgcagag cggcgccgag gtgaagaagc ccggcagcag cgtgaagggtg 60

agctgcaagg ccagcggcgg caccttcagc agctacgcca tcagctgggt gaggcaggcc 120

cccggccagg gcctggagt gatgggcggc atcggccct tcttcggcac cgccaactac 180

gcccagaagt tccagggcag ggtgaccatc accgccgacg agagcaccag caccgcctac	240
atggagctga gcagcctgag gagcgaggac accgccgtgt actactgcgc cagggaacacc	300
ccctacttcg actactgggg ccagggcacc ctggtgaccg tgagcagcgc cagcaccaag	360
ggccccagcg tggtccccct ggccccagc agcaagagca ccagcggcgg caccgccgcc	420
ctgggctgcc tggtgaagga ctacttcccc gagcccgtga ccgtgagctg gaacagcggc	480
gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc	540
ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagacctc catctgcaac	600
gtgaaccaca agcccagcaa caccaaggtg gacaagaggg tggagcccaa gagctgcgac	660
aagaccaca cctgcccccc ctgccccgcc cccgaggccg ccggcggccc cagcgtgttc	720
ctg	723

<210> 110

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 110

agctacgagc tgaccagcc cctgagcgtg agcgtggccc tgggccagac cgccaggatc	60
acctgcagcg gcgacagcat cccaactac tacgtgtact ggtaccagca gaagcccggc	120
caggcccccg tgctggtgat ctacgacgac agcaacaggc ccagcggcat ccccgagagg	180
ttcagcggca gcaacagcgg caacaccgcc accctgacca tcagcagggc ccaggccggc	240
gacgaggccg actactactg ccagagcttc gacagcagcc tgaacgccga ggtgttcggc	300
ggcggcacca agctgaccgt gctgggccag cccaaggccg ccccagcgt gaccctgttc	360
ccccccagca gcgaggagct gcaggccaac aaggccaccc tggtgtgcct gatcagcgac	420
ttctaccccc gcgccgtgac cgtggcctgg aaggccgaca gcagccccgt gaaggccggc	480
gtggagacca ccacccccag caagcagagc aacaacaagt acgccgccag cagctacctg	540
agcctgaccc ccgagcagtg gaagagccac aggagctaca gctgccaggt gaccacagag	600

ggcagcaccg tggagaagac cgtggccccc accgagtgc gc

642

<210> 111
<211> 729
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature
<222> (667)..(729)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (676)..(678)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (679)..(729)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (697)..(729)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(729)
<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 111
gaggtgaagc tggaggagag cggcggcggc ctggtgcagc ccggcggcag catgaagctg 60
agctgcgccg ccagcggcctt caccttcagc gacgcctgga tggactgggt gaggcagagc 120
cccgagaagg gcctggagtg ggtggccgag atcaggagca aggccagcaa ccacgccacc 180

tactacgccg agagcgtgaa gggcagggtc accatcagca gggacgacag caagagcagc	240
gtgtacctgc agatgaacag cctgagggcc gaggacaccg gcatctacta ctgcaccagg	300
tggaggaggt tcttcgacag ctggggccag ggcaccaccc tgaccgtgag cagcgccagc	360
accaagggcc ccagcgtgtt ccccctggcc cccagcagca agagcaccag cggcggcacc	420
gccgccctgg gctgcctggt gaaggactac ttccccgagc ccgtgaccgt gagctggaac	480
agcggcgccc tgaccagcgg cgtgcacacc ttccccgccg tgctgcagag cagcggcctg	540
tacagcctga gcagcgtggt gaccgtgccc agcagcagcc tgggcaccca gacctacatc	600
tgcaacgtga accacaagcc cagcaacacc aaggtggaca agaaggtgga gccaagagc	660
tgcgacaaga cccacacctg cccccctgc cccgcccccg agctgctggg cggccccagc	720
gtgttcctg	729

<210> 112

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 112

cagatcgtgc tgagccagag ccccgccatc ctgagcgcca gccccggcga gaaggtgacc	60
atgacctgca gggccagcag cagcgtgagc tacatgcact ggtaccagca gaagcccggc	120
agcagcccca agccctggat ctacgccacc agcaacctgg ccagcggcgt gcccgtaggg	180
ttcagcggca gcggcagcgg caccagctac agcctgacca tcagcagggt ggaggccgag	240
gacgccgcca cctactactg ccagcagtgg agcagcaacc ccctgacctt cggcgccggc	300
accaagctgg agctgaagag gaccgtggcc gccccagcg tgttcatctt cccccccagc	360
gacgagcagc tgaagagcgg caccgccagc gtggtgtgcc tgctgaacaa cttctacccc	420
agggaggcca aggtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggag	480
agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg	540
agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg	600
agcagccccg tgaccaagag cttcaacagg ggcgagtgc	639

<210> 113
 <211> 738
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (676)..(738)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (685)..(687)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (688)..(738)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (706)..(738)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(738)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 113	
caggtgcagc tggtgcagag cggcgccgag ctgaagaagc ccggcgccag cgtgaaggtg	60
agctgcaaga gcagcggcta ccacttcacc agctactgga tgcactgggt gaagcaggcc	120
cccggccagg gcctggagtg gatcggcgtg atccaccca acagcggcag catcaactac	180
aacgagaagt tcgagagcag ggtgaccatc accgtggaca agagcaccag caccgcctac	240

atggagctga gcagcctgag gagcgaggac accgccgtgt actactgcgc cggcgagagg	300
gacagcaccg aggtgctgcc catggactac tggggccagg gcaccaccgt gaccgtgagc	360
agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcaccg ccgccctggg ctgcctggtg aaggactact tccccgagcc cgtgaccgtg	480
agctggaaca gcggcgccct gaccagcggc gtgcacacct tccccgccgt gctgcagagc	540
agcggcctgt acagcctgag cagcgtggtg accgtgcccc gcagcagcct gggcacccag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaggggtggag	660
cccaagagct gcgacaagac ccacacctgc cccccctgcc ccgccccga gctgctgggc	720
ggccccagcg tgttcctg	738

<210> 114

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 114

gacgtgcaga tcaccagag ccccagcagc ctgagcgcca gcctgggcga gagggccacc	60
atcaactgca gggccagcaa gagcatcaac aagtacctgg cctggtacca gcagaagccc	120
ggcaaggccc ccaagctgct gatctacagc ggcagcacc tgcagagcgg catccccgcc	180
aggttcagcg gcagcggcag cggcaccgac ttaccctga ccatcagcag cctggagccc	240
gaggacttcg ccatgtacta ctgccagcag cacaacgagt accccctgac cttcggccag	300
ggcaccaagc tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc	360
agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac	420
cccagggagg ccaaggtgca gtggaagggtg gacaacgccc tgcagagcgg caacagccag	480
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc	540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc	600
ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc	642

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<210> 115
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polynucleotide"

<220>
<221> misc_feature
<222> (676)..(738)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (685)..(687)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (688)..(738)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (706)..(738)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(738)
<223> /note="Variant nucleotides given in the sequence have no
      preference with respect to those in the annotations
      for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
      substitutions and preferred embodiments"

<400> 115
gaggtgcagc tggtggagag cggcggcggc ctggtgcagc ccggcaggag cctgaggctg      60
agctgcgccg ccagcggctt caccttcgac gactacgcca tgcactgggt gaggcaggcc      120
cccggcaagg gcctggagtg ggtgagcgcc atcacctgga acagcggcca catcgactac      180
gccgacagcg tggagggcag gttcaccatc agcagggaca acgccaagaa cagcctgtac      240

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ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc caaggtgagc	300
tacctgagca ccgccagcag cctggactac tggggccagg gcaccctggt gaccgtgagc	360
agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcaccg ccgccctggg ctgcctggtg aaggactact tccccgagcc cgtgaccgtg	480
agctggaaca gcggcgccct gaccagcggc gtgcacacct tccccgccgt gctgcagagc	540
agcggcctgt acagcctgag cagcgtggtg accgtgcccc gcagcagcct gggcaccag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gaaggtggag	660
cccaagagct gcgacaagac ccacacctgc cccccctgcc ccgccccga gctgctgggc	720
ggccccagcg tgttcctg	738

<210> 116

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 116

gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagggtgacc	60
atcacctgca gggccagcca gggcatcagg aactacctgg cctggtacca gcagaagccc	120
ggcaaggccc ccaagctgct gatctacgcc gccagcacc tgagagcgg cgtgccagc	180
aggttcagcg gcagcggcag cggcaccgac ttaccctga ccatcagcag cctgcagccc	240
gaggacgtgg ccacctacta ctgccagagg tacaacaggg cccctacac cttcggccag	300
ggcaccaagg tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc	360
agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac	420
cccagggagg ccaaggtgca gtggaaggtg gacaacgccc tgagagcgg caacagccag	480
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc	540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc	600
ctgagcagcc ccgtgaccaa gagcttcaac aggggagcagc gc	642

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<210> 117
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

<220>
<221> misc_feature
<222> (673)..(735)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (682)..(684)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (685)..(735)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (703)..(735)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(735)
<223> /note="Variant nucleotides given in the sequence have no
        preference with respect to those in the annotations
        for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
        substitutions and preferred embodiments"

<400> 117
gaggtgaagc tggaggagag cggcggcggc ctggtgcagc ccggcggcag catgaagctg      60
agctgcgtgg ccagcggctt catcttcagc aaccactgga tgaactgggt gaggcagagc      120
cccgagaagg gcctggagtg ggtggccgag atcaggagca agagcatcaa cagcgccacc      180
cactacgccg agagcgtgaa gggcaggttc accatcagca gggacgacag caagagcgcc      240
gtgtacctgc agatgaccga cctgaggacc gaggacaccg gcgtgtacta ctgcagcagg      300

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aactactacg gcagcaccta cgactactgg ggccagggca ccaccctgac cgtgagcagc	360
gccagcacca agggccccag cgtgttcccc ctggccccc gcagcaagag caccagcggc	420
ggcaccgccg ccctgggctg cctgggtgaag gactacttcc ccgagcccgt gaccgtgagc	480
tggaacagcg gcgccctgac cagcggcgtg cacaccttcc ccgccgtgct gcagagcagc	540
ggcctgtaca gcctgagcag cgtggtgacc gtgcccagca gcagcctggg caccagacc	600
tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc	660
aagagctgcg acaagacca cacctgcccc ccctgccccg ccccgagct gctgggcggc	720
cccagcgtgt tcctg	735

<210> 118

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 118

gacatcctgc tgaccagag ccccgccatc ctgagcgtga gcccggcga gagggtgagc	60
ttcagctgca gggccagcca gttcgtgggc agcagcatcc actggtacca gcagaggacc	120
aacggcagcc ccaggctgct gatcaagtac gccagcgaga gcatgagcgg catccccagc	180
aggttcagcg gcagcggcag cggcaccgac ttcaccctga gcatcaacac cgtggagagc	240
gaggacatcg ccgactacta ctgccagcag agccacagct ggcccttcac cttcggcagc	300
ggcaccaacc tggaggtgaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc	360
agcgacgagc agctgaagag cggcaccgcc agcgtgggtg gcctgctgaa caacttctac	420
cccagggagg ccaaggtgca gtggaagggtg gacaacgccc tgcagagcgg caacagccag	480
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc	540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc	600
ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc	642

<210> 119


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<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

<220>
<221> misc_feature
<222> (658)..(720)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (667)..(669)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (670)..(720)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (688)..(720)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(720)
<223> /note="Variant nucleotides given in the sequence have no
        preference with respect to those in the annotations
        for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
        substitutions and preferred embodiments"

<400> 119
agcaagctgc aggtgcagct ggtggagagc ggcggcggcg tggtgcagcc cggcaggagc      60
ctgaggctga gctgcgccgc cagcggcttc atcttcagca gctacgccat gcaactgggtg      120
aggcaggccc ccggcaacgg cctggagtgg gtggccttca tgagctacga cggcagcaac      180
aagaagtacg ccgacagcgt gaagggcagg ttcacatca gcagggacaa cagcaagaac      240
accctgtacc tgcagatgaa cagcctgagg gccgaggaca ccgccgtgta ctactgcgcc      300

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agggacaggg gcatcgccgc cggcggcaac tactactact acggcatgga cgtgtggggc	360
cagggcacca ccgtgaccgt gagcagcgcc agcaccaagg gccccagcgt gttccccctg	420
gccccagca gcaagagcac cagcggcggc accgccgcc tgggctgcct ggtgaaggac	480
tacttccccg agcccgtgac cgtgagctgg aacagcggcg ccctgaccag cggcgtgcac	540
accttccccg ccgtgctgca gagcagcggc ctgtacagcc tgagcagcgt ggtgaccgtg	600
cccagcagca gcctgggcac ccagacctac atctgcaacg tgaaccacaa gcccagcaag	660
accacacct gccccccctg ccccgcccc gagctgctgg gcggccccag cgtgttcctg	720

<210> 120

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 120

gccggcagcg agatcgtgct gacccagagc cccgccaccc tgagcctgag ccccggcgag	60
agggccaccc tgagctgcag ggccagccag agcgtgtaca gctacctggc ctggtaccag	120
cagaagcccc gccaggcccc caggctgctg atctacgacg ccagcaacag ggccaccggc	180
atccccgcca ggttcagcgg cagcggcagc ggcaccgact tcaccctgac catcagcagc	240
ctggagcccc aggacttcgc cgtgtactac tgccagcaga ggagcaactg gcccccttc	300
accttcggcc ccggcaccaa ggtggacatc aagaggaccg tggccgcccc cagcgtgttc	360
atcttcccc ccagcgacga gcagctgaag agcggcaccg ccagcgtggt gtgcctgctg	420
aacaacttct accccaggga ggccaagggt cagtgggaagg tggacaacgc cctgcagagc	480
ggcaacagcc aggagagcgt gaccgagcag gacagcaagg acagcaccta cagcctgagc	540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaggtg	600
accaccagg gcctgagcag ccccgtagcc aagagcttca acaggggcga gtgc	654

<210> 121

<211> 735

<212> DNA

<213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (673)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (682)..(684)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (685)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (703)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(735)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 121
 gaggtgcagc tgggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtgaagggtg 60
 agctgcaagg ccagcggcta caccttcacc agccacggca tcagctgggt gaggcaggcc 120
 cccggccagg gcctggactg gatgggctgg atcagcccct acagcgcaa caccaactac 180
 gccagaagc tgcagggcag ggtgaccatg accaccgaca ccagcaccag caccgcctac 240
 atggagctga gcagcctgag gagcgaggac accgccgtgt actactgcgc cagggtgggc 300
 agcggcccct actactacat ggacgtgtgg ggccagggca ccctggtgac cgtgagcagc 360
 gccagcacca agggccccag cgtgttcccc ctggccccca gcagcaagag caccagcggc 420

ggcaccgccg ccctgggctg cctggtgaag gactacttcc ccgagcccgt gaccgtgagc	480
tggaacagcg gcgccctgac cagcggcgtg cacaccttcc ccgccgtgct gcagagcagc	540
ggcctgtaca gcctgagcag cgtggtgacc gtgcccagca gcagcctggg caccagacc	600
tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagaa ggtggagccc	660
aagagctgcg acaagaccca cacctgcccc ccctgccccg ccccgaggc cgccggcggc	720
cccagcgtgt tcctg	735

<210> 122
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 122	
cagagcgcgc tgaccagcc caggagcgtg agcggcagcc ccggccagag cgtgaccatc	60
agctgcaccg gcaccagcag cagcgtgggc gacagcatct acgtgagctg gtaccagcag	120
caccccgga aggccccaa gctgatgctg tacgacgtga ccaagaggcc cagcggcgtg	180
cccgacaggt tcagcggcag caagagcggc aacaccgcca gcctgaccat cagcggcctg	240
caggccgagg acgaggccga ctactactgc tacagctacg ccggcaccga caccctgttc	300
ggcggcggca ccaaggtgac cgtgctgggc cagcccaagg ccgccccag cgtgaccctg	360
ttcccccca gcagcgagga gctgcaggcc aacaaggcca ccctggtgtg cctgatcagc	420
gacttctacc ccggcgccgt gaccgtggcc tggaaggccg acagcagccc cgtgaaggcc	480
ggcgtggaga ccaccacccc cagcaagcag agcaacaaca agtacgccgc cagcagctac	540
ctgagcctga ccccgagca gtggaagagc cacaggagct acagctgcca ggtgaccac	600
gagggcagca ccgtggagaa gaccgtggcc cccaccgagt gcagc	645

<210> 123
 <211> 735
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (673)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (682)..(684)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (685)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (703)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(735)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 123
 caggtgcagc tgcaggagag cggccccggc ctggtgaagc ccagcgagac cctgagcctg 60
 acctgcagcg tgagcggcgg cagcatcatc agcaggagca gctactgggg ctggatcagg 120
 cagccccccg gcaagggcct ggagtggatc ggcggcatct accacagcgg caacacctac 180
 gacaacccca gcctgaagag caggctgacc atgagcgtgg acaccagcaa gaaccagttc 240
 agcctgaacc tgaggagcgt gaccgccgcc gacaccgccg tgtactactg cgccaggatc 300
 gtgcccggcg gcgacgcctt cgacatctgg ggccagggca ccatggtgac cgtgagcagc 360
 gccagcacca agggccccag cgtgttcccc ctggccccca gcagcaagag caccagcggc 420

ggcaccgccg ccctgggctg cctggtgaag gactacttcc ccgagcccgt gaccgtgagc	480
tggaacagcg gcgccctgac cagcggcgtg cacaccttcc ccgccgtgct gcagagcagc	540
ggcctgtaca gcctgagcag cgtggtgacc gtgcccagca gcagcctggg caccagacc	600
tacatctgca acgtgaacca caagcccagc aacaccaagg tggacaagag ggtggagccc	660
aagagctgcg acaagaccca cacctgcccc ccctgccccg ccccgagct gctgggcggc	720
cccagcgtgt tcctg	735

<210> 124
 <211> 639
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 124	
gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagggtgacc	60
gcctgcaggg ccagccagag cgtgggcacc tacctgaact ggtaccagca gaagaggggc	120
aaggccccca agctgctgat cttcgccgcc agcagcctgc agagcggcgt gccagcagg	180
ttcagcggca gcggcagcgg caccgacttc accctgacca tcagcagcct gcagcccag	240
gacttcgcca cctactactg ccagcagagc tacagcagcc ccccccacctt cggccagggc	300
accaaggtgg agatcaagag gaccgtggcc gccccagcg tgttcatctt cccccagc	360
gacgagcagc tgaagagcgg caccgccagc gtggtgtgcc tgctgaacaa cttctacccc	420
agggaggcca aggtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggag	480
agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg	540
agcaaggccg actacgagaa gcacaaggctg tacgcctgcg aggtgaccca ccagggcctg	600
agcagccccg tgaccaagag cttcaacagg ggcgagtgc	639

<210> 125
 <211> 726
 <212> DNA
 <213> Artificial Sequence

<220>

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (664)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (673)..(675)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (676)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (694)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(726)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 125
 gaggtgcagc tggtggagag cggcggcggc ctgatccagc ccggcggcag cctgaggctg 60
 agctgcgccg ccagcggctt caccttcagc aactacgcca tgagctgggt gaggcaggcc 120
 cccggcaagg gcctggagtg ggtgagcagc atcagcagcg gcggcagcac ctactacccc 180
 gacagcgtga agggcagggt caccatcagc agggacaaca gcaagaacac cctgtacctg 240
 cagatgaaca gcctgagggc cgaggacacc gccgtgtact actgcgccag gtactactac 300
 ggccagtact tcgacttctg gggccagggc accctgggtga ccgtgagcag cgccagcacc 360
 aagggcccca gcgtgttccc cctggccccc agcagcaaga gcaccagcgg cggcaccgcc 420
 gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgag ctggaacagc 480

ggcgccctga ccagcggcgt gcacaccttc cccgccgtgc tgcagagcag cggcctgtac	540
agcctgagca gcgtgggtgac cgtgcccagc agcagcctgg gcacccagac ctacatctgc	600
aacgtgaacc acaagcccag caacaccaag gtggacaaga ggggtggagcc caagagctgc	660
gacaagaccc acacctgccc cccctgcccc gccccgagc tgctgggcgg cccagcgtg	720
ttcctg	726

<210> 126
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 126	
gacatcgtga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagggtgacc	60
atcacctgca aggccagcca ggacgtgagc accaccgtgg cctggtacca gcagaagccc	120
ggcaaggccc ccaagctgct gatctacagc gccagctaca ggagcaccgg cgtgcccagc	180
aggttcagcg gcagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc	240
gaggacttcg ccgtgtacta ctgccagcag cactacagca cccccctgac cttcggcggc	300
ggcaccaagg tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc	360
agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac	420
cccagggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag	480
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc	540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc	600
ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc	642

<210> 127
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (661)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (669)..(672)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (673)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (691)..(723)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(723)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 127

gaggtgcagc tgggtgcagag cggcgccgag gtgaagaagc ccggcagcag cgtgaaggtg 60

agctgcaagg ccagcggcgg caccttcagc agctacgcca tcagctgggt gaggcaggcc 120

cccggccagg gcctggagtg gatgggcggc atcggcccct tcttcggcac cgccaactac 180

gcccagaagt tccagggcag ggtgaccatc accgccgacg agagcaccag caccgcctac 240

atggagctga gcagcctgag gagcgaggac accgccgtgt actactgcgc cagggacacc 300

ccctacttcg actactgggg ccagggcacc ctgggtgaccg tgagcagcgc cagcaccaag 360

ggccccagcg tgttccccct ggcccccagc agcaagagca ccagcggcgg caccgccgcc 420

ctgggctgcc tgggtgaagga ctacttcccc gagcccgtga ccgtgagctg gaacagcggc 480

gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc	540
ctgagcagcg tggtagaccgt gccagcagc agcctgggca cccagaccta catctgcaac	600
gtgaaccaca agcccagcaa caccaaggtg gacaagaggg tggagcccaa gagctgcgac	660
aagaccaca cctgcccccc ctgccccgcc cccgaggccg ccggcggccc cagcgtgttc	720
ctg	723

<210> 128
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 128	
agctacgagc tgaccagcc cctgagcgtg agcgtggccc tgggccagac cgccaggatc	60
acctgcagcg gcgacagcat ccccaactac tacgtgtact ggtaccagca gaagcccggc	120
caggcccccg tgctgggtgat ctacgacgac agcaacaggc ccagcggcat cccgagagg	180
ttcagcggca gcaacagcgg caacaccgcc accctgacca tcagcagggc ccaggccggc	240
gacgaggccg actactactg ccagagcttc gacagcagcc tgaacgccga ggtgttcggc	300
ggcggcacca agctgaccgt gctggggccag cccaaggccg cccccagcgt gaccctgttc	360
ccccccagca gcgaggagct gcaggccaac aaggccaccc tgggtgtgcct gatcagcgac	420
ttctaccccc gcgccgtgac cgtggcctgg aaggccgaca gcagccccgt gaaggccggc	480
gtggagacca ccacccccag caagcagagc aacaacaagt acgccgccag cagctacctg	540
agcctgaccc ccgagcagtg gaagagccac aggagctaca gctgccaggt gaccacagag	600
ggcagcaccg tggagaagac cgtggccccc accgagtgcg gc	642

<210> 129
 <211> 705
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<220>

<221> misc_feature

<222> (673)..(705)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (691)..(705)

<223> /note="This region may be absent in its entirety"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 129

caggtgcagc tgcaggagag cggccccggc ctggtgaagc ccagcgagac cctgagcctg	60
acctgcgccg tgagcggcca cagcatcagc cacgaccacg cctggagctg ggtgaggcag	120
ccccccggcg agggcctgga gtggatcggc ttcacagct acagcggcat caccaactac	180
aaccccagcc tgcagggcag ggtgaccatc agcagggaca acagcaagaa caccctgtac	240
ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc caggagcctg	300
gccaggacca ccgccatgga ctactggggc gagggcaccc tggtagaccgt gagcagcgcc	360
agcaccaagg gccccagcgt gttccccctg gccccagca gcaagagcac cagcggcggc	420
accgccgccc tgggctgcct ggtgaaggac tacttccccg agcccgtgac cgtgagctgg	480
aacagcggcg ccctgaccag cggcgtgcac accttccccg ccgtgctgca gagcagcggc	540
ctgtacagcc tgagcagcgt ggtgaccgtg cccagcagca acttcggcac ccagacctac	600
acctgcaacg tggaccacaa gcccagcaac accaaggtgg acaagaccgt ggagaggaag	660
agctgcgtgg agtgcccccc ctgccccgcc cccccgtgg ccggc	705

<210> 130

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 130
gacatccaga tgaccagag ccccagcagc ctgagcgcca gcgtgggcga cagcgtgacc 60
atcacctgcc aggccagcac cgacatcagc agccaccta actggtacca gcagaagccc 120
ggcaaggccc ccgagctgct gatctactac ggacagccacc tgctgagcgg cgtgcccagc 180
aggttcagcg gcagcggcag cggcaccgac ttcaccttca ccatcagcag cctggaggcc 240
gaggacgccg ccacctacta ctgcggccag ggcaacaggc tgccttacac cttcggccag 300
ggcaccaagg tggagatcga gaggaccgtg gccgccccca gcgtgttcat cttccccccc 360
agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac 420
cccagggagg ccaaggtgca gtggaagggtg gacaacgccc tgacagcgg caacagccag 480
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600
ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 131
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> misc_feature
<222> (661)..(723)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (670)..(672)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (673)..(723)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature

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<222> (691)..(723)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(723)
<223> /note="Variant nucleotides given in the sequence have no
        preference with respect to those in the annotations
        for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
        substitutions and preferred embodiments"

<400> 131
gaggtgcagc tggtggagag cggcggcggc ctggtgcagc ccggcaggag cctgaggctg      60
agctgcgccg ccagcagggt caccttcgac gactacgcca tgcactgggt gaggcaggcc      120
cccggcaagg gcctggagtg ggtgagcggc atcagctgga acagcggcag gatcggctac      180
gccgacagcg tgaagggcag gttcaccatc agcagggaca acgccgagaa cagcctgttc      240
ctgcagatga acggcctgag ggccgaggac accgccctgt actactgcgc caagggcagg      300
gacagcttcg acatctgggg ccagggcacc atggtgaccg tgagcagcgc cagcaccaag      360
ggccccagcg tgttccccct ggccccagc agcaagagca ccagcggcgg caccgccgcc      420
ctgggctgcc tggtgaagga ctacttcccc gagcccgtga ccgtgagctg gaacagcggc      480
gccctgacca gcggcgtgca caccttcccc gccgtgctgc agagcagcgg cctgtacagc      540
ctgagcagcg tggtgaccgt gcccagcagc agcctgggca cccagaccta catctgcaac      600
gtgaaccaca agcccagcaa caccaaggtg gacaagaagg tggagcccaa gagctgcgac      660
aagaccaca cctgcccccc ctgccccgcc cccgagctgc tgggcggccc cagcgtgttc      720
ctg                                                                    723

<210> 132
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
        polynucleotide"

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<400> 132
gacatccaga tgacccagag ccccagcagc gtgagcgcca gcgtgggcga cagggtgacc 60
atcacctgca gggccagcca gggcatcagc agctggctgg cctggtacca gcagaagccc 120
ggcaaggccc ccaagctgct gatctacggc gccagcagcc tggagagcgg cgtgcccagc 180
aggttcagcg gcagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc 240
gaggacttcg ccagctacta ctgccagcag gccaacagct tcccctacac cttcggccag 300
ggcaccaagc tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc 360
agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac 420
cccagggagg ccaaggtgca gtggaaggtg gacaacgccc tgcagagcgg caacagccag 480
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc 540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc 600
ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc 642

<210> 133
<211> 738
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> misc_feature
<222> (676)..(738)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (685)..(687)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (688)..(738)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (706)..(738)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(738)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 133

gaggtgcagc tggtggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg	60
agctgcgccg ccagcggctt caccttcagc agcagctgga tgaactgggt gaggcaggcc	120
cccggcaagg gcctggagtg ggtgggcagg atctaccccg gcgacggcga caccaactac	180
aacgtgaagt tcaagggcag gttcaccatc agcagggacg acagcaagaa cagcctgtac	240
ctgcagatga acagcctgaa gaccgaggac accgccgtgt actactgcgc caggagcggc	300
ttcatcacca ccgtgagggg cttcgactac tggggccagg gcaccctggt gaccgtgagc	360
agcgccagca ccaagggccc cagcgtgttc cccctggccc ccagcagcaa gagcaccagc	420
ggcggcaccg ccgccctggg ctgcctgggt aaggactact tccccgagcc cgtgaccgtg	480
agctggaaca gcggcgccct gaccagcggc gtgcacacct tccccgccgt gctgcagagc	540
agcggcctgt acagcctgag cagcgtgggt accgtgcccc gcagcagcct gggcacccag	600
acctacatct gcaacgtgaa ccacaagccc agcaacacca aggtggacaa gagggtggag	660
ccaagagct gcgacaagac ccacacctgc cccccctgcc ccgccccga gctgctgggc	720
ggccccagcg tggttcctg	738

<210> 134

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 134

gagatcgtgc tgacccagag ccccgacttc cagagcgtga cccccaagga gaaggtgacc	60
atcacctgca gggccagcga gagcgtggac accttcggca tcagcttcat gaactggttc	120
cagcagaagc ccgaccagag ccccaagctg ctgatccacg aggccagcaa ccagggcagc	180
ggcgtgcca gcaggttcag cggcagcggc agcggcaccg acttcaccct gaccatcaac	240
agcctggagg ccgaggacgc cgccacctac tactgccagc agagcaagga ggtgcccttc	300
accttcggcg gcggcaccaa ggtggagatc aagaggaccg tggccgcccc cagcgtgttc	360
atcttcccc ccagcgacga gcagctgaag agcggcaccg ccagcgtggt gtgcctgctg	420
aacaacttct accccagga ggccaaggtg cagtggaagg tggacaacgc cctgcagagc	480
ggcaacagcc aggagagcgt gaccgagcag gacagcaagg acagcaccta cagcctgagc	540
agcaccctga ccctgagcaa ggccgactac gagaagcaca aggtgtacgc ctgcgaggtg	600
accaccagg gcctgagcag ccccgtagacc aagagcttca acaggggcga gtgc	654

<210> 135
 <211> 726
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (664)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (673)..(675)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (676)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (694)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(726)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 135
 gaggtgcagc tggtggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg 60
 agctgcgccg ccagcggcctt cttcatcacc aacaactact ggggctgggt gaggcaggcc 120
 cccggcaagg gcctggagtg ggtgggctac atcagctaca gcggcagcac cagctacaac 180
 cccagcctga agagcagggt caccatcagc agggacacca gcaagaacac cttctacctg 240
 cagatgaaca gcctgagggc cgaggacacc gccgtgtact actgcgccag gaccggcagc 300
 agcggctact tcgacttctg gggccagggc accctggtga ccgtgagcag cgccagcacc 360
 aaggggccca gcgtgttccc cctggccccc agcagcaaga gcaccagcgg cggcaccgcc 420
 gccctgggct gcctggtgaa ggactacttc cccgagcccg tgaccgtgag ctggaacagc 480
 ggcgccctga ccagcggcgt gcacaccttc cccgccgtgc tgcagagcag cggcctgtac 540
 agcctgagca gcgtggtgac cgtgcccagc agcagcctgg gcacccagac ctacatctgc 600
 aacgtgaacc acaagcccag caacaccaag gtggacaaga aggtggagcc caagagctgc 660
 gacaagaccc acacctgccc cccctgcccc gccccgagc tgctgggcgg cccagcgtg 720
 ttcctg 726

<210> 136
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 136
 gacatccaga tgaccagag cccagcagc ctgagcgcca gcgtgggcga cagggtgacc 60

atcacctgca gggccagcga gagcgtggac gacctgctgc actggtacca gcagaagccc	120
ggcaaggccc ccaagctgct gatcaagtac gccagccaga gcatcagcgg cgtgcccagc	180
aggttcagcg gcagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc	240
gaggacttcg ccacctacta ctgccagcag ggcaacagcc tgcccaacac cttcggccag	300
ggcaccaagg tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc	360
agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac	420
cccagggagg ccaaggtgca gtggaagggtg gacaacgccc tgcagagcgg caacagccag	480
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc	540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc	600
ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc	642

<210> 137
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (685)..(717)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (703)..(717)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 137	
gaggtgcagc tggtgcagag cggcgccgag gtgaagaagc ccggcgccag cgtgaagggtg	60
agctgcaagg ccagcggcta caccttcacc gactacaaca tgcactgggt gaggcaggcc	120

cccgccagg gcctggagt gatgggcgag atcaaccca acagcggcgg cgccggctac	180
aaccagaagt tcaagggcag ggtgaccatg accaccgaca ccagcaccag caccgcctac	240
atggagctga ggagcctgag gagcgacgac accgccgtgt actactgcgc caggctgggc	300
tacgacgaca tctacgacga ctggtacttc gacgtgtggg gccagggcac caccgtgacc	360
gtgagcagcg ccagcaccaa gggccccagc gtgttcccc tggccccctg cagcaggagc	420
accagcgaga gcaccgccgc cctgggctgc ctggtgaagg actacttccc cgagcccgtg	480
accgtgagct ggaacagcgg cgccctgacc agcggcgtgc acaccttccc cgccgtgctg	540
cagagcagcg gcctgtacag cctgagcagc gtggtgaccg tgcccagcag caacttcggc	600
accagacct acacctgcaa cgtggaccac aagcccagca acaccaaggt ggacaagacc	660
gtggagagga agtgctgcgt ggagtgcccc ccctgccccg cccccccgt ggccggc	717

<210> 138

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 138

gacatccaga tgaccagag cccagcagc ctgagcgcca gcgtgggcga cagggtgacc	60
atcacctgca gggccagcca ggacatcagc aactacctga actggtacca gcagaagccc	120
ggcaaggccc ccaagctgct gatctactac accagcaggc tgctgagcgg cgtgcccagc	180
aggttcagcg gcagcggcag cggcaccgac ttcaccctga ccatcagcag cctgcagccc	240
gaggacttcg ccacctacta ctgccagcag ggcgacaccc tgccctacac cttcggcggc	300
ggcaccaagg tggagatcaa gaggaccgtg gccgccccca gcgtgttcat cttccccccc	360
agcgacgagc agctgaagag cggcaccgcc agcgtggtgt gcctgctgaa caacttctac	420
cccagggagg ccaaggtgca gtggaagggtg gacaacgccc tgcagagcgg caacagccag	480
gagagcgtga ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc	540
ctgagcaagg ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc	600
ctgagcagcc ccgtgaccaa gagcttcaac aggggcgagt gc	642

<210> 139
<211> 741
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature
<222> (679)..(741)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (688)..(690)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (691)..(741)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (709)..(741)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(741)
<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 139
gaggtgcagc tgctggagag cggcggcggc ctggtgcagc ccggcggcag cctgaggctg 60
agctgcgccg ccagcggcctt caccttcagc cactacatca tgatgtgggt gaggcaggcc 120
cccggcaagg gcctggagtg ggtgagcggc atctacagca gcggcggcat caccgtgtac 180
gccgacagcg tgaagggcag gttcaccatc agcagggaca acagcaagaa caccctgtac 240

ctgcagatga acagcctgag ggccgaggac accgccgtgt actactgcgc ctacaggagg	300
atcggcgtgc ccaggaggga cgagttcgac atctggggcc agggcaccat ggtgaccgtg	360
agcagcgcca gcaccaaggg ccccagcgtg ttccccctgg ccccagcag caagagcacc	420
agcggcggca ccgccgccct gggctgcctg gtgaaggact acttccccga gcccgtagacc	480
gtgagctgga acagcggcgc cctgaccagc ggcgtgcaca ctttccccgc cgtgctgcag	540
agcagcggcc tgtacagcct gagcagcgtg gtgaccgtgc ccagcagcag cctgggcacc	600
cagacctaca tctgcaacgt gaaccacaag cccagcaaca ccaaggtgga caagagggtg	660
gagcccaaga gctgcgacaa gaccacacc tgccccccct gccccgcccc cgagctgctg	720
ggcggcccca gcgtgttcct g	741

<210> 140

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 140

gacatccaga tgaccagag ccccagcacc ctgagcgcca gcgtgggcga cagggtgacc	60
atcacctgca gggccagcca gagcatcagc agctggctgg cctggtacca gcagaagccc	120
ggcaaggccc ccaagctgct gatctacaag gccagcacc tggagagcgg cgtgcccagc	180
aggttcagcg gcagcggcag cggcaccgag ttcaccctga ccatcagcag cctgcagccc	240
gacgacttcg ccacctacta ctgccagcag tacaacacct actggacctt cggccagggc	300
accaaggtgg agatcaagag gaccgtggcc gccccagcg tgttcatctt cccccccagc	360
gacgagcagc tgaagagcgg caccgccagc gtggtgtgcc tgctgaacaa cttctacccc	420
agggaggcca aggtgcagtg gaaggtggac aacgccctgc agagcggcaa cagccaggag	480
agcgtgaccg agcaggacag caaggacagc acctacagcc tgagcagcac cctgaccctg	540
agcaaggccg actacgagaa gcacaaggtg tacgcctgcg aggtgaccca ccagggcctg	600
agcagccccg tgaccaagag cttcaacagg ggcgagtgc	639

<210> 141
 <211> 2205
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 141
 atgtaccgga tgcagctgct gctgctcatt gccctgtctc tggccctggt caccaatagc 60
 gaagtccagc tgctggaatc tggcggcgga cttgttcaac ctggcggctc tctgagactg 120
 agctgtgccg cttccggctt caccttcagc cactatatca tgatgtgggt ccgacaggcc 180
 cctggcaaag gccttgaatg ggtgtccggc atctatagca gcggcggcat cacagtgtac 240
 gccgactctg tgaagggcag attcaccatc agccgggaca acagcaagaa caccctgtac 300
 ctgcagatga acagcctgag agccgaggac accgccgtgt actactgcgc ctatagaaga 360
 atcggcgtgc ccagacggga cgagttcgat atttggggcc agggcaccat ggtcaccgtg 420
 tctagcgcct ctacaaaggg ccctagcgtg ttccctctgg ctccctagcag caagagcaca 480
 agcggaggaa cagccgctct gggctgtctg gtcaaggact actttcccga gcctgtgacc 540
 gtgtcctgga atagcggagc actgacaagc ggcgtgcaca cttttccagc tgtgctgcaa 600
 agcagcggcc tgtactctct gagcagcgtg gtcacagtgc caagctctag cctgggcacc 660
 cagacctaca tctgcaatgt gaaccacaag cctagcaaca ccaaggtgga caagagagtg 720
 gaaccaaga gctgcgacaa gaccacacc tgtcctccat gtcctgctcc agaactgctc 780
 ggcggacctt ccgtgttcct gtttcctcca aagcctaagg acaccctgat gatcagcaga 840
 acccctgaag tgacctgcgt ggtggtggat gtgtcccacg aggatcccga agtgaagttc 900
 aattggtacg tggacggcgt ggaagtgcac aacgccaaga ccaagcctag agaggaacag 960
 tacaacagca cctacagagt ggtgtccgtg ctgaccgtgc tgcaccagga ttggctgaac 1020
 ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgctcctat cgagaaaacc 1080
 atcagcaagg ccaagggcca gcctagggaa cccaggttt acacactgcc tccaagccgg 1140
 gaagagatga ccaagaacca ggtgtccctg acctgcctcg tgaagggtt ctacccttcc 1200
 gatatcgccg tggaatggga gagcaatggc cagccagaga acaactacaa gacaaccctt 1260

cctgtgctgg acagcgacgg ctcattcttc ctgtacagca agctgacagt ggacaagtcc	1320
agatggcagc agggcaacgt gttcagctgc agcgtgatgc acgaggccct gcacaaccac	1380
tacaccaga agagtctgag cctgtctcca ggcctgcgga agagaagggc tcctgtgaag	1440
cagaccctga acttcgacct gctgaaactg gccggcgacg tggaaagcaa ccccgacct	1500
atgtatagaa tgcagctcct cctgctgac gcactgagcc tggctctcgt gaccaacagc	1560
gacatccaga tgacacagag ccccagcaca ctgtctgcc gcgtgggaga cagagtgacc	1620
atcacctgta gagccagcca gtccatctcc tcttggtgg cctggtatca gcaaaagcct	1680
ggcaaggccc ctaagctgct gatctacaag gcctccacac tggaaagcgg ggtgccctcc	1740
agattttctg gcagcggatc tggcaccgag ttcaccctga ccatcagtag cctgcagcct	1800
gacgacttcg ccacctacta ctgccagcag tacaatacct actggacctt cggccaggga	1860
acaaaggtgg aaatcaagcg gactgtggcc gtcceaagcg tgttcatctt tccacctagc	1920
gacgagcagc tgaagtccgg cacagcctct gttgtgtgcc tgctgaacaa cttctacccc	1980
agagaagcca aggtgcagtg gaaagtggac aatgccctgc agagcggcaa ctcccaagag	2040
agcgtgacag agcaggactc caaggattcc acctacagcc tgtctagcac cctgacactg	2100
agcaaggccg actacgagaa gcacaaagtg tatgcctgcg aagtgacca ccagggcctt	2160
agctctccag tgaccaagag cttcaaccgg ggcgagtgtt gataa	2205

<210> 142

<400> 142
000

<210> 143

<211> 738

<212> PRT

<213> Adeno-associated virus 8

<400> 143

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

Glu	Gly	Ile	Arg	Glu	Trp	Trp	Ala	Leu	Lys	Pro	Gly	Ala	Pro	Lys	Pro
			20					25					30		

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
180 185 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
405 410 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
435 440 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly

450

455

460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
 465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
 485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
 515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
 530 535 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
 545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
 580 585 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
 595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
 610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
 625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
 645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
 660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 144

<211> 736

<212> PRT

<213> Adeno-associated virus 9

<400> 144

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

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly

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

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 145
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 145
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
180 185 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
 385 390 395 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
 405 410 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
 420 425 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
 435 440 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
 450 455 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
 465 470 475 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
 485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
 500 505 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
 515 520 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
 530 535 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
 545 550 555 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
 565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
 580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 146

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 146

Met Tyr Arg Met Gln Leu Leu Leu Leu Ile Ala Leu Ser Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 147
<211> 26
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
VEGF-A signal peptide"

<400> 147
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala
20 25

<210> 148
<211> 29
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Fibulin-1 signal peptide"

<400> 148
Met Glu Arg Ala Ala Pro Ser Arg Arg Val Pro Leu Pro Leu Leu Leu
1 5 10 15

Leu Gly Gly Leu Ala Leu Leu Ala Ala Gly Val Asp Ala
20 25

<210> 149
<211> 19
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Vitronectin signal peptide"

<400> 149

Met Ala Pro Leu Arg Pro Leu Leu Ile Leu Ala Leu Leu Ala Trp Val
1 5 10 15

Ala Leu Ala

<210> 150

<211> 18

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Complement Factor H signal peptide"

<400> 150

Met Arg Leu Leu Ala Lys Ile Ile Cys Leu Met Leu Trp Ala Ile Cys
1 5 10 15

Val Ala

<210> 151

<211> 19

<212> PRT

<213> Unknown

<220>

<221> source

<223> /note="Description of Unknown:
Opticin signal peptide"

<400> 151

Met Arg Leu Leu Ala Phe Leu Ser Leu Leu Ala Leu Val Leu Gln Glu
1 5 10 15

Thr Gly Thr

<210> 152

<211> 18

<212> PRT

<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Albumin signal peptide"

<400> 152
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser

<210> 153
<211> 18
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Chymotrypsinogen signal peptide"

<400> 153
Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
1 5 10 15

Phe Gly

<210> 154
<211> 20
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Interleukin-2 signal peptide"

<400> 154
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu
1 5 10 15

Val Thr Asn Ser
20

<210> 155

<211> 15
<212> PRT
<213> Unknown

<220>
<221> source
<223> /note="Description of Unknown:
Trypsinogen-2 signal peptide"

<400> 155
Met Asn Leu Leu Leu Ile Leu Thr Phe Val Ala Ala Ala Val Ala
1 5 10 15

<210> 156
<211> 17
<212> PRT
<213> Homo sapiens

<400> 156
Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
1 5 10 15

Ala

<210> 157
<211> 22
<212> PRT
<213> Homo sapiens

<400> 157
Met Phe Ser Phe Val Asp Leu Arg Leu Leu Leu Leu Ala Ala Thr
1 5 10 15

Ala Leu Leu Thr His Gly
20

<210> 158
<211> 19
<212> PRT
<213> Homo sapiens

<400> 158
Met Lys Leu Val Phe Leu Val Leu Leu Phe Leu Gly Ala Leu Gly Leu
1 5 10 15

Cys Leu Ala

<210> 159
<211> 22
<212> PRT
<213> Homo sapiens

<400> 159
Met Gly Pro Thr Ser Gly Pro Ser Leu Leu Leu Leu Leu Thr His
1 5 10 15

Leu Pro Leu Ala Leu Gly
20

<210> 160
<211> 18
<212> PRT
<213> Homo sapiens

<400> 160
Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr
1 5 10 15

Ser Gly

<210> 161
<211> 27
<212> PRT
<213> Homo sapiens

<400> 161
Met Ala Pro His Arg Pro Ala Pro Ala Leu Leu Cys Ala Leu Ser Leu
1 5 10 15

Ala Leu Cys Ala Leu Ser Leu Pro Val Arg Ala
20 25

<210> 162
<211> 22
<212> PRT
<213> Homo sapiens

<400> 162
Met Trp Ala Thr Leu Pro Leu Leu Cys Ala Gly Ala Trp Leu Leu Gly
1 5 10 15

Val Pro Val Cys Gly Ala
20

<210> 163
<211> 19
<212> PRT
<213> Homo sapiens

<400> 163
Met Gln Ala Leu Val Leu Leu Leu Cys Ile Gly Ala Leu Leu Gly His
1 5 10 15

Ser Ser Cys

<210> 164
<211> 23
<212> PRT
<213> Homo sapiens

<400> 164
Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu Gly Leu Ala Leu
1 5 10 15

Val Phe Gly Glu Gly Ser Ala
20

<210> 165
<211> 20
<212> PRT
<213> Homo sapiens

<400> 165
Met Gln Pro Ser Ser Leu Leu Pro Leu Ala Leu Cys Leu Leu Ala Ala
1 5 10 15

Pro Ala Ser Ala
20

<210> 166
<211> 23
<212> PRT
<213> Homo sapiens

<400> 166

Met Ala Pro Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp
1 5 10 15

Leu Ile Ala Pro Ser Arg Ala
20

<210> 167

<211> 31

<212> PRT

<213> Homo sapiens

<400> 167

Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Leu Ala Val Gln Cys
1 5 10 15

Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys Arg
20 25 30

<210> 168

<211> 15

<212> PRT

<213> Homo sapiens

<400> 168

Met Trp Cys Ile Val Leu Phe Ser Leu Leu Ala Trp Val Tyr Ala
1 5 10 15

<210> 169

<211> 17

<212> PRT

<213> Homo sapiens

<400> 169

Met Asn Pro Thr Leu Ile Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
1 5 10 15

Ala

<210> 170

<211> 17

<212> PRT

<213> Homo sapiens

<400> 170

Met Trp Gln Leu Trp Ala Ser Leu Cys Cys Leu Leu Val Leu Ala Asn
1 5 10 15

Ala

<210> 171
<211> 16
<212> PRT
<213> Homo sapiens

<400> 171
Met Leu Leu Ile Leu Leu Ser Val Ala Leu Leu Ala Phe Ser Ser Ala
1 5 10 15

<210> 172
<211> 20
<212> PRT
<213> Homo sapiens

<400> 172
Met Trp Lys Arg Trp Leu Ala Leu Ala Leu Val Ala Val Ala
1 5 10 15

Trp Val Arg Ala
20

<210> 173
<211> 18
<212> PRT
<213> Homo sapiens

<400> 173
Met Lys Trp Val Thr Phe Ile Ser Leu Leu Phe Leu Phe Ser Ser Ala
1 5 10 15

Tyr Ser

<210> 174
<211> 24
<212> PRT
<213> Homo sapiens

<400> 174
Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys

1 5 10 15

Cys Leu Val Pro Val Ser Leu Ala
20

<210> 175
<211> 18
<212> PRT
<213> Homo sapiens

<400> 175
Met Lys Ala Ala Val Leu Thr Leu Ala Val Leu Phe Leu Thr Gly Ser
1 5 10 15

Gln Ala

<210> 176
<211> 18
<212> PRT
<213> Homo sapiens

<400> 176
Met Lys Leu Leu Ala Ala Thr Val Leu Leu Leu Thr Ile Cys Ser Leu
1 5 10 15

Glu Gly

<210> 177
<211> 27
<212> PRT
<213> Homo sapiens

<400> 177
Met Asp Pro Pro Arg Pro Ala Leu Leu Ala Leu Leu Ala Leu Pro Ala
1 5 10 15

Leu Leu Leu Leu Leu Leu Ala Gly Ala Arg Ala
20 25

<210> 178
<211> 28
<212> PRT
<213> Homo sapiens

<400> 178

Met	Gln	Arg	Val	Asn	Met	Ile	Met	Ala	Glu	Ser	Pro	Gly	Leu	Ile	Thr
1				5					10					15	

Ile	Cys	Leu	Leu	Gly	Tyr	Leu	Leu	Ser	Ala	Glu	Cys
			20					25			

<210> 179

<211> 20

<212> PRT

<213> Homo sapiens

<400> 179

Met	Gly	Pro	Leu	Met	Val	Leu	Phe	Cys	Leu	Leu	Phe	Leu	Tyr	Pro	Gly
1				5					10					15	

Leu	Ala	Asp	Ser
			20

<210> 180

<211> 18

<212> PRT

<213> Homo sapiens

<400> 180

Met	Trp	Leu	Leu	Val	Ser	Val	Ile	Leu	Ile	Ser	Arg	Ile	Ser	Ser	Val
1				5					10					15	

Gly Gly

<210> 181

<211> 18

<212> PRT

<213> Homo sapiens

<400> 181

Met	Leu	Leu	Leu	Phe	Ser	Val	Ile	Leu	Ile	Ser	Trp	Val	Ser	Thr	Val
1				5					10					15	

Gly Gly

<210> 182

<211> 19
<212> PRT
<213> Homo sapiens

<400> 182
Met Phe Ser Met Arg Ile Val Cys Leu Val Leu Ser Val Val Gly Thr
1 5 10 15

Ala Trp Thr

<210> 183
<211> 30
<212> PRT
<213> Homo sapiens

<400> 183
Met Lys Arg Met Val Ser Trp Ser Phe His Lys Leu Lys Thr Met Lys
1 5 10 15

His Leu Leu Leu Leu Leu Cys Val Phe Leu Val Lys Ser
20 25 30

<210> 184
<211> 26
<212> PRT
<213> Homo sapiens

<400> 184
Met Ser Trp Ser Leu His Pro Arg Asn Leu Ile Leu Tyr Phe Tyr Ala
1 5 10 15

Leu Leu Phe Leu Ser Ser Thr Cys Val Ala
20 25

<210> 185
<211> 18
<212> PRT
<213> Homo sapiens

<400> 185
Met Lys Ser Leu Val Leu Leu Leu Cys Leu Ala Gln Leu Trp Gly Cys
1 5 10 15

His Ser

<210> 186
<211> 23
<212> PRT
<213> Homo sapiens

<400> 186
Met Ala Arg Val Leu Gly Ala Pro Val Ala Leu Gly Leu Trp Ser Leu
1 5 10 15

Cys Trp Ser Leu Ala Ile Ala
20

<210> 187
<211> 18
<212> PRT
<213> Homo sapiens

<400> 187
Met Lys Leu Ile Thr Ile Leu Phe Leu Cys Ser Arg Leu Leu Leu Ser
1 5 10 15

Leu Thr

<210> 188
<211> 20
<212> PRT
<213> Homo sapiens

<400> 188
Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala
1 5 10 15

Ala Ser Tyr Ser
20

<210> 189
<211> 19
<212> PRT
<213> Homo sapiens

<400> 189
Met Glu His Lys Glu Val Val Leu Leu Leu Leu Phe Leu Lys Ser
1 5 10 15

Gly Gln Gly

<210> 190
<211> 24
<212> PRT
<213> Homo sapiens

<400> 190
Met Ala His Val Arg Gly Leu Gln Leu Pro Gly Cys Leu Ala Leu Ala
1 5 10 15

Ala Leu Cys Ser Leu Val His Ser
20

<210> 191
<211> 29
<212> PRT
<213> Homo sapiens

<400> 191
Met Ile Ser Arg Met Glu Lys Met Thr Met Met Met Lys Ile Leu Ile
1 5 10 15

Met Phe Ala Leu Gly Met Asn Tyr Trp Ser Cys Ser Gly
20 25

<210> 192
<211> 32
<212> PRT
<213> Homo sapiens

<400> 192
Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val
1 5 10 15

Tyr Leu Leu Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys
20 25 30

<210> 193
<211> 19
<212> PRT
<213> Homo sapiens

<400> 193

Met Arg Leu Ala Val Gly Ala Leu Leu Val Cys Ala Val Leu Gly Leu
1 5 10 15

Cys Leu Ala

<210> 194
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 194
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly
20

<210> 195
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 195
Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly
20

<210> 196
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 196

Glu Pro Lys Ser Cys Asp Lys Thr His Leu
1 5 10

<210> 197

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 197

Glu Pro Lys Ser Cys Asp Lys Thr His Thr
1 5 10

<210> 198

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 198

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

<210> 199

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 199

Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

<210> 200
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 200
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
20 25

<210> 201
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 201
Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu
20 25

<210> 202
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 202
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Ala Gly Ala
20

<210> 203
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 203
Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Ala Gly Ala
20

<210> 204
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 204
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu
20 25

<210> 205
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 205

Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu
20 25

<210> 206
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 206
Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly
20

<210> 207
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 207
Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly
20

<210> 208
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 208

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu
20 25

<210> 209

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 209

Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Phe Glu Gly Gly Pro Ser Val Phe Leu
20 25

<210> 210

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 210

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly
20

<210> 211

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 211

Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly
20

<210> 212

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 212

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
20 25

<210> 213

<211> 27

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 213

Glu Pro Lys Ser Cys Asp Lys Thr His Leu Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
20 25

<210> 214
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 214
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly

<210> 215
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 215
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly

<210> 216
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 216
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala
1 5 10

<210> 217
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 217
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala
1 5 10

<210> 218
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 218
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu
20

<210> 219
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
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<400> 219
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu
20

<210> 220
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 220
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly

<210> 221
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 221
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala
1 5 10

<210> 222
<211> 4
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<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 222
Arg Lys Arg Arg
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<210> 223
<211> 4
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 223

Arg Arg Arg Arg

1

<210> 224

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 224

Arg Arg Lys Arg

1

<210> 225

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 225

Arg Lys Lys Arg

1

<210> 226

<400> 226

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<210> 227

<211> 21

<212> PRT

<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<222> (1)..(3)
<223> /note="This region may be absent in its entirety"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 227
Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15

Glu Asn Pro Gly Pro
20

<210> 228
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<222> (1)..(3)
<223> /note="This region may be absent in its entirety"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 228
Gly Ser Gly Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val
1 5 10 15

Glu Glu Asn Pro Gly Pro
20

<210> 229
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
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<222> (1)..(3)
<223> /note="This region may be absent in its entirety"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 229
Gly Ser Gly Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp
1 5 10 15

Val Glu Ser Asn Pro Gly Pro
20

<210> 230
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> SITE
<222> (1)..(3)
<223> /note="This region may be absent in its entirety"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 230

Gly Ser Gly Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys
1 5 10 15

Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 231

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 231

Arg Lys Arg Arg Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu
1 5 10 15

Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly Pro
20 25

<210> 232

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 232

Cys Pro Pro Cys Pro Ala
1 5

<210> 233

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
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<400> 233
Cys Pro Pro Cys Pro
1 5

<210> 234

<400> 234
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<210> 235

<400> 235
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<210> 236
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 236
Glu Asp Thr Ala Val Tyr Tyr
1 5

<210> 237
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 237
Tyr Cys Ala Ser Gly Asp Tyr Trp
1 5

<210> 238
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 238
Glu Asp Val Gly Val Tyr Tyr
1 5

<210> 239
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 239
Glu Asp Phe Ala Val Tyr Tyr
1 5

<210> 240
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 240
Glu Asp Ser Gly Ile Tyr Tyr
1 5

<210> 241
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 241
Asn Trp Glu Asp Tyr Trp
1 5

<210> 242
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
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peptide"

<400> 242
Glu Asp Phe Ala Thr Tyr Tyr
1 5

<210> 243
<211> 6
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<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 243
Asp Thr Ala Val Tyr Tyr
1 5

<210> 244
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 244
Tyr Tyr Gly Ala Phe Asp
1 5

<210> 245
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 245

Glu Asp Glu Ala Asp Tyr Tyr
1 5

<210> 246

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 246

Tyr Tyr Tyr Gly Arg His Phe Asp
1 5

<210> 247

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 247

Ser Gln Ser Val Asp Tyr Asp Gly Asp Ser Tyr
1 5 10

<210> 248

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 248

Glu Asp Val Ala Val Tyr Tyr
1 5

<210> 249
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 249
Glu Asp Leu Ala Thr Tyr Tyr
1 5

<210> 250
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 250
Glu Asp Thr Ala Val Tyr
1 5

<210> 251
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 251
Asp Asp Phe Ala Thr Tyr Tyr
1 5

<210> 252
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

peptide"

<400> 252

Asp Leu Ser Gly Tyr Tyr
1 5

<210> 253

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 253

Glu Asp Val Ala Thr Tyr Tyr
1 5

<210> 254

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 254

Asp Thr Ala Met Tyr Tyr
1 5

<210> 255

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 255

Asp Glu Ala Asp Tyr Tyr
1 5

<210> 256

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 256
Thr Phe Glu Gly Asp Tyr Val Phe
1 5

<210> 257
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 257
Asp Asn Leu Gly Thr Tyr Tyr Val Glu
1 5

<210> 258

<400> 258
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<210> 259
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<400> 259
Asp Ser Ile Pro Asn Tyr
1 5

<210> 260
<211> 6
<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 260

Tyr Cys Gln Ser Phe Asp
1 5

<210> 261

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 261

Glu Asp Thr Gly Ile Tyr Tyr
1 5

<210> 262

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 262

Glu Asp Ala Ala Thr Tyr Tyr
1 5

<210> 263

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 263

Tyr Asn Glu Lys Phe Glu
1 5

<210> 264
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 264
Glu Asp Phe Ala Met Tyr Tyr
1 5

<210> 265
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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peptide"

<400> 265
Phe Thr Phe Asp Asp Tyr Ala
1 5

<210> 266
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 266
Glu Asp Thr Gly Val Tyr Tyr
1 5

<210> 267
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 267
Glu Asp Ile Ala Asp Tyr Tyr
1 5

<210> 268
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 268
Tyr Tyr Tyr Gly Met Asp
1 5

<210> 269
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 269
Glu Leu Leu Ile Tyr Tyr
1 5

<210> 270
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 270
Glu Asp Thr Ala Leu Tyr Tyr

1

5

<210> 271

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 271

Glu Asp Phe Ala Ser Tyr Tyr

1

5

<210> 272

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 272

Asp Leu Leu His Trp Tyr

1

5

<210> 273

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 273

Asp Asp Thr Ala Val Tyr Tyr

1

5

<210> 274

<211> 736

<212> PRT

<213> Adeno-associated virus 1

<400> 274

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp

420

425

430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
 435 440 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 275

<211> 735

<212> PRT

<213> Adeno-associated virus 2

<400> 275

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

85

90

95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
 100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
 130 135 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
 145 150 155 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
 165 170 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
 180 185 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
 195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
 210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
 225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
 245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
 260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
 275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
 290 295 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
 305 310 315 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
 325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
 340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
 355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
 370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
 435 440 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
 450 455 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
 465 470 475 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
 485 490 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
 500 505 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
515 520 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
530 535 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545 550 555 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
565 570 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
580 585 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
595 600 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
610 615 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625 630 635 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
645 650 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 276

<211> 736

<212> PRT

<213> Adeno-associated virus 3

<400> 276

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

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
130 135 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145 150 155 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
260 265 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
275 280 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
290 295 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305 310 315 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
325 330 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
340 345 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
355 360 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
370 375 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
 385 390 395 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
 405 410 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
 420 425 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
 435 440 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
 450 455 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
 465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
 485 490 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
 500 505 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
 515 520 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
 530 535 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
 545 550 555 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
 565 570 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
 580 585 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln

595

600

605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
 660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
 705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 277

<211> 734

<212> PRT

<213> Adeno-associated virus 4

<400> 277

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
 1 5 10 15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
 20 25 30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
 35 40 45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
50 55 60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65 70 75 80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
115 120 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
130 135 140

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

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
165 170 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
180 185 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
195 200 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
210 215 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225 230 235 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
245 250 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr

260

265

270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
 275 280 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
 290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
 305 310 315 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
 325 330 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
 340 345 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
 355 360 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
 370 375 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
 385 390 395 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
 405 410 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
 420 425 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
 435 440 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
 450 455 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
 465 470 475 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
485 490 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
500 505 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
515 520 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
530 535 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545 550 555 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
565 570 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
580 585 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
595 600 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
610 615 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625 630 635 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
645 650 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
660 665 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
675 680 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
690 695 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705 710 715 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
725 730

<210> 278

<211> 724

<212> PRT

<213> Adeno-associated virus 5

<400> 278

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1 5 10 15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
20 25 30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
35 40 45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
50 55 60

Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65 70 75 80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
85 90 95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
100 105 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
115 120 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
130 135 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
 145 150 155 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
 165 170 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
 180 185 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
 195 200 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
 210 215 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
 225 230 235 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
 245 250 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
 260 265 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
 275 280 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
 290 295 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
 305 310 315 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
 325 330 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
 340 345 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
355 360 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
370 375 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385 390 395 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
405 410 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
420 425 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
435 440 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
450 455 460

Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465 470 475 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
485 490 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
500 505 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
515 520 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
530 535 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545 550 555 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
565 570 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
580 585 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
595 600 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
610 615 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625 630 635 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
645 650 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 279

<211> 736

<212> PRT

<213> Adeno-associated virus 6

<400> 279

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
180 185 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
260 265 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
275 280 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
290 295 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305 310 315 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
325 330 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
340 345 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
355 360 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
370 375 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385 390 395 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
405 410 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
420 425 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg

435

440

445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
 450 455 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
 465 470 475 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
 485 490 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
 500 505 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
 515 520 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
 530 535 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
 545 550 555 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
 565 570 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
 580 585 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
 595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
 625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 280

<211> 737

<212> PRT

<213> Adeno-associated virus 7

<400> 280

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

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly

100

105

110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
 115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
 130 135 140

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

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
 165 170 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
 180 185 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
 195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
 210 215 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
 225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
 245 250 255

Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
 260 265 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
 305 310 315 320

255

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
370 375 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
405 410 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
435 440 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
450 455 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465 470 475 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
485 490 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
500 505 510

Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
515 520 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
530 535 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545 550 555 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
565 570 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
580 585 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
595 600 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
610 615 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625 630 635 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
645 650 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
660 665 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
675 680 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
690 695 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
705 710 715 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
725 730 735

Leu

<210> 281

<211> 736

<212> PRT

<213> Adeno-associated virus

<400> 281

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln

595

600

605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
 610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
 625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
 645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
 660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
 675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
 690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Ser Thr Glu Gly Val
 705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
 725 730 735

<210> 282

<211> 736

<212> PRT

<213> Adeno-associated virus

<400> 282

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

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
 20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
 35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

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

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn

260

265

270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
 275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
 290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
 305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
 325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
 340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
 355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
 370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
 385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
 405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
 420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
 435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
 450 455 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
 465 470 475 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
485 490 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
500 505 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
515 520 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
530 535 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545 550 555 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
565 570 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
580 585 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
595 600 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
610 615 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625 630 635 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
645 650 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 283

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 283

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro

115

120

125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 284

<211> 228

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 284

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
 1 5 10 15

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

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

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

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ser Val
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Pro Gly Lys
225

<210> 285

<211> 229

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 285

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

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

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 286
<211> 2193
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 286
atgtacagaa tgcagctgct gctgctcatt gccctgtctc tggccctggt caccaattct 60
gaggtccagc tgcttgagag tgggtggtgga ctggttcagc ctggtggcag cctgagactg 120
tcttgctgctg cctctggctt caccttcagc cactatatca tgatgtgggt cagacaggcc 180
cctggcaaag gcctggaatg ggtgtcaggc atctacagca gtggtggcat cacagtgtat 240
gctgactctg tgaagggcag attcaccatc agcagagaca acagcaagaa caccctgtac 300
ctgcagatga actccctgag agctgaggac acagcagtgt actactgtgc ctatagaaga 360
attgggggtgc ccagaaggga tgagtttgac atctggggcc agggcaccat ggttacagtg 420
tcctctgcca gcacaaaggg cccctctgtt tttccactgg ctcccagcag caagagcacc 480
agtgggtggaa cagctgccct gggctgtctg gtcaaggatt acttccctga gcctgtgact 540
gtgtcctgga actctggggc tctgacttct ggggtgcaca cctttccagc tgtgctgcag 600
tcctctggcc tgtactctct gtcctctgtg gtcacagtgc ctagctctag cctgggcaca 660
cagacctaca tctgcaatgt gaaccacaag cctagcaaca ccaaggtgga caagagagtg 720
gaaccaaga gctgtgacaa gaccacacc tgtcctccat gtcctgctcc agaactgctt 780
ggaggccctt ctgtgttcct gtttcctcca aagcctaagg acaccctgat gatcagcaga 840

acccctgaag tgacctgtgt ggtggttgat gtgtcccatg aggaccacaga agtgaagttc	900
aattgggtatg tggatgggggt tgaagtgcac aatgccaaga ccaagcctag agaggaacag	960
tacaacagca cctacagagt ggtttctgtg ctgacagtgc tgcaccagga ctggctgaat	1020
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgctcctat tgagaaaacc	1080
atctccaagg ccaagggcca gccaagagaa cccaggttt acaccctgcc acctagcaga	1140
gaagagatga ccaagaacca ggtgtccctg acctgcctgg ttaagggtt ctaccctct	1200
gacattgctg tggaatggga gagcaatggc cagcctgaaa acaactacaa gacaaccct	1260
cctgtgctgg actctgatgg ctcttcttc ctgtacagca agctgactgt ggacaagtcc	1320
agatggcagc agggaaatgt gttcagctgc tctgtgatgc atgaggccct gcacaaccac	1380
tacaccacaga aaagtctgtc tctgtcccct ggcagaaaga gaagaggctc tggagaaggc	1440
agaggctccc tgctgacatg tggggatgtt gaagagaatc ctgggcctat gtataggatg	1500
caactgctcc tcctgattgc tctgagcctg gctcttgtga ccaactctga catccagatg	1560
acacagagcc cctccacact gtctgcatct gtgggagaca gagtgaccat cacctgtaga	1620
gccagccagt ctatctctag ctggctggcc tggatatcagc aaaagcctgg caaggcccct	1680
aagctgctga tctacaaggc cagcacactt gagtcagggg tgcctccag attttctggc	1740
tctggatctg gcacagagtt caccctgacc atcagctccc tgcagccaga tgactttgcc	1800
acctactact gccagcagta caatacctac tggacctttg gccagggaac aaaggtggaa	1860
atcaagagaa cagtggctgc cccatctgtg ttcattctcc caccatctga tgaacagctg	1920
aagtctggca ctgcctctgt tgtgtgcctg ctgaacaact tttaccccag agaagccaag	1980
gtgcagtgga aagtggataa tggcctgcag tctggcaata gccaagaatc tgtgacagag	2040
caggactcca aggattccac ctacagcctg agcagcacc tgacactgag caaggctgac	2100
tatgagaagc acaaagtgtg tgcctgtgaa gtgacacacc agggactgag cagcccagtg	2160
accaagagct tcaacagggg agagtgtgta taa	2193

<210> 287

<211> 2211

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 287

atgtacagaa tgcagctgct gctgctcatt gccctgtctc tggccctggt caccaattct	60
gaggtccagc tgcttgagag tgggtggtgga ctggttcagc ctggtggcag cctgagactg	120
tcttgtgctg cctctggctt caccttcagc cactatatca tgatgtgggt cagacaggcc	180
cctggcaaag gcctggaatg ggtgtcaggc atctacagca gtggtggcat cacagtgtat	240
gctgactctg tgaagggcag attcaccatc agcagagaca acagcaagaa caccctgtac	300
ctgcagatga actccctgag agctgaggac acagcagtgt actactgtgc ctatagaaga	360
attgggggtgc ccagaaggga tgagtttgac atctggggcc agggcaccat ggttacagtg	420
tcctctgcca gcacaaaggg cccctctgtt tttccactgg ctcccagcag caagagcacc	480
agtgggtgaa cagctgccct gggctgtctg gtcaaggatt acttccctga gcctgtgact	540
gtgtcctgga actctggggc tctgacctct ggggtgcaca cttttccagc tgtgctgcag	600
tcctctggcc tgtactctct gtcctctgtg gtcacagtgc ctagctctag cctgggcaca	660
cagacctaca tctgcaatgt gaaccacaag cctagcaaca ccaaggtgga caagagagtg	720
gaaccaaga gctgtgacaa gaccacacc tgtcctccat gtcctgctcc agaactgctt	780
ggaggccctt ctgtgttcct gtttctcca aagcctaagg acaccctgat gatcagcaga	840
accctgaag tgacctgtgt ggtggttgat gtgtcccatg aggaccaga agtgaagtgc	900
aattggtatg tggatggggt tgaagtgcac aatgccaaga ccaagcctag agaggaacag	960
tacaacagca cctacagagt ggtttctgtg ctgacagtgc tgcaccagga ctggctgaat	1020
ggcaaagagt acaagtgcaa ggtgtccaac aaggccctgc ctgctcctat tgagaaaacc	1080
atctccaagg ccaagggcca gccaagagaa cccaggttt acaccctgcc acctagcaga	1140
gaagagatga ccaagaacca ggtgtccctg acctgcctgg ttaagggtt ctaccctct	1200
gacattgctg tggaatggga gagcaatggc cagcctgaaa acaactacaa gacaaccct	1260
cctgtgctgg actctgatgg ctcatcttc ctgtacagca agctgactgt ggacaagtcc	1320
agatggcagc agggaaatgt gttcagctgc tctgtgatgc atgaggccct gcacaaccac	1380
tacaccaga aaagtctgtc tctgtcccct ggcagaaaga gaagaggatc aggggccccca	1440

gtgaagcaga ccctgaactt tgatctgctg aagctggctg gggatgttga gagcaaccct	1500
ggacctatgt ataggatgca actgctcctc ctgattgctc tgagcctggc tcttgtgacc	1560
aactctgaca tccagatgac acagagcccc tccacactgt ctgcatctgt gggagacaga	1620
gtgaccatca cctgtagagc cagccagtct atctcttcct ggctggcctg gtatcagcaa	1680
aagcctggca aggcccctaa gctgctgac tacaaggcca gcacacttga gtcaggggtg	1740
ccctccagat tttctggctc tggatctggc acagagttca ccctgacct cagctccctg	1800
cagccagatg actttgccac ctactactgc cagcagtaca atacctactg gacctttggc	1860
cagggaaaca aggtggaaat caagagaaca gtggctgccc catctgtgtt catcttccca	1920
ccatctgatg aacagctgaa gtctggcact gcctctgttg tgtgcctgct gaacaacttt	1980
taccctagag aagccaaggt gcagtggaaa gtggataatg ccctgcagtc tggcaatagc	2040
caagaatctg tgacagagca ggactccaag gattccacct acagcctgag cagcaccctg	2100
acactgagca aggctgacta tgagaagcac aaagtgtatg cctgtgaagt gacacaccag	2160
ggactgagca gccagtgac caagagcttc aacaggggag agtgctgata a	2211

<210> 288

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 288

Leu Gly Glu Thr Thr Arg Pro

1 5

<210> 289

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 289

Leu Ala Leu Gly Glu Thr Thr Arg Pro
1 5

<210> 290

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 290

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 291

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 291

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 292

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 292

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

275

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
195 200 205

<210> 293
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 293
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 294

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 294

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Ser Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 295
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 295
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln

165

170

175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 195 200 205

<210> 296

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 296

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 35 40 45

Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
 50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 115 120 125

280

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 297

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 297

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
50 55 60

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys

85

90

95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
 145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 195 200 205

<210> 298

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 298

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 35 40 45

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
195 200 205

<210> 299

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 299

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu

1	5	10	15
Val Thr Cys	Val Val Val Asp	Val Ser His Glu Asp	Pro Glu Val Lys
	20	25	30
Phe Asn Trp	Tyr Val Asp Gly	Val Glu Val His Asn	Ala Lys Thr Lys
	35	40	45
Pro Arg Glu	Glu Gln Tyr Asn	Ser Thr Tyr Arg	Val Val Ser Val Leu
	50	55	60
Thr Val Leu	His Gln Asp Trp	Leu Asn Gly Lys	Glu Tyr Lys Cys Lys
65	70	75	80
Val Ser Asn	Lys Ala Leu Pro	Ala Pro Ile Glu	Lys Thr Ile Ser Lys
	85	90	95
Ala Lys Gly	Gln Pro Arg Glu	Pro Gln Val Tyr	Thr Leu Pro Pro Ser
	100	105	110
Arg Asp Glu	Leu Thr Lys Asn	Gln Val Ser Leu	Thr Cys Leu Val Lys
	115	120	125
Gly Phe Tyr	Pro Ser Asp Ile	Ala Val Glu Trp	Glu Ser Asn Gly Gln
	130	135	140
Pro Glu Asn	Asn Tyr Lys Thr	Thr Pro Pro Val	Leu Asp Ser Asp Gly
145	150	155	160
Ser Phe Phe	Leu Tyr Ser Lys	Leu Thr Val Asp	Lys Ser Arg Trp Gln
	165	170	175
Gln Gly Asn	Val Phe Ser Cys	Ser Val Met His	Glu Ala Leu His Asn
	180	185	190
His Tyr Thr	Gln Lys Ser Leu	Ser Leu Ser Pro	Gly Lys
	195	200	205
<210>	300		
<211>	210		

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 300

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
20 25 30

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
35 40 45

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
50 55 60

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
65 70 75 80

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
85 90 95

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

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
115 120 125

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
130 135 140

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
145 150 155 160

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
165 170 175

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
180 185 190

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
195 200 205

Gly Lys
210

<210> 301

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 301

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 195 200 205

<210> 302

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 302

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 303
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 303
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 304

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 304

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 305

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 305
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 306

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 306

Phe Pro Pro Lys Pro Lys Asp Gln Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln

130

135

140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu His Asn
 180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 195 200 205

<210> 307

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 307

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 308

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 308

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu

50

55

60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 309

<211> 208

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 309

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
20 25 30

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
35 40 45

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
50 55 60

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
65 70 75 80

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
85 90 95

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

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
115 120 125

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
130 135 140

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
145 150 155 160

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
165 170 175

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
180 185 190

Glu Ala Leu His Ala His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
195 200 205

<210> 310

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 310

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 311

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 311

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 312

<211> 204

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 312

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
195 200

<210> 313

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 313

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

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
20 25 30

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
35 40 45

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg
50 55 60

Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys
65 70 75 80

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu
85 90 95

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

Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu
115 120 125

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
130 135 140

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met
145 150 155 160

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
165 170 175

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
180 185 190

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
195 200 205

Gly Lys
210

<210> 314

<211> 204

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 314

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
195 200

<210> 315

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 315

aggttaattt ttaaaaagca gtcaaaagtc caagtggccc ttggcagcat ttactctctc	60
tgtttgctct ggtaataat ctcaggagca caaacattcc agatccaggt taatTTTTaa	120
aaagcagtca aaagtccaag tggcccttgg cagcatttac tctctctgtt tgctctgggt	180
aataatctca ggagcacaaa cattccagat ccggcgcgcc agggctggaa gctacctttg	240
tctagaaggc tcagaggcac acaggagttt ctgggctcac cctgccccct tccaaccctt	300
cagttcccat cctccagcag ctgtttgtgt gctgcctctg aagtccacac tgaacaaact	360
tcagcctact catgtcccta aaatgggcaa acattgcaag cagcaaacag caaacacaca	420
gccctccctg cctgctgacc ttggagctgg ggagaggtc agagacctct ctggggccat	480
gccacctcca acatccactc gacccttgg aatttcggtg gagaggagca gaggttgtcc	540
tggcgtgggt taggtagtgt gagaggggta cccggggatc ttgctaccag tggaacagcc	600
actaaggatt ctgcagttag agcagagggc cagctaagtg gtactctccc agagactgtc	660
tgactcacgc cccccctcc accttgga caaggacgtg tggtttctga gccaggtaca	720
atgactcctt tcggttaagt cagtggaagc tgtacactgc ccaggcaaag cgtccgggca	780
gcgtaggcgg gcgactcaga tcccagccag tggacttagc ccctgtttgc tcctccgata	840
actgggggtga ccttggttaa tattcaccag cagcctcccc cgttgcccct ctggatccac	900
tgcttaaata cggacgagga cagggccctg tctcctcagc ttcaggcacc accactgacc	960
tgggacagt	969

<210> 316

<211> 1050

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 316
aggctcagag gcacacagga gtttctgggc tcaccctgcc cccttccaac ccctcagttc 60
ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc 120
tactcatgtc ctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc 180
cctgcctgct gaccttggag ctggggcaga ggtcagagac ctctctgggc ccatgccacc 240
tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagagggt gtcctggcgt 300
ggtttaggta gtgtgagagg gtctagaagg ctgagaggca cacaggagtt tctgggctca 360
ccctgcccc ttccaacccc tcagttcca tcctccagca gctgtttgtg tgctgcctct 420
gaagtccaca ctgaacaaac ttcagcctac tcatgtccct aaaatgggca aacattgcaa 480
gcagcaaaca gcaaacacac agccctccct gcctgctgac cttggagctg gggcagagggt 540
cagagacctc tctgggcccc tgccacctcc aacatccact cgaccccttg gaatttcggt 600
ggagaggagc agaggttgtc ctggcgtgggt ttaggtagtg tgagaggggt acccggggat 660
cttgctacca gtggaacagc cactaaggat tctgcagtga gagcagaggg ccagctaagt 720
ggtactctcc cagagactgt ctgactcacg ccaccccctc caccttggac acaggacgct 780
gtggtttctg agccaggtac aatgactcct ttcggtaagt gcagtggaag ctgtacactg 840
cccaggcaaa gcgtccgggc agcgtaggcg ggcgactcag atcccagcca gtggacttag 900
cccctgtttg ctctccgat aactggggtg accttggtta atattcacca gcagcctccc 960
ccgttgcccc tctggatcca ctgcttaaatac acggacgagg acagggccct gtctcctcag 1020
cttcaggcac caccactgac ctgggacagt 1050

<210> 317
<211> 1089
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 317
aggttaattt ttaaaaagca gtcaaaagtc caagtggccc ttggcagcat ttactctctc 60
tgtttgctct ggttaataat ctcaggagca caaacattcc agatccaggt taatttttaa 120

aaagcagtca aaagtccaag tggcccttgg cagcatttac tctctctgtt tgctctggtt	180
aataatctca ggagcacaaa cattccagat ccggcgcgcc agggctggaa gctacctttg	240
acatcatttc ctctgcgaat gcatgtataa tttctacaga acctattaga aaggatcacc	300
cagcctctgc ttttgtacaa ctttccctta aaaaactgcc aattccactg ctgtttggcc	360
caatagttag aacttttttc tgctgcctct tgggtgctttt gcctatggcc cctattctgc	420
ctgctgaaga cactcttgcc agcatggact taaaccctc cagctctgac aatcctcttt	480
ctcttttgtt ttacatgaag ggtctggcag ccaaagcaat cactcaaagt tcaaacctta	540
tcattttttg ctttgttcct cttggccttg gttttgtaca tcagctttga aaataccatc	600
ccagggttaa tgctgggggtt aatttataac taagagtgtc ctagttttgc aatacaggac	660
atgctataaa aatggaaaga tgttgctttc tgagaggatc ttgctaccag tggaacagcc	720
actaaggatt ctgcagttag agcagagggc cagctaagtg gtactctccc agagactgtc	780
tgactcacgc caccctctcc accttgaca caggacgtg tggtttctga gccaggtaca	840
gtgactcctt tcggtaagtg cagtggaagc tgtacactgc ccaggcaaag cgtccgggca	900
gcgtaggcgg gcgactcaga tcccagccag tggacttagc ccctgtttgc tcctccgata	960
actgggggtga ccttggttaa tattcaccag cagcctcccc cgttgcccct ctggatccac	1020
tgcttaaata cggacgagga cagggccctg tctcctcagc ttcaggcacc accactgacc	1080
tgggacagt	1089

<210> 318

<211> 1430

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 318

aggctcagag gcacacagga gtttctgggc tcaccctgcc cccttccaac ccctcagttc	60
ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc	120
tactcatgtc ctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc	180
cctgcctgct gaccttgag ctggggcaga ggtcagagac ctctctgggc ccatgccacc	240

tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagaggtt gtcctggcgt	300
ggtttaggta gtgtgagagg gtctagagcc cttaagctag caggttaatt tttaaaaagc	360
agtcaaaagt ccaagtggcc cttggcagca ttactctct ctgtttgctc tggttaataa	420
tctcaggagc acaaacattc cagatccagg ttaattttta aaaagcagtc aaaagtccaa	480
gtggcccttg gcagcattta ctctctctgt ttgctctggt taataatctc aggagcacia	540
acattccaga tccggcgcg cagggctgga agctacctt gacatcattt cctctgcgaa	600
tgcatgtata atttctacag aacctattag aaaggatcac ccagcctctg cttttgtaca	660
actttccctt aaaaaactgc caattccact gctgtttggc ccaatagtga gaactttttc	720
ctgctgcctc ttggtgcttt tgcctatggc ccctattctg cctgctgaag acactcttgc	780
cagcatggac ttaaaccctt ccagctctga caatcctctt tctcttttgt ttacatgaa	840
gggtctggca gccaaagcaa tcaactcaaag ttcaaactt atcatttttt gctttgttcc	900
tcttggcctt ggttttgtac atcagctttg aaaataccat cccagggtta atgctggggt	960
taatttataa ctaagagtgc tctagttttg caatacagga catgctataa aaatggaaag	1020
atgttgcttt ctgagaggat cttgctacca gtggaacagc cactaaggat tctgcagtga	1080
gagcagaggg ccagctaagt ggtactctcc cagagactgt ctgactcacg ccacccctc	1140
caccttggac acaggacgt gtggtttctg agccaggtag agtgactcct ttcggtaagt	1200
gcagtggaag ctgtacactg cccaggcaaa gcgtccgggc agcgtaggcg ggcgactcag	1260
atcccagcca gtggacttag cccctgtttg ctctccgat aactggggtg accttggtta	1320
atattcacca gcagcctccc ccgttgcccc tctggatcca ctgcttaaatt acggacgagg	1380
acagggccct gtctcctcag cttcaggcac caccactgac ctgggacagt	1430

<210> 319

<211> 1318

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 319

aggttaat	ttaaaaagca	gtcaaaagtc	caagtggccc	ttggcagcat	ttactctctc	60
tgtttgctct	ggttaataat	ctcaggagca	caaacattcc	agatccaggt	taatTTTTaa	120
aaagcagtca	aaagtccaag	tggcccttgg	cagcatttac	tctctctgtt	tgctctggtt	180
aataatctca	ggagcacaaa	cattccagat	ccggcgcgcc	agggctggaa	gctacctttg	240
acatcatttc	ctctgcgaat	gcatgtataa	tttctacaga	acctattaga	aaggatcacc	300
cagcctctgc	ttttgtacaa	ctttccctta	aaaaactgcc	aattccactg	ctgtttggcc	360
caatagttag	aactttttcc	tgctgcctct	tggtgctttt	gcctatggcc	cctattctgc	420
ctgctgaaga	cactcttgcc	agcatggact	taaaccctc	cagctctgac	aatcctcttt	480
ctcttttgtt	ttacatgaag	ggtctggcag	caaagcaat	cactcaaagt	tcaaacctta	540
tcattttttg	ctttgttcct	cttggccttg	gttttgtaca	tcagctttga	aaataccatc	600
ccagggttaa	tgctgggggt	aatttataac	taagagtgtc	ctagttttgc	aatacaggac	660
atgctataaa	aatggaaaga	tgttgctttc	tgagaggatc	ttgctaccag	tggaacagcc	720
actaaggatt	ctgcagttag	agcagagggc	cagctaagt	gtactctccc	agagactgtc	780
tgactcacgc	cacccctcc	accttgga	caggacgctg	tggtttctga	gccaggtaca	840
gtgactcctt	tcggtaagt	cagtggaagc	tgtacactgc	ccaggcaaag	cgccgggca	900
gcgtaggcgg	gcgactcaga	tcccagccag	tggaacttagc	ccctgtttgc	tcctccgata	960
actgggggtga	ccttggttaa	tattcaccag	cagcctcccc	cgttgcccct	ctggatccac	1020
tgcttaaata	cggacgagga	cagggccctg	tctcctcagc	ttcaggcacc	accactgacc	1080
tgggacagta	aaacaggtaa	gtccgctgtt	tgtgtgctgc	ctctgaagtc	cacactgaac	1140
aaacttcagc	ctactcatgt	ccctaaaatg	ggcaaacatt	gcaagcagca	aacagcaaac	1200
acacagccct	ccctgcctgc	tgaccttgga	gctggggcag	aggtcagaga	cctctctggc	1260
ctctactaac	catgttcatt	ttttcttttt	ttttctacag	gtcctgggtg	acgaacag	1318

<210> 320

<211> 1579

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 320

aggctcagag gcacacagga gtttctgggc tcaccctgcc cccttccaac ccctcagttc	60
ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc	120
tactcatgtc cctaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc	180
cctgcctgct gaccttggag ctggggcaga ggtcagagac ctctctgggc ccatgccacc	240
tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagagggt gtcctggcgt	300
ggtttaggta gtgtgagagg gccactacgg gtttaggctg cccatgtaag gaggcaaggc	360
ctggggacac ccgagatgcc tggttataat taaccagac atgtggctgc ccccccccc	420
cccaacacct gctgcctcta aaaataacct tgtccctggt ggatcccact acgggttttag	480
gctgcccattg taaggaggca aggcctgggg acacccgaga tgcctggtta taattaacct	540
agacatgtgg ctgcccccc ccccccaac acctgctgcc tctaaaaata accctgtccc	600
tggtggatcc cactacgggt ttaggctgcc catgtaagga ggcaaggcct ggggacaccc	660
gagatgcctg gttataatta acccagacat gtggctgccc ccccccccc caacacctgc	720
tgcctctaaa aataaccctg tccctggtgg atcccctgca tgcgaagatc ttcgaacaag	780
gctgtggggg actgagggca ggctgtaaca ggcttggggg ccagggtta tacgtgcctg	840
ggactcccaa agtattactg ttccatgttc ccggcgaagg gccagctgtc ccccgccagc	900
tagactcagc acttagttta ggaaccagtg agcaagtcag cccttggggc agcccataca	960
aggccatggg gctgggcaag ctgcacgcct gggtccgggg tgggcacggt gcccgggcaa	1020
cgagctgaaa gctcatctgc tctcaggggc ccctccctgg ggacagcccc tcctggctag	1080
tcacaccctg taggctcctc tatataacct aggggcacag gggctgccct cattctacca	1140
ccacctccac agcacagaca gacactcagg agccagccag cgtcgagatc ttgctaccag	1200
tggaacagcc actaaggatt ctgcagttag agcagagggc cagctaagtg gtactctccc	1260
agagactgtc tgactcacgc cccccctcc accttggaaca caggacgtg tggtttctga	1320
gccaggtaca gtgactcctt tcggtaagtg cagtgggaagc tgtacactgc ccaggcaaag	1380
cgtccgggca gcgtaggcgg gcgactcaga tcccagccag tggacttagc ccctgtttgc	1440
tcctccgata actggggtga ccttggttaa tattcaccag cagcctcccc cgttgccct	1500

ctggatccac tgcttaaata cggacgagga cagggccctg tctcctcagc ttcaggcacc	1560
accactgacc tgggacagt	1579

<210> 321
 <211> 1080
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 321	
aggctcagag gcacacagga gtttctgggc tcaccctgcc cccttccaac ccctcagttc	60
ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc	120
tactcatgtc ctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc	180
cctgcctgct gaccttggag ctggggcaga ggtcagagac ctctctgggc ccatgccacc	240
tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagagggt gtcctggcgt	300
ggtttaggta gtgtgagagg ggtacccggg gatcttgcta ccagtctaga ggccgtccgc	360
cctcggcacc atcctcacga cacccaaata tggcgacggg tgaggaatgg tggggagtta	420
tttttagagc ggtgaggaag gtgggcaggc agcaggtgtt ggcgctctaa aaataactcc	480
cgggagttat ttttagagcg gaggaatggg ggacacccaa atatggcgac ggttcctcac	540
ccgtcgccat atttgggtgt ccgccctcgg ccggggccgc attcctgggg gccgggcggt	600
gctcccgccc gcctcgataa aaggctccgg ggccggcggc ggcccacgag ctacccggag	660
gagcgggagg cgccaagcgt gagtatcgat cttgctacca gtggaacagc cactaaggat	720
tctgcagtga gagcagaggg ccagctaagt ggtactctcc cagagactgt ctgactcacg	780
ccacccccctc caccttggac acaggacgct gtggtttctg agccaggtac agtgactcct	840
ttcggtaaagt gcagtggaag ctgtacactg cccaggcaaa gcgtccgggc agcgtaggcg	900
ggcgactcag atcccagcca gtggacttag cccctgtttg ctctccgat aactgggggtg	960
accttgggta atattcacca gcagcctccc ccgttgcccc tctggatcca ctgcttaaat	1020
acggacgagg acagggccct gtctcctcag cttcaggcac caccactgac ctgggacagt	1080

<210> 322
 <211> 568
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 322
 gaatggtgga cacccaaata tggcgacggt tcctcacccg tcgcatatt tgggtgtccg 60
 ccctcggccg gggccgcatt cctggggggc gggcggtgct cccgcccgcc tcgataaaag 120
 gctccggggc cggcggcggc ccacgagcta cccggaggag cgggaggcgc caagcgatct 180
 tgctaccagt ggaacagcca ctaaggattc tgcagtgaga gcagagggcc agctaagtgg 240
 tactctcca gagactgtct gactcacgcc accccctcca ccttggacac aggacgtgt 300
 ggtttctgag ccaggtacag tgactccttt cggttaagtgc agtggaagct gtacactgcc 360
 caggcaaagc gtccgggcag cgtaggcggg cgactcagat cccagccagt ggacttagcc 420
 cctgtttgct cctccgataa ctgggggtgac cttgggttaat attcaccagc agcctcccc 480
 gttgcccctc tggatccact gcttaaatac ggacgaggac agggccctgt ctctcagct 540
 tcaggcacca ccactgacct gggacagt 568

<210> 323
 <211> 895
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 323
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 ccatacctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc 120
 tactcatgtc ctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc 180
 cctgcctgct gaccttggag ctggggcaga ggtcagagac ctctctgggc ccatgccacc 240
 tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagaggtt gtcctggcgt 300

ggttttaggta gtgtgagagg gtctagagaa tggtggacac ccaaatatgg cgacggttcc	360
tcacccgtcg ccatatttgg gtgtccgccc tcggccgggg ccgcattcct gggggccggg	420
cggtgctccc gccgcctcg ataaaaggct ccggggccgg cggcggccca cgagctaccc	480
ggaggagcgg gaggcgcaa gcgatcttgc taccagtgga acagccacta aggattctgc	540
agtgagagca gagggccagc taagtggtag tctcccagag actgtctgac tcacgccacc	600
ccctccacct tggacacagg acgctgtggt ttctgagcca ggtacagtga ctcctttcgg	660
taagtgcagt ggaagctgta cactgcccag gcaaagcgtc cgggcagcgt aggcgggcga	720
ctcagatccc agccagtgga cttagcccct gtttgctcct ccgataactg gggtgacctt	780
ggttaatatt caccagcagc ctccccgtt gccctctgg atccactgct taaatacggg	840
cgaggacagg gccctgtctc ctcagcttca ggcaccacca ctgacctggg acagt	895

<210> 324

<211> 1291

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 324

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ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc	120
tactcatgtc cctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc	180
cctgcctgct gaccttggag ctggggcaga ggtcagagac ctctctgggc ccatgccacc	240
tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagaggtt gtcctggcgt	300
ggttttaggta gtgtgagagg gccactacgg gtttaggctg cccatgtaag gaggcaaggc	360
ctggggacac ccgagatgcc tggttataat taaccagac atgtggctgc ccccccccc	420
cccaacacct gctgcctcta aaaataacct tgtccctggt ggatcccctg catgcgaaga	480
tcttcgaaca aggctgtggg ggactgaggg caggctgtaa caggcttggg ggccagggct	540
tatacgtgcc tgggactccc aaagtattac tgttccatgt tcccggcgaa gggccagctg	600
tccccgcca gctagactca gcacttagtt taggaaccag tgagcaagtc agcccttggg	660

gcagcccata caaggccatg gggctgggca agctgcacgc ctgggtccgg ggtgggcacg	720
gtgcccgggc aacgagctga aagctcatct gctctcaggg gccctccct ggggacagcc	780
cctcctggct agtcacaccc ttaggctcc tctatataac ccaggggcac aggggctgcc	840
ctcattctac caccacctcc acagcacaga cagacactca ggagccagcc agcgtcgaga	900
tcttgctacc agtggaacag ccactaagga ttctgcagtg agagcagagg gccagctaag	960
tggtactctc ccagagactg tctgactcac gccacccct ccaccttga cacaggacgc	1020
tgtggtttct gagccaggta cagtgactcc tttcggttaag tgcagtggaa gctgtacact	1080
gcccaggcaa agcgtccggg cagcgtaggc gggcgactca gatcccagcc agtggactta	1140
gcccctgttt gtcctccga taactggggg gaccttggtt aatattcacc agcagcctcc	1200
cccgttgccc ctctggatcc actgcttaaa tacggacgag gacagggccc tgtctcctca	1260
gcttcaggca ccaccactga cctgggacag t	1291

<210> 325

<211> 1147

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 325

aggctcagag gcacacagga gtttctgggc tcaccctgcc ccctccaac ccctcagttc	60
ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc	120
tactcatgtc ctaaaatgg gaaacattg caagcagcaa acagcaaaca cacagccctc	180
cctgcctgct gaccttgag ctggggcaga ggtcagagac ctctctgggc ccatgccacc	240
tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagagggt gtcctggcgt	300
ggtttaggta gtgtgagagg gccctgcatg cgaagatctt cgaacaaggc tgtgggggac	360
tgagggcagg ctgtaacagg cttggggggc agggcttata cgtgcctggg actcccaaag	420
tattactgtt ccatgttccc ggcgaagggc cagctgtccc ccgccagcta gactcagcac	480
ttagtttagg aaccagtgag caagtcagcc cttggggcag ccatacaag gccatggggc	540

tgggcaagct gcacgcctgg gtccgggggtg ggcacggtgc ccgggcaacg agctgaaagc	600
tcatctgctc tcagggggccc ctccctgggg acagcccctc ctggctagtc acaccctgta	660
ggctcctcta tataaaccag gggcacaggg gctgccctca ttctaccacc acctccacag	720
cacagacaga cactcaggag ccagccagcg tcgagatctt gctaccagtg gaacagccac	780
taaggattct gcagtgagag cagagggcca gctaagtggc actctcccag agactgtctg	840
actcacgcca cccctccac cttggacaca ggacgctgtg gtttctgagc caggtacagt	900
gactcctttc ggtaagtga gtggaagctg tacactgccc aggcaaagcg tccgggcagc	960
gtaggcgggc gactcagatc ccagccagtg gacttagccc ctgtttgctc ctccgataac	1020
tggggtgacc ttggttaata ttcaccagca gcctccccg ttgcccctct ggatccactg	1080
cttaaatacg gacgaggaca gggccctgtc tcctcagctt caggcaccac cactgacctg	1140
ggacagt	1147

<210> 326

<211> 1490

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 326

aggctcagag gcacacagga gtttctgggc tcaccctgcc cccttccaac ccctcagttc	60
ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc	120
tactcatgtc cctaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc	180
cctgcctgct gaccttggag ctggggcaga ggtcagagac ctctctgggc ccatgccacc	240
tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagagggt gtcctggcgt	300
ggtttaggta gtgtgagagg gcccttcaga ttaaaaataa ctgaggtaag ggcctgggta	360
ggggaggtgg tgtgagacgc tcctgtctct cctctatctg cccatcggcc ctttggggag	420
gaggaatgtg cccaaggact aaaaaaaggc catggagcca gaggggagag ggcaacagac	480
ctttcatggg caaaccttgg ggccctgctg aagctttggc ccactacggg tttaggctgc	540
ccatgtaagg aggcaaggcc tggggacacc cgagatgcct gggtataatt aaccagaca	600

tgtggctgcc ccccccccc ccaacacctg ctgcctctaa aaataaccct gtccctggtg	660
gatccccctgc atgcgaagat cttcgaacaa ggctgtgggg gactgagggc aggctgtaac	720
aggcttgggg gccagggctt atacgtgcct gggactccca aagtattact gttccatgtt	780
cccggaag gccagctgt ccccgccag ctagactcag cacttagttt aggaaccagt	840
gagcaagtca gcccttgggg cagcccatac aaggccatgg ggctgggcaa gctgcacgcc	900
tgggtccggg gtgggcacgg tgccgggca acgagctgaa agctcatctg ctctcagggg	960
cccctccctg gggacagccc ctcttggtta gtcacacct gtaggctcct ctatataacc	1020
caggggcaca ggggctgccc tcattctacc accacctcca cagcacagac agacactcag	1080
gagccagcca gcgtcgagat cttgctacca gtggaacagc cactaaggat tctgcagtga	1140
gagcagaggg ccagctaagt ggtactctcc cagagactgt ctgactcacg ccaccccctc	1200
caccttgga acaggacgt gtggtttctg agccaggtac agtgactcct ttcggtaagt	1260
gcagtggaag ctgtactctg cccaggcaaa gcgtccgggc agcgtaggcg ggcgactcag	1320
atcccagcca gtggacttag cccctgtttg ctctccgat aactggggtg accttggtta	1380
atattcacca gcagcctccc ccgttgcccc tctggatcca ctgcttaa at acggacgagg	1440
acagggccct gtctcctcag cttcaggcac caccactgac ctgggacagt	1490

<210> 327

<211> 969

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 327

aggttaattt ttaaaaagca gtcaaaagtc caagtggccc ttggcagcat ttactctctc	60
tgtttgctct ggtaataat ctcaggagca caaacattcc agatccaggt taatttttta	120
aaagcagtca aaagtccaag tggcccttgg cagcatttac tctctctgtt tgctctggtt	180
aataatctca ggagcacaaa cattccagat ccggcgcgcc agggctggaa gctacctttg	240
tctagaaggc tcagaggcac acaggagttt ctgggctcac cctgccccct tccaaccctt	300

cagttcccat cctccagcag ctgtttgtgt gctgcctctg aagtccacac tgaacaaact	360
tcagcctact catgtcccta aaatgggcaa acattgcaag cagcaaacag caaacacaca	420
gccctccctg cctgctgacc ttggagctgg ggcagaggtc agagacctct ctgggcccat	480
gccacctcca acatccactc gacccttgg aatttcggtg gagaggagca gaggttgtcc	540
tggcgtggtt taggtagtgt gagaggggta cccggggatc ttgctaccag tggaacagcc	600
actaaggatt ctgcagtgag agcagagggc cagctaagtg gtactctccc agagactgtc	660
tgactcacgc caccctcc accttgga caggacgctg tggtttctga gccaggtaca	720
atgactcctt tcggtaaagt cagtggaagc tgtacactgc ccaggcaaag cgtccgggca	780
gcgtaggcgg gcgactcaga tcccagccag tggacttagc ccctgtttgc tcctccgata	840
actgggggtga ccttggttaa tattcaccag cagcctcccc cgttgcccct ctggatccac	900
tgcttaaata cggacgagga cagggccctg tctctcagc ttcaggcacc accactgacc	960
tgggacagt	969

<210> 328

<211> 2074

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 328

aggctcagag gcacacagga gtttctgggc tcaccctgcc cccttccaac ccctcagttc	60
ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc aactgaaca aacttcagcc	120
tactcatgtc cctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc	180
cctgcctgct gaccttgag ctggggcaga ggtcagagac ctctctgggc ccatgccacc	240
tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagagggt gtcctggcgt	300
ggtttaggta gtgtgagagg gcacacatac acgaacacac atacatatac atacattcac	360
atatatgcac acacatacac atatacacgc atacacgtac acacaaatgc aactcacac	420
atgcacacac atacataata tacacactct cacacatgca catacacaca tacatacaca	480
tacatgtgca tgcacacaca caaatacaca tgcatacatc cacattcaca cagatgcaga	540

cacaaatgca cacacacaca cacacacaca cacacacaca cacacacaca cgcacactgc	600
caccctgaac tagtggtggc taaatgaaca ataagtctcc atcaccagct tggggggagg	660
taggtggtag tgtaggtgcc cccattgtgt gatcatgttc attgtatgag tttgtctgtg	720
ttcattcatc atagtacag tccccatgtg ggtagcagag agtacgtgtg catgcatcat	780
ctccgtgttt gtcacatgagt gtgtatgtca gtgtgtttcca gtctttctgt gtgagtgtcg	840
tccccaatcc cccatcccc cccccagatc tctaattagt ggtttggggg ttgttccttt	900
tccctcctgt tcctttcctc agcagcgcgg cagcagcggc ggagcctcg gtggtagcag	960
cagcagcagc agcagcagca gcagcagcag cagcagcagc agcaacagaa gctgccgcgc	1020
cgctgagtag cagcaaggac tccgagtcaa gagtaggatt gtaggattgg atctgagtgg	1080
gaacaagagt gagctggcct gagagaggag cagatgcctc ccagcgcctt caggccaccc	1140
attgccagta atcttcaagc cagacctctt gagaggagac gggacagcca accctagcct	1200
accaggtac agacactggg cagttctggg ggactgcca cagatgccta ttggattcct	1260
ggggtatgta ggactcccg gtctaccagc ctttttcacc tttccccata gcacccccaa	1320
ggaagctctg acaacttgcc catattcctg tttccaccc gtcccctggg caccctctt	1380
tcttctctcc ctcccagatc ctttctttgg ggagctcagc aaatggagca ggaaatttg	1440
accctctgcc tccctctctc gccttcctca ttggatccgg agtcttctcc gctgggaaag	1500
ctgtaattag aggggtggatc cctacagaca gagagcagcc ccccccaccc cccccccag	1560
tcccttctaa ctttagatct cttctctccc attctcccat tctccctccc tctcccttct	1620
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agatcttgct accagtggaa cagccactaa ggattctgca gtgagagcag agggccagct	1740
aagtgggtact ctcccagaga ctgtctgact cacgccaccc cctccacctt ggacacagga	1800
cgctgtgggt tctgagccag gtacagtac tcctttcggg aagtgcagtg gaagctgtac	1860
actgccagg caaagcgtcc gggcagcgta ggcgggcgac tcagatcca gccagtggac	1920
ttagcccctg tttgctctc cgataactgg ggtgacctg gttaatatc accagcagcc	1980
tccccgttg cccctctgga tccactgctt aaatacggac gaggacaggg ccctgtctcc	2040
tcagcttcag gcaccaccac tgacctggga cagt	2074

<210> 329
 <211> 1360
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 329
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 acacactctc acacatgcac atacacacat acatacacat acatgtgcat gcacacacac 180
 aaatacacat gcatacatcc acattcacac agatgcagac acaaatgcac acacacacac 240
 acacacacac acacacacac acacacacac gcacactgcc accctgaact agtggtggct 300
 aaatgaacaa taagtctcca tcaccagctt ggggggaggt aggtggtagt gtaggtgccc 360
 ccattgtgtg atcatgttca ttgtatgagt ttgtctgtgt tcattcatca tagtgacagt 420
 ccccatgtgg gtagcagaga gtacgtgtgc atgcatcatc tccgtgtttg ctcagtagtg 480
 tgtatgtcag tgtgttccag tctttctgtg tgagtgtcgt cccaatccc ccatcccccc 540
 cccagatct ctaattagt gtttggggtt tgttcctttt cctcctgtt cttttcctca 600
 gcagcgcggc agcagcggcg gcagcctcgg tggtagcagc agcagcagca gcagcagcag 660
 cagcagcagc agcagcagca gcaacagaag ctgccgcgcc gctgagtagc agcaaggact 720
 ccgagtcaag agtaggattg taggattgga tctgagtggg aacaagagtg agctggcctg 780
 agagaggagc agatgcctcc cagcgccctc aggccacca ttgccagtaa tcttcaagcc 840
 agacctcttg agaggagacg ggacagccaa ccctagccta cccaggtaca gacactgggc 900
 agttctgggg gactgcccac agatgcctat tggattcctg gggtatgtag gactcccggg 960
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 atattcctgt ttcccacccg tcccctgggc accccctttt cttctctccc tcccagatcc 1080
 cttctttggg gagctcagca aatggagcag gaaatttgga ccctctgcct ccctctctcg 1140
 ccttcctcat tggatccgga gtcttctccg ctgggaaagc tgtaattaga gggtggatcc 1200
 ctacagacag agagcagccc cccaccccc accccccagt cccttctaac tttagatctc 1260

ttctctccca ttctccatt ctccctcct ctcccttctc cctctccac tggctcctcg	1320
gttctctcca tctgcctgac tccttgggac ccggtcccca	1360

<210> 330
 <211> 756
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 330	
cgcggcagca gcggcggcag cctcgggtgg agcagcagca gcagcagcag cagcagcagc	60
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gtcaagagta ggattgtagg attggatctg agtgggaaca agagttagct ggcctgagag	180
aggagcagat gcctcccagc gccctcaggc caccattgc cagtaatctt caagccagac	240
ctcttgagag gagacgggac agccaaccct agcctacca ggtacagaca ctgggcagtt	300
ctgggggact gcccacagat gcctattgga ttcttgggggt atgtaggact cccgggtcta	360
ccagcccttt tcacctttcc ccatagcacc cccaaggaag ctctgacaac ttgcccata	420
tcctgtttcc caccgtccc ctgggcaccc ctttttcttc tctccctccc agatcccttc	480
tttggggagc tcagcaaatg gagcaggaaa tttggaccct ctgcctcctt ctctgcctt	540
cctcattgga tccggagtct tctccgctgg gaaagctgta attagagggt ggatccctac	600
agacagagag cagccccccc acccccaccc ccagtcctt tctaacttta gatctcttct	660
ctcccattct ccattctcc ctccctctcc cttctccctc tcccactggc tcctcggttc	720
tctccatctg cctgactcct tgggacccgg tcccca	756

<210> 331
 <211> 244
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> SITE
 <222> (224)..(244)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> VARIANT
 <222> (227)..(227)
 <223> /replace="Leu"

<220>
 <221> SITE
 <222> (228)..(244)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (234)..(244)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> SITE
 <222> (1)..(244)
 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 331
 Glu Val Gln Leu Val Glu Ser Gly Gly Lys Leu Leu Lys Pro Gly Gly
 1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Phe
 20 25 30

Ala Met Ser Trp Phe Arg Gln Ser Pro Glu Lys Arg Leu Glu Trp Val
 35 40 45

Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Thr Val
 50 55 60

Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Glu Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Trp Gly Tyr Tyr Ala Leu Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu

<210> 332

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 332

Gln Ile Val Leu Ile Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Arg Leu Leu Ile Tyr
35 40 45

Asp Thr Ser Asn Leu Ala Ser Gly Val Pro Val Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Gly Tyr Pro Tyr Thr
85 90 95

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

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

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys
130 135 140

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu
145 150 155 160

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser
165 170 175

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
180 185 190

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe

Asn Arg Gly Glu Cys
210

<210> 333
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> SITE
<222> (225)..(245)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (228)..(228)
<223> /replace="Leu"

<220>
<221> SITE
<222> (229)..(245)
<223> /note="This region may be absent in its entirety"

<220>
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<222> (235)..(245)
<223> /note="This region may be absent in its entirety"

<220>
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<222> (1)..(245)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 333
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Leu Ser Asn Tyr
20 25 30

Tyr Val Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Ile Ile Tyr Gly Ser Asp Glu Thr Ala Tyr Ala Thr Ser Ala Ile
50 55 60

Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Asp Asp Ser Ser Asp Trp Asp Ala Lys Phe Asn Leu Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp
210 215 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Leu
245

<210> 334

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 334

Ala Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Asn Asn Glu
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Arg Ala Ser Thr Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Ser Leu Arg Asn
85 90 95

Ile Asp Asn Ala Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu
115 120 125

Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro

130

135

140

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

Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
 165 170 175

Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
 180 185 190

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val
 195 200 205

Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 335

<211> 244

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<220>

<221> SITE

<222> (224)..(244)

<223> /note="This region may be absent in its entirety"

<220>

<221> VARIANT

<222> (227)..(227)

<223> /replace="Leu"

<220>

<221> SITE

<222> (228)..(244)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (234)..(244)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (1)..(244)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 335

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Pro Phe
20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Lys Ile Ser Pro Gly Gly Ser Trp Thr Tyr Tyr Ser Asp Thr Val
50 55 60

Thr Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gln Leu Trp Gly Tyr Tyr Ala Leu Asp Ile Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu

<210> 336
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 336
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Ser Ala Ser Ile Ser Val Ser Tyr Met
20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
35 40 45

Asp Met Ser Asn Leu Ala Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro Glu

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

<210> 337
 <211> 242
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
 <221> SITE
 <222> (223)..(242)

<223> /note="This region may be absent in its entirety"

<220>

<221> VARIANT

<222> (228)..(228)

<223> /replace="Ser"

<220>

<221> SITE

<222> (232)..(242)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (1)..(242)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 337

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5						10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asn	Phe	Asn	Asp	Tyr
			20					25					30		

Phe	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			

Ala	Gln	Met	Arg	Asn	Lys	Asn	Tyr	Gln	Tyr	Gly	Thr	Tyr	Tyr	Ala	Glu
	50					55					60				

Ser	Leu	Glu	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asp	Ser	Lys	Asn	Ser
65					70					75				80	

Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Lys	Thr	Glu	Asp	Thr	Ala	Val	Tyr
			85						90					95	

Tyr	Cys	Ala	Arg	Glu	Ser	Tyr	Tyr	Gly	Phe	Thr	Ser	Tyr	Trp	Gly	Gln
			100					105					110		

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu

<210> 338

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 338

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Gly Ile Ser
20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asn Ala Asn Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln His Asn Ser Ala Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 339

<211> 247

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> SITE

<222> (227)..(247)

<223> /note="This region may be absent in its entirety"

<220>

<221> VARIANT

<222> (230)..(230)

<223> /replace="Leu"

<220>

<221> SITE

<222> (231)..(247)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (237)..(247)

<223> /note="This region may be absent in its entirety"

<220>

<221> SITE

<222> (1)..(247)

<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 339

Glu Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Thr Ser Arg
20 25 30

Tyr Tyr Ala Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35 40 45

Trp Ile Gly Val Ile Asp Tyr Asp Gly Asp Thr Tyr Tyr Ser Pro Ser
50 55 60

Leu Lys Ser Arg Val Ser Ile Ser Trp Asp Thr Ser Lys Asn Gln Phe
65 70 75 80

Ser Leu Lys Leu Ser Ser Val Thr Pro Ala Asp Thr Ala Val Tyr Tyr
85 90 95

Cys Ala Arg Asp Pro Asp Val Val Thr Gly Phe His Tyr Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
225 230 235 240

Gly Gly Pro Ser Val Phe Leu
245

<210> 340

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 340
Gln Ser Ala Leu Thr Gln Pro Pro Ser Val Ser Gly Thr Pro Gly Gln
1 5 10 15

Ser Val Thr Ile Ser Cys Ala Gly Ala Asn Asn Asp Ile Gly Thr Tyr
20 25 30

Ala Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu
35 40 45

Met Ile Tyr Lys Val Thr Thr Arg Ala Ser Gly Ile Pro Asp Arg Phe
50 55 60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65 70 75 80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Tyr Arg Asn Phe
85 90 95

Asn Asn Ala Val Phe Gly Thr Gly Thr Lys Leu Thr Val Leu Gly Gln
100 105 110

Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu
115 120 125

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

Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys
145 150 155 160

Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr
165 170 175

Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His
180 185 190

Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys
195 200 205

Thr Val Ala Pro Thr Glu Cys Ser
210 215

<210> 341
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> SITE
<222> (224)..(244)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (227)..(227)
<223> /replace="Leu"

<220>
<221> SITE
<222> (228)..(244)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (234)..(244)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (1)..(244)
<223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 341

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Tyr Ser Ile Thr Ser Asp
20 25 30

His Ala Trp Ser Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Ser Tyr Ser Gly Ile Thr Thr Tyr Asn Pro Ser Leu
50 55 60

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

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Leu Ala Arg Thr Thr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Ser Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro

195

200

205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240

Ser Val Phe Leu

<210> 342

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 342

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

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

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 343
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>
<221> misc_feature
<222> (670)..(732)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (679)..(681)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (682)..(732)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (700)..(732)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(732)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 343

gaagtgcagc tggtggaaag cggcggcaaa ctgctgaaac cgggcggcag cctgaaactg 60

agctgcgcgg cgagcggctt tacctttagc agctttgcga tgagctggtt tcgccagagc 120

ccggaaaaac gcctggaatg ggtggcggaa attagcagcg gcggcagcta tacctattat 180

ccggataaccg tgaccggccg ctttaccatt agccgcgata acgcgaaaaa caccctgtat 240

ctggaaatga gcagcctgcg cagcgaagat accgcgatgt attattgcgc gcgcggcctg 300

tggggctatt atgcgctgga ttattggggc cagggcacca gcgtgaccgt gagcagcgcg 360

agcaccaaag gcccagcgt gtttccgctg gcgccgagca gcaaaagcac cagcggcggc 420

accgcggcgc tgggctgcct ggtgaaagat tattttccgg aaccggtgac cgtgagctgg 480

aacagcggcg cgctgaccag cggcgtgcat acctttccgg cgggtgctgca gagcagcggc 540

ctgtatagcc tgagcagcgt ggtgaccgtg ccgagcagca gcctgggcac ccagacctat 600

atttgcaacg tgaaccataa accgagcaac accaaagtgg ataaaaaagt ggaaccgaaa 660

agctgcgata agaccacac ctgccccccc tgccccgccc ccgagctgct gggcggcccc 720

agcgtgttcc tg 732

<210> 344

<211> 639

<212> DNA

<213> Artificial Sequence

<220>

<221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 344
 cagattgtgc tgattcagag cccggcgatt atgagcgca gcccgggcga aaaagtgacc 60
 atgacctgca gcgcgagcag cagcgtgagc tatatgtatt ggtatcagca gaaaccgggc 120
 agcagcccg gcctgctgat ttatgatacc agcaacctgg cgagcggcgt gccggtgcgc 180
 tttagcggca gcggcagcgg caccagctat agcctgacca ttagccgcat ggaagcggaa 240
 gatgcggcga cctattattg ccagcagtgg agcggctatc cgtatacctt tggcggcggc 300
 accaaactgg aaattaaacg caccgtggcg gcgccgagcg tgttttat tccgccgagc 360
 gatgaacagc tgaaaagcgg caccgcgagc gtggtgtgcc tgctgaacaa cttttatccg 420
 cgcgaagcga aagtgcagtg gaaagtggat aacgcgctgc agagcggcaa cagccaggaa 480
 agcgtgaccg aacaggatag caaagatagc acctatagcc tgagcagcac cctgaccctg 540
 agcaaagcgg attatgaaaa acataaagtg tatgcgtgcg aagtgacca tcagggcctg 600
 agcagcccgg tgacaaaaag cttaaccgc ggcgaatgc 639

<210> 345
 <211> 735
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (673)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (682)..(684)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (685)..(735)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (703)..(735)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> misc_feature
 <222> (1)..(735)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 345
 gaagtgcagc tgggtggaaag cggcggcggc ctggtgcagc cgggcggcag cctgcgcctg 60
 agctgcgcgg cgagcggctt tagcctgagc aactattatg tgacctgggt gcgccaggcg 120
 ccgggcaaag gcctggaatg ggtgggcatt atttatggca gcgatgaaac cgcgtatgcg 180
 accagcgcga ttggccgctt taccattagc cgcgataaca gcaaaaacac cctgtatctg 240
 cagatgaaca gcctgcgcgc ggaagatacc gcggtgtatt attgcgcgcg cgatgatagc 300
 agcgattggg atgcgaaatt taacctgtgg ggccagggca ccctggtgac cgtgagcagc 360
 gcgagcacca aaggcccag cgtgtttccg ctggcgccga gcagcaaaag caccagcggc 420
 ggcaccgcgg cgctgggctg cctggtgaaa gattattttc cggaaccggt gaccgtgagc 480
 tggaacagcg gcgcgctgac cagcggcgtg catacctttc cggcggtgct gcagagcagc 540
 ggctgtata gcctgagcag cgtggtgacc gtgccgagca gcagcctggg caccagacc 600
 tatatttgca acgtgaacca taaaccgagc aacaccaaag tggataaacg cgtggaaccg 660
 aaaagctgcg ataagacca cacctgcccc ccctgccccg ccccgagct gctgggcggc 720
 cccagcgtgt tcctg 735

<210> 346
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (670)..(732)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (679)..(681)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (682)..(732)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (700)..(732)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(732)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 346

gcgattcaga tgaccagag cccgagcagc ctgagcgca gcgtgggcga tcgcgtgacc 60

attacctgcc aggcgagcca gagcattaac aacgaactga gctggtatca gcagaaaccg 120

ggcaaagcgc cgaaactgct gatttatcgc gcgagcacc tggcgagcgg cgtgccgagc 180

cgcttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240

gatgattttg cgacctatta ttgccagcag ggctatagcc tgcgcaacat tgataacgcg 300

tttggcggcg gcaccaaagt ggaaattaa cgcaccgtgg cggcgccgag cgtgtttatt 360

tttccgccga gcgatgaaca gctgaaaagc ggcaccgcga gcgtggtgtg cctgctgaac 420

aacttttatc cgcgcaagc gaaagtgcag tggaaagtgg ataacgcgct gcagagcggc 480

aacagccagg aaagcgtgac cgaacaggat agcaaagata gcacctatag cctgagcagc	540
accctgaccc tgagcaaagc ggattatgaa aaacataaag tgtatgcgtg cgaagtgacc	600
catcagggcc tgagcagccc ggtgaccaa agctttaacc gcggcgaatg cgaaccgaaa	660
agctgcgata agaccacac ctgccccccc tgccccgccc ccgagctgct gggcggcccc	720
agcgtgttcc tg	732

<210> 347
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (670)..(732)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (679)..(681)
 <223> /replace="ctg"

<220>
 <221> misc_feature
 <222> (682)..(732)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (700)..(732)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(732)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 347
gaagtgcagc tggtggaaag cggcggcggc ctggtgcagc cgggcggcag cctg'gcctg 60
agctgcgcgg cgagcggcctt taccttttagc ccgtttgcga tgagctgggt gcgccaggcg 120
ccgggcaaag gcctggaatg ggtggcgaaa attagcccgg gcggcagctg gacctattat 180
agcgataaccg tgaccggccg ctttaccatt agccgcgata acgcgaaaaa cagcctgtat 240
ctgcagatga acagcctgcg cgcggaagat accgcggtgt attattgcgc gcgccagctg 300
tggggctatt atgcgctgga tatttggggc cagggcacca ccgtgaccgt gagcagcgcg 360
agcaccaaag gcccgagcgt gtttccgctg gcgccgagca gcaaaagcac cagcggcggc 420
accgcggcgc tgggctgcct ggtgaaagat tattttccgg aaccggtgac cgtgagctgg 480
aacagcggcg cgctgaccag cggcgtgcat acctttccgg cggctgctgca gagcagcggc 540
ctgtatagcc tgagcagcgt ggtgaccgtg ccgagcagca gcctgggcac ccagacctat 600
atttgcaacg tgaaccataa accgagcaac accaaagtgg ataaaaaagt ggaaccgaaa 660
agctgcgata agaccacac ctgccccccc tgccccgcc ccgagctgct gggcggcccc 720
agcgtgttcc tg 732

<210> 348
<211> 639
<212> DNA
<213> Artificial Sequence
<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 348
gaaattgtgc tgaccagag cccggcgacc ctgagcctga gcccgggcga acgcgcgacc 60
ctgagctgca gcgcgagcat tagcgtgagc tatatgtatt ggtatcagca gaaaccgggc 120
caggcggcgc gcctgctgat ttatgatatg agcaacctgg cgagcggcat tccggcgcgc 180
ttagcggca gcggcagcgg caccgatttt accctgacca ttagcagcct ggaaccggaa 240
gattttgcgg tgtattattg catgcagtgg agcggctatc cgtatacctt tggcggcggc 300
accaaagtgg aaattaaacg caccgtggcg gcgccgagcg tgtttatttt tccgccgagc 360
gatgaacagc tgaaaagcgg caccgcgagc gtggtgtgcc tgctgaacaa cttttatccg 420

cgcgaaagcga aagtgcagtg gaaagtggat aacgcgctgc agagcggcaa cagccaggaa	480
agcgtgaccg aacaggatag caaagatagc acctatagcc tgagcagcac cctgaccctg	540
agcaaagcgg attatgaaaa acataaagtg tatgcgtgcg aagtgacca tcagggcctg	600
agcagcccgg tgaccaaaaag ctttaaccgc ggcgaatgc	639

<210> 349
 <211> 726
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
 <221> misc_feature
 <222> (667)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (682)..(683)
 <223> /replace="ag"

<220>
 <221> misc_feature
 <222> (694)..(726)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(726)
 <223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 349	
gaagtgcagc tggtggaaag cggcggcggc ctggtgcagc cgggcggcag cctgcgcctg	60
agctgcgcgg cgagcggctt taactttaac gattatttta tgaactgggt gcgccaggcg	120

ccgggcaaag gcctggaatg ggtggcgag atgcgcaaca aaaactatca gtatggcacc	180
tattatgcgg aaagcctgga aggccgcttt accattagcc gcgatgatag caaaaacagc	240
ctgtatctgc agatgaacag cctgaaaacc gaagataccg cgggtgtatta ttgcgcgcgc	300
gaaagctatt atggctttac cagctattgg ggccaggga ccctggtgac cgtgagcagc	360
gcgagcacca aaggcccag cgtgtttccg ctggcgccgt gcagccgcag caccagcgaa	420
agcaccgcgg cgctgggctg cctggtgaaa gattattttc cggaaccggt gaccgtgagc	480
tggaacagcg gcgcgctgac cagcggcgtg catacctttc cggcggtgct gcagagcagc	540
ggcctgtata gcctgagcag cgtggtgacc gtgccgagca gcagcctggg caccaaaacc	600
tatacctgca acgtggatca taaaccgagc aacaccaaag tgataaacg cgtggagagc	660
aagtacggcc cccctgccc cccctgcccc gccccgagt tcctgggcgg cccagcgtg	720
ttcctg	726

<210> 350

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 350

gatattcaga tgaccagag cccgagcagc ctgagcgca gcgtgggcga tcgcgtgacc	60
attacctgcc aggcgagcca ggatattggc attagcctga gctggtatca gcagaaaccg	120
ggcaaagcgc cgaaactgct gatttataac gcgaacaacc tggcggatgg cgtgccgagc	180
cgcttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg	240
gaagattttg cgacctatta ttgcctgcag cataacagcg cgccgtatac ctttggccag	300
ggcaccaaac tggaatttaa acgcaccgtg gcggcgccga gcgtgtttat ttttcgccg	360
agcgatgaac agctgaaaag cggcaccgcg agcgtggtgt gcctgctgaa caacttttat	420
ccgcgcgaag cgaaagtga gtggaaagtg gataacgcgc tgcaagcgg caacagccag	480
gaaagcgtga ccgaacagga tagcaaagat agcacctata gcctgagcag caccctgacc	540
ctgagcaaag cggattatga aaaacataaa gtgtatgcgt gcgaagtgac ccatcagggc	600

ctgagcagcc cggtgaccaa aagctttaac cgcggcgaat gc

642

<210> 351

<211> 741

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (679)..(741)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (688)..(690)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (691)..(741)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (709)..(741)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(741)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 351

gaagtgcagc tgcaggaaag cggcccgggc ctggtgaaac cgagccagac cctgagcctg 60

acctgcaccg tgagcggcgg cagcattacc agccgctatt atgcgtggag ctggattcgc 120

cagccgccgg gcaaaggcct ggaatggatt ggcgtgattg attatgatgg cgatacctat 180

tatagcccga gcctgaaaag ccgcgtgagc attagctggg ataccagcaa aaaccagttt	240
agcctgaaac tgagcagcgt gaccccggcg gataccgcgg tgtattattg cgcgcgcgat	300
ccggatgtgg tgaccggcctt tcattatgat tattggggcc agggcaccat ggtgaccgtg	360
agcagcgcga gcaccaaagg cccgagcgtg tttccgctgg cgccgagcag caaaagcacc	420
agcggcggca ccgcggcgct gggctgcctg gtgaaagatt attttccgga accggtgacc	480
gtgagctgga acagcggcgc gctgaccagc ggcgtgcata cttttccggc ggtgctgcag	540
agcagcggcc tgtatagcct gagcagcgtg gtgaccgtgc cgagcagcag cctgggcacc	600
cagacctata tttgcaacgt gaaccataaa ccgagcaaca ccaaagtgga taaaaaagtg	660
gaaccgaaaa gctgcgataa gaccacacc tgccccccct gccccgcccc cgagctgctg	720
ggcggcccca gcgtgttcct g	741

<210> 352

<211> 648

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 352

cagagcgcgc tgaccagcc gccgagcgtg agcggcaccc cgggccagag cgtgaccatt	60
agctgcgcgg gcgcgaacaa cgatattggc acctatgcgt atgtgagctg gtatcagcag	120
ctgccgggca ccgcgccgaa actgatgatt tataaagtga ccaccgcgc gagcggcatt	180
ccggatcgct ttagcggcag caaaagcggc aacaccgcga gcctgaccat tagcggcctg	240
caggcggaag atgaagcgga ttattattgc gcgagctatc gcaactttaa caacgcggtg	300
tttggcaccg gcaccaaact gaccgtgctg ggccagccga aagcggcgcc gagcgtgacc	360
ctgtttccgc cgagcagcga agaactgcag gcgaacaaag cgaccctggt gtgcctgatt	420
agcgatTTTT atccgggcgc ggtgaccgtg gcgtggaaag cggatagcag cccggtgaaa	480
gcgggcgtgg aaaccaccac cccgagcaaa cagagcaaca acaaatatgc ggcgagcagc	540
tatctgagcc tgaccccgga acagtggaaa agccatcgca gctatagctg ccaggtgacc	600

catgaaggca gcaccgtgga aaaaaccgtg gcgccgaccg aatgcagc

648

<210> 353
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature
<222> (670)..(732)
<223> /note="This region may be absent in its entirety"

<220>
<221> variation
<222> (679)..(681)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (682)..(732)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (700)..(732)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(732)
<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 353
caggtgcagc tgcaggaaag cggcccgggc ctggtgcgcc cgagccagac cctgagcctg 60
acctgcaccg tgagcggcta tagcattacc agcgatcatg cgtggagctg ggtgcgccag 120
ccgccgggcc gcggcctgga atggattggc tatattagct atagcggcat taccacctat 180

aacccgagcc tgaaaagccg cgtgaccatg ctgcgcgata ccagcaaaaa ccagtttagc	240
ctgcgcctga gcagcgtgac cgcggcggat accgcggtgt attattgcgc gcgcagcctg	300
gcgcgcacca ccgcgatgga ttattggggc cagggcagcc tggtagaccgt gagcagcgcg	360
agcaccaaag gcccgagcgt gtttccgctg gcgccgagca gcaaaagcac cagcggcggc	420
accgcggcgc tgggctgcct ggtgaaagat tattttccgg aaccggtgac cgtgagctgg	480
aacagcggcg cgctgaccag cggcgtgcat acctttccgg cggctgtgca gagcagcggc	540
ctgtatagcc tgagcagcgt ggtgaccgtg ccgagcagca gcctgggcac ccagacctat	600
atttgcaacg tgaaccataa accgagcaac accaaagtgg ataaaaaagt ggaaccgaaa	660
agctgcgata agaccacac ctgcccccc tgccccgcc ccgagctgct gggcggcccc	720
agcgtgttcc tg	732

<210> 354

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 354

gatattcaga tgaccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc	60
attacctgcc gcgcgagcca ggatattagc agctatctga actggtatca gcagaaaccg	120
ggcaaagcgc cgaaactgct gatttattat accagccgcc tgcatagcgg cgtgccgagc	180
cgcttttagcg gcagcggcag cggcaccgat tttaccttta ccattagcag cctgcagccg	240
gaagatattg cgacctatta ttgccagcag ggcaacaccc tgccgtatac ctttggccag	300
ggcaccaaag tggaaattaa acgcaccgtg gcggcgccga gcgtgtttat ttttccgccg	360
agcgaatgaac agctgaaaag cggcaccgcg agcgtggtgt gcctgctgaa caacttttat	420
ccgcgcgaag cgaaagtga gtggaaagtg gataacgcgc tgcagagcgg caacagccag	480
gaaagcgtga ccgaacagga tagcaaagat agcacctata gcctgagcag caccctgacc	540
ctgagcaaag cggattatga aaaacataaa gtgtatgcgt gcgaagtgac ccatcagggc	600
ctgagcagcc cggtagcaaa aagctttaac cgcggcgaat gc	642

<210> 355
 <211> 205
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 355
 Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 356

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 356

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 195 200 205

<210> 357

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 357

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
 20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
 50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 358
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 358
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
195 200 205

<210> 359

<211> 204

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 359

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
195 200

<210> 360

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> SITE
<222> (229)..(249)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (233)..(249)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (239)..(249)
<223> /note="This region may be absent in its entirety"

<220>
<221> source
<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 360
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Thr Phe Ser Ser Phe
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Ser Ser Thr Ile Tyr Tyr Gly Asp Thr Val
50 55 60

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

Leu Gln Met Ser Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Gly Tyr Tyr Tyr Gly Arg Ser Tyr Tyr Thr Met Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
130 135 140

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
145 150 155 160

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
180 185 190

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
195 200 205

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu
245

<210> 361

<211> 219

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 361

Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Ala Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Ile Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Pro Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys
100 105 110

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

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
130 135 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
165 170 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
180 185 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys

210

215

<210> 362
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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 <222> (228)..(238)
 <223> /note="This region may be absent in its entirety"

<220>
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 <223> /note="This region may be absent in its entirety"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 362
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly His Ile Phe Ser Asn Tyr
 20 25 30

Trp Ile Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Glu Ile Leu Pro Gly Ser Gly His Thr Glu Tyr Thr Glu Asn Phe
 50 55 60

Lys Asp Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Tyr Phe Phe Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
210 215 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
225 230 235

<210> 363
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 363
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala

20

25

30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn Thr Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 364

<211> 246

<212> PRT
 <213> Artificial Sequence

 <220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polypeptide"

 <220>
 <221> SITE
 <222> (226)..(246)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> VARIANT
 <222> (229)..(229)
 <223> /replace="Leu"

 <220>
 <221> SITE
 <222> (230)..(246)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> SITE
 <222> (236)..(246)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> SITE
 <222> (1)..(246)
 <223> /note="Variant residues given in the sequence have no preference with respect to those in the annotations for variant positions"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

 <400> 364
 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1 5 10 15

 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

 Val Ile His Trp Val Arg Gln Arg Pro Gly Gln Gly Leu Ala Trp Met
 35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Arg Phe
50 55 60

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

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Leu Cys
85 90 95

Gly Arg Glu Gly Ile Arg Tyr Tyr Gly Leu Leu Gly Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225 230 235 240

Gly Pro Ser Val Phe Leu
245

<210> 365
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 365
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gly Thr Ser Glu Asp Ile Ile Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Gly Tyr Thr Leu Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

365

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 366
<211> 238
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> SITE
<222> (219)..(238)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (224)..(224)
<223> /replace="Ser"

<220>
<221> SITE
<222> (228)..(238)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (1)..(238)
<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 366

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Leu Ser Leu Thr Ser Asn
20 25 30

Ser Val Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Gly Leu Ile Trp Ser Asn Gly Asp Thr Asp Tyr Asn Ser Ala Ile Lys
50 55 60

Ser Arg Phe Thr Ile Ser Arg Asp Thr Ser Lys Ser Thr Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Glu Tyr Tyr Gly Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro

210

215

220

Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu
 225 230 235

<210> 367

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 367

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Leu Ala Ser Glu Gly Ile Ser Ser Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Gly Ala Asn Ser Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Ala Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Lys Phe Pro Asn
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 368
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> SITE
<222> (225)..(244)
<223> /note="This region may be absent in its entirety"

<220>
<221> VARIANT
<222> (230)..(230)
<223> /replace="Ser"

<220>
<221> SITE
<222> (234)..(244)
<223> /note="This region may be absent in its entirety"

<220>
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<223> /note="Variant residues given in the sequence have no
preference with respect to those in the annotations
for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 368

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Gly Leu Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Asn Asn Gly Asp Thr Asn Tyr Gly Gln Glu Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Ser Ser Ser Trp Ala Arg Trp Phe Phe Asp Leu Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

370

Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
210 215 220

Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Leu

<210> 369

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 369

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

Thr Ala Arg Ile Thr Cys Gly Gly Asn Ile Ile Gly Ser Lys Leu Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
35 40 45

Asp Asp Gly Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Thr Gly Ser Asp Pro
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 370
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> SITE
<222> (227)..(237)
<223> /note="This region may be absent in its entirety"

<220>
<221> SITE
<222> (233)..(237)
<223> /note="This region may be absent in its entirety"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 370

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

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Ile Met Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Leu Ile Asn Pro Tyr Asn Gly Gly Thr Asp Tyr Asn Pro Gln Phe
50 55 60

Gln Asp Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Asp Asp Gly Pro Tyr Thr Leu Glu Thr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130 135 140

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Ser Cys
210 215 220

Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
225 230 235

<210> 371
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 371
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Glu Asp Ile Tyr Ser Phe
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asn Ala Gln Thr Glu Ala Gln Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln His His Tyr Asp Ser Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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

115

120

125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 372

<211> 242

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>

<221> SITE

<222> (222)..(242)

<223> /note="This region may be absent in its entirety"

<220>

<221> VARIANT

<222> (225)..(225)

<223> /replace="Leu"

<220>

<221> SITE

<222> (226)..(242)

<223> /note="This region may be absent in its entirety"

<220>
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 <223> /note="This region may be absent in its entirety"

 <220>
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 <223> /note="Variant residues given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

 <220>
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 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

 <400> 372
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

 Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Tyr Ser Ile Thr Ser Gly
 20 25 30

 Tyr Ser Trp Asn Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 35 40 45

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

 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Phe Tyr
 65 70 75 80

 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

 Ala Arg Gly Ser His Tyr Phe Gly His Trp His Phe Ala Val Trp Gly
 100 105 110

 Gln Gly Thr Leu Val Thr Val Ser Ser Gly Pro Ser Val Phe Pro Leu
 115 120 125

 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
 130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Lys Ala Glu Pro Lys Ser Cys Asp Lys Thr His
210 215 220

Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
225 230 235 240

Phe Leu

<210> 373

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 373

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Asp Tyr Asp
20 25 30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
35 40 45

Lys Leu Leu Ile Tyr Ala Ala Ser Tyr Leu Glu Ser Gly Val Pro Ser

50

55

60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser His
85 90 95

Glu Asp Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105 110

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr
130 135 140

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

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
180 185 190

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg
210 215

<210> 374

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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 <222> (228)..(238)
 <223> /note="This region may be absent in its entirety"

<220>
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 <222> (234)..(238)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 374
 Gln Met Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Arg Thr Tyr
 20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

Lys Gly Arg Phe Thr Ile Thr Arg Asp Asn Ser Lys Asn Thr Leu Asn
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ala Pro Gln Trp Glu Leu Val His Glu Ala Phe Asp Ile Trp
 100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
 130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys
210 215 220

Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly
225 230 235

<210> 375

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 375

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

Thr Ala Arg Ile Thr Cys Gly Gly Asn Asn Leu Gly Ser Lys Ser Val
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Val Tyr
35 40 45

Asp Asp Ser Asp Arg Pro Ser Trp Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg Gly Glu Ala Gly
65 70 75 80

380

Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser Asp His
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys
100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln
115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly
130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly
145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala
165 170 175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser
180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val
195 200 205

Ala Pro Thr Glu Cys Ser
210

<210> 376

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<220>

<221> misc_feature

<222> (685)..(747)

<223> /note="This region may be absent in its entirety"

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<220>
<221> variation
<222> (694)..(696)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (697)..(747)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (715)..(747)
<223> /note="This region may be absent in its entirety"

<220>
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<222> (1)..(747)
<223> /note="Variant nucleotides given in the sequence have no
        preference with respect to those in the annotations
        for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
        substitutions and preferred embodiments"

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<400> 376
gaagtgcagc tggtggaaag cggcggcggc ctggtgcagc cgggcggcag cctg'gcctg      60
agctgcagcg cgagcggcctt tacctttagc agctttggca tgcattgggt gcgccaggcg      120
ccgggcaaag gcctggaatg ggtggcgat attagcagcg gcagcagcac catttattat      180
ggcgataccg tgaaaggccg ctttaccatt agccgcgata acgcgaaaaa cagcctgttt      240
ctgcagatga gcagcctgcg cgcggaagat accgcggtgt attattgcgc gcgcgaaggc      300
ggctattatt atggccgcag ctattatacc atggattatt ggggccaggg caccaccgtg      360
accgtgagca gcgcgagcac caaaggcccc agcgtgtttc cgctggcgcc gagcagcaaa      420
agcaccagcg gcggcaccgc ggcgctgggc tgcctggtga aagattattt tccggaaccg      480
gtgaccgtga gctggaacag cggcgcgctg accagcggcg tgcatacctt tccggcggtg      540
ctgcagagca gcggcctgta tagcctgagc agcgtggtga ccgtgccgag cagcagcctg      600
ggcacccaga cctatatattg caacgtgaac cataaaccga gcaacaccaa agtggataaa      660
cgcgtggaac cgaaaagctg cgataagacc cacacctgcc cccctgcccg cgcccccgag      720

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ctggccggcg cccccagcgt gttcctg

747

<210> 377

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 377

gatgtggtga tgaccagag cccgctgagc ctgccggtga ccccgggcgc gccggcgagc 60

attagctgcc gcagcagcca gagcattgtg catagcaacg gcaacaccta tctggaatgg 120

tatctgcaga aaccgggcca gagcccgaac ctgctgattt ataaagttag caaccgcttt 180

agcggcgtgc cggatcgctt tagcggcagc ggcagcggca ccgattttac cctgcgcatt 240

agccgcgtgg aagcggaaga tgtgggcatt tattattgct ttcagggcag ccatgtgccg 300

ccgacctttg gcccgggcac caaactggaa attaaacgca ccgtggcggc gccgagcgtg 360

tttatttttc cgccgagcga tgaacagctg aaaagcggca ccgcgagcgt ggtgtgcctg 420

ctgaacaact tttatccgcg cgaagcgaac gtgcagtgga aagtggataa cgcgctgcag 480

agcggcaaca gccaggaaag cgtgaccgaa caggatagca aagatagcac ctatagcctg 540

agcagcaccg tgaccctgag caaagcggat tatgaaaaac ataaagtgta tgcgtgcgaa 600

gtgacccatc agggcctgag cagcccgggtg accaaaagct ttaaccgcgg cgaatgc 657

<210> 378

<211> 714

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (682)..(714)

<223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (700)..(714)
 <223> /note="This region may be absent in its entirety"

 <220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 378
 caggtgcagc tggtgcagag cggcgcgga gtgaaaaaac cgggcgcgag cgtgaaagtg 60
 agctgcaaag cgagcggcca tatttttagc aactattgga ttcagtgggt gcgccaggcg 120
 ccgggccagg gcctggaatg gatgggcgaa attctgccgg gcagcggcca taccgaatat 180
 accgaaaact ttaaagatcg cgtgaccatg acccgcgata ccagcaccag caccgtgtat 240
 atggaactga gcagcctgcg cagcgaagat acccggtgtt attattgcgc gcgctatatt 300
 tttggcagca gcccgaactg gtattttgat gtgtggggcc agggcaccct ggtgaccgtg 360
 agcagcgcga gcaccaaagg cccgagcgtg tttccgctgg cgccgtgcag ccgcagcacc 420
 agcgaagca ccgcggcgct gggctgcctg gtgaaagatt attttccgga accggtgacc 480
 gtgagctgga acagcggcgc gctgaccagc ggcgtgcata cttttccggc ggtgctgcag 540
 agcagcggcc tgtatagcct gagcagcgtg gtgaccgtgc cgagcagcaa ctttggcacc 600
 cagacctata cctgcaacgt ggatcataaa ccgagcaaca ccaaagtgga taaaaccgtg 660
 gaacgcaaat gctgcgtgga atgccccccc tgccccgcc ccccggtggc cggc 714

<210> 379
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 379
 gatattcaga tgaccagag cccgagcagc ctgagcgcga gcgtgggcga tcgctgacc 60
 attacctgcg gcgcgagcga aaacatttat ggcgcgtga actggtatca gcagaaaccg 120
 ggcaaagcgc cgaaactgct gatttatggc gcgaccaacc tggcggatgg cgtgccgagc 180

cgctttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg	240
gaagattttg cgacctatta ttgccagaac gtgctgaaca ccccgctgac ctttggccag	300
ggcaccaaag tggaaattaa acgcaccgtg gcggcgccga gcgtgtttat ttttccgccg	360
agcgatgaac agctgaaaag cggcaccgcg agcgtggtgt gcctgctgaa caacttttat	420
ccgcgcgaag cgaaagtgca gtggaaagtg gataacgcgc tgcaagcgg caacagccag	480
gaaagcgtga ccgaacagga tagcaaagat agcacctata gcctgagcag caccctgacc	540
ctgagcaaag cggattatga aaaacataaa gtgtatgcgt gcgaagtgac ccatcagggc	600
ctgagcagcc cggtgaccaa aagctttaac cgcggcgaat gc	642

<210> 380

<211> 738

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (676)..(738)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (685)..(687)

<223> /replace="ctg"

<220>

<221> misc_feature

<222> (688)..(738)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (706)..(738)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(738)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations"

for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 380

gaagtgcagc tggtgcagag cggcgcgga gtgaaaaaac cgggcgcgag cgtgaaagtg	60
agctgcaaag cgagcggcta tacctttacc agctatgtga ttcattgggt gcgccagcgc	120
ccgggccagg gcctggcgtg gatgggctat attaaccgt ataacgatgg caccaaata	180
aacgaacgct ttaaaggcaa agtgaccatt accagcgatc gcagcaccag caccgtgtat	240
atggaactga gcagcctgcg cagcgaagat accgcggtgt atctgtgcgg ccgcgaaggc	300
attcgctatt atggcctgct gggcgattat tggggccagg gcaccctggt gaccgtgagc	360
agcgcgagca ccaaaggccc gagcgtgttt ccgctggcgc cgagcagcaa aagcaccagc	420
ggcggcaccg cggcgctggg ctgcctggtg aaagattatt ttccggaacc ggtgaccgtg	480
agctggaaca gcggcgcgct gaccagcggc gtgcatacct ttccggcggt gctgcagagc	540
agcggcctgt atagcctgag cagcgtggtg accgtgccga gcagcagcct gggcaccag	600
acctatattt gcaacgtgaa ccataaacg agcaacacca aagtggataa aaaagtggaa	660
ccgaaaagct gcgataagac ccacacctgc cccccctgcc ccgccccga gctggccggc	720
gccccagcg tgttcctg	738

<210> 381

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 381

gatattcaga tgaccagag cccgagcagc ctgagcgca gcgtgggcga tcgcgtgacc	60
attacctgcg gcaccagcga agatattatt aactatctga actggtatca gcagaaaccg	120
ggcaaagcgc cgaaactgct gatttatcat accagccgcc tgagagcgg cgtgccgagc	180
cgctttagcg gcagcggcag cggcaccgat ttaccctga ccattagcag cctgcagccg	240

gaagattttg cgacctatta ttgccagcag ggctataccc tgccgtatac ctttggccag	300
ggcaccaaag tggaaattaa acgcaccgtg gcggcgccga gcgtgtttat ttttccgccg	360
agcgatgaac agctgaaaag cggcaccgcg agcgtggtgt gcctgctgaa caacttttat	420
ccgcgcgaag cgaaagtga gtggaaagtg gataacgcgc tgcagagcgg caacagccag	480
gaaagcgtga ccgaacagga tagcaaagat agcacctata gcctgagcag caccctgacc	540
ctgagcaaag cggattatga aaaacataaa gtgtatgcgt gcgaagtgac ccatcagggc	600
ctgagcagcc cggtgaccaa aagctttaac cgcggcgaat gc	642

<210> 382

<211> 726

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (667)..(726)

<223> /note="This region may be absent in its entirety"

<220>

<221> variation

<222> (682)..(683)

<223> /replace="ag"

<220>

<221> misc_feature

<222> (694)..(726)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (1)..(726)

<223> /note="Variant nucleotides given in the sequence have no preference with respect to those in the annotations for variant positions"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 382
gaagtgcagc tgggtggaaag cggcggcggc ctggtgcagc cgggcggcag cctgcgcctg 60
agctgcgcgg tgagcggcct gaggctgacc agcaacagcg tgaactggat tcgccaggcg 120
ccgggcaaag gcctggaatg ggtgggcctg atttggagca acggcgatac cgattataac 180
agcgcgatta aaagccgctt taccattagc cgcgatacca gcaaaagcac cgtgtatctg 240
cagatgaaca gcctgcgcgc ggaagatacc gcggtgtatt attgcgcgcg cgaatattat 300
ggctattttg attattgggg ccagggcacc ctggtgaccg tgagcagcgc gaggacaaaa 360
ggcccgagcg tgtttccgct ggcgccgtgc agccgcagca ccagcgaaag caccgcggcg 420
ctgggctgcc tggtgaaaga ttattttccg gaaccggtga ccgtgagctg gaacagcggc 480
gcgctgacca gcggcgtgca tacctttccg gcggtgctgc agagcagcgg cctgtatagc 540
ctgagcagcg tggtgaccgt gccgagcagc agcctgggca ccaaaaccta tacctgcaac 600
gtggatcata aaccgagcaa caccaaagtg gataaacgcg tggaagcaa atatgagagc 660
aagtacggcc cccctgccc cccctgcccc gccccgagt tcctgggcgg cccagcgtg 720
ttcctg 726

<210> 383
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 383
gatattcaga tgaccagag cccgagcagc ctgagcgcga gcgtgggcga tcgcgtgacc 60
attacctgcc tggcgagcga aggcattagc agctatctgg cgtggtatca gcagaaaccg 120
ggcaaagcgc cgaaactgct gatttatggc gcgaacagcc tgagaccgg cgtgccgagc 180
cgcttttagcg gcagcggcag cgcgaccgat tataccctga ccattagcag cctgcagccg 240
gaagattttg cgacctatta ttgccagcag agctataaat ttccgaacac ctttggccag 300
ggcaccaaag tggaagtga acgcaccgtg gcggcgccga gcgtgtttat ttttccgccg 360
agcgatgaac agctgaaaag cggcaccgcg agcgtggtgt gcctgctgaa caacttttat 420

ccgcgcgaag cgaaagtgca gtggaaagtg gataacgcgc tgcagagcgg caacagccag	480
gaaagcgtga ccgaacagga tagcaaagat agcacctata gcctgagcag caccctgacc	540
ctgagcaaag cggattatga aaaacataaa gtgtatgcgt gcgaagtgac ccatcagggc	600
ctgagcagcc cggtgaccaa aagctttaac cgcggcgaat gc	642

<210> 384
 <211> 732
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<220>
 <221> misc_feature
 <222> (673)..(732)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> variation
 <222> (688)..(689)
 <223> /replace="ag"

<220>
 <221> misc_feature
 <222> (700)..(732)
 <223> /note="This region may be absent in its entirety"

<220>
 <221> misc_feature
 <222> (1)..(732)
 <223> /note="Variant nucleotides given in the sequence have no
 preference with respect to those in the annotations
 for variant positions"

<220>
 <221> source
 <223> /note="See specification as filed for detailed description of
 substitutions and preferred embodiments"

<400> 384	
caggtgcagc tggtgcagag cggcgcggaa gtgaaaaaac cgggcgcgag cgtgaaagtg	60
agctgcaaag cgagcggcta tacctttacc aactatggcc tgagctgggt gcgccaggcg	120

ccgggccagg gcctggaatg gatgggctgg attagcgcga acaacggcga taccaactat	180
ggccaggaat ttcagggccg cgtgaccatg accaccgata ccagcaccag caccgcgtat	240
atggaactgc gcagcctgcg cagcgatgat accgcggtgt attattgcgc gcgcgatagc	300
agcagcagct gggcgcgctg gttttttgat ctgtggggcc gcggcaccct ggtgaccgtg	360
agcagcgcga gcaccaaagg cccgagcgtg tttccgctgg cgccgtgcag ccgcagcacc	420
agcgaaagca ccgcggcgct gggctgcctg gtgaaagatt attttccgga accggtgacc	480
gtgagctgga acagcggcgc gctgaccagc ggcgtgcata cttttccggc ggtgctgcag	540
agcagcggcc tgtatagcct gagcagcgtg gtgaccgtgc cgagcagcag cctgggcacc	600
aaaacctata cctgcaacgt ggatcataaa ccgagcaaca ccaaagtgga taaacgcgtg	660
gagagcaagt acggccccc ctgcccccc tgccccgcc ccgagttcct gggcggcccc	720
agcgtgttcc tg	732

<210> 385

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 385

agctatgtgc tgaccagcc gccgagcgtg agcgtggcgc cgggcaaac cgcgcgcat	60
acctgcggcg gcaacattat tggcagcaaa ctggtgcatt ggtatcagca gaaaccgggc	120
caggcgccgg tgctggtgat ttatgatgat ggcgatcgcc cgagcggcat tccggaacgc	180
tttagcggca gcaacagcgg caacaccgcg accctgacca ttagccgcgt ggaagcgggc	240
gatgaagcgg attattattg ccaggtgtgg gataccggca gcgatccggt ggtgtttggc	300
ggcggcacca aactgaccgt gctgggccag ccgaaagcgg cgccgagcgt gaccctgttt	360
ccgccgagca gcgaagaact gcaggcgaac aaagcgaccc tgggtgtgcct gattagcgat	420
ttttatccgg gcgcggtgac cgtggcgtgg aaagcggata gcagcccgggt gaaagcgggc	480
gtggaaacca ccaccccgag caaacagagc aacaacaaat atgcggcgag cagctatctg	540
agcctgaccc cggaacagtg gaaaagccat cgcagctata gctgccaggt gacccatgaa	600

ggcagcaccg tggaaaaaac cgtggcgccg accgaatgca gc

642

<210> 386

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>

<221> misc_feature

<222> (679)..(711)

<223> /note="This region may be absent in its entirety"

<220>

<221> misc_feature

<222> (697)..(711)

<223> /note="This region may be absent in its entirety"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 386

caggtgcagc tgggtgcagag cggcgcgga	gtgaaaaaac cggcgcgag cgtgaaagt	60
agctgcaaag cgagcggcta tacctttacc	ggctatatatta tgaactgggt gcgccaggcg	120
ccgggccagg gcctggaatg gatgggcctg	attaaccctg ataacggcgg caccgattat	180
aacccgcagt ttcaggatcg cgtgaccatt	accgcggata aaagcaccag caccgcgtat	240
atggaactga gcagcctgcg cagcgaagat	accgcggtgt attattgcgc gcgcgatggc	300
tatgatgatg gcccgtatac cctggaaacc	tggggccagg gcaccctggt gaccgtgagc	360
agcgcgagca ccaaaggccc gagcgtgttt	ccgctggcgc cgagcagcaa aagcaccagc	420
ggcggcaccg cggcgctggg ctgcctggtg	aaagattatt ttccggaacc ggtgaccgtg	480
agctggaaca gcggcgcgct gaccagcggc	gtgcatacct ttccggcggt gctgcagagc	540
agcggcctgt atagcctgag cagcgtggtg	accgtgccga gcagcaactt tggcaccag	600
acctatacct gcaacgtgga tcataaaccg	agcaacacca aagtggataa aaccgtggaa	660

cgcaaaagct gcgtggaatg cccccctgc cccgcccccc ccgtggccgg c 711

<210> 387
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 387
gatattcaga tgaccagag cccgagcagc ctgagcgca gcgtgggcga tcgcgtgacc 60
attacctgcc aggcgagcga agatatttat agctttgtgg cgtggtatca gcagaaaccg 120
ggcaaagcgc cgaaactgct gatttataac gcgcagaccg aagcgcaggg cgtgccgagc 180
cgcttttagcg gcagcggcag cggcaccgat tttaccctga ccattagcag cctgcagccg 240
gaagattttg cgacctatta ttgccagcat cattatgata gcccgtgac ctttggcggc 300
ggcaccaaag tggaaattaa acgcaccgtg gcggcgccga gcgtgtttat tttccgccg 360
agcgatgaac agctgaaaag cggcaccgcg agcgtggtgt gcctgctgaa caacttttat 420
ccgcgcgaag cgaaagtga gtggaaagtg gataacgcgc tgcagagcgg caacagccag 480
gaaagcgtga ccgaacagga tagcaaagat agcacctata gcctgagcag caccctgacc 540
ctgagcaaag cggattatga aaaacataaa gtgtatgcgt gcgaagtgac ccatcagggc 600
ctgagcagcc cggtgaccaa aagctttaac cgcggcgaat gc 642

<210> 388
<211> 708
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature
<222> (646)..(708)
<223> /note="This region may be absent in its entirety"


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<220>
<221> variation
<222> (655)..(657)
<223> /replace="ctg"

<220>
<221> misc_feature
<222> (658)..(708)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (676)..(708)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (1)..(708)
<223> /note="Variant nucleotides given in the sequence have no
      preference with respect to those in the annotations
      for variant positions"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
      substitutions and preferred embodiments"

<400> 388
gaagtgcagc tggtggaaag cggcggcggc ctggtgcagc cgggcggcag cctgcgcctg      60
agctgcgcgg tgagcggcta tagcattacc agcggctata gctggaactg gattcgccag      120
gcgccgggca aaggcctgga atgggtggcg agcattacct atgatggcag caccaactat      180
gcggatagcg tgaaaggccg ctttaccatt agccgcgatg atagcaaaaa caccttttat      240
ctgcagatga acagcctgcg cgcggaagat accgcggtgt attattgcgc gcgcggcagc      300
cattattttg gccattggca ttttgcggtg tggggccagg gcaccctggt gaccgtgagc      360
agcggcccga gcgtgtttcc gctggcgccg agcagcaaaa gcaccagcgg cggcaccgcg      420
gcgctgggct gcctggtgaa agattatttt ccggaaccgg tgaccgtgag ctggaacagc      480
ggcgcgctga ccagcggcgt gcataccttt ccggcgggtgc tgcagagcag cggcctgtat      540
agcctgagca gcgtggtgac cgtgccgagc agcagcctgg gcaccagac ctatatttgc      600
aacgtgaacc ataaaccgag caacaccaaa gtggataaaa aagcgaagac ccacacctgc      660
ccccctgcc ccgccccga gctggccggc gccccagcg tgttcctg      708

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<210> 389
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 389
gatattcagc tgaccagag cccgagcagc ctgagcgca gcgtgggcga tcgcgtgacc 60
attacctgcc gcgcgagcca gagcgtggat tatgatggcg atagctatat gaactggtat 120
cagcagaaac cgggcaaagc gccgaaactg ctgatttatg cggcgagcta tctggaaagc 180
ggcgtgccga gccgcttttag cggcagcggc agcggcaccg attttaccct gaccattagc 240
agcctgcagc cggaagattt tgcgacctat tattgccagc agagccatga agatccgtat 300
acctttggcc agggcaccaa agtggaaatt aaacgcaccg tggcggcgcc gagcgtgttt 360
atttttccgc cgagcgatga acagctgaaa agcggcaccg cgagcgtggt gtgcctgctg 420
aacaactttt atccgcgcga agcgaaagtg cagtggaaag tggataacgc gctgcagagc 480
ggcaacagcc aggaaagcgt gaccgaacag gatagcaaag atagcaccta tagcctgagc 540
agcaccctga ccctgagcaa agcggattat gaaaaacata aagtgtatgc gtgcgaagtg 600
acccatcagg gcctgagcag cccggtgacc aaaagcttta accgc 645

<210> 390
<211> 693
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> misc_feature
<222> (661)..(693)
<223> /note="This region may be absent in its entirety"

<220>
<221> misc_feature
<222> (679)..(693)

<223> /note="This region may be absent in its entirety"

<220>

<221> source

<223> /note="See specification as filed for detailed description of substitutions and preferred embodiments"

<400> 390

cagatgcagc	tggtggaaag	cggcggcggc	gtggtgcagc	cgggccgcag	cctg'gcctg	60
agctgcgcgg	cgagcggctt	tacctttcgc	acctatggca	tgattgggt	gcgccaggcg	120
ccgggcaaag	gcctggaatg	ggtggcgggtg	atttggtatg	atggcagcaa	caaacattat	180
gcggatagcg	tgaaaggccg	ctttaccatt	acccgcgata	acagcaaaaa	caccctgaac	240
ctgcagatga	acagcctgcg	cgcggaagat	accgcggtgt	attattgcgc	gcgcgcgccg	300
cagtgggaac	tggtgcatga	agcgtttgat	atttggggcc	agggcaccat	ggtgaccgtg	360
agcagcgcga	gcaccaaagg	cccgagcgtg	tttccgctgg	cgccgtgcag	ccgcagcacc	420
agcgaagca	ccgcggcgct	gggctgcctg	gtgaaagatt	attttccgga	accggtgacc	480
gtgagctgga	acagcggcgc	gctgaccagc	ggcgtgcata	cctttccggc	ggtgctgcag	540
agcagcggcc	tgtatagcct	gagcagcgtg	gtgaccgtgc	cgagcagcaa	ctttggcacc	600
cagacctata	cctgcaacgt	ggatcataaa	ccgagcaaca	ccaaagtgga	taaaaccgtg	660
tgccccccct	gccccgcccc	ccccgtggcc	ggc			693

<210> 391

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 391

agctatgtgc	tgaccagcc	gccgagcgtg	agcgtggcgc	cgggccagac	cgcgcgcat	60
acctgcggcg	gcaacaacct	gggcagcaaa	agcgtgcatt	ggtatcagca	gaaaccgggc	120
caggcgccgg	tgctggtggt	gtatgatgat	agcgatcgcc	cgagctggat	tccggaacgc	180
tttagcggca	gcaacagcgg	caacaccgcg	accctgacca	ttagccgcgg	cgaagcgggc	240
gatgaagcgg	attattattg	ccaggtgtgg	gatagcagca	gcgatcatgt	ggtgtttggc	300

ggcggcacca aactgaccgt gctgggccag ccgaaagcgg cgccgagcgt gaccctgttt 360
ccgccgagca gcgaagaact gcaggcgaac aaagcgaccc tgggtgtgcct gattagcgat 420
ttttatccgg gcgcggtgac cgtggcgtgg aaagcggata gcagcccggg gaaagcgggc 480
gtggaaacca ccaccccag caaacagagc aacaacaaat atgcggcgag cagctatctg 540
agcctgaccc cggaacagt gaaaagccat cgcagctata gctgccaggt gacccatgaa 600
ggcagcaccg tggaaaaaac cgtggcgccg accgaatgca gc 642

<210> 392

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 392

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 393

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 393

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Glu Gly Asn Val Phe Ser Cys Ser Val Leu His Glu Ala Leu His Ser
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
195 200 205

<210> 394

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 394

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
195 200 205

<210> 395

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 395

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
195 200 205

400

<210> 396
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 396
Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
85 90 95

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln

165

170

175

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 195 200 205

<210> 397

<211> 203

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
 polypeptide"

<400> 397

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
 1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
 20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
 35 40 45

Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu
 50 55 60

Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
 65 70 75 80

Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys
 85 90 95

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly
145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
165 170 175

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
195 200

<210> 398

<211> 205

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<400> 398

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
1 5 10 15

Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys
20 25 30

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
35 40 45

Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu
50 55 60

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
65 70 75 80

Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys

85

90

95

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

Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 115 120 125

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
 130 135 140

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
 145 150 155 160

Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln
 165 170 175

Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
 180 185 190

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 195 200 205

<210> 399

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 399

Glu Lys His Lys Val Tyr
 1 5

<210> 400

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 400

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

Ala Gly Gly

<210> 401

<400> 401

000

Ala Gly Gly

<210> 402

<400> 402

000

<210> 403

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 403

Glu Asp Ile Ala Thr Tyr Tyr
1 5

<210> 404

<400> 404

000

<210> 405

<400> 405

000

<210> 406

<400> 406

000

<210> 407

<400> 407

000

<210> 408

<400> 408

000

<210> 409

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 409

Glu Asp Val Gly Ile Val Tyr Tyr

1

5

<210> 410

<400> 410

000

<210> 411

<211> 1725

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 411

gacattgatt attgactagt tattaatagt aatcaattac ggggtcatta gttcatagcc	60
catatatgga gttccgcgtt acataactta cggtaaatgg cccgcctggc tgaccgcca	120
acgacccccg cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga	180
ctttccattg acgtcaatgg gtggagtatt tacggtaaac tgcccacttg gcagtacatc	240
aagtgtatca tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgctt	300
ggcattatgc ccagtacatg accttatggg acttttctac ttggcagtac atctacgtat	360
tagtcatcgc tattaccatg gtcgaggtga gcccacgtt ctgcttcact ctccccatct	420
cccccccctc cccaccccc aTTTTgtatt tatttatttt ttaattattt tgtgcagcga	480
tgggggcggg gggggggggg gggcgcgcg caggcggggc ggggcggggc gaggggcggg	540
gcggggcgag gcggagaggt gcggcggcag ccaatcagag cggcgcgctc cgaaagtttc	600
cttttatggc gaggcggcgg cggcggcggc cctataaaaa gcgaagcgcg cggcgggcgg	660
gagtcgctgc gcgctgcctt cgccccgtgc cccgctccgc cgccgcctcg cgccgccgcg	720
cccggctctg actgaccgcg ttactccac aggtgagcgg gcgggacggc ctttctctc	780
cgggctgtaa ttagcgcttg gtttaatgac ggcttgtttc ttttctgtgg ctgcgtgaaa	840
gccttgaggg gctccgggag ggccctttgt gcggggggag cggctcgggg ggtgcgtgcg	900
tgtgtgtgtg cgtggggagc gccgcgtgcg gctccgcgct gccggcggcg tgtgagcgct	960
gcggggcgcg cgcggggctt tgtgcgctcc gcagtgtgcg cgaggggagc gcggccgggg	1020
gcggtgcccc gcggtgcggg gggggctgcg aggggaacaa aggctgcgtg cggggtgtgt	1080
gcgtgggggg gtgagcaggg ggtgtgggcg cgtcggtcgg gctgcaacc cccctgcacc	1140
cccctcccc agttgctgag cacggcccgg cttcgggtgc ggggctccgt acggggcgtg	1200
gcgcggggct cgccgtgccg ggcggggggt ggcggcaggt gggggtgccg ggcggggcgg	1260
ggccgcctcg ggccggggag ggctcggggg aggggcgcgg cggcccccg agcgccggcg	1320
gctgtcgagg cgcggcgagc cgagccatt gccttttatg gtaatcgtgc gagaggcgcg	1380
agggacttcc tttgtccaa atctgtgcgg agccgaaatc tgggagcgcg cgccgcaccc	1440
cctctagcgg gcgcggggcg aagcggtgcg gcgccggcag gaaggaaatg ggcggggagg	1500

gccttcgtgc gtcgccgcgc cgccgtcccc ttctccctct ccagcctcgg ggctgtccgc	1560
ggggggacgg ctgccttcgg gggggacggg gcagggcggg gttcggcttc tggcgtgtga	1620
ccggcggctc tagagcctct gctaaccatg ttcatgcctt cttctttttc ctacagctcc	1680
tgggcaacgt gctggttatt gtgctgtctc atcattttgg caaag	1725

<210> 412
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 412	
aggctcagag gcacacagga gtttctgggc tcaccctgcc cccttccaac ccctcagttc	60
ccatcctcca gcagctgttt gtgtgctgcc tctgaagtcc acactgaaca aacttcagcc	120
tactcatgtc cctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc	180
cctgcctgct gaccttggag ctggggcaga ggtcagagac ctctctgggc ccatgccacc	240
tccaacatcc actcgacccc ttggaatttc ggtggagagg agcagagggt gtcctggcgt	300
ggtttaggta gtgtgagagg ggtacccggg gatcttgcta ccagtggaac agccactaag	360
gattctgcag tgagagcaga gggccagcta agtggtactc tcccagagac tgtctgactc	420
acgccacccc ctccaccttg gacacaggac gctgtggttt ctgagccagg tacaatgact	480
cctttcggtg agtgacgtgg aagctgtaca ctgcccaggc aaagcgtccg ggcagcgtag	540
gcgggcgact cagatcccag ccagtggact tagcccctgt ttgctcctcc gataactggg	600
gtgaccttgg ttaatatcca ccagcagcct cccccgttgc ccctctggat ccactgctta	660
aatacggacg aggacagggc cctgtctcct cagcttcagg caccaccact gacctgggac	720
agt	723

<210> 413
 <211> 865
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 413
 ccactacggg tttaggctgc ccatgtaagg aggcaaggcc tggggacacc cgagatgcct 60
 gggtataatt aaccagaca tgttgctgcc ccccccccc ccaacacctg ctgcctctaa 120
 aaataaccct gtccctggtg gatcccacta cgggttttagg ctgcccattgt aaggaggcaa 180
 ggcttgggga caccgagat gcctgggttat aattaacca gacatgtggc tgcccccccc 240
 ccccccaaca cctgctgcct ctaaaaataa ccctgtccct ggtggatccc actacgggtt 300
 taggctgccc atgtaaggag gcaaggcctg gggacacccg agatgcctgg ttataattaa 360
 ccagacatg tggctgcccc ccccccccc aacacctgct gcctctaaaa ataaccctgt 420
 ccctggtgga tcccctgcat gcgaagatct tcgaacaagg ctgtggggga ctgagggcag 480
 gctgtaacag gcttgggggc cagggttat acgtgcctgg gactcccaa gtattactgt 540
 tccatgttcc cggcgaaggg ccagctgtcc cccgccagct agactcagca cttagtttag 600
 gaaccagtga gcaagtcagc ccttggggca gccatacaa ggccatgggg ctgggcaagc 660
 tgcacgcctg ggtccggggt gggcacggtg cccgggcaac gagctgaaag ctcatctgct 720
 ctgaggggcc cctccctggg gacagcccct cctggctagt cacaccctgt aggctcctct 780
 atataacca ggggcacagg ggctgccctc attctaccac cacctccaca gcacagacag 840
 aactcagga gccagccagc gtcga 865

<210> 414
 <211> 251
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 414
 atggaggcgg tactatgtag atgagaattc aggagcaaac tgggaaaagc aactgcttcc 60
 aaatatttgt gatatttaca gtgtagtttt ggaaaaactc ttagcctacc aattcttcta 120
 agtgttttaa aatgtgggag ccagtacaca tgaagttata gagtgtttta atgaggctta 180

aatattttacc gtaactatga aatgctacgc atatcatgct gttcaggctc cgtggccacg 240
caactcatac t 251

<210> 415
<211> 212
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 415
gggcagagcg cacatcgccc acagtccccg agaagttggg gggagggggtc ggcaattgaa 60
cgggtgccta gagaaggtgg cgcggggtaa actgggaaag tgatgtcgtg tactggctcc 120
gcctttttcc cgagggtggg ggagaaccgt atataagtgc agtagtcgcc gtgaacgttc 180
tttttcgcaa cgggtttgcc gccagaacac ag 212

<210> 416
<211> 133
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 416
gtaagtatca aggttacaag acaggtttta ggagaccaat agaaactggg cttgtcgaga 60
cagagaagac tcttgcgttt ctgataggca cctattgggtc ttactgacat ccactttgcc 120
tttctctcca cag 133

<210> 417
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 417
 gtgagtatct cagggatcca gacatgggga tatgggaggt gcctctgata ccagggctca 60
 ctgtgggtct ctctgttcac ag 82

<210> 418
 <211> 130
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 418
 ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgctc ggcgaccttt 60
 ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gaggggccaa ctccatcact 120
 aggggttcct 130

<210> 419
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 419
 ctgcgcgctc gctcgctcac tgaggccgcc cgggcaaagc ccgggcgctc ggcgaccttt 60
 ggtcgcccgg cctcagtgag cgagcgagcg cgcagagagg gagggg 106

<210> 420
 <211> 143
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 polynucleotide"

<400> 420
 gaaccctag tgatggagtt ggccactccc tctctgcgcg ctgctcgct cactgaggcc 60

gcccgggcaa agcccgggcg tcgggcgacc tttggtcgcc cggcctcagt gagcgagcga 120

gcgcgcagag agggagtggc caa 143

<210> 421

<211> 110

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 421

ttggccactc cctctctgcg cgctcgctcg ctactgagg cgggcgacc aaaggtcgcc 60

cgacgcccgg gctttgcccg ggcggcctca gtgagcgagc gagcgcgag 110

<210> 422

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 422

atgtatagga tgcaactgct cctcctgatt gctctgagcc tggctcttgt gaccaactct 60

<210> 423

<211> 460

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 423

gggctggaag ctacctttga catcatttcc tctgcgaatg catgtataat ttctacagaa 60

cctattagaa aggatcacc agcctctgct tttgtacaac tttcccttaa aaaactgcc 120

attccactgc tgtttgccc aatagtgaga actttttcct gctgcctctt ggtgcttttg 180

cctatggccc ctattctgcc tgctgaagac actcttgcca gcatggactt aaacccctcc	240
agctctgaca atcctctttc tcttttgttt tacatgaagg gtctggcagc caaagcaatc	300
actcaaagtt caaaccttat ctttttttgc tttgttcctc ttggccttgg tttgtacat	360
cagctttgaa aataccatcc cagggttaat gctggggtta atttataact aagagtgtc	420
tagttttgca atacaggaca tgctataaaa atggaaagat	460

<210> 424
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 424	
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gagaatcctg ggcct	75

<210> 425
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 425	
agaaagagaa ga	12

<210> 426
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic
 oligonucleotide"

<400> 426	
agaaagagaa gaggctctgg a	21

<210> 427
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 427
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9

<210> 428
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
oligonucleotide"

<400> 428
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54

<210> 429
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> SITE
<222> (5)..(7)
<223> /note="This region may be absent in its entirety"

<220>
<221> source
<223> /note="See specification as filed for detailed description of
substitutions and preferred embodiments"

<400> 429
Arg Lys Arg Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys

1 5 10 15

Gly Asp Val Glu Glu Asn Pro Gly Pro
20 25

<210> 430
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 430
Cys Pro Pro Cys Ala
1 5

<210> 431
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 431
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala
1 5 10 15

Ala Gly Gly

<210> 432
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 432
Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Ala

1 5 10 15

Ala Gly Gly

<210> 433
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 433
Glu Arg Lys Ser Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly

<210> 434
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<400> 434
Glu Arg Lys Ser Cys Val Glu Cys Pro Pro Cys Pro Ala
1 5 10

<210> 435
<211> 4196
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 435
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atagcccata tatggagttc cgcgttacat aacttacggt aaatggcccg cctggctgac	120
cgcccaacga ccccgccca ttgacgtcaa taatgacgta tgttcccata gtaacgcaa	180
tagggacttt ccattgacgt caatgggtgg agtatttacg gtaaactgcc cacttggcag	240
tacatcaagt gtatcatatg ccaagtacgc cccctattga cgtcaatgac ggtaaattggc	300
ccgcctggca ttatgcccag tacatgacct tatgggactt tcctacttgg cagtacatct	360
acgtattagt catcgctatt accatggctg aggtgagccc cacgttctgc ttcactctcc	420
ccatctcccc cccctccca cccccaattt tgtatttatt ttttttttaa ttattttgtg	480
cagcgatggg ggcggggggg gggggggggc gcgcgccagg cggggcgggg cggggcgagg	540
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ctctgccaaa aattatgggg acatcatgaa gccccttgag catctgactt ctggctaata	4140
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<210> 436

<211> 4106

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 436

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acgacccccc cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga	180
ctttccattg acgtcaatgg gtggagtatt tacggtaaac tgcccacttg gcagtacatc	240

aagtgtatca tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgctt	300
ggcattatgc ccagtacatg accttatggg actttcctac ttggcagtac atctacgtat	360
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tgtgttgga ttttttgtgt ctctca	4106

<210> 437

<211> 4092

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 437

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acgacccccg cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga	180
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<210> 438

<211> 3397

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 438

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<210> 439

<211> 3227

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 439

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<210> 440
 <211> 3472
 <212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 440

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<210> 441

<211> 3553

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 441

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<210> 442

<211> 3592

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic

polynucleotide"

<400> 442

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<210> 443

<211> 4083

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 443

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tactcatgtc ctaaaatgg gcaaacattg caagcagcaa acagcaaaca cacagccctc	180
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tca	4083

<210> 444
 <211> 1353
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 444	
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<210> 445
 <211> 363
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 445	
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ctgcagatga actccctgag agctgaggac acagcagtgt actactgtgc caaggtgtcc	300
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tct	363

<210> 446
 <211> 294
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 446	
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<210> 447
 <211> 651
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 447	
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tacaagacaa cccctcctgt gctggactct gatggctcat tcttcctgta cagcaagctg	540
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<210> 448
 <211> 642
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 448
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cctagagaag ccaagggtgca gtggaagggt gacaatgccc tgcagtctgg caatagccaa 480
gaatctgtga cagagcagga ctccaaggat tccacctaca gcctgagcag caccctgaca 540
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<210> 449
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polynucleotide"

<400> 449
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atcacatgca gagccagcca gggaatcaga aactacctgg cctggtatca gcaaaagcct 120
ggcaaggccc ctaagctgct gatctatgca gccagcacac tgcagtcagg ggtgccaagc 180
agattttcag gctctggctc tggcacagac ttcaccctga ccatttctag cctgcagcct 240
gaggatgtgg ccacctacta ctgccagaga tacaacagag ccccatcac ctttggacag 300
ggcaciaaagg tggaaatcaa g 321

<210> 450
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 450
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 ggcaactgcct ctgttgtgtg cctgctgaac aacttctacc ccagagaagc caaggtgcag 120
 tggaagggttg acaatgccct gcagtcaggc aacagccaag aatctgtgac tgaacaggat 180
 tccaaggata gcacctacag cctgagcagc accctgacac tgagcaaggc tgactatgag 240
 aagcaciaag tgtatgcctg tgaagtgacc caccagggac tgagcagccc agtgaccaag 300
 agcttcaaca ggggagagtg ctga 324

<210> 451
 <211> 4092
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 451
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 catatatgga gttccgcgtt acataactta cggtaaattgg cccgcctggc tgaccgccca 120
 acgacccccg cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga 180
 ctttccattg acgtcaatgg gtggagtatt tacggtaaac tgcccacttg gcagtacatc 240
 aagtgtatca tatgccaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgctt 300
 ggcaattatgc ccagtacatg accttatggg actttcctac ttggcagtac atctacgtat 360
 tagtcatcgc tattaccatg gtcgaggtga gcccacggtt ctgcttcact ctccccatct 420
 cccccccctc cccacccccca attttgtatt tatttatattt ttaattattt tgtgcagcga 480
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 gcggggcgag gcgggagaggt gcggcggcag ccaatcagag cggcgcgctc cgaaagtttc 600
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cccggtcttg actgaccgcg ttactccac aggtgagcgg gcgggacggc ctttctctc	780
cgggctgtaa ttagcgcttg gtttaatgac ggcttgtttc ttttctgtgg ctgcgtgaaa	840
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gtctctcact cg	4092

<210> 452

<211> 2193

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 452

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tcttgtgctg cctctggctt cacctttgat gactatgcc a tgactgggt cagacaggcc	180
cctggcaaag gactggaatg ggtgtcagcc atcacctgga actctggcca cattgactat	240
gctgactctg tggaaggcag attcaccatc agcagagaca atgccaagaa cagcctgtac	300
ctgcagatga actccctgag agctgaggac acagcagtgt actactgtgc caaggtgtcc	360
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tcttggaaact caggggctct gacctctggg gtgcacacat ttccagctgt gctgcagtcc	600
tctggcctgt actctctgtc ctctgtggtc acagtgccta gctctagcct gggcacccag	660
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cctgaagtga cctgtgtggt ggttgatgtg tcccatgagg acccagaagt gaagttcaat	900
tggtatgtgg atggggttga agtgcacaat gctaagacca agcctagaga ggaacagtac	960

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gagcaggact ccaaggattc cacctacagc ctgagcagca ccctgacact gagcaaggct	2100
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gtgaccaaga gcttcaacag gggagagtgc tga	2193

<210> 453

<211> 3423

<212> DNA

<213> Artificial Sequence

<220>

<221> source

<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<400> 453

gacattgatt attgactagt tattaatagt aatcaattac ggggtcatta gttcatagcc	60
catatatgga gttccgcgtt acataactta cggtaaattgg cccgcctggc tgaccgcccc	120
acgacccccg cccattgacg tcaataatga cgtatgttcc catagtaacg ccaataggga	180
ctttccattg acgtcaatgg gtggagtatt tacggtaaac tgcccacttg gcagtacatc	240
aagtgtatca tatgccaaagt acgcccccta ttgacgtcaa tgacggtaaa tggcccgctt	300
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cccccccctc cccaccccc aattttgtatt tattttatttt ttaattattt tgtgcagcga	480
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<210> 454
 <211> 1524
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> source
 <223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

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