

SEQUENCE LISTING

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<120> PD-1 HOMING ENDONUCLEASE VARIANTS, COMPOSITIONS, AND METHODS OF USE

<130> BLBD-076/02W0

<150> US 62/414,279
<151> 2016-10-28

<150> US 62/385,079
<151> 2016-09-08

<160> 123

<170> PatentIn version 3.5

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<213> Ophiostoma novo-ulmi subsp. americana (mitochondrion)

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Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

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

Ala Phe Cys Val Met Glu Asn Lys Glu His Leu Lys Ile Asn Gly Ile
115 120 125

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

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

Gly Glu Gly Cys Phe Phe Val Asn Leu Ile Lys Ser Lys Ser Lys Leu
180 185 190

Gly Val Gln Val Gln Leu Val Phe Ser Ile Thr Gln His Ile Lys Asp
195 200 205

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

Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
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<213> Ophiostoma novo-ulmi subsp. americana (mitochondrion)

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Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

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

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

Gly Glu Gly Cys Phe Phe Val Asn Leu Ile Lys Ser Lys Ser Lys Leu
180 185 190

Gly Val Gln Val Gln Leu Val Phe Ser Ile Thr Gln His Ile Lys Asp

195

200

205

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

Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
 225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
 245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
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Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe
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<213> Ophiostoma novo-ulmi subsp. americana (mitochondrion)

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Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

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

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

Gly Glu Gly Cys Phe Phe Val Asn Leu Ile Lys Ser Lys Ser Lys Leu
180 185 190

Gly Val Gln Val Gln Leu Val Phe Ser Ile Thr Gln His Ile Lys Asp
195 200 205

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

Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Val Phe
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Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

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

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

Gly Glu Gly Cys Phe Phe Val Asn Leu Ile Lys Ser Lys Ser Lys Leu
180 185 190

Gly Val Gln Val Gln Leu Val Phe Ser Ile Thr Gln His Ile Lys Asp
195 200 205

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

Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
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Asn Lys Ser Ser Val Gly Tyr Ser Thr Glu Leu Gly Phe Gln Ile Thr
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
 115 120 125

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

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
 165 170 175

Gly Glu Gly Cys Phe Phe Val Asn Leu Ile Lys Ser Lys Ser Lys Leu
180 185 190

Gly Val Gln Val Gln Leu Val Phe Ser Ile Thr Gln His Ile Lys Asp
195 200 205

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

Lys Glu Lys Asn Lys Ser Glu Phe Ser Trp Leu Asp Phe Val Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
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Asn Pro Asn Ile Pro Arg Tyr Lys Thr Arg Leu Arg Phe Glu Ile Asp
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
 115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
 130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
 165 170 175

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

Pro Val Gln Val Arg Leu Arg Phe Ala Ile Gly Gln His Ile Arg Asp
 195 200 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Arg Ile

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215

220

Arg Glu Lys Asn Ile Ser Glu Lys Ser Trp Leu Glu Phe Glu Val Thr
 225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
 245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
 260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
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Asn Pro Asn Ile Pro Arg Tyr Arg Thr Arg Leu Arg Phe Glu Ile Asp
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asp Ile Gln Ser Thr Trp
50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

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

Pro Val Gln Val Arg Leu Arg Phe Ala Ile Gly Gln His Ile Arg Asp
195 200 205

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

Arg Glu Lys Asn Ile Ser Glu Lys Ser Trp Leu Glu Phe Glu Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
290 295 300

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Asn Pro Asn Ile Pro Arg Tyr Arg Thr Arg Leu Arg Phe Glu Ile Asp
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asp Ile Gln Ser Thr Trp
50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys

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90

95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
 115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
 130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
 165 170 175

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

Pro Val Gln Val Arg Leu Arg Phe Ala Ile Gly Gln His Ile Arg Asp
 195 200 205

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

Arg Glu Lys Asn Ile Ser Glu Lys Ser Trp Leu Glu Phe Glu Val Thr
 225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
 245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
 260 265 270

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 275 280 285

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Asn Pro Asn Ile Pro Arg Tyr Arg Thr Arg Leu Arg Phe Glu Ile Asp
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asp Ile Gln Ser Thr Trp
 50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
 115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

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

Pro Val Gln Val Arg Leu Arg Phe Ala Ile Gly Gln His Ile Arg Asp
195 200 205

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

Arg Glu Lys Asn Lys Ser Glu Lys Ser Trp Leu Glu Phe Glu Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
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Asn Pro Asn Ile Pro Arg Tyr Arg Thr Arg Leu Arg Phe Glu Ile Asp
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asp Ile Gln Ser Thr Trp
 50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
 115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
 130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
 165 170 175

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

Pro Val Gln Val Arg Leu Arg Phe Met Ile Gly Gln His Ile Lys Asp
195 200 205

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

Arg Glu Lys Asn Lys Ser Glu Lys Ser Trp Leu Glu Phe Glu Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
290 295 300

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Asn Arg Gly Thr Ala Arg Tyr His Thr Arg Leu Ser Phe Ala Ile Val
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
 115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
 130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
 165 170 175

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

Arg Val Arg Val Gln Leu Val Phe Glu Ile Ser Gln His Ile Arg Asp
 195 200 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly His Ile
 210 215 220

Tyr Glu Gly Asn Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg Val Glu
 225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
 245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
 260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
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Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
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Asn Arg Gly Thr Ala Arg Tyr His Thr Arg Leu Ser Phe Thr Ile Val
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

Lys Glu Leu Ala Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

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

Arg Val Arg Val Gln Leu Val Phe Glu Ile Ser Gln His Ile Arg Asp
195 200 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly His Ile
210 215 220

Tyr Glu Gly Asn Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg Val Glu
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val

260

265

270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
 275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
 290 295 300

<210> 13

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized I-OnuI variant PD-1.IgV.exon2_RD1_G5

<220>

<221> MOD_RES

<222> (1)..(4)

<223> Any amino acid or absent

<220>

<221> MOD_RES

<222> (302)..(303)

<223> Any amino acid or absent

<400> 13

Xaa Xaa Xaa Xaa Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
 1 5 10 15

Gly Phe Ala Asp Ala Glu Gly Ser Phe Gln Leu Tyr Ile Ser Asn Val
 20 25 30

Asn Asn Asn Arg Ser Arg Tyr Arg Ala Arg Leu Arg Phe Ala Ile Glu
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

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

Val Gly Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

Gly Asp Gly Asn Phe Tyr Val His Leu Lys Lys Ser Gly Arg Thr Thr
180 185 190

Arg Val Tyr Val Gln Leu Arg Phe Ser Ile Ala Gln His Ile Arg Asp
195 200 205

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

Asn Glu Trp Asn Ala Ser Glu Arg Ser Ala Leu Glu Phe Arg Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
290 295 300

<210> 14
 <211> 303
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Synthesized I-OnuI variant PD-1.IgV.exon2_RD1_PS3

<220>
 <221> MOD_RES
 <222> (1)..(4)
 <223> Any amino acid or absent

<220>
 <221> MOD_RES
 <222> (302)..(303)
 <223> Any amino acid or absent

<400> 14

Xaa Xaa Xaa Xaa Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
 1 5 10 15

Gly Phe Ala Asp Ala Glu Gly Cys Phe Leu Leu His Ile Arg Asn Leu
 20 25 30

Asn Arg Thr Ser Thr Lys Tyr Arg Thr Arg Leu Ser Phe Glu Ile Glu
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

Lys Val Gly Ile Ile Asn Asn Ile Gly Asn Arg Arg Val Arg Leu Ser
 65 70 75 80

Val Arg Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Leu Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
 115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp

130

135

140

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

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
 165 170 175

Gly Asp Gly Asn Phe Tyr Val His Leu Lys Lys Ser Gly Arg Thr Thr
 180 185 190

Arg Val Tyr Val Gln Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
 195 200 205

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

Thr Glu Ser Asn Pro Ser Glu Arg Ser Asp Leu Glu Phe Arg Val Thr
 225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
 245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
 260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
 275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
 290 295 300

<210> 15

<211> 870

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized megaTAL PD-1.ITSM.ex5_RD1_CV3-08

<400> 15

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg

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

Ile Ala Ser Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
 225 230 235 240

Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val
 245 250 255

Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
 260 265 270

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
 275 280 285

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
 290 295 300

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
 305 310 315 320

Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
 325 330 335

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu
 340 345 350

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
 355 360 365

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His
 370 375 380

Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly
 385 390 395 400

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
 405 410 415

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn
 420 425 430

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu

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

Lys Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys
660 665 670

Leu Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn
675 680 685

Lys Glu His Leu Lys Glu Asn Gly Ile Lys Glu Leu Val Arg Ile Lys
690 695 700

Ala Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro
705 710 715 720

Glu Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn
725 730 735

Leu Lys Trp Leu Ala Gly Phe Thr Ser Gly Glu Gly His Phe Gly Val
740 745 750

Ile Leu Ala Lys Arg Arg Pro Ala Ser Pro Val Gln Val Arg Leu Arg
755 760 765

Phe Ala Ile Gly Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu
770 775 780

Ile Thr Tyr Leu Gly Cys Gly Arg Ile Arg Glu Lys Asn Ile Ser Glu
785 790 795 800

Lys Ser Trp Leu Glu Phe Glu Val Thr Lys Phe Ser Asp Ile Asn Asp
805 810 815

Lys Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu
820 825 830

Glu Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys
835 840 845

Lys His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu
850 855 860

Asn Met Asn Lys Gly Arg

865

870

<210> 16

<211> 870

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized megaTAL PD-1.ITSM.ex5_RD2_73

<400> 16

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg
 1 5 10 15

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
 35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
 65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
 85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
 100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
 115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
 130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
 145 150 155 160

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val

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

Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly
 385 390 395 400

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
 405 410 415

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn
 420 425 430

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
 435 440 445

Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser
 450 455 460

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
 465 470 475 480

Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
 485 490 495

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile Val Ala Gln
 500 505 510

Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu
 515 520 525

Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys
 530 535 540

Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val Asn Arg Arg
 545 550 555 560

Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg Ser Arg Arg
 565 570 575

Glu Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly
 580 585 590

Ser Phe Gln Leu Glu Ile Arg Asn Val Asn Pro Asn Ile Pro Arg Tyr

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

Lys Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu
820 825 830

Glu Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys
835 840 845

Lys His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu
850 855 860

Asn Met Asn Lys Gly Arg
865 870

<210> 17
<211> 870
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized megaTAL PD-1.ITSM.ex5_RD3_03

<400> 17

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg
1 5 10 15

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145 150 155 160

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

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
180 185 190

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
195 200 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
210 215 220

Ile Ala Ser Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu
225 230 235 240

Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val
245 250 255

Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln
260 265 270

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
275 280 285

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
290 295 300

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
305 310 315 320

Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu

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

Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val Asn Arg Arg
 545 550 555 560

Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg Ser Arg Arg
 565 570 575

Glu Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly
 580 585 590

Ser Phe Gln Leu Glu Ile Arg Asn Val Asn Pro Asn Ile Pro Arg Tyr
 595 600 605

Arg Thr Arg Leu Arg Phe Glu Ile Asp Leu His Asn Lys Asp Lys Ser
 610 615 620

Ile Leu Glu Asp Ile Gln Ser Thr Trp Lys Val Gly Lys Ile Tyr Asn
 625 630 635 640

Gln Gly Asp Ser Tyr Val Lys Leu Arg Val Thr Arg Phe Glu Asp Leu
 645 650 655

Lys Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys
 660 665 670

Leu Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn
 675 680 685

Lys Glu His Leu Lys Glu Asn Gly Ile Lys Glu Leu Val Arg Ile Lys
 690 695 700

Ala Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro
 705 710 715 720

Glu Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn
 725 730 735

Leu Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly His Phe Gly Val
 740 745 750

Ile Leu Ala Lys Arg Arg Pro Ala Ser Pro Val Gln Val Arg Leu Arg

755

760

765

Phe Ala Ile Gly Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu
 770 775 780

Ile Thr Tyr Leu Gly Cys Gly Arg Thr Arg Glu Lys Asn Ile Ser Glu
 785 790 795 800

Lys Ser Trp Leu Glu Phe Glu Val Thr Lys Phe Ser Asp Ile Asn Asp
 805 810 815

Lys Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu
 820 825 830

Glu Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys
 835 840 845

Lys His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu
 850 855 860

Asn Met Asn Lys Gly Arg
 865 870

<210> 18

<211> 870

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized megaTAL PD-1.ITSM.ex5_RD4_CV23

<400> 18

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg
 1 5 10 15

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
 35 40 45

Thr His Ala His Ile Val Ala Leu Ser Gln His Pro Ala Ala Leu Gly

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

Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln
275 280 285

Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr
290 295 300

Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro
305 310 315 320

Asp Gln Val Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu
325 330 335

Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu
340 345 350

Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln
355 360 365

Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His
370 375 380

Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly
385 390 395 400

Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln
405 410 415

Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn
420 425 430

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
435 440 445

Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser
450 455 460

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
465 470 475 480

Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile

485

490

495

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile Val Ala Gln
 500 505 510

Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu
 515 520 525

Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys
 530 535 540

Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val Asn Arg Arg
 545 550 555 560

Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg Ser Arg Arg
 565 570 575

Glu Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly
 580 585 590

Ser Phe Gln Leu Glu Ile Arg Asn Val Asn Pro Asn Ile Pro Arg Tyr
 595 600 605

Arg Thr Arg Leu Arg Phe Glu Ile Asp Leu His Asn Lys Asp Lys Ser
 610 615 620

Ile Leu Glu Asp Ile Gln Ser Thr Trp Lys Val Gly Lys Ile Tyr Asn
 625 630 635 640

Gln Gly Asp Ser Tyr Val Lys Leu Arg Val Thr Arg Phe Glu Asp Leu
 645 650 655

Lys Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys
 660 665 670

Leu Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn
 675 680 685

Lys Glu His Leu Lys Glu Asn Gly Ile Lys Glu Leu Val Arg Ile Lys
 690 695 700

Ala Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro
705 710 715 720

Glu Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn
725 730 735

Leu Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly His Phe Gly Val
740 745 750

Ile Leu Ala Lys Arg Arg Pro Ala Ser Pro Val Gln Val Arg Leu Arg
755 760 765

Phe Ala Ile Gly Gln His Ile Arg Asp Lys Asn Leu Met Asn Ser Leu
770 775 780

Ile Thr Tyr Leu Gly Cys Gly Arg Ile Arg Glu Lys Asn Lys Ser Glu
785 790 795 800

Lys Ser Trp Leu Glu Phe Glu Val Thr Lys Phe Ser Asp Ile Asn Asp
805 810 815

Lys Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu
820 825 830

Glu Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys
835 840 845

Lys His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu
850 855 860

Asn Met Asn Lys Gly Arg
865 870

<210> 19
<211> 870
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized megaTAL PD-1.ITSM.ex5_RD5_CV23MK

<400> 19

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg
 1 5 10 15

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
 35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
 65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
 85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
 100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
 115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
 130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
 145 150 155 160

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

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
 180 185 190

Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
 195 200 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala

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

Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu
435 440 445

Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser
450 455 460

Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro
465 470 475 480

Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile
485 490 495

Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Ser Ile Val Ala Gln
500 505 510

Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu
515 520 525

Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys
530 535 540

Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val Asn Arg Arg
545 550 555 560

Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg Ser Arg Arg
565 570 575

Glu Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp Ala Glu Gly
580 585 590

Ser Phe Gln Leu Glu Ile Arg Asn Val Asn Pro Asn Ile Pro Arg Tyr
595 600 605

Arg Thr Arg Leu Arg Phe Glu Ile Asp Leu His Asn Lys Asp Lys Ser
610 615 620

Ile Leu Glu Asp Ile Gln Ser Thr Trp Lys Val Gly Lys Ile Tyr Asn
625 630 635 640

Gln Gly Asp Ser Tyr Val Lys Leu Arg Val Thr Arg Phe Glu Asp Leu

645	650	655
Lys Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Ile Thr Gln Lys		
660	665	670
Leu Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val Met Glu Asn		
675	680	685
Lys Glu His Leu Lys Glu Asn Gly Ile Lys Glu Leu Val Arg Ile Lys		
690	695	700
Ala Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys Ala Phe Pro		
705	710	715
Glu Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn Ile Pro Asn		
725	730	735
Leu Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly His Phe Gly Val		
740	745	750
Ile Leu Ala Lys Arg Arg Pro Ala Ser Pro Val Gln Val Arg Leu Arg		
755	760	765
Phe Met Ile Gly Gln His Ile Lys Asp Lys Asn Leu Met Asn Ser Leu		
770	775	780
Ile Thr Tyr Leu Gly Cys Gly Arg Ile Arg Glu Lys Asn Lys Ser Glu		
785	790	795
Lys Ser Trp Leu Glu Phe Glu Val Thr Lys Phe Ser Asp Ile Asn Asp		
805	810	815
Lys Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly Val Lys Leu		
820	825	830
Glu Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile Glu Glu Lys		
835	840	845
Lys His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys Ile Lys Leu		
850	855	860

Asn Met Asn Lys Gly Arg
865 870

<210> 20
<211> 841
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized megaTAL PD-1.ile3.exon1_RD1 B1

<400> 20

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg
1 5 10 15

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145 150 155 160

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

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
180 185 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
195 200 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
210 215 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225 230 235 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
245 250 255

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
260 265 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
275 280 285

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
290 295 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305 310 315 320

Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
325 330 335

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
340 345 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
355 360 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp

370

375

380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly
 385 390 395 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
 405 410 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
 420 425 430

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
 435 440 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
 450 455 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Ser Ile Val Ala Gln Leu
 465 470 475 480

Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val
 485 490 495

Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys Lys
 500 505 510

Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val Asn Arg Arg Ile
 515 520 525

Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg Val Gly Gly Ser
 530 535 540

Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp
 545 550 555 560

Ala Glu Gly Ser Phe Gly Leu Ser Ile Leu Asn Arg Asn Arg Gly Thr
 565 570 575

Ala Arg Tyr His Thr Arg Leu Ser Phe Ala Ile Val Leu His Asn Lys
 580 585 590

Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Ile
 595 600 605

Ile Thr Asn Asp Gly Asp Arg Tyr Val Arg Leu Arg Val Thr Arg Phe
 610 615 620

Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Val
 625 630 635 640

Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val
 645 650 655

Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile Lys Glu Leu Val
 660 665 670

Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys
 675 680 685

Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu Ile Asn Lys Asn
 690 695 700

Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser
 705 710 715 720

Phe Phe Val Arg Leu Arg Lys Ser Asn Val Asn Ala Arg Val Arg Val
 725 730 735

Gln Leu Val Phe Glu Ile Ser Gln His Ile Arg Asp Lys Asn Leu Met
 740 745 750

Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly His Ile Tyr Glu Gly Asn
 755 760 765

Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg Val Glu Lys Phe Ser Asp
 770 775 780

Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly
 785 790 795 800

Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile

805

810

815

Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys
 820 825 830

Ile Lys Leu Asn Met Asn Lys Gly Arg
 835 840

<210> 21

<211> 841

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized megaTAL PD-1.ile3.exon1_RD2_B1H8

<400> 21

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg
 1 5 10 15

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
 35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
 65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
 85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
 100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
 115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly

130

135

140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
 145 150 155 160

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

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
 180 185 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
 195 200 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
 210 215 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
 225 230 235 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
 245 250 255

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
 260 265 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
 275 280 285

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
 290 295 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
 305 310 315 320

Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
 325 330 335

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
 340 345 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
 355 360 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
 370 375 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly
 385 390 395 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
 405 410 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
 420 425 430

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
 435 440 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
 450 455 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Ser Ile Val Ala Gln Leu
 465 470 475 480

Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn Asp His Leu Val
 485 490 495

Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp Ala Val Lys Lys
 500 505 510

Gly Leu Pro His Ala Pro Glu Leu Ile Arg Arg Val Asn Arg Arg Ile
 515 520 525

Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg Val Gly Gly Ser
 530 535 540

Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr Gly Phe Ala Asp
 545 550 555 560

Ala Glu Gly Ser Phe Gly Leu Ser Ile Leu Asn Arg Asn Arg Gly Thr

565

570

575

Ala Arg Tyr His Thr Arg Leu Ser Phe Thr Ile Val Leu His Asn Lys
 580 585 590

Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp Lys Val Gly Ile
 595 600 605

Ile Thr Asn Asp Gly Asp Arg Tyr Val Arg Leu Cys Val Thr Arg Phe
 610 615 620

Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys Tyr Pro Leu Val
 625 630 635 640

Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln Ala Phe Ser Val
 645 650 655

Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile Lys Glu Leu Ala
 660 665 670

Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp Glu Leu Lys Lys
 675 680 685

Ala Phe Pro Glu Asn Ile Gly Lys Glu Arg Pro Leu Ile Asn Lys Asn
 690 695 700

Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser Gly Asp Gly Ser
 705 710 715 720

Phe Phe Val Arg Leu Arg Lys Ser Asn Val Asn Ala Arg Val Arg Val
 725 730 735

Gln Leu Val Phe Glu Ile Ser Gln His Ile Arg Asp Lys Asn Leu Met
 740 745 750

Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly His Ile Tyr Glu Gly Asn
 755 760 765

Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg Val Glu Lys Phe Ser Asp
 770 775 780

Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn Thr Leu Ile Gly
785 790 795 800

Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val Ala Lys Leu Ile
805 810 815

Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp Glu Ile Lys Lys
820 825 830

Ile Lys Leu Asn Met Asn Lys Gly Arg
835 840

<210> 22
<211> 909
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthesized megaTAL PD-1.IgV.exon2_RD1_G5

<400> 22

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg
1 5 10 15

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
 115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
 130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
 145 150 155 160

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

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
 180 185 190

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
 195 200 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
 210 215 220

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
 225 230 235 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
 245 250 255

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
 260 265 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
 275 280 285

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
 290 295 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
 305 310 315 320

Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala

335

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Ser Ile
530 535 540

Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu Thr Asn
545 550 555 560

Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala Met Asp
565 570 575

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

Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile Ser Arg
595 600 605

Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
610 615 620

Gly Phe Ala Asp Ala Glu Gly Ser Phe Gln Leu Tyr Ile Ser Asn Val
625 630 635 640

Asn Asn Asn Arg Ser Arg Tyr Arg Ala Arg Leu Arg Phe Ala Ile Glu
645 650 655

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
660 665 670

Lys Val Gly Val Ile Asn Asn Ile Gly Asp Thr Ser Val Arg Leu Ser
675 680 685

Val Gly Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
690 695 700

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705 710 715 720

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
725 730 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
740 745 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu

755

760

765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
770 775 780

Gly Asp Gly Asn Phe Tyr Val His Leu Lys Lys Ser Gly Arg Thr Thr
785 790 795 800

Arg Val Tyr Val Gln Leu Arg Phe Ser Ile Ala Gln His Ile Arg Asp
805 810 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Tyr Ile
820 825 830

Asn Glu Trp Asn Ala Ser Glu Arg Ser Ala Leu Glu Phe Arg Val Thr
835 840 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
850 855 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865 870 875 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
885 890 895

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg
900 905

<210> 23

<211> 909

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized megaTAL PD-1.IgV.exon2_RD1_PS3

<400> 23

Met Gly Ser Ala Pro Pro Lys Lys Lys Arg Lys Val Val Asp Leu Arg
1 5 10 15

Thr Leu Gly Tyr Ser Gln Gln Gln Gln Glu Lys Ile Lys Pro Lys Val

20

25

30

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145 150 155 160

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

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
180 185 190

Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
195 200 205

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Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225 230 235 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
245 250 255

Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala Leu Glu Thr Val
260 265 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
275 280 285

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
290 295 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305 310 315 320

Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly Gly Lys Gln Ala
325 330 335

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
340 345 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys
355 360 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
370 375 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Ile Gly
385 390 395 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
405 410 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
420 425 430

Ile Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
435 440 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala

450						455									460
Ser	His	Asp	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg	Leu	Leu
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Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val	Val	Ala
				485					490					495	
Ile	Ala	Ser	Asn	Gly	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Thr	Val	Gln	Arg
			500					505					510		
Leu	Leu	Pro	Val	Leu	Cys	Gln	Asp	His	Gly	Leu	Thr	Pro	Asp	Gln	Val
		515					520					525			
Val	Ala	Ile	Ala	Ser	Asn	Asn	Gly	Gly	Lys	Gln	Ala	Leu	Glu	Ser	Ile
	530					535					540				
Val	Ala	Gln	Leu	Ser	Arg	Pro	Asp	Pro	Ala	Leu	Ala	Ala	Leu	Thr	Asn
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Asp	His	Leu	Val	Ala	Leu	Ala	Cys	Leu	Gly	Gly	Arg	Pro	Ala	Met	Asp
				565					570					575	
Ala	Val	Lys	Lys	Gly	Leu	Pro	His	Ala	Pro	Glu	Leu	Ile	Arg	Arg	Val
			580					585					590		
Asn	Arg	Arg	Ile	Gly	Glu	Arg	Thr	Ser	His	Arg	Val	Ala	Ile	Ser	Arg
		595					600					605			
Val	Gly	Gly	Ser	Ser	Arg	Arg	Glu	Ser	Ile	Asn	Pro	Trp	Ile	Leu	Thr
	610					615					620				
Gly	Phe	Ala	Asp	Ala	Glu	Gly	Cys	Phe	Leu	Leu	His	Ile	Arg	Asn	Leu
625					630					635					640
Asn	Arg	Thr	Ser	Thr	Lys	Tyr	Arg	Thr	Arg	Leu	Ser	Phe	Glu	Ile	Glu
				645					650					655	
Leu	His	Asn	Lys	Asp	Lys	Ser	Ile	Leu	Glu	Asn	Ile	Gln	Ser	Thr	Trp
			660					665					670		

Lys Val Gly Ile Ile Asn Asn Ile Gly Asn Arg Arg Val Arg Leu Ser
675 680 685

Val Arg Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
690 695 700

Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
705 710 715 720

Ala Phe Ser Leu Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
725 730 735

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
740 745 750

Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg Pro Leu
755 760 765

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
770 775 780

Gly Asp Gly Asn Phe Tyr Val His Leu Lys Lys Ser Gly Arg Thr Thr
785 790 795 800

Arg Val Tyr Val Gln Leu Arg Phe Ser Ile Ser Gln His Ile Arg Asp
805 810 815

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly Tyr Ile
820 825 830

Thr Glu Ser Asn Pro Ser Glu Arg Ser Asp Leu Glu Phe Arg Val Thr
835 840 845

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
850 855 860

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
865 870 875 880

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp

885

890

895

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg
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<212> PRT

<213> Mus musculus

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 35 40 45

Gly Ser Leu Val Leu Pro Arg Val Leu Asp Lys Leu Thr Leu Cys Met
 50 55 60

Cys Pro Glu Arg Pro Phe Thr Ala Lys Ala Ser Glu Ile Thr Gly Leu
 65 70 75 80

Ser Ser Glu Ser Leu Met His Cys Gly Lys Ala Gly Phe Asn Gly Ala
 85 90 95

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

Cys Leu Val Ala His Asn Gly Phe Asp Tyr Asp Phe Pro Leu Leu Cys
 115 120 125

Thr Gly Leu Gln Arg Leu Gly Ala His Leu Pro Gln Asp Thr Val Cys
 130 135 140

Leu Asp Thr Leu Pro Ala Leu Arg Gly Leu Asp Arg Ala His Ser His
 145 150 155 160

Gly Thr Arg Ala Gln Gly Arg Lys Ser Tyr Ser Leu Ala Ser Leu Phe
165 170 175

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

Asp Val His Thr Leu Leu Leu Ile Phe Leu His Arg Ala Pro Glu Leu
195 200 205

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210 215 220

Met Tyr Val Pro Pro Asp Gly Pro Ser Leu Glu Ala
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gaagcccucg ugggucaugg auucacgcac gcccacaucg uggcccuguc gcagcauccg	180
gccgcccugg gcaccguggc ggugaccuac cagcacauca ucaccgccc u gcccgaagcc	240
acccacgagg acaucguggg agugggcaag cagugguccg gagcacgcgc ccuggaggcc	300
cugcugaccg acgccgggga acugcgcggc ccgccucugc agcuggauac cggccaacug	360
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gcucugaccg gugccccgcu caaucugacu ccggaccagg ugguggcuau cgccagcaac	480
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cacgggcuga cucccgacca ggucguggcc auugccagcc acgacggcgg caagcaggcu	600
uuggagacug ugcagcggcu ccugccagug cugugccaag aucacggucu gaccccagau	660
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cugccggugc uuugucagga ucacggccug accccugauc agggugguggc caucgcgucc	780
aauaacgggg ggaagcaggc acucgagacu guccagaggc uccugccugu gcucugccag	840
gaccacgggc ucacacccga ucaggucguc gcuaucgcgu cgcacgacgg uggaaagcag	900
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gaucaggucg ucgcgaucgc aucuaauggu ggaggaaagc aggcccugga gacaguccag	1020
cgccugcucc cgguguugug ccaagaccuau ggucuuaacc cugaccaggu ggucgcuauu	1080
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ugccaggaua auggauugac cccagaccag gugguggcga uugccagcaa caacggcggg	1200
aagcaagcgu uggaaaccgu ccagagacug cuuccugugc ugugccaaga ccacgguuug	1260
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gccaucgcaa gcaacaucgg uggcaaacag gcucuggaaa cuguccaaag acugcugccc	1440
gugcuuugcc aggaccacgg acugacuccu gaccaagugg uggcaauugc cuccaacauc	1500
ggaggcaagc aagcgcucga auccaucgug gcgcagcuca gccggccaga ccccgcccug	1560

gccgcccuga cuaacgauca ccugguggcc cuggcgugcc ucggcgugcg ccccgcuau	1620
gacgcgguga agaaggggcu gccccacgcc cccgagcuca uucggcggggu gaaccgccgg	1680
aucggagaaa gaaccuccca ucggguggcc aucucgagau cacggcggga auccauuaac	1740
cccuggaucc ugacuggcuu ugccgacgcc gagggauccu uccagcucga aauccggaac	1800
gugaacccaa acaucccccg guaucgcacc agacugcggu ucgagaucga ccuucacaac	1860
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cagggggacu cauacugaa gcugcgggug acccgcuucg aagaucuaa agugaucauc	1980
gaccuuucg agaaguaccc ccugaucacu cagaagcuug gagacuaca acuguucaag	2040
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guguuccagg aaaacacccu gauuggcgug aagcuggagg acuucgagga uuggugcaag	2520
guggccaagc uaucgaaga aaagaagcac cugacugaau ccggcuugga cgagaucaag	2580
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<212> RNA

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gaggcccuug ugggccacgg cuucacacau gcacacaucg ucgcccuguc gcagcauucc	180

gccgcccugg ggaccguggc cgugaccuau caacacauca uuaccgccc	gccggaggcc	240
acccacgagg acaucguggg uguggggaag caguggagcg gagccagggc	acucgaagcc	300
cuccucacug acgcuggaga acugcgcgga ccgccucucc agcuggacac	cggacagcug	360
gugaaaaucg ccaagcgggg aggagugacc gccauggaag ccgugcacgc	cucgaggaac	420
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cauggucuga ccccgacca ggucgucgcc auugcaucca acaauggugg	caagcaggca	600
cuggagacug uccagaggcu gcucccgug cugugccagg accacgggcu	caccccgga	660
caaguggucg ccaucgccuc caacggagga ggaaaacaag cucuggagac	ugugcaacgc	720
cugcugccug uguugugcca agaccacgga cugacgcccg aucagguggu	ggcgauccga	780
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ccagaccaag ucguggccau ugcuuccaac aacgguggca aacaggcgcu	cgaaacgguc	1020
cagcggcugu ugcccugcu uugccaggau cacggacuca cccugauca	ggugguggca	1080
auugcgucca acaacggugg aaagcaggcc cuggaaacgg ugcagcggcu	gcuuccgguc	1140
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gccgaagggu ccuucggccu cucgauccug aaccggaacc gggguaccgc	ucgguaccac	1740
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gagcaccuga aggagaacgg caucaaggag cucgcccgga ucaaggccaa gaugaacugg	2040
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aucaacaaga acaucccgaa cuucaagugg cuugccggau ucaccuccgg cgacggaucc	2160
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gugaagcuug aggauuucga ggacuggugc aagguggcca agcugauuga agagaagaag	2460
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gaggcccucg ugggccaugg auucacucac gcccauauagc uggcccuguc ccagcaccgc	180
gccgcccugg gcaccguggc ggugaccuac cagcacauca ucaccgcgcu gccugaagcc	240
accacagagg acaucgucgg uguggguaag cagugguccg gagccagagc ccuggaggcu	300
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aacucccuga	ucaccuaccu	cggguugcgga	uacaucaacg	aauggaacgc	cagcgagaga	2520
ucggcccugg	aguucagggg	gacuaaguuc	uccgacauca	acgacaagau	uaucggcgug	2580
uuucaggaaa	auaccucacu	cggcgugaag	cuggaggacu	uugaggacug	gugcaaggug	2640
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<212> DNA

<213> Artificial Sequence

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Asn Pro Pro Thr Phe Ser Pro Ala Leu Leu Val Val Thr Glu Gly Asp
 35 40 45

Asn Ala Thr Phe Thr Cys Ser Phe Ser Asn Thr Ser Glu Ser Phe Val
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Leu Asn Trp Tyr Arg Met Ser Pro Ser Asn Gln Thr Asp Lys Leu Ala
 65 70 75 80

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

Val Thr Gln Leu Pro Asn Gly Arg Asp Phe His Met Ser Val Val Arg
100 105 110

Ala Arg Arg Asn Asp Ser Gly Thr Tyr Leu Cys Gly Ala Ile Ser Leu
115 120 125

Ala Pro Lys Ala Gln Ile Lys Glu Ser Leu Arg Ala Glu Leu Arg Val
130 135 140

Thr Glu Arg Arg Ala Glu Val Pro Thr Ala His Pro Ser Pro Ser Pro
145 150 155 160

Arg Pro Ala Gly Gln Phe Gln Thr Leu Val Val Gly Val Val Gly Gly
165 170 175

Leu Leu Gly Ser Leu Val Leu Leu Val Trp Val Leu Ala Val Ile Arg
180 185 190

Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro
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Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro
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Arg Asp Phe Ala Ala Tyr Arg Ser
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<210> 60
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<220>
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Asn Pro Asn Ile Pro Arg Tyr Lys Thr Arg Leu Arg Phe Glu Ile Asp
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

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

Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
 115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
 130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Leu Lys Trp Leu Ala Gly Phe Thr Ser
 165 170 175

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

Pro Val Gln Val Arg Leu Arg Phe Ala Ile Gly Gln His Ile Arg Asp
195 200 205

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

Arg Glu Lys Asn Ile Ser Glu Lys Ser Trp Leu Glu Phe Glu Val Thr
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
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Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
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Asn Arg Gly Thr Ala Arg Tyr His Thr Arg Leu Ser Phe Thr Ile Met
35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
50 55 60

Lys Val Gly Ser Ile Leu Asn Asn Gly Asp His Tyr Val Ser Leu Val
65 70 75 80

Val Tyr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

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

Arg Val Arg Val Gln Leu Val Phe Glu Ile Ser Gln His Ile Arg Asp
195 200 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly His Ile
210 215 220

Tyr Glu Gly Asn Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg Val Glu
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
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Asn Arg Gly Thr Gly Arg Tyr His Thr Arg Leu Ser Phe Thr Ile Met
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Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
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Lys Val Gly Ser Ile Thr Asn Asn Gly Asp His Tyr Val Ser Leu Val
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Val Tyr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
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Tyr Pro Leu Ile Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe Lys Gln
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Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
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Gly Asp Gly Ser Phe Phe Val Arg Leu Arg Lys Ser Asn Val Asn Ala
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Arg Val Arg Val Gln Leu Val Phe Glu Ile Ser Gln His Ile Arg Asp
195 200 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly His Ile
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Tyr Glu Gly Asn Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg Val Glu
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp

275

280

285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
 290 295 300

<210> 63

<211> 303

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized I-OnuI variant PD-1.ile3.exon1_RD3_B1 G2C5

<220>

<221> MOD_RES

<222> (1)..(4)

<223> Any amino acid or absent

<220>

<221> MOD_RES

<222> (302)..(303)

<223> Any amino acid or absent

<400> 63

Xaa Xaa Xaa Xaa Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile Leu Thr
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Gly Phe Ala Asp Ala Glu Gly Ser Phe Gly Leu Ser Ile Leu Asn Arg
 20 25 30

Asn Arg Gly Thr Ala Arg Tyr His Thr Arg Leu Ser Phe Thr Ile Met
 35 40 45

Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser Thr Trp
 50 55 60

Lys Val Gly Ser Ile Tyr Asn Asn Gly Asp His Tyr Val Ser Leu Glu
 65 70 75 80

Val Phe Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe Glu Lys
 85 90 95

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

Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn Gly Ile
115 120 125

Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu Asn Asp
130 135 140

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

Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe Thr Ser
165 170 175

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

Arg Val Arg Val Gln Leu Val Phe Glu Ile Ser Gln His Ile Arg Asp
195 200 205

Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly His Ile
210 215 220

Tyr Glu Gly Asn Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg Val Glu
225 230 235 240

Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln Glu Asn
245 250 255

Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys Lys Val
260 265 270

Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly Leu Asp
275 280 285

Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg Xaa Xaa
290 295 300

<210> 64
<211> 943
<212> PRT
<213> Artificial Sequence

<220>

<223> Synthesized megaTAL PD-1.ile3.exon1_RD1_B1G2 construct

<400> 64

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

Arg Ser Thr Val Ala Gln His His Glu Ala Leu Val Gly His Gly Phe
35 40 45

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

Thr Val Ala Val Thr Tyr Gln His Ile Ile Thr Ala Leu Pro Glu Ala
65 70 75 80

Thr His Glu Asp Ile Val Gly Val Gly Lys Gln Trp Ser Gly Ala Arg
85 90 95

Ala Leu Glu Ala Leu Leu Thr Asp Ala Gly Glu Leu Arg Gly Pro Pro
100 105 110

Leu Gln Leu Asp Thr Gly Gln Leu Val Lys Ile Ala Lys Arg Gly Gly
115 120 125

Val Thr Ala Met Glu Ala Val His Ala Ser Arg Asn Ala Leu Thr Gly
130 135 140

Ala Pro Leu Asn Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
145 150 155 160

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

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
180 185 190

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
195 200 205

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
210 215 220

Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
225 230 235 240

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
245 250 255

Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val
260 265 270

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
275 280 285

Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu
290 295 300

Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr
305 310 315 320

Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys Gln Ala
325 330 335

Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly
340 345 350

Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn Asn Gly Gly Lys
355 360 365

Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys Gln Asp
370 375 380

His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser His Asp Gly
385 390 395 400

Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val Leu Cys
405 410 415

Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala Ser Asn
420 425 430

Gly Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu Pro Val
435 440 445

Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala Ile Ala
450 455 460

Ser Asn Asn Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg Leu Leu
465 470 475 480

Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val Val Ala
485 490 495

Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu Thr Val Gln Arg
500 505 510

Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp Gln Val
515 520 525

Val Ala Ile Ala Ser Asn Gly Gly Gly Lys Gln Ala Leu Glu Thr Val
530 535 540

Gln Arg Leu Leu Pro Val Leu Cys Gln Asp His Gly Leu Thr Pro Asp
545 550 555 560

Gln Val Val Ala Ile Ala Ser His Asp Gly Gly Lys Gln Ala Leu Glu
565 570 575

Ser Ile Val Ala Gln Leu Ser Arg Pro Asp Pro Ala Leu Ala Ala Leu
580 585 590

Thr Asn Asp His Leu Val Ala Leu Ala Cys Leu Gly Gly Arg Pro Ala
595 600 605

Met Asp Ala Val Lys Lys Gly Leu Pro His Ala Pro Glu Leu Ile Arg
610 615 620

Arg Val Asn Arg Arg Ile Gly Glu Arg Thr Ser His Arg Val Ala Ile
625 630 635 640

Ser Arg Val Gly Gly Ser Ser Arg Arg Glu Ser Ile Asn Pro Trp Ile
645 650 655

Leu Thr Gly Phe Ala Asp Ala Glu Gly Ser Phe Gly Leu Ser Ile Leu
660 665 670

Asn Arg Asn Arg Gly Thr Ala Arg Tyr His Thr Arg Leu Ser Phe Thr
675 680 685

Ile Met Leu His Asn Lys Asp Lys Ser Ile Leu Glu Asn Ile Gln Ser
690 695 700

Thr Trp Lys Val Gly Ile Ile Thr Asn Asn Gly Asp His Tyr Val Thr
705 710 715 720

Leu Arg Val Thr Arg Phe Glu Asp Leu Lys Val Ile Ile Asp His Phe
725 730 735

Glu Lys Tyr Pro Leu Val Thr Gln Lys Leu Gly Asp Tyr Lys Leu Phe
740 745 750

Lys Gln Ala Phe Ser Val Met Glu Asn Lys Glu His Leu Lys Glu Asn
755 760 765

Gly Ile Lys Glu Leu Val Arg Ile Lys Ala Lys Met Asn Trp Gly Leu
770 775 780

Asn Asp Glu Leu Lys Lys Ala Phe Pro Glu Asn Ile Ser Lys Glu Arg
785 790 795 800

Pro Leu Ile Asn Lys Asn Ile Pro Asn Phe Lys Trp Leu Ala Gly Phe
805 810 815

Thr Ser Gly Asp Gly Ser Phe Phe Val Arg Leu Arg Lys Ser Asn Val
820 825 830

Asn Ala Arg Val Arg Val Gln Leu Val Phe Glu Ile Ser Gln His Ile
835 840 845

Arg Asp Lys Asn Leu Met Asn Ser Leu Ile Thr Tyr Leu Gly Cys Gly
850 855 860

His Ile Tyr Glu Gly Asn Lys Ser Glu Arg Ser Trp Leu Gln Phe Arg
865 870 875 880

Val Glu Lys Phe Ser Asp Ile Asn Asp Lys Ile Ile Pro Val Phe Gln
885 890 895

Glu Asn Thr Leu Ile Gly Val Lys Leu Glu Asp Phe Glu Asp Trp Cys
900 905 910

Lys Val Ala Lys Leu Ile Glu Glu Lys Lys His Leu Thr Glu Ser Gly
915 920 925

Leu Asp Glu Ile Lys Lys Ile Lys Leu Asn Met Asn Lys Gly Arg
930 935 940

<210> 65
<211> 2832
<212> RNA
<213> Artificial Sequence

<220>
<223> Synthesized PD-1 Exon1 RD2_B1G2 megaTAL mRNA construct

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gaggcacugg ugggccaugg guuuacacac gcgcacaucg uugcgcucag ccaacacccg 180
gcagcguuag ggaccgucgc ugucacguau cagcacauaa ucacggcggu gccagaggcg 240
acacacgaag acaucguugg cgucggcaaa cagugguccg gcgcacgcgc ccuggaggcc 300
uugcucacgg augcggggga guugagaggu ccgccguuac aguuggacac aggccaacuu 360
gugaagauug caaaacgugg cggcgugacc gcaauggagg cagugcaugc aucgcgcaau 420
gcacugacgg gugcccccu gaaccuaacc ccugaucagg uagucgcuaau agcuucaaac 480
aacgggggca agcaagcacu ggagaccguu caacgacucc ugccagugcu cugccaagac 540
cacggacuua cgccagauca ggugguugcu auugccucca acaauggcgg gaaacaagcg 600

uuggaaacug	ugcagagacu	guuaccuguc	uugugucaag	accacggccu	cacgccagau	660
caggugguag	ccauagcguc	gaauggaggu	gguaagcaag	cccuugaaac	gguccagcgu	720
cuucugccgg	uguugugcca	ggaccacgga	cuaacgccgg	aucaggucgu	agccauugcu	780
ucaaauaacg	gcggcaaaca	ggcgcuagag	acaguccagc	gccucuugcc	uguguuauhc	840
caggaucacg	gcuaaaccac	agaccaaguu	guggcuauug	caucuaacaa	ugguggcaaa	900
caagccuugg	agacagugca	acgauuacug	ccugucuuau	gucaggauca	uggccugacg	960
cccgaucagg	uaguggcaau	cgcaucuaau	aauggaggua	agcaagcacu	ggagacuguc	1020
cagagauugu	uacccguacu	augucaagau	caugguuuga	cgccugauca	gguuguugcg	1080
auagccagca	acaacggagg	gaaacaggcu	cuugaaaccg	uacagcgacu	ucucccaguc	1140
uugugccaag	aucacgggcu	uacuccugau	caagucguag	cuaucgccag	ccacgacggg	1200
gggaaacagg	cccuggaaac	cguacaacgu	cuccucccag	uacuuuguca	agaccacggg	1260
uugacuccgg	aucaagucgu	cgcgauccg	agcaauaggag	gggggaagca	ggcgucggaa	1320
acuguucaga	gacugcugcc	uguacuugu	caggaccaug	gucugacacc	ugaccaaguu	1380
guggcgauag	ccaguaacaa	ugggggaaaa	caggcacuag	agacggauca	aagguuguug	1440
cccguucugu	gccaggacca	cggcuugaca	ccggaucagg	ugguagcuau	cgcuucacac	1500
gauggcggaa	aacaggcuuu	agaaacaguc	caaagacuuc	ucccaguccu	uugucaggac	1560
cacggauuga	cuccagauca	agucguugcu	auugcaagua	augguggugg	uaagcaagcu	1620
uuagaaaccg	uacagaggcu	uuugccagug	cugugccagg	accauggacu	gaccccugau	1680
caagugguag	caauugcauc	ucaugaugga	ggaaaacaag	cucuggaaag	cauuguggcc	1740
cagcugagcc	ggccugaucc	ggcguuggcc	gcguugacca	acgaccaccu	cgucgccuug	1800
gccugccucg	gcggacgucc	ugccauggau	gcagugaaaa	agggauugcc	gcacgcgccg	1860
gaauugauca	gaagagucaa	ucgccguauu	ggcgaacgca	cgucccaucg	cguugcgaua	1920
ucuagagugg	gaggaagcuc	ucgcagagag	uccaucaacc	cauggauucu	gacugguuuc	1980
gcugaugccg	aaggaucauu	cgggcuaagc	auccucaaca	gaaacagagg	uacugcuaga	2040
uaccacacuc	gacugucauu	cacaaucaug	cugcacaaca	aggacaaauc	gauucuggag	2100
aaauuccagu	cgacuuggaa	ggucggcaua	aucaccaaca	acggcgacca	cuacgucacc	2160
cugcgcguca	cccguuucga	agauuugaaa	gugauuauhc	accacuucga	gaaauauccg	2220

cugguaacac agaaauuggg cgauuacaag uuguuuuaac aggcauucag cgucauggag	2280
aacaaagaac aucuuaagga gaaugggauu aaggagcucg uacgaaucaa agcuaagaug	2340
aauggggguc ucaaugacga auugaaaaaa gcauuuccag agaacauuag caaagagcgc	2400
ccccuuauca auaagaacau uccgaauuuc aaauggcugg cuggauucac aucuggugau	2460
ggcuccuucu ucgugcgccu aagaaagucu aauguuaaug cuagaguacg ugugcaacug	2520
guauucgaga ucucacagca caucagagac aagaaccuga ugaauucauu gauaacauac	2580
cuaggcugug gucacauca cgagggaaac aaaucugagc gcaguuggcu ccaauucaga	2640
guagaaaaau ucagcgauau caacgacaag aucauuccgg uauuccagga aaauacucug	2700
auuggcguca aacucgagga cuuugaagau uggugcaagg uugccaaaau gaucgaagag	2760
aagaaacacc ugaccgauc cgguuuggau gagauuaaga aaaucaagcu gaacaugaac	2820
aaaggucguu ga	2832

<210> 66
 <211> 2832
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthesized PD-1 Exon1 RD2_B1G2C4 megaTAL mRNA construct

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gaggcacugg ugggccaugg guuuacacac gcgcacaucg uugcgcucag ccaacacccg	180
gcagcguuag ggaccgucgc ugucacguau cagcacauaa ucacggcguu gccagaggcg	240
acacacgaag acaucguugg cgucggcaaa cagugguccg gcgcacgcgc ccuggaggcc	300
uugcucacgg augcggggga guugagaggu ccgccguuac aguuggacac aggccaacuu	360
gugaagauug caaaacgugg cggcgugacc gcaauaggagg cagugcaugc aucgcgcaau	420
gcacugacgg gugcccccu gaaccuaacc ccugaucagg uagucgcuau agcuucaaac	480
aacgggggca agcaagcacu ggagaccguu caacgacucc ugccagugcu cugccaagac	540
cacggacuua cgccagauca ggugguugcu auugccucca acaauggcgg gaaacaagcg	600
uuggaaacug ugcagagacu guuaccuguc uugugucaag accacggccu cacgccagau	660

caggugguag ccauagcguc gaauggaggu gguaagcaag cccuugaaac gguccagcgu	720
cuucugccgg uguugugcca ggaccacgga cuaacgccgg aucaggucgu agccauugcu	780
ucaaauaacg gcggcaaaca ggcgcuagag acaguccagc gccucuugcc uguguuaugc	840
caggauacag gcuaaacccc agaccaaguu guggcuauug caucuaacaa ugguggcaaa	900
caagccuugg agacagugca acgauuacug ccugucuauu gucaggauca uggccugacg	960
cccgaucagg uaguggcaau cgcaucuaau aauggaggua agcaagcacu ggagacuguc	1020
cagagauugu uacccguacu augucaagau caugguuuga cgccugauca gguuguugcg	1080
auagccagca acaacggagg gaaacaggcu cuugaaaccg uacagcgacu ucucccaguc	1140
uugugccaag aucacgggcu uacuccugau caagucguag cuaucgccag ccacgacggu	1200
gggaaacagg cccuggaaac cguacaacgu cuccucccag uacuuuguca agaccacggg	1260
uugacuccgg aucaagucgu cgcgauccg agcaauaggag gggggaagca ggcgucggaa	1320
acuguucaga gacugcugcc uguacuugu caggaccaug gucugacacc ugaccaaguu	1380
guggcgauag ccaguaacaa ugggggaaaa caggcacuag agacgguuca aagguuguug	1440
cccguucugu gccaggacca cggcuugaca ccggaucagg ugguagcuau cgcuucacac	1500
gauggcgga aacaggcuuu agaaacaguc caaagacuuc ucccaguccu uugucaggac	1560
cacggauuga cuccagauca agucguugcu auugcaagua augguggugg uaagcaagcu	1620
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cagcugagcc ggccugaucc ggcgauuggc gcguugacca acgaccaccu cgucgccuug	1800
gccugccucg gcggacgucc ugccauggau gcagugaaaa agggauugcc gcacgcgccg	1860
gaauugauca gaagagucaa ucgccguauu ggcgaaacga cgucccaucg cguugcgaua	1920
ucuagagugg gaggaagcuc ucgcagagag uccaucaacc cauggauucu gacugguuuc	1980
gcugaugccg aaggaucauu cgggcuaagc auccucaaca gaaacagagg uacugcuaga	2040
uaccacacuc gacugucauu cacaaucaug cugcacaaca aggacaaauc gauucuggag	2100
aaauuccagu cgacuuggaa ggucggcagc auccucaaca auggcgacca cuacgucucg	2160
cugguggucu accguuucga agauuugaaa gugauuauug accacuucga gaaauauccg	2220
cugauaacac agaaauuggg cgauuacaag uuguuuuuaac aggcuuucag cgucauggag	2280

aacaaagaac aucuuaagga gaaugggauu aaggagcucg uacgaaucaa agcuaagaug	2340
aaauugggguc ucaaugacga auugaaaaaa gcauuuccag agaacauuag caaagagcgc	2400
ccccuuauca auaagaacau uccgaauuuc aaauggcugg cuggauucac aucuggugau	2460
ggcuccuucu ucgugcgccu aagaaagucu aauguuaaug cuagaguacg ugugcaacug	2520
guauucgaga ucucacagca caucagagac aagaaccuga ugaauucauu gauaacauac	2580
cuaggcugug gucacauca cgagggaaac aaaucugagc gcaguuggcu ccaauucaga	2640
guagaaaaau ucagcgauau caacgacaag aucauuccgg uauuccagga aaauacucug	2700
auuggcguca aacucgagga cuuugaagau uggugcaagg uugccaaaau gaucgaagag	2760
aagaaacacc ugaccgauc cgguuuggau gagauuaaga aaaucaagcu gaacaugaac	2820
aaaggucguu ga	2832

<210> 67
 <211> 2832
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthesized PD-1 Exon1 RD2_B1G2C11 megaTAL mRNA construct

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gaggcacugg ugggccaugg guuuacacac gcgcacaucg uugcgcucag ccaacacccg	180
gcagcguuag ggaccgucgc ugucacguau cagcacauaa ucacggcguu gccagaggcg	240
acacacgaag acaucguugg cgucggcaaa cagugguccg gcgcacgcgc ccuggaggcc	300
uugcucacgg augcggggga guugagaggu ccgccguuac aguuggacac aggccaacuu	360
gugaagauug caaaacgugg cggcgugacc gcaauaggagg cagugcaugc aucgcgcaau	420
gcacugacgg gugcccccu gaaccuaacc ccugaucagg uagucgcuaau agcuucaaac	480
aacggggggca agcaagcacu ggagaccguu caacgacucc ugccagugcu cugccaagac	540
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uuggaaacug ugcaagagacu guuaccuguc uugugucaag accacggccu cacgccagau	660
caggugguag ccuagcgcg gaauggaggu gguaagcaag cccuugaaac gguccagcgu	720

cuucugccgg	uguugugcca	ggaccacgga	cuaacgccgg	aucaggucgu	agccauugcu	780
ucaaauaacg	gctggcaaaca	ggcgcuagag	acaguccagc	gccucuugcc	uguguuaugc	840
caggauacag	gcuaaacccc	agaccaaguu	guggcuauug	caucuaaca	ugguggcaaa	900
caagccuugg	agacagugca	acgauuacug	ccugucuau	gucaggauca	uggccugacg	960
cccgaucagg	uaguggcaau	cgcaucuaau	aauggaggua	agcaagcacu	ggagacuguc	1020
cagagauugu	uacccguacu	augucaagau	caugguuuga	cgccugauca	gguguugcg	1080
auagccagca	acaacggagg	gaaacaggcu	cuugaaaccg	uacagcgacu	ucucccaguc	1140
uugugccaag	aucacgggcu	uacuccugau	caagucguag	cuacgccag	ccacgacggu	1200
gggaaacagg	cccuggaaac	cguacaacgu	cuccucccag	uacuuuguca	agaccacggg	1260
uugacuccgg	aucaagucgu	cgcgauccg	agcaauaggag	gggggaagca	ggcgucggaa	1320
acuguucaga	gacugcugcc	uguacuugu	caggaccaug	gucugacacc	ugaccaaguu	1380
guggcgauag	ccaguaaca	ugggggaaaa	caggcacuag	agacgguuc	aagguuguug	1440
cccguucugu	gccaggacca	cggcuugaca	ccggauccag	ugguagcuau	cgcuucacac	1500
gauggcggaa	aacaggcuuu	agaaacaguc	caaagacuuc	ucccaguccu	uugucaggac	1560
cacggauuga	cuccagauca	agucguugcu	auugcaagua	augguggugg	uaagcaagcu	1620
uuagaaaccg	uacagaggcu	uuugccagug	cugugccagg	accauggacu	gacccugau	1680
caagugguag	caauugcauc	ucaugaugga	ggaaaacaag	cucuggaaag	cauuguggcc	1740
cagcugagcc	ggccugaucc	ggcgauuggcc	gcguugacca	acgaccaccu	cgucgccuug	1800
gccugccucg	gcggacgucc	ugccauggau	gcagugaaaa	agggauugcc	gcacgcgccg	1860
gaauugauca	gaagagucaa	ucgccguauu	ggcgaacgca	cgucccaucg	cguugcgaua	1920
ucuagagugg	gaggaagcuc	ucgcagagag	uccaucaacc	cauggauucu	gacugguuuc	1980
gcugaugccg	aaggaucauu	cgggcuaagc	auccucaaca	gaaacagagg	uacugguaga	2040
uaccacacuc	gacugucauu	cacaaucaug	cugcacaaca	aggacaaauc	gauucuggag	2100
aaauuccagu	cgacuuggaa	ggucggcucg	aucacgaaca	acggcgacca	cuacgucagc	2160
cuggucgucu	accguuucga	agauuugaaa	gugauuauug	accacuucga	gaaauauccg	2220
cugauaacac	agaaauuggg	cgauuacaag	uuguuuuuac	aggcauucag	cgucauggag	2280
aacaaagaac	aucuuuagga	gaaugggauu	aaggagcucg	uacgaaucaa	agcuuagaug	2340

aaauggggguc ucaaugacga auugaaaaaa gcauuuccag agaacauuag caaagagcgc	2400
ccccuuauca auaagaacau uccgaauuuc aaaugggcugg cuggauucac aucuggugau	2460
ggcuccuucu ucgugcgccu aagaaagucu aauguuaaug cuagaguacg ugugcaacug	2520
guauucgaga ucucacagca caucagagac aagaaccuga ugaauucauu gauaacauac	2580
cuaggcugug gucacauca cgaggggaaac aaaucugagc gcaguuggcu ccaauucaga	2640
guagaaaaau ucagcgauau caacgacaag aucauuccgg uauuccagga aaauacucug	2700
auuggcguca aacucgagga cuuugaagau uggugcaagg uugccaaau gaucgaagag	2760
aagaaacacc ugaccgauc cgguuuggau gagauuaaga aaaucaagcu gaacaugaac	2820
aaaggucguu ga	2832

<210> 68
 <211> 2832
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthesized PD-1 Exon1 RD2_B1G2C5 megaTAL mRNA construct

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<220>
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<400> 70

Asp Gly Gly Gly Ser
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<210> 71
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 <212> PRT
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<220>
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<400> 71

Thr Gly Glu Lys Pro
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<210> 72

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary linker sequence

<400> 72

Gly Gly Arg Arg
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<210> 73

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary linker sequence

<400> 73

Gly Gly Gly Gly Ser
1 5

<210> 74

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary linker sequence

<400> 74

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Val Asp
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<210> 75

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary linker sequence

<400> 75

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

<210> 76

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary linker sequence

<400> 76

Gly Gly Arg Arg Gly Gly Gly Ser
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<210> 77

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary linker sequence

<400> 77

Leu Arg Gln Arg Asp Gly Glu Arg Pro
1 5

<210> 78

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Exemplary linker sequence

<400> 78

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

<210> 79
<211> 16
<212> PRT
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<220>
<223> Exemplary linker sequence

<400> 79

Leu	Arg	Gln	Lys	Asp	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Arg	Pro
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<210> 80
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<222> (2)..(3)
<223> Xaa is any amino acid

<220>
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<222> (5)..(5)
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<220>
<221> MISC_FEATURE
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<223> Xaa = Gly or Ser

<400> 80

Glu	Xaa	Xaa	Tyr	Xaa	Gln	Xaa
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<210> 81
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<220>
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Glu Asn Leu Tyr Phe Gln Gly
1 5

<210> 82
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<212> PRT
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<220>
<223> Cleavage sequence by TEV protease

<400> 82

Glu Asn Leu Tyr Phe Gln Ser
1 5

<210> 83
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 83

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
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<210> 84
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 84

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1 5 10 15

Pro Gly Pro

<210> 85
<211> 14
<212> PRT
<213> Artificial Sequence

<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 85

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

<210> 86
<211> 21
<212> PRT
<213> Artificial Sequence

<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 86

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
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<210> 87
<211> 18
<212> PRT
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<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 87

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
1 5 10 15

Gly Pro

<210> 88
<211> 13
<212> PRT
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Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
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<210> 89

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 89

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
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<210> 90

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 90

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1 5 10 15

Asn Pro Gly Pro
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<210> 91

<211> 14

<212> PRT

<213> Artificial Sequence

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<400> 91

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

<210> 92

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 92

Gly Ser Gly Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala
1 5 10 15

Gly Asp Val Glu Ser Asn Pro Gly Pro
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<210> 93

<211> 22

<212> PRT

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<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 93

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val
1 5 10 15

Glu Ser Asn Pro Gly Pro
20

<210> 94

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 94

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

<210> 95
<211> 19
<212> PRT
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<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 95

Leu	Leu	Asn	Phe	Asp	Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val	Glu	Ser	Asn
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Pro Gly Pro

<210> 96
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 96

Thr	Leu	Asn	Phe	Asp	Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val	Glu	Ser	Asn
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Pro Gly Pro

<210> 97
<211> 14
<212> PRT
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<220>
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<400> 97

Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val	Glu	Ser	Asn	Pro	Gly	Pro
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<210> 98
<211> 17

<212> PRT
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<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 98

Asn	Phe	Asp	Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val	Glu	Ser	Asn	Pro	Gly
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Pro

<210> 99
<211> 20
<212> PRT
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<220>

<223> Self-cleaving polypeptide comprising 2A site

<400> 99

Gln	Leu	Leu	Asn	Phe	Asp	Leu	Leu	Lys	Leu	Ala	Gly	Asp	Val	Glu	Ser
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Asn	Pro	Gly	Pro
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<223> Self-cleaving polypeptide comprising 2A site

<400> 100

Ala	Pro	Val	Lys	Gln	Thr	Leu	Asn	Phe	Asp	Leu	Leu	Lys	Leu	Ala	Gly
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Asp	Val	Glu	Ser	Asn	Pro	Gly	Pro
							20

<210> 101
<211> 40

<212> PRT
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<220>
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<400> 101

Val Thr Glu Leu Leu Tyr Arg Met Lys Arg Ala Glu Thr Tyr Cys Pro
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Arg Pro Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys
20 25 30

Ile Val Ala Pro Val Lys Gln Thr
35 40

<210> 102
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 102

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

Gly Pro

<210> 103
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Self-cleaving polypeptide comprising 2A site

<400> 103

Leu Leu Ala Ile His Pro Thr Glu Ala Arg His Lys Gln Lys Ile Val
1 5 10 15

Ala Pro Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Leu Ala Gly
20 25 30

Asp Val Glu Ser Asn Pro Gly Pro
35 40

<210> 104
<211> 33
<212> PRT
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<220>
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<400> 104

Glu Ala Arg His Lys Gln Lys Ile Val Ala Pro Val Lys Gln Thr Leu
1 5 10 15

Asn Phe Asp Leu Leu Lys Leu Ala Gly Asp Val Glu Ser Asn Pro Gly
20 25 30

Pro

<210> 105
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<210> 106
<211> 8
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<213> Homo sapiens

<400> 106

Glu Gln Thr Glu Tyr Ala Thr Ile
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<210> 107
<211> 43
<212> DNA

<213> Homo sapiens
 <400> 107
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<210> 108
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 <212> DNA
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<220>
 <223> Made in Lab

<400> 108
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<210> 109
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<400> 109
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<210> 110
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 nnnnnnnnna tactccgtct gc 22

<210> 111
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<223> Made in Lab

<400> 111
aatggtggca tactccgtct gc 22

<210> 112
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<400> 112
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<210> 113
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<400> 113
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<210> 114
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<400> 114

Met Gln Ile Pro Gln Ala Pro
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<210> 115
<211> 44
<212> DNA
<213> Homo sapiens

<400> 115
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<210> 116

<211> 44
 <212> DNA
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 <220>
 <223> Made in Lab

 <400> 116
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 <210> 117
 <211> 8
 <212> PRT
 <213> Homo sapiens

 <400> 117

 Asn Gly Arg Asp Phe His Met Ser
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 <210> 118
 <211> 43
 <212> DNA
 <213> Homo sapiens

 <400> 118
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 <210> 119
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 <400> 119
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 <210> 120
 <211> 32
 <212> DNA
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 <400> 120
 gctccaggca tgcagatccc acaggcgccc tg 32

 <210> 121
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<212> DNA
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 <400> 121
 actccaaaca tacaaatccc acaaacaccc ta 32

 <210> 122
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 <212> DNA
 <213> Homo sapiens

 <400> 122
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 <210> 123
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 <223> Made in Lab

 <400> 123
 acccaacgaa cgtaacttcc acataaacgt a 31