

SEQUENCE LISTING

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<120> Penicillin-G Acylases

<130> CX2-149W01

<150> US 62/158,118

<151> 2015-05-07

<160> 15

<170> PatentIn version 3.5

<210> 1

<211> 2541

<212> DNA

<213> Kluyvera citrophila

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 <212> PRT
 <213> *Kluyvera citrophila*

<400> 2

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 20 25 30

Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala Asp
 35 40 45

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

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

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

Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu Ser
 100 105 110

Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn Ala

115

120

125

Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln Gln
 130 135 140

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

Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser Thr
 165 170 175

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

Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu Val
 195 200 205

Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr Pro
 210 215 220

Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala Ala Leu Leu Pro Arg
 225 230 235 240

Tyr Asp Gln Pro Ala Pro Met Leu Asp Arg Pro Ala Lys Gly Thr Asp
 245 250 255

Gly Ala Leu Leu Ala Leu Thr Ala Asp Gln Asn Arg Glu Thr Ile Ala
 260 265 270

Ala Gln Phe Ala Gln Ser Gly Ala Asn Gly Leu Ala Gly Tyr Pro Thr
 275 280 285

Thr Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys
 290 295 300

Ala Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Ala Pro Ala Tyr
 305 310 315 320

Thr Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn
325 330 335

Thr Pro Phe Ala Tyr Pro Gly Leu Val Phe Gly His Asn Gly Thr Ile
340 345 350

Ser Trp Gly Ser Thr Ala Gly Phe Gly Asp Asp Val Asp Ile Phe Ala
355 360 365

Glu Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu
370 375 380

Trp Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly
385 390 395 400

Gln Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile
405 410 415

Lys Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp
420 425 430

Asp Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys
435 440 445

Ala Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu
450 455 460

Thr Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val
465 470 475 480

His Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu
485 490 495

Pro Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe
500 505 510

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

515

520

525

Trp Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala
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Phe Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu
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Asp Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg
 565 570 575

Gln Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu
 580 585 590

Lys Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu
 595 600 605

Val Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp
 610 615 620

Gly Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu
 625 630 635 640

Thr Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe
 645 650 655

Gly Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro
 660 665 670

Thr Gly Ser Leu Asn Ile Ser Val Gly Ala Lys Ile Leu Tyr Glu Ala
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Leu Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly
 690 695 700

Gly Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp
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Gln Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr
725 730 735

Pro Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro
740 745 750

Gln Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg
755 760 765

Gly Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg
770 775 780

Pro Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile
785 790 795 800

Ala Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met
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Tyr Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val
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Asp Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Arg
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<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic PGA nucleotide sequence for variant 1

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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetic PGA protein sequence for variant 1

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
 35 40 45

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

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
 65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln

275

280

285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
 290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
 305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
 325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
 340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
 355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
 370 375 380

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

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
 405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
 420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
 435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
 450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
 465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
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Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp

675

680

685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
 690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
 705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
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Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
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Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr
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<210> 5
 <211> 2295
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic PGA nucleotide sequence for variant 6

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 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540

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tacggcaagc agcagggcat ggcgggtcttt aaccagctga aatggctggt taatccttcc      2220
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acgcaaacgg cgtaa                                                         2295

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<210> 6
<211> 764
<212> PRT
<213> Artificial Sequence

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<220>
<223> synthetic PGA protein sequence for variant 6

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<400> 6

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

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

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Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65          70          75          80

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Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85          90          95

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Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100         105         110

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Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys

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115

120

125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
 130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
 145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
 165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
 180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
 195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
 210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
 225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
 245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
 260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
 275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
 290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
 305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

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

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr

515

520

525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 7
<211> 2295
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic PGA nucleotide sequence for variant 53

<400> 7
agcaatatgt ggggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatggtcaat 60
gggccgcagt ttggttggtt taatccggcg tacacctacg gtatcggcct gcacggcgcg 120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctggt tggtcacaac 180
ggcaccatatt catggggatc caccgccggt ggtggtgatg atgtcgatat ctttgccgaa 240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat taactggtac 540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
cccggccacg acccgcttt gccggttccc ggactggaa aatgggactg gaaagggttg 660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagt cgggctatat cgccaactgg 720
aacaactcgc cgcaaaaaga ctaccgggcc tctgatctgt tcgcgttcct gtggggcggt 780
gcggatcgag ttactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat 840

caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta	900
ccggcgctga aggacgccac cgcgaacctg gcggaaaacg atccgcgccg ccaactgggtg	960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag	1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacgggtggtt	1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag	1140
gacgggccaa ccggctcgct gaacatcagc gtgggggcga aaatcctcta cgaagctctg	1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag	1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac	1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggccaa taacttcttc	1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt	1440
acggaaaacg acatgattgt cttctcaccg acgtcgggta accgcccggg tcttgccctgg	1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac	1560
tatgacgatc agctgaaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct	1620
caggacgttg acgagcacca agagtctcag gaagtgctgc aggtacagtt ggatcagacc	1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgatacctat	1740
cgactgtttt acggctatgg ctacgtgggtg gcgcaggatc gcctgttcca gatggaaatg	1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcttt cgtttctttt	1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc	1920
tccgtgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat	1980
aaagtgaacg ccagccccga taagctgtta cccagcaggt tctccacctt tggttttaaa	2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcgaaaccgt	2100
ttctctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa	2160
tacggcaagc agcagggcag ggcggtcttt aaccagctga aatggctggg taatccttcc	2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac	2280
acgcaaacgg cgtaa	2295

<210> 8
<211> 764
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic PGA protein sequence for variant 5

<400> 8

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Phe Asn Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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

Trp Gly Ser Thr Ala Gly Gly Gly Asp Asp Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Val Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

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

355

360

365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
 370 375 380

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

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
 405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
 420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
 435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
 450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
 465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
 485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
 500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
 515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
 530 535 540

Glu His Gln Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
 545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala

<210> 9
 <211> 2295
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> synthetic PGA nucleotide sequence for variant 261

<400> 9
 agcaatatgt ggggtgattgg caaaaacaaa gcccaggatg cgaaggccat tatgggtcaat 60
 gggccgcagt ttggttggtta taatccggcg tatacctacg gtatcggcct gcacggcgcg 120
 ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctttt tggtcacaac 180
 ggcaccattt catggggatc caccgccggg gccgggtgatg tcgtcgatat ctttgccgaa 240
 aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg 300
 agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc 360
 acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg 420
 cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc 480
 aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac 540
 tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag 600
 cccggccacg acccgcgttt gccggttccc ggcaactggaa aatgggactg gaaagggttg 660
 ctgtcgtttg atttgaatcc gaaagtgtat aaccgcgagt cgggctatat cgccaactgg 720
 aacaactcgc cgcaaaaaga ctaccgggcc tctgatctgt tcgcgttcct gtggggcggt 780
 gcggatcgag cgactgagat cgacacgac ctcgataagc aaccgcgctt caccgccgat 840
 caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta 900
 ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg 960
 gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag 1020
 caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt 1080
 gccgcggtcc cagcgcctt tggtaagtgg tacagcgcca gtggctatga aaccaccag 1140

gacggggccaa ccggctcgct gaacatcagc gtggggggcga aaatcctcta cgaagctctg	1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag	1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac	1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccggggccaa taacttcttc	1380
ggcgtgccgc aggcgggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt	1440
acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggg tcttgccctgg	1500
gatgtggtgg cgccggggca aagcggtttt atcgcgccgg atggcaaagc cgataagcac	1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct	1620
caggacgttg acgagcacia agagtctcag gaagtgctgc aggtacagtt ggatcagacc	1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata ttacgccga tgataacctat	1740
cgactgtttt acggctatgg ctacgtgggtg gcgcaggatc gcctgttcca gatggaaatg	1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgtttcattt	1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccctc	1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat	1980
aaagtgaacg ccagccccga taagctgtta cccagcagt tctccacctt tggttttaaa	2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggcaaccgt	2100
ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa	2160
tacggcaagc agcagggcat ggcggtcttt aaccagctga aatggctggg taatccttcc	2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac	2280
acgcaaacgg cgtaa	2295

<210> 10

<211> 764

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetic PGA protein sequence for variant 261

<400> 10

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Tyr Asn Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

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

Trp Gly Ser Thr Ala Gly Ala Gly Asp Val Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195

200

205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
 210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
 225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
 245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
 260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
 275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
 290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
 305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
 325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
 340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
 355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
 370 375 380

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

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595

600

605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Ser Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 11

<211> 2295

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic PGA nucleotide sequence for variant 258

<400> 11

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gggccgcagt ttggttggta taatccggcg tatacctacg gtatcggcct gcacggcgcg	120
ggctatgacg tcaccggcaa tacgccgttt gcctatccgg gcctcctttt tggtcacaac	180
ggcaccatth catggggatc caccgccgtt gccggtgata gcgtcgatat ctttgccgaa	240
aaactttccg ccgagaagcc gggctattac cagcataacg gcgagtgggt gaagatgttg	300
agccgcaagg agactattgc ggtcaaagac ggccagccgg agacctttac cgtttggcgc	360
acgctgcacg gcaacgtcat taaaaccgat actgcgacgc agaccgccta tgccaaagcg	420
cgcgcctggg atggcaaaga ggtggcgtcc ctgctggcgt ggacgcacca gatgaaggcc	480
aaaaactggc cggagtggac gcagcaggcg gccaaacagg cgctgaccat caactggtac	540
tacgccgatg tgaacggcaa tatcggctat gtgcataccg gcgcctatcc ggatcgccag	600
cccggccacg acccgcgtht gccggttccc ggcactggaa aatgggactg gaaagggttg	660
ctgtcgtttg atttgaatcc gaaagtgtat aaccgcagt cgggctatat cgccaactgg	720
aacaactcgc cgcaaaaaga ctacccggcc tctgatctgt tcgcgttcct gtggggcggt	780
gcggatcgag cgactgagat cgacacgatc ctcgataagc aaccgcgctt caccgccgat	840
caggcgtggg atgtgatccg ccaaaccagc cgtcgggatc tcaacctgcg gttgttctta	900
ccggcgctga aggacgccac cgccaacctg gcggaaaacg atccgcgccg ccaactggtg	960
gataaactgg cgagctggga cggcgaaaac cttgtcaacg atgacggaaa aacctatcag	1020
caaccgggat cggcgattct taacgcctgg ctgaccagca tgctcaagcg cacggtggtt	1080
gccgcggtcc cagcgccgtt tggtaagtgg tacagcgcca gtggctatga aaccacccag	1140
gacggggcaa ccggctcgct gaacatcagc gtggggggcg aaatcctcta cgaagctctg	1200
cagggtgata agtcgccaat cccgcaggcg gtcgatctgt ttggcgggaa accgcagcag	1260
gaagtaatac tggcggcgct ggacgacgct tggcagacgc tgtcaaaacg ctacggtaac	1320
gacgtcaccg gctggaaaac ccctgccatg gcgcttacct tccgggcaa taacttcttc	1380
ggcgtgccgc aggcggcagc aaaagaggcg cgtcatcagg cggagtacca gaaccgcggt	1440

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acggaaaaca acatgattgt cttctcaccg acgtcgggta accgcccggg tcttgccctgg      1500
gatgtggtgg cgccggggca aagcgggttt atcgcgccgg atggcaaagc cgataagcac      1560
tatgacgatc agctgaaaat gtacgagagc tttggccgta aatcgctgtg gttaacgcct      1620
caggacgttg acgagcacia agagtctcag gaagtgctgc aggtacagtt ggatcagacc      1680
gaggttaaga tcgttcgcga tgaatacggc atgccgcata tttacgccga tgataacctat      1740
cgactgtttt acggctatgg ctacgtgggtg gcgcaggatc gcctgttcca gatggaaatg      1800
gcgcgccgca gtactcaggg gaccgtctcc gaggtgctgg gcaaagcatt cgттааgттt      1860
gataaagata ttcgccagaa ctactggccg gattctattc gcgcgcagat agcttccttc      1920
tccgctgagg ataaatccat tctgcagggc tatgccgatg gcatgaatgc gtggatcgat      1980
aaagtgaacg ccagccccga taagctgtta cccagcaggt tctccacctt tggttttaaa      2040
cccaagcatt gggaaccgtt tgatgtggcg atgatttttg tcggcaccat ggсgaaccgt      2100
ttttctgaca gcaccagcga aattgataac ctggcgctgc tgacggcgct aaaagacaaa      2160
tacggcaagc agcagggcat ggсgtcttt aaccagctga aatggctggт таатсттсс      2220
gcgccaacca ccattgcggc gcgggaaagc gcctatccgc tgaagtttga tctgcaaaac      2280
acgcaaacgg cgtaa                                                                2295

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<211> 764
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<213> Artificial Sequence

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<220>
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<400> 12

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

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Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr

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35

40

45

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

Trp Gly Ser Thr Ala Gly Ala Gly Asp Ser Val Asp Ile Phe Ala Glu
 65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
 85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
 100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
 115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
 130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
 145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
 165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
 180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
 195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
 210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
 225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

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

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro

435

440

445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
 450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
 465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
 485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
 500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
 515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
 530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
 545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
 565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
 580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
 595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Val Lys Phe Asp Lys Asp Ile
 610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
 625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
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<223> Xaa can be Val or Asn

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<223> Xaa can be Thr or Asp

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<223> Xaa can be Pro or His

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<223> Xaa can be Val, Ile or Leu

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<223> Xaa can be Gly, Phe or Ala

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<222> (126)..(126)

<223> Xaa can be Val or Ile

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<223> Xaa can be Ile or Val

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<223> Xaa can be Thr, Lys or Trp

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<223> Xaa can be Ala, Arg or Thr

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<223> Xaa can be Gln, His or Ser

<220>

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<222> (156)..(156)

<223> Xaa can be His or Arg

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<222> (160)..(160)

<223> Xaa can be Ala or Ser

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<223> Xaa can be Trp or Phe

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<223> Xaa can be Leu, Phe, Ser, Thr, Val, or Trp

<220>

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<223> Xaa can be Phe or Trp

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<223> Xaa can be Ala, Phe, Gly, Leu, Met, Arg, Ser, Val, or Tyr

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<222> (367)..(367)

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<222> (370)..(370)

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<222> (372)..(372)

<223> Xaa can be Ser, Ala or Leu

<220>

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<223> Xaa can be Ala, Gln, or Tyr

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<223> Xaa can be Ile or Pro

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<223> Xaa can be Val, Asn, or Pro

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<223> Xaa can be Pro or Gln

<220>
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<222> (453)..(453)
<223> Xaa can be Thr or Arg

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<222> (454)..(454)
<223> Xaa can be Phe or Tyr

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<222> (456)..(456)
<223> Xaa can be Ala or Thr

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<223> Xaa can be Asp or Asn

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<223> Xaa can be Gln or Lys

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<222> (557)..(557)
<223> Xaa can be Leu or Ser

<220>
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<223> Xaa can be Phe or Leu

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<222> (616)..(616)
<223> Xaa can be Ala or Asp

<220>
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<222> (618)..(618)
<223> Xaa can be Val or Ile

<220>
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<223> Xaa can be Ser or Lys

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<223> Xaa can be Met or Arg

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<220>
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<220>
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<223> Xaa can be Leu or Pro

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

Xaa Phe Ala Tyr Pro Gly Leu Xaa Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Xaa Gly Asp Xaa Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Xaa Thr Val Trp Arg Thr Leu His Gly Asn Xaa Xaa Lys
115 120 125

Xaa Xaa Xaa Xaa Xaa Xaa Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp
130 135 140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr Xaa Gln Met Lys Xaa
145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro

195

200

205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
 210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Xaa
 225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Xaa Xaa Xaa Xaa
 245 250 255

Xaa Trp Gly Gly Ala Asp Arg Xaa Thr Glu Ile Asp Thr Ile Leu Asp
 260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
 275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
 290 295 300

Asp Ala Thr Xaa Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
 305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
 325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Xaa Ala Trp Leu Thr
 340 345 350

Ser Met Leu Lys Arg Thr Val Xaa Ala Ala Val Pro Xaa Pro Xaa Xaa
 355 360 365

Xaa Xaa Tyr Xaa Xaa Ser Gly Tyr Glu Xaa Xaa Xaa Xaa Gly Pro Xaa
 370 375 380

Gly Ser Xaa Xaa Xaa Ser Xaa Gly Ala Lys Ile Leu Tyr Glu Ala Leu
 385 390 395 400

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Xaa Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Xaa Xaa Arg Xaa Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Xaa Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
530 535 540

Glu His Xaa Glu Ser Gln Glu Val Leu Gln Val Gln Xaa Asp Gln Thr
545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
580 585 590

Asp Arg Leu Xaa Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr

595

600

605

Val Ser Glu Val Leu Gly Lys Xaa Phe Xaa Xaa Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Xaa Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Xaa Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Xaa Ala Tyr
740 745 750

Pro Xaa Lys Phe Asp Leu Gln Asn Thr Gln Thr
755 760

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<222> (56)..(56)
<223> Xaa can be Val or Leu

<220>
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<222> (71)..(71)
<223> Xaa can be Gly or Ala

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<223> Xaa can be Asp, Asn, Ser, Thr or Val

<220>
<221> VARIANT
<222> (139)..(139)
<223> Xaa can be Lys or Ile

<220>
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<222> (445)..(445)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> VARIANT
<222> (455)..(455)
<223> Xaa can be Arg or Trp

<220>
<221> VARIANT
<222> (618)..(618)
<223> Xaa can be Val or Ile

<220>
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<222> (619)..(619)
<223> Xaa can be Ser or Lys

<400> 14

Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala

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

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
245 250 255

Leu Trp Gly Gly Ala Asp Arg Ala Thr Glu Ile Asp Thr Ile Leu Asp
260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

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

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

405

410

415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
 420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Xaa Lys Thr Pro
 435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
 450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
 465 470 475 480

Thr Glu Asn Asn Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
 485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
 500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
 515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Asp
 530 535 540

Glu His Lys Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
 545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
 565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
 580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
 595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Xaa Xaa Phe Asp Lys Asp Ile
610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
725 730 735

Val Asn Pro Ser Ala Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760

<210> 15

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<212> PRT

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<223> Xaa can be Asn or Val

<220>
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<223> Xaa can be Leu or Ile

<220>
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<222> (71)..(71)
<223> Xaa can be Gly or Ala

<220>
<221> VARIANT
<222> (74)..(74)
<223> Xaa can be Asp, Asn, Ser Thr, or Val

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<222> (264)..(264)
<223> Xaa can be Val or Ala

<220>
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<222> (484)..(484)
<223> Xaa can be Asp or Asn

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<222> (547)..(547)
<223> Xaa can be Gln or Lys

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<223> Xaa can be Val or Ile

<220>
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<222> (619)..(619)
<223> Xaa can be Ser or Lys

<220>
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<222> (741)..(741)
<223> Xaa can be Ala or Thr

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Ser Asn Met Trp Val Ile Gly Lys Asn Lys Ala Gln Asp Ala Lys Ala
1 5 10 15

Ile Met Val Asn Gly Pro Gln Phe Gly Trp Xaa Xaa Pro Ala Tyr Thr
20 25 30

Tyr Gly Ile Gly Leu His Gly Ala Gly Tyr Asp Val Thr Gly Asn Thr
35 40 45

Pro Phe Ala Tyr Pro Xaa Leu Leu Phe Gly His Asn Gly Thr Ile Ser
50 55 60

Trp Gly Ser Thr Ala Gly Xaa Gly Asp Xaa Val Asp Ile Phe Ala Glu
65 70 75 80

Lys Leu Ser Ala Glu Lys Pro Gly Tyr Tyr Gln His Asn Gly Glu Trp
85 90 95

Val Lys Met Leu Ser Arg Lys Glu Thr Ile Ala Val Lys Asp Gly Gln
100 105 110

Pro Glu Thr Phe Thr Val Trp Arg Thr Leu His Gly Asn Val Ile Lys
115 120 125

Thr Asp Thr Ala Thr Gln Thr Ala Tyr Ala Lys Ala Arg Ala Trp Asp

130

135

140

Gly Lys Glu Val Ala Ser Leu Leu Ala Trp Thr His Gln Met Lys Ala
 145 150 155 160

Lys Asn Trp Pro Glu Trp Thr Gln Gln Ala Ala Lys Gln Ala Leu Thr
 165 170 175

Ile Asn Trp Tyr Tyr Ala Asp Val Asn Gly Asn Ile Gly Tyr Val His
 180 185 190

Thr Gly Ala Tyr Pro Asp Arg Gln Pro Gly His Asp Pro Arg Leu Pro
 195 200 205

Val Pro Gly Thr Gly Lys Trp Asp Trp Lys Gly Leu Leu Ser Phe Asp
 210 215 220

Leu Asn Pro Lys Val Tyr Asn Pro Gln Ser Gly Tyr Ile Ala Asn Trp
 225 230 235 240

Asn Asn Ser Pro Gln Lys Asp Tyr Pro Ala Ser Asp Leu Phe Ala Phe
 245 250 255

Leu Trp Gly Gly Ala Asp Arg Xaa Thr Glu Ile Asp Thr Ile Leu Asp
 260 265 270

Lys Gln Pro Arg Phe Thr Ala Asp Gln Ala Trp Asp Val Ile Arg Gln
 275 280 285

Thr Ser Arg Arg Asp Leu Asn Leu Arg Leu Phe Leu Pro Ala Leu Lys
 290 295 300

Asp Ala Thr Ala Asn Leu Ala Glu Asn Asp Pro Arg Arg Gln Leu Val
 305 310 315 320

Asp Lys Leu Ala Ser Trp Asp Gly Glu Asn Leu Val Asn Asp Asp Gly
 325 330 335

Lys Thr Tyr Gln Gln Pro Gly Ser Ala Ile Leu Asn Ala Trp Leu Thr
340 345 350

Ser Met Leu Lys Arg Thr Val Val Ala Ala Val Pro Ala Pro Phe Gly
355 360 365

Lys Trp Tyr Ser Ala Ser Gly Tyr Glu Thr Thr Gln Asp Gly Pro Thr
370 375 380

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

Gln Gly Asp Lys Ser Pro Ile Pro Gln Ala Val Asp Leu Phe Gly Gly
405 410 415

Lys Pro Gln Gln Glu Val Ile Leu Ala Ala Leu Asp Asp Ala Trp Gln
420 425 430

Thr Leu Ser Lys Arg Tyr Gly Asn Asp Val Thr Gly Trp Lys Thr Pro
435 440 445

Ala Met Ala Leu Thr Phe Arg Ala Asn Asn Phe Phe Gly Val Pro Gln
450 455 460

Ala Ala Ala Lys Glu Ala Arg His Gln Ala Glu Tyr Gln Asn Arg Gly
465 470 475 480

Thr Glu Asn Asp Met Ile Val Phe Ser Pro Thr Ser Gly Asn Arg Pro
485 490 495

Val Leu Ala Trp Asp Val Val Ala Pro Gly Gln Ser Gly Phe Ile Ala
500 505 510

Pro Asp Gly Lys Ala Asp Lys His Tyr Asp Asp Gln Leu Lys Met Tyr
515 520 525

Glu Ser Phe Gly Arg Lys Ser Leu Trp Leu Thr Pro Gln Asp Val Xaa

530

535

540

Glu His Xaa Glu Ser Gln Glu Val Leu Gln Val Gln Leu Asp Gln Thr
 545 550 555 560

Glu Val Lys Ile Val Arg Asp Glu Tyr Gly Met Pro His Ile Tyr Ala
 565 570 575

Asp Asp Thr Tyr Arg Leu Phe Tyr Gly Tyr Gly Tyr Val Val Ala Gln
 580 585 590

Asp Arg Leu Phe Gln Met Glu Met Ala Arg Arg Ser Thr Gln Gly Thr
 595 600 605

Val Ser Glu Val Leu Gly Lys Ala Phe Xaa Xaa Phe Asp Lys Asp Ile
 610 615 620

Arg Gln Asn Tyr Trp Pro Asp Ser Ile Arg Ala Gln Ile Ala Ser Leu
 625 630 635 640

Ser Ala Glu Asp Lys Ser Ile Leu Gln Gly Tyr Ala Asp Gly Met Asn
 645 650 655

Ala Trp Ile Asp Lys Val Asn Ala Ser Pro Asp Lys Leu Leu Pro Gln
 660 665 670

Gln Phe Ser Thr Phe Gly Phe Lys Pro Lys His Trp Glu Pro Phe Asp
 675 680 685

Val Ala Met Ile Phe Val Gly Thr Met Ala Asn Arg Phe Ser Asp Ser
 690 695 700

Thr Ser Glu Ile Asp Asn Leu Ala Leu Leu Thr Ala Leu Lys Asp Lys
 705 710 715 720

Tyr Gly Lys Gln Gln Gly Met Ala Val Phe Asn Gln Leu Lys Trp Leu
 725 730 735

Val Asn Pro Ser Xaa Pro Thr Thr Ile Ala Ala Arg Glu Ser Ala Tyr
740 745 750

Pro Leu Lys Phe Asp Leu Gln Asn Thr Gln Thr Ala
755 760