

KWS 0119 PCT.txt
SEQUENCE LISTING

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<150> DE 10 2012 003 848.8
<151> 2012-02-29
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<211> 488

<212> PRT

<213> Erwinia herbicola

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35 40 45

Asn Arg Thr Ser Pro Arg Val Ser Leu Asp Arg Leu Arg Ala Phe Asn

50 55 60

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

65 70 75 80

Gly Gln Ala Ala Gln His Leu Gln Gln Leu Glu Ala Glu Leu Asn Asn

85 90 95

Gly Ser Asn Ile Arg Glu Leu Leu Asp Gly Pro Gly Phe Gly Gly Leu

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Leu Thr His Val Ile Asp Asp Ile Ala Ser Ile Ser Asn Ala Glu Asn

115 120 125

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130 135 140

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

145 150 155 160

Phe Gly Leu Tyr Ala Val Arg Glu Lys Leu Gln Gly Glu Ala Glu Leu

165 170 175

Ala Gly Ser Met Gln Thr His Pro Ala Phe Gln Ser Phe Pro Val Ala

180 185 190

Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu His Trp Gly Asp Tyr Gly

195 200 205

Ala Ala Ser Gly Met Arg Phe Asp Asn Glu Pro Gly Tyr Met Gly Ser

210 215 220

Met Phe Arg Gly Leu Lys Phe Val Ile Asp Ser Glu Ala Gly Ser Ser

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 Arg Gln Glu Ile Ala Asp Ser Pro Leu Ser Arg Ser Gly Arg Ser Ser
 35 40 45
 Asn Arg Thr Ser Pro Arg Val Ser Leu Asp Arg Leu Arg Ala Phe Asn
 50 55 60
 Pro Pro Ser Gly Ala Ser Val Gly Ala Leu Arg Asn Trp Phe Trp Gln
 65 70 75 80
 Gly Gln Ala Ala Gln His Leu Gln Gln Leu Glu Ala Glu Leu Asn Asn
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 Ser Arg Lys Lys Gly Glu Ile Asp Ala Thr Trp Leu Glu Asn Leu His
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 260 265 270

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Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly Tyr
305 310 315 320

Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn Leu
325 330 335

Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser Arg Phe Ala
340 345 350

Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg Pro Ile Asp Trp Asp
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 35 40 45

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

Pro Pro Ser Gly Ala Ser Val Gly Ala Leu Arg Asn Trp Phe Trp Gln
 65 70 75 80

Gly Gln Ala Ala Gln His Leu Gln Gln Leu Glu Ala Glu Leu Asn Asn
 85 90 95

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

Leu Thr His Val Ile Asp Asp Ile Ala Ser Ile Ser Asn Ala Glu Asn
 115 120 125

Leu Ser Pro Ile Glu Val Ala Glu Glu Leu Arg Gln Ala Ile Ser Thr
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130

135

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140

Gly Arg Gly Ala Asn Asn Leu Asp Ile Ser Leu Lys Asn Val Leu Gln
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Phe Gly Leu Tyr Ala Val Arg Glu Lys Leu Gln Gly Glu Ala Glu Leu
165 170 175

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180 185 190

Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu His Trp Gly Asp Tyr Gly
195 200 205

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

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

Leu Lys Asn Val Leu Gln Phe Gly Leu Tyr Ala Val Arg Glu Lys Leu
65 70 75 80

Gln Gly Glu Ala Glu Leu Ala Gly Ser Met Gln Thr His Pro Ala Phe
85 90 95

Gln Ser Phe Pro Val Ala Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu
100 105 110

His Trp Gly Asp Tyr Gly Ala Ala Ser Gly Met Arg Phe Asp Asn Glu
115 120 125

Pro Gly Tyr Met Gly Ser Met Phe Arg Gly Leu Lys Phe Val Ile Asp
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Glu Lys Leu Gln Gly Glu Ala Glu Leu Ala Gly Ser Met Gln Thr His
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Pro Ala Phe Gln Ser Phe Pro Val Ala Gln Ala Trp Lys Phe Cys Ile
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Glu Gln Glu His Trp Gly Asp Tyr Gly Ala Ala Ser Gly Met Arg Phe
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Asp Asn Glu Pro Gly Tyr Met Gly Ser Met Phe Arg Gly Leu Lys Phe
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20

25

30

Asp Ile Ser Leu Lys Asn Val Leu Gln Phe Gly Leu Tyr Ala Val Arg
 35 40 45

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 50 55 60

Pro Ala Phe Gln Ser Phe Pro Val Ala Gln Ala Trp Lys Phe Cys Ile
 65 70 75 80

Glu Gln Glu His Trp Gly Asp Tyr Gly Ala Ala Ser Gly Met Arg Phe
 85 90 95

Asp Asn Glu Pro Gly Tyr Met Gly Ser Met Phe Arg Gly Leu Lys Phe
 100 105 110

Val Ile Asp Ser Glu Ala Gly Ser Ser Ser Arg Lys Lys Gly Glu Ile
 115 120 125

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

Phe Gln Arg Arg Val Met His Asp Trp Gln Phe Gly Ala Asn Val Glu
 145 150 155 160

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

Ser Asp Lys Val Arg Ser Ala Ala Ser Ala Ile Phe Tyr Leu Pro Glu
 180 185 190

His Leu Trp Pro Leu Glu Gly Gly Tyr Arg Gln Gly Gln Leu Val Gln
 195 200 205

Phe Lys Leu Val Tyr Pro Lys Asn Leu Thr Pro Ala Gly Leu Gly Asp
 210 215 220

Leu Gln Lys Phe Gln Ser Arg Phe Ala Gly Trp Ala Glu Phe Arg Ser
 225 230 235 240

Val Gly Asn Arg Pro Ile Asp Trp Asp Glu Val Glu Arg Gly Asn Ala
 245 250 255

Gln Val Met Trp Ala Cys Thr Gly Lys Ser Arg Lys Glu Val Met Lys
 260 265 270

Leu Val Lys Asn Val Leu Gln Thr His Tyr Asn Asp Ile Lys Arg Thr
 275 280 285

Thr Asn Ala Glu Ala Ala Leu His Val Val Ala Arg Thr Cys Ala Thr
 290 295 300

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300

290

295

Leu Glu Arg Ala His Val Phe Met Asp Gly Ser Ala Arg Thr Phe Gly
305 310 315 320
Cys Leu Leu Leu Asn Lys Leu Leu Leu Ser Ala Gly Leu Ser Pro Cys
325 330 335
Met Ala Pro Asp Ala Asn Glu Phe Asp Gly Tyr Ser Asn Glu Glu Leu
340 345 350
Val Ala Arg Ile Gln Glu Gly Gln Asn Ile Phe Arg Ala His Cys His
355 360 365

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<210> 15
<211> 1209
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_92-488

<400> 15
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gcggattgct gacccatgtg atcgacgata tcgcctcgat ttcaaacgcg gaaaattttgt 120
cgccgatcga ggctgcagag gagctaaggc aagctattag caccgggcgc ggggcgaaca 180
at ttggatat atctttgaaa aacgtttctac aattcggact ttatgcggtc agggaaaaac 240
tgcaagggga agccgagctc gccggctcga tgcaaacaca ccctgctttt cagtctttcc 300
cggtggccca ggcctggaaa ttttgattg agcaagagca ttggggtgat tacggcgccg 360
catccggcat gcgatttgac aacgagcccg gctacatggg tagtatgttt cgcggttaa 420
aattcgtcat cgactcggaa gcgggttcct cgtcccga aaaggcgaa atcgatgcta 480
cttggttgga gaatttgac gacatcgctg tcaatggcgt gttccagcgc agagtcatgc 540
atgattggca gttcggcgcc aatgtcgaag aagctgtgaa tgcatcgcc gcccttaccg 600
cgctggcag caatattagc gataaggta ggagcgcagc gtcggcaatc ttctatttgc 660
cggaacacct atggccattg gaggggtgggt atcgacaagg ccagttggtc cagttcaaac 720
tggtttatcc caagaatctg actccggctg ggctcggcga tctgcaaaag ttccagtccc 780
ggttcgccgg gtgggctgag tttcgaagtg tcggtaatcg tccgatcgac tgggatgagg 840
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tgaagctggg gaaaaatgtg ctcaaacgc attataacga tataaaaagg actaccaacg 960
cagaggccgc actgcatgtg gtggcacgaa cgtgcgctac cctggagcgc gcgcacgtgt 1020
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caggcttatc accatgcatg gcccctgatg ccaacgaatt cgacggttac tcgaacgaag1140

aactggtggc gcggattcag gaaggacaga atatattccg ggcacattgc catgcatagc1200

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<210> 16

<211> 398

<212> PRT

<213> Artificial Sequence

<220>

<223> PthG_92-488

<400> 16

Met Ala Glu Leu Asn Asn Gly Ser Asn Ile Arg Glu Leu Leu Asp Gly115

Pro Gly Phe Gly Gly Leu Leu Thr His Val Ile Asp Asp Ile Ala Ser202530

Ile Ser Asn Ala Glu Asn Leu Ser Pro Ile Glu Val Ala Glu Glu Leu354045

Arg Gln Ala Ile Ser Thr Gly Arg Gly Ala Asn Asn Leu Asp Ile Ser505560

Leu Lys Asn Val Leu Gln Phe Gly Leu Tyr Ala Val Arg Glu Lys Leu65707580

Gln Gly Glu Ala Glu Leu Ala Gly Ser Met Gln Thr His Pro Ala Phe859095

Gln Ser Phe Pro Val Ala Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu100105110

His Trp Gly Asp Tyr Gly Ala Ala Ser Gly Met Arg Phe Asp Asn Glu115120125

Pro Gly Tyr Met Gly Ser Met Phe Arg Gly Leu Lys Phe Val Ile Asp130135140

Ser Glu Ala Gly Ser Ser Ser Arg Lys Lys Gly Glu Ile Asp Ala Thr145150155160

Trp Leu Glu Asn Leu His Asp Ile Ala Val Asn Gly Val Phe Gln Arg165170175

Arg Val Met His Asp Trp Gln Phe Gly Ala Asn Val Glu Glu Ala Val180185190

Asn Ala Val Ala Ala Leu Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys195200205

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Val Arg Ser Ala Ala Ser Ala Ile Phe Tyr Leu Pro Glu His Leu Trp
210 215 220

Pro Leu Glu Gly Gly Tyr Arg Gln Gly Gln Leu Val Gln Phe Lys Leu
225 230 235 240

Val Tyr Pro Lys Asn Leu Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys
245 250 255

Phe Gln Ser Arg Phe Ala Gly Trp Ala Glu Phe Arg Ser Val Gly Asn
260 265 270

Arg Pro Ile Asp Trp Asp Glu Val Glu Arg Gly Asn Ala Gln Val Met
275 280 285

Trp Ala Cys Thr Gly Lys Ser Arg Lys Glu Val Met Lys Leu Val Lys
290 295 300

Asn Val Leu Gln Thr His Tyr Asn Asp Ile Lys Arg Thr Thr Asn Ala
305 310 315 320

Glu Ala Ala Leu His Val Val Ala Arg Thr Cys Ala Thr Leu Glu Arg
325 330 335

Ala His Val Phe Met Asp Gly Ser Ala Arg Thr Phe Gly Cys Leu Leu
340 345 350

Leu Asn Lys Leu Leu Leu Ser Ala Gly Leu Ser Pro Cys Met Ala Pro
355 360 365

Asp Ala Asn Glu Phe Asp Gly Tyr Ser Asn Glu Glu Leu Val Ala Arg
370 375 380

Ile Gln Glu Gly Gln Asn Ile Phe Arg Ala His Cys His Ala
385 390 395

<210> 17
<211> 999
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_162-488

<400> 17
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agcaagagca ttggggtgat tacggcgccg catccggcat gcgatttgac aacgagcccg 180
gctacatggg tagtatgttt cgcggttaa aattcgtcac cgactcggaa gcgggttcct 240
cgtcccga aaaggcgaa atcgatgcta cttggttgga gaattgcac gacatcgctg 300

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tcaatggcgt gttccagcgc agagtcatgc atgattggca gttcggcgcc aatgtcgaag 360
aagctgtgaa tgcagtcgcc gcccttaccg cgcttgccag caatattagc gataagggtca 420
ggagcgcagc gtcggcaatc ttctatttgc cggaacacct atggccattg gaggggtgggt 480
atcgacaagg ccagttggtc cagttcaaac tggtttatcc caagaatctg actccggctg 540
ggctcggcga tctgcaaaag ttccagtccc ggttcgccgg gtgggctgag tttcgaagtg 600
tcggtaatcg tccgatcgac tgggatgagg tagaacgcgg caacgcccag gttatgtggg 660
cgtgcacggg aaaaagccga aaagagggtta tgaagctggt gaaaaatgtg ctccaaacgc 720
attataacga tataaaaagg actaccaacg cagaggccgc actgcatgtg gtggcacgaa 780
cgtgcgctac cctggagcgc gcgcacgtgt tcatggatgg cagcgcacga acttttcggtt 840
gcctgctcct caataaaactt ttgctttccg caggcttatc accatgcatg gcccttgatg 900
ccaacgaatt cgacggttac tcgaacgaag aactggtggc gcggattcag gaaggacaga 960
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<210> 18
<211> 328
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_162-488

<400> 18

Met Gly Leu Tyr Ala Val Arg Glu Lys Leu Gln Gly Glu Ala Glu Leu
1 5 10 15

Ala Gly Ser Met Gln Thr His Pro Ala Phe Gln Ser Phe Pro Val Ala
20 25 30

Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu His Trp Gly Asp Tyr Gly
35 40 45

Ala Ala Ser Gly Met Arg Phe Asp Asn Glu Pro Gly Tyr Met Gly Ser
50 55 60

Met Phe Arg Gly Leu Lys Phe Val Ile Asp Ser Glu Ala Gly Ser Ser
65 70 75 80

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

Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg Val Met His Asp Trp
100 105 110

Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn Ala Val Ala Ala Leu
115 120 125

Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val Arg Ser Ala Ala Ser
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140

130

135

Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly Tyr
145 150 155 160Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn Leu
165 170 175Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser Arg Phe Ala
180 185 190Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg Pro Ile Asp Trp Asp
195 200 205Glu Val Glu Arg Gly Asn Ala Gln Val Met Trp Ala Cys Thr Gly Lys
210 215 220Ser Arg Lys Glu Val Met Lys Leu Val Lys Asn Val Leu Gln Thr His
225 230 235 240Tyr Asn Asp Ile Lys Arg Thr Thr Asn Ala Glu Ala Ala Leu His Val
245 250 255Val Ala Arg Thr Cys Ala Thr Leu Glu Arg Ala His Val Phe Met Asp
260 265 270Gly Ser Ala Arg Thr Phe Gly Cys Leu Leu Leu Asn Lys Leu Leu Leu
275 280 285Ser Ala Gly Leu Ser Pro Cys Met Ala Pro Asp Ala Asn Glu Phe Asp
290 295 300Gly Tyr Ser Asn Glu Glu Leu Val Ala Arg Ile Gln Glu Gly Gln Asn
305 310 315 320Ile Phe Arg Ala His Cys His Ala
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<213> Artificial Sequence<220>
<223> pthG_205-488

<400> 19	
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aaaaaggcga aatcgatgct acttggttgg agaatttgca cgacatcgct gtcaatggcg	180
tgttccagcg cagagtcag catgattggc agttcggcgc caatgtcgaa gaagctgtga	240

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atgcagtcgc cgcccttacc ggcctggca gcaatattag cgataaggctc aggagcgag 300
cgctcggaat cttctatttg ccggaacacc tatggccatt ggaggggtggg tatcgacaag 360
gccagttggt ccagttcaaa ctggtttatc ccaagaatct gactccggct gggctcggcg 420
atctgcaaaa gttccagtcc cggttcgccg ggtgggctga gtttcgaagt gtcggtaatc 480
gtccgatcga ctgggatgag gtagaacgcg gcaacgcccc ggttatgtgg gcgtgcacgg 540
gaaaaagccg aaaagagggt atgaagctgg tgaaaaatgt gtcctcaaag cattataacg 600
atataaaaag gactaccaac gcagaggccg cactgcatgt ggtggcacga acgtgcgcta 660
ccctggagcg cgcgcacgtg ttcattggatg gcagcgcacg aactttcggg tgctgtctcc 720
tcaataaact tttgctttcc gcaggcttat caccatgcat ggcccctgat gccaacgaat 780
tcgacggtta ctcgaacgaa gaactggtgg cgcggtattca ggaaggacag aatatattcc 840
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<210> 20
<211> 285
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_205-488

<400> 20

Met Gly Asp Tyr Gly Ala Ala Ser Gly Met Arg Phe Asp Asn Glu Pro
1 5 10 15

Gly Tyr Met Gly Ser Met Phe Arg Gly Leu Lys Phe Val Ile Asp Ser
20 25 30

Glu Ala Gly Ser Ser Ser Arg Lys Lys Gly Glu Ile Asp Ala Thr Trp
35 40 45

Leu Glu Asn Leu His Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg
50 55 60

Val Met His Asp Trp Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn
65 70 75 80

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

Arg Ser Ala Ala Ser Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro
100 105 110

Leu Glu Gly Gly Tyr Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val
115 120 125

Tyr Pro Lys Asn Leu Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe
130 135 140

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Gln Ser Arg Phe Ala Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg
145 150 155 160

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

Ala Cys Thr Gly Lys Ser Arg Lys Glu Val Met Lys Leu Val Lys Asn
180 185 190

Val Leu Gln Thr His Tyr Asn Asp Ile Lys Arg Thr Thr Asn Ala Glu
195 200 205

Ala Ala Leu His Val Val Ala Arg Thr Cys Ala Thr Leu Glu Arg Ala
210 215 220

His Val Phe Met Asp Gly Ser Ala Arg Thr Phe Gly Cys Leu Leu Leu
225 230 235 240

Asn Lys Leu Leu Leu Ser Ala Gly Leu Ser Pro Cys Met Ala Pro Asp
245 250 255

Ala Asn Glu Phe Asp Gly Tyr Ser Asn Glu Glu Leu Val Ala Arg Ile
260 265 270

Gln Glu Gly Gln Asn Ile Phe Arg Ala His Cys His Ala
275 280 285

<210> 21
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_245-488

<400> 21
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atgcagtcgc cgcccttacc gcgcctggca gcaatattag cgataaggtc aggagcgCag 180
cgtcggcaat cttctatttg ccggaacacc tatggccatt ggaggggtggg tatcgacaag 240
gccagttggt ccagttcaaa ctggtttatc ccaagaatct gactccggct gggctcggcg 300
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gtccgatcga ctgggatgag gtagaacgcg gcaacgcca ggttatgtgg gcgtgcacgg 420
gaaaaagccg aaaagagggt atgaagctgg tgaaaaatgt gtcctcaaacg cattataacg 480
atataaaaag gactaccaac gcagaggccg cactgcatgt ggtggcacga acgtgcgcta 540
ccctggagcg cgcgcacgtg ttcatggatg gcagcgcacg aactttcggt tgctgtctcc 600
tcaataaact ttgtctttcc gcaggcttat caccatgcat ggccccgat gccaacgaat 660

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tcgacgggta ctcgaacgaa gaactgggtg cgcggtattca ggaaggacag aatatattcc 720
gggcacattg ccatgcatag cgatggatcc 750

<210> 22
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_245-488

<400> 22

Met Gly Glu Ile Asp Ala Thr Trp Leu Glu Asn Leu His Asp Ile Ala
1 5 10 15

Val Asn Gly Val Phe Gln Arg Arg Val Met His Asp Trp Gln Phe Gly
20 25 30

Ala Asn Val Glu Glu Ala Val Asn Ala Val Ala Ala Leu Thr Ala Pro
35 40 45

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

Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly Tyr Arg Gln Gly
65 70 75 80

Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn Leu Thr Pro Ala
85 90 95

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

Glu Phe Arg Ser Val Gly Asn Arg Pro Ile Asp Trp Asp Glu Val Glu
115 120 125

Arg Gly Asn Ala Gln Val Met Trp Ala Cys Thr Gly Lys Ser Arg Lys
130 135 140

Glu Val Met Lys Leu Val Lys Asn Val Leu Gln Thr His Tyr Asn Asp
145 150 155 160

Ile Lys Arg Thr Thr Asn Ala Glu Ala Ala Leu His Val Val Ala Arg
165 170 175

Thr Cys Ala Thr Leu Glu Arg Ala His Val Phe Met Asp Gly Ser Ala
180 185 190

Arg Thr Phe Gly Cys Leu Leu Leu Asn Lys Leu Leu Leu Ser Ala Gly
195 200 205

Leu Ser Pro Cys Met Ala Pro Asp Ala Asn Glu Phe Asp Gly Tyr Ser

210

215

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220

Asn Glu Glu Leu Val Ala Arg Ile Gln Glu Gly Gln Asn Ile Phe Arg
225 230 235 240

Ala His Cys His Ala
245

<210> 23
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_253-488

<400> 23
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ctggcagcaa tattagcgat aaggtcagga gcgcagcgtc ggcaatcttc tatttgccgg 180
aacacctatg gccattggag ggtgggtatc gacaaggcca gttggtccag ttcaaactgg 240
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tcgccgggtg ggctgagttt cgaagtgtcg gtaatcgtcc gatcgactgg gatgaggtag 360
aacgcggcaa cgcccagggt atgtgggcgt gcacgggaaa aagccgaaaa gaggttatga 420
agctggtgaa aaatgtgtct caaacgcatt ataacgatat aaaaaggact accaacgcag 480
aggccgcact gcatgtggtg gcacgaacgt gcgctaccct ggagcgcgcg cacgtgttca 540
tggtatggcag cgcacgaact ttcggttgcc tgctcctcaa taaacttttg ctttccgcag 600
gcttatcacc atgcatggcc cctgatgcca acgaattcga cggttactcg aacgaagaac 660
tggtggcgcg gattcaggaa ggacagaata tattccgggc acattgccat gcatagcgat 720
ggatcc 726

<210> 24
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_253-488

<400> 24

Met Glu Asn Leu His Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg
1 5 10 15

Val Met His Asp Trp Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn
20 25 30

Ala Val Ala Ala Leu Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val
35 40 45

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Arg Ser Ala Ala Ser Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro
50 55 60

Leu Glu Gly Gly Tyr Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val
65 70 75 80

Tyr Pro Lys Asn Leu Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe
85 90 95

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

Pro Ile Asp Trp Asp Glu Val Glu Arg Gly Asn Ala Gln Val Met Trp
115 120 125

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

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

Ala Ala Leu His Val Val Ala Arg Thr Cys Ala Thr Leu Glu Arg Ala
165 170 175

His Val Phe Met Asp Gly Ser Ala Arg Thr Phe Gly Cys Leu Leu Leu
180 185 190

Asn Lys Leu Leu Leu Ser Ala Gly Leu Ser Pro Cys Met Ala Pro Asp
195 200 205

Ala Asn Glu Phe Asp Gly Tyr Ser Asn Glu Glu Leu Val Ala Arg Ile
210 215 220

Gln Glu Gly Gln Asn Ile Phe Arg Ala His Cys His Ala
225 230 235

<210> 25
<211> 720
<212> DNA
<213> Artificial sequence

<220>
<223> pthG_G+256-488

<400> 25
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agttcggcgc caatgtcgaa gaagctgtga atgcagtcgc cgcccttacc ggcctggca 120
gcaatattag cgataaggtc aggagcgcag cgtcggcaat cttctatttg ccggaacacc 180
tatggccatt ggaggggtggg tatcgacaag gccagttggg ccagttcaaa ctggtttatc 240
ccaagaatct gactccggct gggctcggcg atctgcaaaa gttccagtcc cggttcgccg 300

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tgaaaaatgt gctccaaacg cattataacg atataaaaag gactaccaac gcagaggccg 480
cactgcatgt ggtggcacga acgtgcgcta ccctggagcg cgcgcacgtg ttcattggatg 540
gcagcgcacg aactttcggg tgcctgctcc tcaataaaact ttgtctttcc gcaggcttat 600
caccatgcat ggcccctgat gccaacgaat tcgacgggta ctcgaacgaa gaactggtgg 660
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<210> 26
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_G+256-488

<400> 26

Met Gly His Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg Val Met
1 5 10 15

His Asp Trp Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn Ala Val
20 25 30

Ala Ala Leu Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val Arg Ser
35 40 45

Ala Ala Ser Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu
50 55 60

Gly Gly Tyr Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro
65 70 75 80

Lys Asn Leu Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser
85 90 95

Arg Phe Ala Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg Pro Ile
100 105 110

Asp Trp Asp Glu Val Glu Arg Gly Asn Ala Gln Val Met Trp Ala Cys
115 120 125

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

Gln Thr His Tyr Asn Asp Ile Lys Arg Thr Thr Asn Ala Glu Ala Ala
145 150 155 160

Leu His Val Val Ala Arg Thr Cys Ala Thr Leu Glu Arg Ala His Val
165 170 175

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Phe Met Asp Gly Ser Ala Arg Thr Phe Gly Cys Leu Leu Leu Asn Lys
180 185 190

Leu Leu Leu Ser Ala Gly Leu Ser Pro Cys Met Ala Pro Asp Ala Asn
195 200 205

Glu Phe Asp Gly Tyr Ser Asn Glu Glu Leu Val Ala Arg Ile Gln Glu
210 215 220

Gly Gln Asn Ile Phe Arg Ala His Cys His Ala
225 230 235

<210> 27
<211> 714
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_257-488

<400> 27
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ttagcgataa ggtcaggagcgcagcgctcggcaatcttcta tttgccggaa cacctatggc180
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cccaggttat gtgggcgtgc acgggaaaaa gccgaaaaga ggttatgaag ctggtgaaaa420
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atgtggtggc acgaacgtgc gctaccctgg agcgcgcgca cgtgttcatg gatggcagcg540
cacgaacttt cggttgctcgtcctctcaata aacttttgct ttccgcaggc ttatcaccat600
gcatggcccc tgatgccaac gaattcgacg gttactcgaa cgaagaactg gtggcgcgga660
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<210> 28
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_257-488

<400> 28
Met Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg Val Met His Asp
1 5 10 15

Trp Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn Ala Val Ala Ala
20 25 30

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Leu Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val Arg Ser Ala Ala
35 40 45

Ser Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly
50 55 60

Tyr Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn
65 70 75 80

Leu Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser Arg Phe
85 90 95

Ala Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg Pro Ile Asp Trp
100 105 110

Asp Glu Val Glu Arg Gly Asn Ala Gln Val Met Trp Ala Cys Thr Gly
115 120 125

Lys Ser Arg Lys Glu Val Met Lys Leu Val Lys Asn Val Leu Gln Thr
130 135 140

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

Val Val Ala Arg Thr Cys Ala Thr Leu Glu Arg Ala His Val Phe Met
165 170 175

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

Leu Ser Ala Gly Leu Ser Pro Cys Met Ala Pro Asp Ala Asn Glu Phe
195 200 205

Asp Gly Tyr Ser Asn Glu Glu Leu Val Ala Arg Ile Gln Glu Gly Gln
210 215 220

Asn Ile Phe Arg Ala His Cys His Ala
225 230

<210> 29
<211> 1065
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_1-350

<400> 29
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accacgacga tcggagttcg atagggcagg aaagccccag gcaagagatt gctgatagtc 120
cgctgagtcg atcaggccgt tcatccaata gaacctctcc ccgcgtatcg ctggacaggc 180

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tcagagcttt caatcccca agcggcgcg	cagtggcg	tttgagaa	tggttctggc	240
aaggacaggc tgctcaacat ctgcagcagc	tcgaagcaga	gctcaacaac	ggttcgaaca	300
ttcgcgagct gttggacggc cctggatttg	gcggattgct	gacccatgtg	atcgacgata	360
tcgcctcgat ttcaaacgcg gaaaatttgt	cgccgatcga	ggtcgcagag	gagctaaggc	420
aagctattag caccggggcg ggggcgaaca	atttggatat	atctttgaaa	aacgttctac	480
aattcggact ttatgcggtc agggaaaaac	tgcaagggga	agccgagctc	gccggctcga	540
tgcaaacaca ccctgctttt cagtctttcc	cggtggccca	ggcctggaaa	ttttgcattg	600
agcaagagca ttgggggtgat tacggcgccg	catccggcat	gcgatttgac	aacgagcccc	660
gctacatggg tagtatgttt cgcggcttaa	aattcgtcat	cgactcggaa	gcgggttcct	720
cgtcccgaaa aaaaggcgaa atcgatgcta	cttggttgga	gaatttgcac	gacatcgctg	780
tcaatggcgt gttccagcgc agagtcatgc	atgattggca	gttcggcgcc	aatgtcgaag	840
aagctgtgaa tgcagtcgcc gcccttaccg	cgctggcag	caatattagc	gataaggcca	900
ggagcgcagc gtcggcaatc ttctatttgc	cggaacacct	atggccattg	gaggggtgggt	960
atcgacaagg ccagttggtc cagttcaaac	tggtttatcc	caagaatctg	actccggctg	1020
ggctcggcga tctgcaaaag ttccagtccc	ggtagcgatg	gatcc		1065

<210> 30
<211> 350
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_1-350

<400> 30

Met Gly Cys Phe Asn Val Thr Gly Ala Ser Gly Arg Ala Asn Asn Tyr	1	5	10	15
Val Val Glu His His Asp Asp Arg Ser Ser Ile Gly Gln Glu Ser Pro	20	25	30	
Arg Gln Glu Ile Ala Asp Ser Pro Leu Ser Arg Ser Gly Arg Ser Ser	35	40	45	
Asn Arg Thr Ser Pro Arg Val Ser Leu Asp Arg Leu Arg Ala Phe Asn	50	55	60	
Pro Pro Ser Gly Ala Ser Val Gly Ala Leu Arg Asn Trp Phe Trp Gln	65	70	75	80
Gly Gln Ala Ala Gln His Leu Gln Gln Leu Glu Ala Glu Leu Asn Asn	85	90	95	
Gly Ser Asn Ile Arg Glu Leu Leu Asp Gly Pro Gly Phe Gly Gly Leu	100	105	110	

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Leu Thr His Val Ile Asp Asp Ile Ala Ser Ile Ser Asn Ala Glu Asn
 115 120 125

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

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

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

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

Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu His Trp Gly Asp Tyr Gly
 195 200 205

Ala Ala Ser Gly Met Arg Phe Asp Asn Glu Pro Gly Tyr Met Gly Ser
 210 215 220

Met Phe Arg Gly Leu Lys Phe Val Ile Asp Ser Glu Ala Gly Ser Ser
 225 230 235 240

Ser Arg Lys Lys Gly Glu Ile Asp Ala Thr Trp Leu Glu Asn Leu His
 245 250 255

Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg Val Met His Asp Trp
 260 265 270

Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn Ala Val Ala Ala Leu
 275 280 285

Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val Arg Ser Ala Ala Ser
 290 295 300

Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly Tyr
 305 310 315 320

Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn Leu
 325 330 335

Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser Arg
 340 345 350

<210> 31
 <211> 1155
 <212> DNA
 <213> Artificial sequence

<220>
 <223> pthG_1-380

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<400> 31
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cgctgagtcg atcaggccgt tcatccaata gaacctctcc ccgcgtatcg ctggacaggc 180
tcagagcttt caatccccca agcggcgcggt cagttggcgc tttgagaaat tggttctggc 240
aaggacaggc tgctcaacat ctgcagcagc tcgaagcaga gctcaacaac ggttcgaaca 300
ttcgcgagct gttggacggc cctggatttg gcggattgct gacccatgtg atcgacgata 360
tcgcctcgat ttcaaacgcg gaaaatttgt cgccgatcga ggtcgcagag gagctaaggc 420
aagctattag caccgggcg cggggaaca atttgatat atctttgaaa aacgttctac 480
aattcggact ttatgcggtc agggaaaaac tgcaagggga agccgagctc gccggctcga 540
tgcaaacaca ccctgctttt cagtctttcc cggtggccca ggccctggaaa ttttgattg 600
agcaagagca ttgggggtgat tacggcgccg catccggcat gcgatttgac aacgagccccg 660
gctacatggg tagtatgttt cgcggtctaa aattcgtcat cgactcggaa gcgggttcct 720
cgtcccgaaa aaaaggcgaa atcgatgcta cttggttgga gaatttgac gacatcgctg 780
tcaatggcgt gttccagcgc agagtcatgc atgattggca gttcggcgcc aatgtcgaag 840
aagctgtgaa tgcagtcgcc gcccttaccg gccttgccag caatattagc gataagggtca 900
ggagcgcagc gtcggcaatc ttctatttgc cggaacacct atggccattg gagggtggtt 960
atcgacaagg ccagttggtc cagttcaaac tggtttatcc caagaatctg actccggctg 1020
ggctcggcga tctgcaaaag ttccagtccc ggctcggcgg gtgggctgag tttcgaagtg 1080
tcggtaatcg tccgatcgac tgggatgagg tagaacgcgg caacgcccag gttatgtggg 1140
cgtagcgatg gatcc 1155

<210> 32
<211> 380
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_1-380

<400> 32

Met Gly Cys Phe Asn Val Thr Gly Ala Ser Gly Arg Ala Asn Asn Tyr
1 5 10 15

Val Val Glu His His Asp Asp Arg Ser Ser Ile Gly Gln Glu Ser Pro
20 25 30

Arg Gln Glu Ile Ala Asp Ser Pro Leu Ser Arg Ser Gly Arg Ser Ser
35 40 45

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

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Pro Pro Ser Gly Ala Ser Val Gly Ala Leu Arg Asn Trp Phe Trp Gln
 65 70 75 80
 Gly Gln Ala Ala Gln His Leu Gln Gln Leu Glu Ala Glu Leu Asn Asn
 85 90 95
 Gly Ser Asn Ile Arg Glu Leu Leu Asp Gly Pro Gly Phe Gly Gly Leu
 100 105 110
 Leu Thr His Val Ile Asp Asp Ile Ala Ser Ile Ser Asn Ala Glu Asn
 115 120 125
 Leu Ser Pro Ile Glu Val Ala Glu Glu Leu Arg Gln Ala Ile Ser Thr
 130 135 140
 Gly Arg Gly Ala Asn Asn Leu Asp Ile Ser Leu Lys Asn Val Leu Gln
 145 150 155 160
 Phe Gly Leu Tyr Ala Val Arg Glu Lys Leu Gln Gly Glu Ala Glu Leu
 165 170 175
 Ala Gly Ser Met Gln Thr His Pro Ala Phe Gln Ser Phe Pro Val Ala
 180 185 190
 Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu His Trp Gly Asp Tyr Gly
 195 200 205
 Ala Ala Ser Gly Met Arg Phe Asp Asn Glu Pro Gly Tyr Met Gly Ser
 210 215 220
 Met Phe Arg Gly Leu Lys Phe Val Ile Asp Ser Glu Ala Gly Ser Ser
 225 230 235 240
 Ser Arg Lys Lys Gly Glu Ile Asp Ala Thr Trp Leu Glu Asn Leu His
 245 250 255
 Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg Val Met His Asp Trp
 260 265 270
 Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn Ala Val Ala Ala Leu
 275 280 285
 Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val Arg Ser Ala Ala Ser
 290 295 300
 Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly Tyr
 305 310 315 320
 Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn Leu
 325 330 335

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Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser Arg Phe Ala
340 345 350

Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg Pro Ile Asp Trp Asp
355 360 365

Glu Val Glu Arg Gly Asn Ala Gln Val Met Trp Ala
370 375 380

<210> 33
<211> 1251
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_1-412

<400> 33
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accacgacga tcggagttcg atagggcagg aaagccccag gcaagagatt gctgatagtc 120
cgctgagtcg atcaggccgt tcatccaata gaacctctcc ccgcgatcgc ctggacaggc 180
tcagagcttt caatcccca agcggcgcgt cagttggcgc tttgagaaat tggttctggc 240
aaggacaggc tgctcaacat ctgcagcagc tcgaagcaga gctcaacaac ggttcgaaca 300
ttcgcgagct gttggacggc cctggatttg gcggattgct gacccatgtg atcgacgata 360
tcgcctcgat ttcaaacgcg gaaaatttgt cgccgatcga ggtcgcagag gagctaaggc 420
aagctattag caccgggcgc ggggcgaaca atttgatat atctttgaaa aacgttctac 480
aattcggact ttatgcggtc agggaaaaac tgcaagggga agccgagctc gccggctcga 540
tgcaaacaca ccctgctttt cagtctttcc cggtggtcca ggcttgaaaa ttttgcatg 600
agcaagagca ttgggggtgat tacggcgccg catccggcat gcgatttgac aacgagcccc 660
gctacatggg tagtatgttt cgcggttaa aattcgtcat cgactcggaa gcgggttcct 720
cgtcccga aaaggcgaa atcgatgcta cttggttgga gaatttgac gacatcgctg 780
tcaatggcgt gttccagcgc agagtcatgc atgattggca gttcggcgcc aatgtcgaag 840
aagctgtgaa tgcagtcgcc gcccttaccg cgcttgag caatattagc gataaggcca 900
ggagcgcagc gtcggcaatc ttctatttgc cggaacacct atggccattg gaggggtggg 960
atcgacaagg ccagttggtc cagttcaaac tggtttatcc caagaatctg actccggctg 1020
ggctcggcga tctgcaaaag ttccagtccc ggctcgccgg gtgggctgag tttcgaagt 1080
tcggtaatcg tccgatcgac tgggatgagg tagaacgcgg caacgcccag gttatgtgg 1140
cgtgcacggg aaaaagccga aaagaggta tgaagctggt gaaaaatgtg ctccaaacgc 1200
attataacga tataaaaagg actaccaacg cagaggccta gcgatggatc c 1251

<210> 34
<211> 412
<212> PRT

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<213> Artificial Sequence

<220>

<223> PthG_1-412

<400> 34

Met Gly Cys Phe Asn Val Thr Gly Ala Ser Gly Arg Ala Asn Asn Tyr
 1 5 10 15

Val Val Glu His His Asp Asp Arg Ser Ser Ile Gly Gln Glu Ser Pro
 20 25 30

Arg Gln Glu Ile Ala Asp Ser Pro Leu Ser Arg Ser Gly Arg Ser Ser
 35 40 45

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

Pro Pro Ser Gly Ala Ser Val Gly Ala Leu Arg Asn Trp Phe Trp Gln
 65 70 75 80

Gly Gln Ala Ala Gln His Leu Gln Gln Leu Glu Ala Glu Leu Asn Asn
 85 90 95

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

Leu Thr His Val Ile Asp Asp Ile Ala Ser Ile Ser Asn Ala Glu Asn
 115 120 125

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

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

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

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

Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu His Trp Gly Asp Tyr Gly
 195 200 205

Ala Ala Ser Gly Met Arg Phe Asp Asn Glu Pro Gly Tyr Met Gly Ser
 210 215 220

Met Phe Arg Gly Leu Lys Phe Val Ile Asp Ser Glu Ala Gly Ser Ser
 225 230 235 240

Ser Arg Lys Lys Gly Glu Ile Asp Ala Thr Trp Leu Glu Asn Leu His
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245

250

255

Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg Val Met His Asp Trp
260 265 270

Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn Ala Val Ala Ala Leu
275 280 285

Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val Arg Ser Ala Ala Ser
290 295 300

Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly Tyr
305 310 315 320

Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn Leu
325 330 335

Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser Arg Phe Ala
340 345 350

Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg Pro Ile Asp Trp Asp
355 360 365

Glu Val Glu Arg Gly Asn Ala Gln Val Met Trp Ala Cys Thr Gly Lys
370 375 380

Ser Arg Lys Glu Val Met Lys Leu Val Lys Asn Val Leu Gln Thr His
385 390 395 400

Tyr Asn Asp Ile Lys Arg Thr Thr Asn Ala Glu Ala
405 410

<210> 35
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_1-440

<400> 35

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cgctgagtcg atcaggccgt tcatccaata gaacctctcc ccgcgtatcg ctggacaggc 180

tcagagcttt caatcccca agcggcgcgt cagttggcgc tttgagaaat tggttctggc 240

aaggacaggc tgctcaacat ctgcagcagc tcgaagcaga gctcaacaac gggtcgaaca 300

ttcgcgagct gttggacggc cctggatttg gcggattgct gacccatgtg atcgacgata 360

tcgcctcgat ttcaaacgcg gaaaatttgt cgccgatcga ggtcgcagag gagctaaggc 420

aagctattag caccgggcgc ggggcgaaca atttgatat atctttgaaa aacgttctac 480

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aattcggact ttatgcggtc agggaaaaac tgcaagggga agccgagctc gccggctcga 540
tgcaaacaca ccctgctttt cagtctttcc cggtggccca ggccctggaaa ttttgcatcg 600
agcaagagca ttggggatgat tacggcgccg catccggcat gcgatttgac aacgagcccc 660
gctacatggg tagtatgttt cgcggcctaa aattcgtcat cgactcggaa gcgggttcct 720
cgtcccgaaa aaaaggcgaa atcgatgcta cttggttga gaatttgac gacatcgctg 780
tcaatggcgt gttccagcgc agagtcatgc atgattggca gttcggcgcc aatgtcgaag 840
aagctgtgaa tgcagtcgcc gcccttaccg cgccctggcag caatattagc gataaggta 900
ggagcgcagc gtcggcaatc ttctatttgc cggaacacct atggccattg gaggggtgggt 960
atcgacaagg ccagttggtc cagttcaaac tggtttatcc caagaatctg actccggctg 1020
ggctcggcga tctgcaaaag ttccagtccc ggctcgccgg gtgggctgag tttcgaagt 1080
tcggtaatcg tccgatcgac tgggatgagg tagaacgcgg caacgcccag gttatgtggg 1140
cgtgcacggg aaaaagccga aaagaggta tgaagctggt gaaaaatgtg ctccaaacgc 1200
attataacga tataaaaagg actaccaacg cagaggccgc actgcatgtg gtggcacgaa 1260
cgtgcgctac cctggagcgc gcgcacgtgt tcatggatgg cagcgcacga actttcggtt 1320
gctagcgatg gatcc 1335

<210> 36
<211> 440
<212> PRT
<213> Artificial Sequence

<220>
<223> PthG_1-440
<400> 36

Met Gly Cys Phe Asn Val Thr Gly Ala Ser Gly Arg Ala Asn Asn Tyr
1 5 10 15
Val Val Glu His His Asp Asp Arg Ser Ser Ile Gly Gln Glu Ser Pro
20 25 30
Arg Gln Glu Ile Ala Asp Ser Pro Leu Ser Arg Ser Gly Arg Ser Ser
35 40 45
Asn Arg Thr Ser Pro Arg Val Ser Leu Asp Arg Leu Arg Ala Phe Asn
50 55 60
Pro Pro Ser Gly Ala Ser Val Gly Ala Leu Arg Asn Trp Phe Trp Gln
65 70 75 80
Gly Gln Ala Ala Gln His Leu Gln Gln Leu Glu Ala Glu Leu Asn Asn
85 90 95
Gly Ser Asn Ile Arg Glu Leu Leu Asp Gly Pro Gly Phe Gly Gly Leu
100 105 110

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Leu Thr His Val Ile Asp Asp Ile Ala Ser Ile Ser Asn Ala Glu Asn
115 120 125

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

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

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

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

Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu His Trp Gly Asp Tyr Gly
195 200 205

Ala Ala Ser Gly Met Arg Phe Asp Asn Glu Pro Gly Tyr Met Gly Ser
210 215 220

Met Phe Arg Gly Leu Lys Phe Val Ile Asp Ser Glu Ala Gly Ser Ser
225 230 235 240

Ser Arg Lys Lys Gly Glu Ile Asp Ala Thr Trp Leu Glu Asn Leu His
245 250 255

Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg Val Met His Asp Trp
260 265 270

Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn Ala Val Ala Ala Leu
275 280 285

Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val Arg Ser Ala Ala Ser
290 295 300

Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly Tyr
305 310 315 320

Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn Leu
325 330 335

Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser Arg Phe Ala
340 345 350

Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg Pro Ile Asp Trp Asp
355 360 365

Glu Val Glu Arg Gly Asn Ala Gln Val Met Trp Ala Cys Thr Gly Lys
370 375 380

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Ser Arg Lys Glu Val Met Lys Leu Val Lys Asn Val Leu Gln Thr His
385 390 395 400

Tyr Asn Asp Ile Lys Arg Thr Thr Asn Ala Glu Ala Ala Leu His Val
405 410 415

Val Ala Arg Thr Cys Ala Thr Leu Glu Arg Ala His Val Phe Met Asp
420 425 430

Gly Ser Ala Arg Thr Phe Gly Cys
435 440

<210> 37
<211> 1473
<212> DNA
<213> Artificial Sequence

<220>
<223> pthG_1-486

<400> 37
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cgctgagtcg atcaggccgt tcatccaata gaacctctcc ccgcgtatcg ctggacaggc 180
tcagagcttt caatccccca agcggcgcggt cagttggcgc tttgagaaat tggttctggc 240
aaggacaggc tgctcaacat ctgcagcagc tcgaagcaga gctcaacaac ggttcgaaca 300
ttcgcgagct gttggacggc cctggatttg gcggattgct gacctatgtg atcgacgata 360
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aattcggact ttatgcggtc agggaaaaac tgcaagggga agccgagctc gccggctcga 540
tgcaaacaca ccctgctttt cagtctttcc cgggtggcca ggcctggaaa ttttgattg 600
agcaagagca ttggggtgat tacggcgccg catccggcat gcgatttgac aacgagcccg 660
gctacatggg tagtatgttt cgcggttaa aattcgatc cgactcggaa gcgggttctt 720
cgtcccgaaa aaaaggcgaa atcgatgcta cttggttgga gaatttgac gacatcgctg 780
tcaatggcgt gttccagcgc agagtcatgc atgattggca gttcggcgcc aatgtcgaag 840
aagctgtgaa tgcagtcgcc gcccttaccg cgcttgag caatattagc gataaggta 900
ggagcgcagc gtcggcaatc ttctatttgc cggaacacct atggccattg gaggggtggg 960
atcgacaagg ccagttggtc cagttcaaac tggtttatcc caagaatctg actccggctg 1020
ggctcggcga tctgcaaaag ttccagtcgc ggttcgccgg gtgggctgag tttcgaagt 1080
tcggtaatcg tccgatcgac tgggatgagg tagaacgcgg caacgcccag gttatgtggg 1140
cgtgcacggg aaaaagccga aaagagggtta tgaagctggg gaaaaatgtg ctccaaacgc 1200
attataacga tataaaaagg actaccaacg cagaggccgc actgcatgtg gtggcacgaa 1260

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cgtgcgctac cctggagcgc gcgcacgtgt tcatggatgg cagcgcacga actttcggtt 1320
 gcctgtctct caataaactt ttgctttccg caggcttatc accatgcatg gcccctgatg 1380
 ccaacgaatt cgacggttac tcgaacgaag aactggtggc gcggattcag gaaggacaga 1440
 atatattccg ggcacattgc tagcgatgga tcc 1473

<210> 38
 <211> 486
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PthG_1-486

<400> 38

Met Gly Cys Phe Asn Val Thr Gly Ala Ser Gly Arg Ala Asn Asn Tyr
 1 5 10 15

Val Val Glu His His Asp Asp Arg Ser Ser Ile Gly Gln Glu Ser Pro
 20 25 30

Arg Gln Glu Ile Ala Asp Ser Pro Leu Ser Arg Ser Gly Arg Ser Ser
 35 40 45

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

Pro Pro Ser Gly Ala Ser Val Gly Ala Leu Arg Asn Trp Phe Trp Gln
 65 70 75 80

Gly Gln Ala Ala Gln His Leu Gln Gln Leu Glu Ala Glu Leu Asn Asn
 85 90 95

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

Leu Thr His Val Ile Asp Asp Ile Ala Ser Ile Ser Asn Ala Glu Asn
 115 120 125

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

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

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

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

Gln Ala Trp Lys Phe Cys Ile Glu Gln Glu His Trp Gly Asp Tyr Gly
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195

200

205

Ala Ala Ser Gly Met Arg Phe Asp Asn Glu Pro Gly Tyr Met Gly Ser
 210 215 220

Met Phe Arg Gly Leu Lys Phe Val Ile Asp Ser Glu Ala Gly Ser Ser
 225 230 235 240

Ser Arg Lys Lys Gly Glu Ile Asp Ala Thr Trp Leu Glu Asn Leu His
 245 250 255

Asp Ile Ala Val Asn Gly Val Phe Gln Arg Arg Val Met His Asp Trp
 260 265 270

Gln Phe Gly Ala Asn Val Glu Glu Ala Val Asn Ala Val Ala Ala Leu
 275 280 285

Thr Ala Pro Gly Ser Asn Ile Ser Asp Lys Val Arg Ser Ala Ala Ser
 290 295 300

Ala Ile Phe Tyr Leu Pro Glu His Leu Trp Pro Leu Glu Gly Gly Tyr
 305 310 315 320

Arg Gln Gly Gln Leu Val Gln Phe Lys Leu Val Tyr Pro Lys Asn Leu
 325 330 335

Thr Pro Ala Gly Leu Gly Asp Leu Gln Lys Phe Gln Ser Arg Phe Ala
 340 345 350

Gly Trp Ala Glu Phe Arg Ser Val Gly Asn Arg Pro Ile Asp Trp Asp
 355 360 365

Glu Val Glu Arg Gly Asn Ala Gln Val Met Trp Ala Cys Thr Gly Lys
 370 375 380

Ser Arg Lys Glu Val Met Lys Leu Val Lys Asn Val Leu Gln Thr His
 385 390 395 400

Tyr Asn Asp Ile Lys Arg Thr Thr Asn Ala Glu Ala Ala Leu His Val
 405 410 415

Val Ala Arg Thr Cys Ala Thr Leu Glu Arg Ala His Val Phe Met Asp
 420 425 430

Gly Ser Ala Arg Thr Phe Gly Cys Leu Leu Leu Asn Lys Leu Leu Leu
 435 440 445

Ser Ala Gly Leu Ser Pro Cys Met Ala Pro Asp Ala Asn Glu Phe Asp
 450 455 460

Gly Tyr Ser Asn Glu Glu Leu Val Ala Arg Ile Gln Glu Gly Gln Asn
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470

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