

10486.204-WO.ST25
SEQUENCE LISTING

<110> Novozymes A/S
 <120> Recombinant Production of Antimicrobial Agents
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Lys Xaa Xaa Xaa Xaa Gln Xaa Xaa Met Lys Lys
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Arg Arg Trp Gln Trp Arg Met Lys Lys Leu Gly Ala Pro Ser Ile Thr
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Cys Val Arg Arg Ala Phe
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Met Lys Lys Leu Gly Ala Pro Ser Ile Thr Cys Val Arg Arg Ala Phe
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Val Ser Gln Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met
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Ile Gln Cys Ile

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

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Thr Cys Val

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20 25 30

Ala Gly His Cys Gly Arg Val Gly Thr Gln Val Thr Ile Gly Asn Gly
35 40 45

Arg Gly Val Phe Glu Gln Ser Val Phe Pro Gly Asn Asp Ala Ala Phe
50 55 60

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

Asn Thr Gly Gly Tyr Ala Ala Val Ala Gly His Asn Gln Ala Pro Ile
85 90 95

Gly Ser Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
100 105 110

Thr Ile Gln Ala Arg Gly Gln Ser Val Ser Tyr Pro Glu Gly Thr Val
115 120 125

Thr Asn Met Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
130 135 140

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Gly Ser Tyr Ile Ser Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly
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Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe Tyr Gln Glu Val Thr
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Pro Met Val Asn Ser Trp Gly Val Arg Leu Arg Thr
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Ala Glu Ala Glu Glu Leu Leu Ser Ala Gln Glu Ala Ala Ile Glu
-135 -130 -125

Thr Asp Ala Glu Ala Thr Glu Ala Ala Gly Glu Ala Tyr Gly Gly
-120 -115 -110

Ser Leu Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp
-105 -100 -95

Ala Ser Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gln Ala Thr Val
-90 -85 -80 -75

Val Ser His Gly Thr Glu Gly Leu Thr Glu Val Val Glu Asp Leu Asn
-70 -65 -60

Gly Ala Glu Val Pro Glu Ser Val Leu Gly Trp Tyr Pro Asp Val Glu
-55 -50 -45

Ser Asp Thr Val Val Val Glu Val Leu Glu Gly Ser Asp Ala Asp Val
-40 -35 -30

Ala Ala Leu Leu Ala Asp Ala Gly Val Asp Ser Ser Ser Val Arg Val
-25 -20 -15

Glu Glu Ala Glu Glu Ala Pro Gln Val Tyr Ala Asp Ile Ile Gly Gly
-10 -5 -1 1 5

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Leu Ala Tyr Tyr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr
10 15 20

Asn Ser Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr
25 30 35

Val Gly Thr Gly Val Thr Ile Gly Asn Gly Thr Gly Thr Phe Gln Asn
40 45 50

Ser Val Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn
55 60 65 70

Phe Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Gln
75 80 85

Ser Val Thr Gly Thr Ser Gln Ala Pro Ala Gly Ser Ala Val Cys Arg
90 95 100

Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Asn
105 110 115

Gln Thr Val Arg Tyr Pro Gln Gly Thr Val Tyr Ser Leu Thr Arg Thr
120 125 130

Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly
135 140 145 150

Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Val
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Gly Gly Thr Thr Tyr Tyr Gln Glu Val Thr Pro Met Ile Asn Ser Trp
170 175 180

Gly Val Arg Ile Arg Thr
185

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Ala Thr Thr Met Val Glu Ala Leu Gln Arg Asp Leu Gly Leu Ser
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Pro Ser Gln Ala Asp Glu Leu Leu Glu Ala Gln Ala Glu Ser Phe
-135 -130 -125

Glu Ile Asp Glu Ala Ala Thr Ala Ala Ala Asp Ser Tyr Gly
-120 -115 -110

Gly Ser Ile Phe Asp Thr Asp Ser Leu Thr Leu Thr Val Leu Val Thr
-105 -100 -95

Asp Ala Ser Ala Val Glu Ala Val Glu Ala Ala Gly Ala Glu Ala Lys
-90 -85 -80

Val Val Ser His Gly Met Glu Gly Leu Glu Glu Ile Val Ala Asp Leu
-75 -70 -65 -60

Asn Ala Ala Asp Ala Gln Pro Gly Val Val Gly Trp Tyr Pro Asp Ile
-55 -50 -45

His Ser Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp
-40 -35 -30

Val Asp Ser Leu Leu Ala Asp Ala Gly Val Asp Thr Ala Asp Val Lys
-25 -20 -15

Val Glu Ser Thr Thr Glu Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly
-10 -5 -1 1 5

Gly Leu Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala
10 15 20

Thr Asn Ala Ser Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly
25 30 35

Thr Val Gly Thr Pro Val Ser Ile Gly Asn Gly Gln Gly Val Phe Glu
40 45 50

Arg Ser Val Phe Pro Gly Asn Asp Ser Ala Phe Val Arg Gly Thr Ser
55 60 65

Asn Phe Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr
70 75 80 85

Ala Thr Val Ser Gly Ser Ser Gln Ala Ala Ile Gly Ser Gln Ile Cys
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Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Val Gln Ala Arg
105 110 115

Gly Gln Thr Val Ser Tyr Pro Gln Gly Thr Val Gln Asn Leu Thr Arg
120 125 130

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Thr Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser
135 140 145

Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser
150 155 160 165

Phe Gly Gly Thr Thr Tyr Tyr Gln Glu Val Asn Pro Met Leu Ser Ser
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Trp Gly Leu Thr Leu Arg Thr
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Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Thr Pro
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Leu Glu Ala Asp Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu
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Val Asp Glu Ala Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly
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Ser Val Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp
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Ala Ala Ser Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu
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Val Ser Tyr Gly Ile Glu Gly Leu Asp Glu Ile Ile Gln Asp Leu Asn
-70 -65 -60

Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala
-55 -50 -45

Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val
-40 -35 -30

Ser Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val
-25 -20 -15 -10

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Thr Ser Ser Ala Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu
-5 -1 1 5

Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn
10 15 20

Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val
25 30 35

Gly Thr Gln Val Ser Ile Gly Asn Gly Gln Gly Val Phe Glu Gln Ser
40 45 50 55

Ile Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe
60 65 70

Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr
75 80 85

Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser
90 95 100

Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln
105 110 115

Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr
120 125 130 135

Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Asn
140 145 150

Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly
155 160 165

Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly
170 175 180

Val Arg Leu Arg Thr
185

<210> 63
<211> 353
<212> PRT
<213> Nocardiosis prasina

<220>
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<222> (166)..(353)

<400> 63

Ala Thr Gly Pro Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala
-165 -160 -155

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Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Thr Pro
-150 -145 -140

Leu Glu Ala Asp Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu
-135 -130 -125

Val Asp Glu Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly
-120 -115 -110

Ser Val Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp
-105 -100 -95 -90

Ser Ala Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu
-85 -80 -75

Val Ser Tyr Gly Ile Thr Gly Leu Asp Glu Ile Val Glu Glu Leu Asn
-70 -65 -60

Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala
-55 -50 -45

Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val
-40 -35 -30

Gly Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val
-25 -20 -15 -10

Thr Thr Thr Glu Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu
-5 -1 1 5

Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn
10 15 20

Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val
25 30 35

Gly Thr Gln Val Thr Ile Gly Asn Gly Arg Gly Val Phe Glu Gln Ser
40 45 50 55

Ile Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe
60 65 70

Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr
75 80 85

Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser
90 95 100

Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln
105 110 115

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Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr
120 125 130 135

Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Asn
140 145 150

Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly
155 160 165

Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly
170 175 180

Val Arg Leu Arg Thr
185

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<213> Peniophora lycii

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<400> 64

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-10 -5 -1 1

Ile Pro Ala Gln Asn Thr Ser Asn Trp Gly Pro Tyr Asp Pro Phe Phe
5 10 15

Pro Val Glu Pro Tyr Ala Ala Pro Pro Glu Gly Cys Thr Val Thr Gln
20 25 30

Val Asn Leu Ile Gln Arg His Gly Ala Arg Trp Pro Thr Ser Gly Ala
35 40 45 50

Arg Ser Arg Gln Val Ala Ala Val Ala Lys Ile Gln Met Ala Arg Pro
55 60 65

Phe Thr Asp Pro Lys Tyr Glu Phe Leu Asn Asp Phe Val Tyr Lys Phe
70 75 80

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

Gly Thr Asp Met Tyr Thr Arg Tyr Ser Thr Leu Phe Glu Gly Gly Asp
100 105 110

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Val Pro Phe Val Arg Ala Ala Gly Asp Gln Arg Val Val Asp Ser Ser
115 120 125 130

Thr Asn Trp Thr Ala Gly Phe Gly Asp Ala Ser Gly Glu Thr Val Leu
135 140 145

Pro Thr Leu Gln Val Val Leu Gln Glu Glu Gly Asn Cys Thr Leu Cys
150 155 160

Asn Asn Met Cys Pro Asn Glu Val Asp Gly Asp Glu Ser Thr Thr Trp
165 170 175

Leu Gly Val Phe Ala Pro Asn Ile Thr Ala Arg Leu Asn Ala Ala Ala
180 185 190

Pro Ser Ala Asn Leu Ser Asp Ser Asp Ala Leu Thr Leu Met Asp Met
195 200 205 210

Cys Pro Phe Asp Thr Leu Ser Ser Gly Asn Ala Ser Pro Phe Cys Asp
215 220 225

Leu Phe Thr Ala Glu Glu Tyr Val Ser Tyr Glu Tyr Tyr Tyr Asp Leu
230 235 240

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

Gly Val Gly Tyr Val Asn Glu Leu Leu Ala Arg Leu Thr Gly Gln Ala
260 265 270

Val Arg Asp Glu Thr Gln Thr Asn Arg Thr Leu Asp Ser Asp Pro Ala
275 280 285 290

Thr Phe Pro Leu Asn Arg Thr Phe Tyr Ala Asp Phe Ser His Asp Asn
295 300 305

Thr Met Val Pro Ile Phe Ala Ala Leu Gly Leu Phe Asn Ala Thr Ala
310 315 320

Leu Asp Pro Leu Lys Pro Asp Glu Asn Arg Leu Trp Val Asp Ser Lys
325 330 335

Leu Val Pro Phe Ser Gly His Met Thr Val Glu Lys Leu Ala Cys Ser
340 345 350

Gly Lys Glu Ala Val Arg Val Leu Val Asn Asp Ala Val Gln Pro Leu
355 360 365 370

Glu Phe Cys Gly Gly Val Asp Gly Val Cys Glu Leu Ser Ala Phe Val
375 380 385

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Glu Ser Gln Thr Tyr Ala Arg Glu Asn Gly Gln Gly Asp Phe Ala Lys
390 395 400

Cys Gly Phe Val Pro Ser Glu
405

<210> 65
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<400> 65

Arg Arg Arg Pro Arg Pro Pro Tyr Leu Pro Arg Pro Arg Pro Pro Pro
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Phe Phe Pro Pro Arg Leu Pro Pro Arg Ile Pro Pro Gly Phe Pro Pro
20 25 30

Arg Phe Pro Pro Arg Phe Pro
35

<210> 66
<211> 44
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44

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<211> 47
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<220>
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<400> 67

10486.204-WO.ST25
catagcacca tggatgaaag gagacgtccc cgacccccat atttgcc 47

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<220>
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<400> 68
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<210> 69
<211> 53
<212> DNA
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<400> 69
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<400> 71

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<400> 72
ctctcatccg ccaaaacagc c 21

<210> 73
<211> 18
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<400> 73

Lys Asn Leu Arg Arg Ile Ile Arg Lys Gly Ile His Ile Ile Lys Lys
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Tyr Gly

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10486.204-WO.ST25

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 ccc 63

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Pro Glu Pro Thr

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Glu Pro Thr Pro

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<400> 81

Pro Thr Glu Pro

1

<210> 82

<211> 4

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<400> 82

Thr Pro Glu Pro

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<211> 8
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<400> 84

Gln Ser His Val Gln Ser Ala Pro
1 5

<210> 85
<211> 4
<212> PRT
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<400> 85

Gln Ser Ala Pro
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<210> 86
<211> 6
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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<400> 86

Xaa Asp Asp Asp Lys Xaa
1 5

<210> 87
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<400> 87

Xaa Lys Arg Xaa
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<210> 88
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Xaa Ile Glu Gly Arg Xaa
1 5

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<400> 89

Pro Xaa Gly Pro Xaa Xaa
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<210> 90
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<400> 90

Xaa Gly Val Arg Gly Pro Arg Xaa
1 5

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Ser Asn Gly Xaa
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<400> 92

Asp Asp Glu Glu Glu
1 5

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<400> 93

Asp Asp Asp Glu Glu
1 5

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<211> 5
<212> PRT
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<223> Peptide

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<400> 94

Asp Asp Asp Asp Glu
 1 5

<210> 95
 <211> 5
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<400> 95

Glu Glu Asp Asp Glu
 1 5

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<400> 96

Asp Asp Glu Glu Asp
 1 5

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Glu Asp Glu Asp Glu
 1 5

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<400> 98

Asp Asp Asp Glu Glu Glu
 1 5

<210> 99
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Asp Glu Asp Glu Asp Glu
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 <211> 6
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Glu Glu Asp Asp Glu Glu
 1 5

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<220>
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<223> Protection peptide

<400> 101

Asp Asp Asp Asp Asp Pro
1 5

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<211> 7
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<400> 102

Glu Glu Glu Glu Glu Asp Pro
1 5

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Asp Asp Asp Glu
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Asp Glu Asp Glu Asp Glu Asp Pro
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<210> 105

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Asp Asp Asp Gly Gly Glu Glu Glu Gly Gly Asp Asp Asp Pro
1 5 10

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<400> 106

Asp Asp Asp Gly Gly Asp Asp Asp Pro Pro Asp Asp Asp Glu
1 5 10

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<211> 31
<212> DNA
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<220>
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<400> 107
tatagagctc cattgaaagg ggaggagaat c

31

<210> 108
<211> 33
<212> DNA
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<220>
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<400> 108
tatactgcag aatgaggcag caagaagatg agc

33

<210> 109
<211> 33
<212> DNA
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<400> 109
tatactgcag ccgcggcagc ttctgcctta aac 33

<210> 110
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 110
tatagctagc tggattgatt ttgccgactc cg 32

<210> 111
<211> 1227
<212> DNA
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<223> DNA fragment (PP1223-9 SacI MluI)

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gagctccatt gaaaggggag gagaatc atg aaa caa caa aaa cgg ctt tac gcc 54
Met Lys Gln Gln Lys Arg Leu Tyr Ala
-25

cga ttg ctg acg ctg tta ttt gcg ctc atc ttc ttg ctg cct cat tct 102
Arg Leu Leu Thr Leu Leu Phe Ala Leu Ile Phe Leu Leu Pro His Ser
-20 -15 -10 -5

gca gcc gcg gca gct tct gcc tta aac tcg ggc aaa gta aat ccg ctt 150
Ala Ala Ala Ala Ala Ser Ala Leu Asn Ser Gly Lys Val Asn Pro Leu
-1 1 5 10

gcc gac ttc agc tta aaa ggc ttt gcc gca cta aac ggc gga aca acg 198
Ala Asp Phe Ser Leu Lys Gly Phe Ala Ala Leu Asn Gly Gly Thr Thr
15 20 25

ggc gga gaa ggc ggt cag acg gta acc gta aca acg gga gat cag ctg 246
Gly Gly Glu Gly Gly Gln Thr Val Thr Val Thr Thr Gly Asp Gln Leu
30 35 40

att gcg gca tta aaa aat aag aat gca aat acg cct tta aaa att tat 294
Ile Ala Ala Leu Lys Asn Lys Asn Ala Asn Thr Pro Leu Lys Ile Tyr
45 50 55 60

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gtc aac ggc acc att aca aca tca aat aca tcc gca tca aag att gac Val Asn Gly Thr Ile Thr Thr Ser Asn Thr Ser Ala Ser Lys Ile Asp 65 70 75	342
gtc aaa gac gtg tca aac gta tcg att gtc gga tca ggg acc aaa ggg Val Lys Asp Val Ser Asn Val Ser Ile Val Gly Ser Gly Thr Lys Gly 80 85 90	390
gaa ctc aaa ggg atc ggc atc aaa ata tgg cgg gcc aac aac atc atc Glu Leu Lys Gly Ile Gly Ile Lys Ile Trp Arg Ala Asn Asn Ile Ile 95 100 105	438
atc cgc aac ttg aaa att cac gag gtc gcc tca ggc gat aaa gac gcg Ile Arg Asn Leu Lys Ile His Glu Val Ala Ser Gly Asp Lys Asp Ala 110 115 120	486
atc ggc att gaa ggc cct tct aaa aac att tgg gtt gat cat aat gag Ile Gly Ile Glu Gly Pro Ser Lys Asn Ile Trp Val Asp His Asn Glu 125 130 135 140	534
ctt tac cac agc ctg aac gtt gac aaa gat tac tat gac gga tta ttt Leu Tyr His Ser Leu Asn Val Asp Lys Asp Tyr Tyr Asp Gly Leu Phe 145 150 155	582
gac gtc aaa aga gat gcg gaa tat att aca ttc tct tgg aac tat gtg Asp Val Lys Arg Asp Ala Glu Tyr Ile Thr Phe Ser Trp Asn Tyr Val 160 165 170	630
cac gat gga tgg aaa tca atg ctg atg ggt tca tcg gac agc gat aat His Asp Gly Trp Lys Ser Met Leu Met Gly Ser Ser Asp Ser Asp Asn 175 180 185	678
tac aac agg acg att aca ttc cat cat aac tgg ttt gag aat ctg aat Tyr Asn Arg Thr Ile Thr Phe His His Asn Trp Phe Glu Asn Leu Asn 190 195 200	726
tcg cgt gtg ccg tca ttc cgt ttc gga gaa ggc cat att tac aac aac Ser Arg Val Pro Ser Phe Arg Phe Gly Glu Gly His Ile Tyr Asn Asn 205 210 215 220	774
tat ttc aat aaa atc atc gac agc gga att aat tcg agg atg ggc gcg Tyr Phe Asn Lys Ile Ile Asp Ser Gly Ile Asn Ser Arg Met Gly Ala 225 230 235	822
cgc atc aga att gag aac aac ctc ttt gaa aac gcc aaa gat ccg att Arg Ile Arg Ile Glu Asn Asn Leu Phe Glu Asn Ala Lys Asp Pro Ile 240 245 250	870
gtc tct tgg tac agc agt tca ccg ggc tat tgg cat gta tcc aac aac Val Ser Trp Tyr Ser Ser Ser Pro Gly Tyr Trp His Val Ser Asn Asn 255 260 265	918
aaa ttt gta aac tct agg ggc agt atg ccg act acc tct act aca acc Lys Phe Val Asn Ser Arg Gly Ser Met Pro Thr Thr Ser Thr Thr Thr 270 275 280	966
tat aat ccg cca tac agc tac tca ctc gac aat gtc gac aat gta aaa Tyr Asn Pro Pro Tyr Ser Tyr Ser Leu Asp Asn Val Asp Asn Val Lys 285 290 300	1014
tca atc gtc aag caa aat gcc gga gtc ggc aaa atc aat cca gct agc Ser Ile Val Lys Gln Asn Ala Gly Val Gly Lys Ile Asn Pro Ala Ser 305 310 315	1062
gaa gcc acc tac ccc ggc aag tgc tac aag aag gac aac atc tgc aag Glu Ala Thr Tyr Pro Gly Lys Cys Tyr Lys Lys Asp Asn Ile Cys Lys 320 325 330	1110

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tac aag gcc cag tcc ggc aag acc ggc atc tgc aag tgc tac gtc aag 1158
Tyr Lys Ala Gln Ser Gly Lys Thr Gly Ile Cys Lys Cys Tyr Val Lys
335 340 345

cgc tgc ccc cgc gac ggc gcc aag tgc gac ctc gac tcc tac aag ggc 1206
Arg Cys Pro Arg Asp Gly Ala Lys Cys Asp Leu Asp Ser Tyr Lys Gly
350 355 360

aag tgc cac tgc tagacgcgt 1227
Lys Cys His Cys
365

<210> 112
<211> 397
<212> PRT
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<223> Synthetic Construct

<400> 112

Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
-25 -20 -15

Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Ser Ala
-10 -5 -1 1

Leu Asn Ser Gly Lys Val Asn Pro Leu Ala Asp Phe Ser Leu Lys Gly
5 10 15

Phe Ala Ala Leu Asn Gly Gly Thr Thr Gly Gly Glu Gly Gly Gln Thr
20 25 30 35

Val Thr Val Thr Thr Gly Asp Gln Leu Ile Ala Ala Leu Lys Asn Lys
40 45 50

Asn Ala Asn Thr Pro Leu Lys Ile Tyr Val Asn Gly Thr Ile Thr Thr
55 60 65

Ser Asn Thr Ser Ala Ser Lys Ile Asp Val Lys Asp Val Ser Asn Val
70 75 80

Ser Ile Val Gly Ser Gly Thr Lys Gly Glu Leu Lys Gly Ile Gly Ile
85 90 95

Lys Ile Trp Arg Ala Asn Asn Ile Ile Ile Arg Asn Leu Lys Ile His
100 105 110 115

Glu Val Ala Ser Gly Asp Lys Asp Ala Ile Gly Ile Glu Gly Pro Ser
120 125 130

Lys Asn Ile Trp Val Asp His Asn Glu Leu Tyr His Ser Leu Asn Val
135 140 145

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Asp Lys Asp Tyr Tyr Asp Gly Leu Phe Asp Val Lys Arg Asp Ala Glu
150 155 160

Tyr Ile Thr Phe Ser Trp Asn Tyr Val His Asp Gly Trp Lys Ser Met
165 170 175

Leu Met Gly Ser Ser Asp Ser Asp Asn Tyr Asn Arg Thr Ile Thr Phe
180 185 190 195

His His Asn Trp Phe Glu Asn Leu Asn Ser Arg Val Pro Ser Phe Arg
200 205 210

Phe Gly Glu Gly His Ile Tyr Asn Asn Tyr Phe Asn Lys Ile Ile Asp
215 220 225

Ser Gly Ile Asn Ser Arg Met Gly Ala Arg Ile Arg Ile Glu Asn Asn
230 235 240

Leu Phe Glu Asn Ala Lys Asp Pro Ile Val Ser Trp Tyr Ser Ser Ser
245 250 255

Pro Gly Tyr Trp His Val Ser Asn Asn Lys Phe Val Asn Ser Arg Gly
260 265 270 275

Ser Met Pro Thr Thr Ser Thr Thr Thr Tyr Asn Pro Pro Tyr Ser Tyr
280 285 290

Ser Leu Asp Asn Val Asp Asn Val Lys Ser Ile Val Lys Gln Asn Ala
295 300 305

Gly Val Gly Lys Ile Asn Pro Ala Ser Glu Ala Thr Tyr Pro Gly Lys
310 315 320

Cys Tyr Lys Lys Asp Asn Ile Cys Lys Tyr Lys Ala Gln Ser Gly Lys
325 330 335

Thr Gly Ile Cys Lys Cys Tyr Val Lys Arg Cys Pro Arg Asp Gly Ala
340 345 350 355

Lys Cys Asp Leu Asp Ser Tyr Lys Gly Lys Cys His Cys
360 365

<210> 113
<211> 26
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<213> Artificial

<220>
<223> Primer

<400> 113
tataacgcgt ctagcagtgg cacttg

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<210> 114
<211> 1297
<212> DNA
<213> Artificial

<220>
<223> DNA fragment (PP1331-2 SacI MluI)

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<222> (114)..(1289)

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<223> Pectate lyase

<220>
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<222> (1236)..(1289)
<223> G10 novispirin

<400> 114
gagctcattg aaaggggagg agaatc atg aaa caa caa aaa cgg ctt tac gcc 53
Met Lys Gln Gln Lys Arg Leu Tyr Ala
-25

cga ttg ctg acg ctg tta ttt gcg ctc atc ttc ttg ctg cct cat tct 101
Arg Leu Leu Thr Leu Leu Phe Ala Leu Ile Phe Leu Leu Pro His Ser
-20 -15 -10 -5

gca gcc gcg gca gct tct gcc tta aac tcg ggc aaa gta aat ccg ctt 149
Ala Ala Ala Ala Ala Ser Ala Leu Asn Ser Gly Lys Val Asn Pro Leu
-1 1 5 10

gcc gac ttc agc tta aaa ggc ttt gcc gca cta aac ggc gga aca acg 197
Ala Asp Phe Ser Leu Lys Gly Phe Ala Ala Leu Asn Gly Gly Thr Thr
15 20 25

ggc gga gaa ggc ggt cag acg gta acc gta aca acg gga gat cag ctg 245
Gly Gly Glu Gly Gly Gln Thr Val Thr Val Thr Thr Gly Asp Gln Leu
30 35 40

att gcg gca tta aaa aat aag aat gca aat acg cct tta aaa att tat 293
Ile Ala Ala Leu Lys Asn Lys Asn Ala Asn Thr Pro Leu Lys Ile Tyr
45 50 55 60

gtc aac ggc acc att aca aca tca aat aca tcc gca tca aag att gac 341
Val Asn Gly Thr Ile Thr Thr Ser Asn Thr Ser Ala Ser Lys Ile Asp
65 70 75

gtc aaa gac gtg tca aac gta tcg att gtc gga tca ggg acc aaa ggg 389
Val Lys Asp Val Ser Asn Val Ser Ile Val Gly Ser Gly Thr Lys Gly
80 85 90

gaa ctc aaa ggg atc ggc atc aaa ata tgg cgg gcc aat aac atc atc 437
Glu Leu Lys Gly Ile Gly Ile Lys Ile Trp Arg Ala Asn Asn Ile Ile
95 100 105

atc cgc aac ttg aaa att cac gag gtc gcc tca ggc gat aaa gac gcg 485
Ile Arg Asn Leu Lys Ile His Glu Val Ala Ser Gly Asp Lys Asp Ala
110 115 120

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atc ggc att gaa ggc cct tct aaa aac att tgg gtt gat cat aat gag Ile Gly Ile Glu Gly Pro Ser Lys Asn Ile Trp Val Asp His Asn Glu 125 130 135 140	533
ctt tac cac agc ctg aac gtt gac aaa gat tac tat gac gga tta ttt Leu Tyr His Ser Leu Asn Val Asp Lys Asp Tyr Tyr Asp Gly Leu Phe 145 150 155	581
gac gtc aaa aga gat gcg gaa tat att aca ttc tct tgg aac tat gtg Asp Val Lys Arg Asp Ala Glu Tyr Ile Thr Phe Ser Trp Asn Tyr Val 160 165 170	629
cac gat gga tgg aaa tca atg ctg atg ggt tca tcg gac agc gat aat His Asp Gly Trp Lys Ser Met Leu Met Gly Ser Ser Asp Ser Asp Asn 175 180 185	677
tac aac agg acg att aca ttc cat cat aac tgg ttt gag aat ctg aat Tyr Asn Arg Thr Ile Thr Phe His His Asn Trp Phe Glu Asn Leu Asn 190 195 200	725
tcg cgt gtg tcg tca ttc cgt ttc gga gaa ggc cat att tac aac aac Ser Arg Val Ser Ser Phe Arg Phe Gly Glu His Ile Tyr Asn Asn 205 210 215 220	773
tat ttc aat aaa atc atc gac agc gga att aat tcg agg atg ggc gcg Tyr Phe Asn Lys Ile Ile Asp Ser Gly Ile Asn Ser Arg Met Gly Ala 225 230 235	821
cgc atc aga att gag aac aac ctc ttt gaa aac gcc aaa gat ccg att Arg Ile Arg Ile Glu Asn Asn Leu Phe Glu Asn Ala Lys Asp Pro Ile 240 245 250	869
gtc tct tgg tac agc agt tca ccg ggc tat tgg cat gta tcc aac aac Val Ser Trp Tyr Ser Ser Ser Pro Gly Tyr Trp His Val Ser Asn Asn 255 260 265	917
aaa ttt gta aac tct agg ggc agt atg ccg act acc tct act aca acc Lys Phe Val Asn Ser Arg Gly Ser Met Pro Thr Thr Ser Thr Thr Thr 270 275 280	965
tat aat ccg cca tac agc tac tca ctc gac aat gtc gac aat gta aaa Tyr Asn Pro Pro Tyr Ser Tyr Ser Leu Asp Asn Val Asp Asn Val Lys 285 290 295 300	1013
tca atc gtc aag caa aat gcc gga gtc ggc aaa atc aat cca gct agc Ser Ile Val Lys Gln Asn Ala Gly Val Gly Lys Ile Asn Pro Ala Ser 305 310 315	1061
ttg gat aaa aga gag gct gaa gct tgt gag gaa gag aga aat gca gaa Leu Asp Lys Arg Glu Ala Glu Ala Cys Glu Glu Glu Arg Asn Ala Glu 320 325 330	1109
gaa gaa aga aga gat gaa cca gat gaa agg gat gct caa gtg gaa cat Glu Glu Arg Arg Asp Glu Pro Asp Glu Arg Asp Ala Gln Val Glu His 335 340 345	1157
aat gcg cgc gag gct gaa gct gat gcg gaa gcg gtg ggc ccg gaa gcg Asn Ala Arg Glu Ala Glu Ala Asp Ala Glu Ala Val Gly Pro Glu Ala 350 355 360	1205
ttt gcg gat gaa gat ctg gat cca tgg gaa aag aac ctc aga cga atc Phe Ala Asp Glu Asp Leu Asp Pro Trp Glu Lys Asn Leu Arg Arg Ile 365 370 375 380	1253
ata agg aaa ggt ata cac atc att aag aaa tac gga taacgcgt Ile Arg Lys Gly Ile His Ile Ile Lys Lys Tyr Gly 385 390	1297

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<210> 115
<211> 421
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 115

Met Lys Gln Gln Lys Arg Leu Tyr Ala Arg Leu Leu Thr Leu Leu Phe
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Ala Leu Ile Phe Leu Leu Pro His Ser Ala Ala Ala Ala Ala Ser Ala
-10 -5 -1 1

Leu Asn Ser Gly Lys Val Asn Pro Leu Ala Asp Phe Ser Leu Lys Gly
5 10 15

Phe Ala Ala Leu Asn Gly Gly Thr Thr Gly Gly Glu Gly Gly Gln Thr
20 25 30 35

Val Thr Val Thr Thr Gly Asp Gln Leu Ile Ala Ala Leu Lys Asn Lys
40 45 50

Asn Ala Asn Thr Pro Leu Lys Ile Tyr Val Asn Gly Thr Ile Thr Thr
55 60 65

Ser Asn Thr Ser Ala Ser Lys Ile Asp Val Lys Asp Val Ser Asn Val
70 75 80

Ser Ile Val Gly Ser Gly Thr Lys Gly Glu Leu Lys Gly Ile Gly Ile
85 90 95

Lys Ile Trp Arg Ala Asn Asn Ile Ile Ile Arg Asn Leu Lys Ile His
100 105 110 115

Glu Val Ala Ser Gly Asp Lys Asp Ala Ile Gly Ile Glu Gly Pro Ser
120 125 130

Lys Asn Ile Trp Val Asp His Asn Glu Leu Tyr His Ser Leu Asn Val
135 140 145

Asp Lys Asp Tyr Tyr Asp Gly Leu Phe Asp Val Lys Arg Asp Ala Glu
150 155 160

Tyr Ile Thr Phe Ser Trp Asn Tyr Val His Asp Gly Trp Lys Ser Met
165 170 175

Leu Met Gly Ser Ser Asp Ser Asp Asn Tyr Asn Arg Thr Ile Thr Phe
180 185 190 195

His His Asn Trp Phe Glu Asn Leu Asn Ser Arg Val Ser Ser Phe Arg

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                                10486.204-WO.ST25
                                205
                200                                210

Phe Gly Glu Gly His Ile Tyr Asn Asn Tyr Phe Asn Lys Ile Ile Asp
                215                                220                                225

Ser Gly Ile Asn Ser Arg Met Gly Ala Arg Ile Arg Ile Glu Asn Asn
                230                                235                                240

Leu Phe Glu Asn Ala Lys Asp Pro Ile Val Ser Trp Tyr Ser Ser Ser
                245                                250                                255

Pro Gly Tyr Trp His Val Ser Asn Asn Lys Phe Val Asn Ser Arg Gly
                260                                265                                270                                275

Ser Met Pro Thr Thr Ser Thr Thr Thr Tyr Asn Pro Pro Tyr Ser Tyr
                280                                285                                290

Ser Leu Asp Asn Val Asp Asn Val Lys Ser Ile Val Lys Gln Asn Ala
                295                                300                                305

Gly Val Gly Lys Ile Asn Pro Ala Ser Leu Asp Lys Arg Glu Ala Glu
                310                                315                                320

Ala Cys Glu Glu Glu Arg Asn Ala Glu Glu Glu Arg Arg Asp Glu Pro
                325                                330                                335

Asp Glu Arg Asp Ala Gln Val Glu His Asn Ala Arg Glu Ala Glu Ala
                340                                345                                350                                355

Asp Ala Glu Ala Val Gly Pro Glu Ala Phe Ala Asp Glu Asp Leu Asp
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Pro Trp Glu Lys Asn Leu Arg Arg Ile Ile Arg Lys Gly Ile His Ile
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Ile Lys Lys Tyr Gly
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<212> DNA
<213> Artificial

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<220>
<223> Primer

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28

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<210> 117
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<212> PRT
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<223> Quenching domain

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<223> Linker

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<222> (15)..()
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Arg Pro Arg Pro Pro Tyr Leu Pro Arg Pro Arg Pro Pro Pro Phe Phe
20 25 30

Pro Pro Arg Leu Pro Pro Arg Ile Pro Pro Gly Phe Pro Pro Arg Phe
35 40 45

Pro Pro Arg Phe Pro
50

<210> 118
<211> 57
<212> PRT
<213> Artificial

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<223> Quenching domain

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<223> Linker

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<223> PR39

<400> 118

Asp Asp Asp Asp Glu Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
1 5 10 15

Gly Glu Arg Arg Arg Pro Arg Pro Pro Tyr Leu Pro Arg Pro Arg Pro

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25