

32491wo\_ST25  
SEQUENCE LISTING

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 Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Asp  
 50 55 60  
 Asn Asn Gln His Gln Asp Met Gln Asp Ala Leu Glu Leu Ile Glu Met  
 65 70 75 80  
 Leu Asn Ile Glu His Tyr Thr Ile Ser Ile Gln Pro Ala Tyr Glu Ala  
 85 90 95  
 Phe Leu Ala Ser Thr Gln Ser Phe Thr Asn Leu Gln Asn Asn Arg Gln  
 100 105 110  
 Leu Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
 115 120 125  
 Tyr Ala Tyr Ala Gln Gln Tyr Asn Arg Ile Val Ile Gly Thr Asp Asn  
 130 135 140  
 Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
 145 150 155 160  
 Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu  
 165 170 175

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Leu Gly Lys Tyr Leu Asp Val Pro Lys Asn Ile Leu Asp Lys Ala Pro  
180 185 190

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
195 200 205

Thr Tyr Gln Glu Ile Asp Asp Phe Leu Asp Gly Lys Gln Val Ser Ala  
210 215 220

Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys  
225 230 235 240

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

Leu Ser Lys Thr Asp Leu Pro Thr Thr Ala Phe Ile Leu Pro Ser Lys  
 50 55 60

Asn Asn Ser Asp Gln Asp Met Ile Asp Ala Leu Glu Leu Ile Asn Lys  
 65 70 75 80

Leu Asn Ile Pro Tyr His Ile Ile Pro Ile Gln Pro Val Tyr Glu Ser  
 85 90 95

Phe Leu Lys Ser Thr Gln Leu Phe Thr Asn Pro Gln Asn Asp Arg Gln  
 100 105 110

Asn Val Ile Lys Gly Asn Ala Gln Ala Arg Phe Arg Met Met Tyr Leu  
 115 120 125

Tyr Ala Tyr Ala Gln Gln Asn Asn Arg Ile Val Val Gly Thr Asp Asn  
 130 135 140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
 145 150 155 160

Ala Asp Ile Leu Pro Leu Ile Asn Leu Lys Lys Ser Gln Val Phe Glu  
 165 170 175

Leu Gly Lys Tyr Leu Asp Val Pro Arg Asn Ile Leu Thr Lys Ala Pro  
 180 185 190

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Gly Glu Met Gly Val  
 195 200 205

Thr Tyr Gln Glu Ile Asp Asn Phe Leu Asp Gly Lys Glu Val Ser Pro  
 210 215 220

Ala Thr Phe Glu Lys Ile Ser Tyr Trp His Asn Arg Ser His His Lys

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Ile Lys Trp Leu Lys Glu Asn Cys Ile Lys Tyr Pro Ala Glu Gly Phe  
20 25 30

Val Ile Gly Ile Ser Gly Gly Ile Asp Ser Ala Val Ala Ala Ser Leu  
35 40 45

Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Lys  
50 55 60

Asn Asn Gln Asp Gln Asp Met Arg Asp Gly Ile Glu Leu Ile Glu Asn  
65 70 75 80

Leu Asn Ile Glu Tyr His Thr Val Ser Ile Gln Pro Ala Tyr Asp Thr  
85 90 95

Phe Ile Glu Ser Thr Phe Asn Phe Thr Asn Ser Gln Asn Asp Arg Gln  
100 105 110

His Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
115 120 125

Tyr Ala Tyr Ala Gln Gln Asn Asn Arg Ile Val Ile Gly Thr Asp Asn  
130 135 140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
145 150 155 160

Ala Asp Ile Leu Pro Leu Ile Asn Leu Lys Lys Ser Gln Val Phe Glu  
165 170 175

Leu Gly Lys Tyr Leu Lys Val Pro Lys Asn Ile Ile Gln Lys Asp Pro  
180 185 190

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195

200

205

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

Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Lys  
 50 55 60

Asn Asn Gln Asp Gln Asp Met Lys Asp Gly Leu Glu Leu Ile Lys Asn  
 65 70 75 80

Leu Asp Ile Glu His His Ile Val Pro Ile Gln Pro Ala Tyr Asp Thr  
 85 90 95

Phe Ile Glu Ser Thr Leu Asn Phe Thr Asn Ser Gln Asn Asp Arg Gln  
 100 105 110

His Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
 115 120 125

Tyr Ala Tyr Ala Gln Gln Asn Asn Arg Ile Val Ile Gly Thr Asp Asn  
 130 135 140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
 145 150 155 160

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Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu  
165 170 175

Met Gly Lys Tyr Leu Lys Val Pro Gln Asn Ile Ile Asp Lys Ala Pro  
180 185 190

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
195 200 205

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

Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys  
225 230 235 240

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

Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Lys  
50 55 60

Asn Asn Gln Asp Gln Asp Met Lys Asp Gly Leu Glu Leu Ile Lys Asn  
65 70 75 80

Leu Asp Ile Glu His His Ile Val Pro Ile Gln Pro Ala Tyr Asp Thr  
85 90 95

Phe Ile Glu Ser Thr Leu Asn Phe Thr Asn Ser Gln Asn Asp Arg Gln  
100 105 110

His Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
115 120 125

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Tyr Ala Tyr Ala Gln Gln Asn Asn Arg Ile Val Ile Gly Thr Asp Asn  
130 135 140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
145 150 155 160

Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu  
165 170 175

Met Gly Glu Tyr Leu Lys Val Pro Gln Asn Ile Ile Asp Lys Ala Pro  
180 185 190

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
195 200 205

Thr Tyr Gln Glu Ile Asp Asn Phe Leu Asp Gly Lys Glu Val Ser Ala  
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Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys  
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Arg Ser Met Ala Phe Thr Pro Asn Phe  
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Val Ile Gly Ile Ser Gly Gly Ile Asp Ser Ala Val Ala Ala Ser Leu  
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Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Lys  
50 55 60

Asn Asn Gln Asp Gln Asp Met Lys Asp Gly Leu Glu Leu Ile Lys Asn  
65 70 75 80

Leu Asp Ile Glu His His Ile Val Pro Ile Gln Pro Ala Tyr Asp Thr  
85 90 95



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Phe Ile Glu Ser Thr Phe Asn Phe Thr Asn Ala Gln Asn Asn Arg Gln  
100 105 110

His Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
115 120 125

Tyr Ala Tyr Ala Gln Gln Asn Asn Arg Ile Val Ile Gly Thr Asp Asn  
130 135 140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
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Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu  
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Leu Gly Lys Tyr Leu Lys Val Pro Gln Asn Ile Ile Asp Lys Ala Pro  
180 185 190

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
195 200 205

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

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

50

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Asn Asn Gln Asp Gln Asp Met Lys Asp Gly Leu Glu Leu Ile Lys Asn  
65 70 75 80

Leu Asp Ile Glu His His Ile Val Pro Ile Gln Pro Ala Tyr Asp Thr  
85 90 95

Phe Ile Glu Ser Thr Phe Asn Phe Thr Asn Ala Gln Asn Asn Arg Gln  
100 105 110

His Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
115 120 125

Tyr Ala Tyr Ala Gln Gln Asn Asn Arg Ile Val Ile Gly Thr Asp Asn  
130 135 140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
145 150 155 160

Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu  
165 170 175

Leu Gly Lys Tyr Leu Lys Val Pro Gln Asn Ile Ile Asp Lys Ala Pro  
180 185 190

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
195 200 205

Ser Tyr Lys Glu Ile Asp Asp Phe Leu Asp Gly Lys Glu Val Ser Glu  
210 215 220

Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys  
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Arg Ser Ile Ala Phe Thr Pro Asp Phe  
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Page 10

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Val Ile Gly Leu Ser Gly Gly Ile Asp Ser Ala Val Ala Ala Ser Leu  
35 40 45  
Ala Val Lys Thr Gly Leu Ser Thr Thr Ala Leu Ile Leu Pro Ser Lys  
50 55 60  
Asn Asn Gln His Gln Asp Ile Gln Asp Ala Leu Glu Leu Ala Asp Lys  
65 70 75 80  
Ile Asn Ile Glu His His Thr Ile Thr Ile Gln Thr Val Tyr Glu Thr  
85 90 95  
Phe Leu Ala Ser Ile Lys Lys Ile Thr Asn Thr Glu Arg Asp Arg Gln  
100 105 110  
Leu Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
115 120 125  
Tyr Ala Tyr Ala Gln Gln Tyr Asn Arg Val Val Ile Gly Thr Asp Asn  
130 135 140  
Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
145 150 155 160  
Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser His Val Phe Glu  
165 170 175  
Leu Gly Lys Tyr Leu Gly Val Pro Lys Asn Ile Leu Asp Lys Ala Pro  
180 185 190  
Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
195 200 205  
Thr Tyr Gln Glu Ile Asp Asp Phe Leu Asp Gly Lys Gln Val Ser Ala  
210 215 220  
Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys  
225 230 235 240  
Arg Lys Leu Ala Leu Ile Pro Asn Phe  
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 Val Ile Gly Ile Ser Gly Gly Ile Asp Ser Ala Val Ala Ala Ser Leu  
 35 40 45  
 Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Lys  
 50 55 60  
 Asn Asn Gln His Gln Asp Ile Gln Asp Ala Leu Glu Leu Val Glu Lys  
 65 70 75 80  
 Leu Asn Ile Glu His His Ile Val Thr Ile Gln Pro Ala Tyr Glu Asn  
 85 90 95  
 Phe Leu Ala Ser Thr Gln Glu Phe Ile Asn Thr Asp Asn Asn Arg Gln  
 100 105 110  
 Leu Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
 115 120 125  
 Tyr Ala Tyr Ala Gln Gln Tyr Asn Arg Ile Val Ile Gly Thr Asp Asn  
 130 135 140  
 Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
 145 150 155 160  
 Ala Asp Ile Phe Pro Leu Ile Asn Leu Lys Lys Ser Gln Val Phe Glu  
 165 170 175  
 Leu Gly Lys Tyr Leu Asp Val Pro Lys Asn Ile Ile Asp Lys Ala Pro  
 180 185 190  
 Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
 195 200 205  
 Thr Tyr Gln Glu Ile Asp Asp Phe Leu Asp Gly Lys Gln Ile Ser Ala  
 210 215 220  
 Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys  
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Val Asn Trp Leu Ser Asp Ser Cys Met Asn Tyr Pro Ala Glu Gly Phe  
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 35 40 45

Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Asp  
 50 55 60

Asn Asn Gln His Gln Asp Met Gln Asp Ala Leu Asp Leu Ile Glu Met  
 65 70 75 80

Leu Asn Ile Glu His Tyr Thr Ile Ser Ile Gln Pro Ala Tyr Glu Ala  
 85 90 95

Phe Leu Ala Ser Thr Gln Arg Phe Thr Asn Leu Gln Asn Asn Arg Gln  
 100 105 110

Leu Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
 115 120 125

Tyr Ala Tyr Ala Gln Gln Tyr Asn Arg Ile Val Ile Gly Thr Asp Asn  
 130 135 140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
 145 150 155 160

Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu  
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Leu Gly Lys Tyr Leu Asp Val Pro Lys Asn Ile Leu Asp Lys Ala Pro  
 180 185 190

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
 195 200 205

Thr Tyr Gln Glu Ile Asp Asp Phe Leu Asp Gly Lys Gln Val Ser Ala  
 210 215 220

Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys

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Val Asn Trp Leu Ser Asp Ser Cys Met Asn Tyr Pro Ala Glu Gly Phe
         20           25           30

Val Ile Gly Leu Ser Gly Gly Ile Asp Ser Ala Val Ala Ala Ser Leu
       35           40           45

Ala Val Lys Thr Gly Leu Pro Ile Thr Ala Leu Ile Leu Pro Ser Asp
     50           55           60

Asn Asn Gln His Gln Asp Met Gln Asp Ala Leu Asp Leu Ile Glu Met
65           70           75           80

Leu Asn Ile Glu His Tyr Thr Ile Ser Ile Gln Pro Ala Tyr Glu Ala
            85           90           95

Phe Leu Ala Ser Thr Gln Ser Phe Thr Asn Leu Gln Asn Asn Arg Gln
        100           105           110

Leu Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu
      115           120           125

Tyr Ala Tyr Ala Gln Gln Tyr Asn Arg Ile Val Ile Gly Thr Asp Asn
    130           135           140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala
145           150           155           160

Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu
        165           170           175

Leu Gly Lys Tyr Leu Asp Val Pro Lys Asn Ile Leu Asp Lys Ala Pro
    180           185           190

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 Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
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Thr Tyr Gln Glu Ile Asp Asp Phe Leu Asp Gly Lys Gln Val Ser Ala  
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Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys  
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Arg Lys Leu Ala Leu Thr Pro Asn Phe  
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 strain NIH B-38, NadE

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Val Ile Gly Leu Ser Gly Gly Ile Asp Ser Ala Val Ala Ala Ser Leu  
 35 40 45

Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Asp  
 50 55 60

Asn Asn Gln His Gln Asp Met Gln Asp Ala Leu Glu Leu Ile Glu Met  
 65 70 75 80

Leu Asn Ile Glu His Tyr Thr Ile Ser Ile Gln Leu Ala Tyr Glu Ala  
 85 90 95

Phe Leu Ala Ser Thr Gln Ser Phe Thr Asn Leu Gln Asn Asn Arg Gln  
 100 105 110

Leu Val Ile Lys Gly Asn Ala Gln Ala Arg Leu Arg Met Met Tyr Leu  
 115 120 125

Tyr Ala Tyr Ala Gln Gln Tyr Asn Arg Ile Val Ile Gly Thr Asp Asn  
 130 135 140

Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
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32491wo\_ST25

Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu  
165 170 175

Leu Gly Lys Tyr Leu Asp Val Pro Lys Asn Ile Leu Asp Lys Ala Pro  
180 185 190

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
195 200 205

Thr Tyr Gln Glu Ile Asp Asp Phe Leu Asp Gly Lys Gln Val Ser Ala  
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Lys Ala Leu Glu Ile Ile Asn Phe Trp His Asn Arg Ser His His Lys  
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Arg Lys Leu Ala Leu Thr Pro Asn Phe  
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<223> CP003932.1\_translation Francisella tularensis subsp. holarctica  
F92, NadE

<400> 15

Met Lys Ile Val Lys Asp Phe Ser Pro Lys Glu Tyr Ser Gln Lys Leu  
1 5 10 15

Val Asn Trp Leu Ser Asp Ser Cys Met Asn Tyr Pro Ala Glu Gly Phe  
20 25 30

Val Ile Gly Leu Ser Gly Gly Ile Asp Ser Ala Val Ala Ala Ser Leu  
35 40 45

Ala Val Lys Thr Gly Leu Pro Thr Thr Ala Leu Ile Leu Pro Ser Asp  
50 55 60

Asn Asn Gln His Gln Asp Met Gln Asp Ala Leu Glu Leu Ile Glu Met  
65 70 75 80

Leu Asn Ile Glu His Tyr Thr Ile Ser Ile Gln Pro Ala Tyr Glu Ala  
85 90 95

Phe Leu Ala Ser Thr Gln Ser Phe Thr Asn Leu Gln Asn Asn Arg Gln  
100 105 110

Leu Val Ile Lys Gly Asn Ala Gln Thr Arg Leu Arg Met Met Tyr Leu  
115 120 125



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Tyr Ala Tyr Ala Gln Gln Tyr Asn Arg Ile Val Ile Gly Thr Asp Asn  
 130 135 140  
 Ala Cys Glu Trp Tyr Met Gly Tyr Phe Thr Lys Phe Gly Asp Gly Ala  
 145 150 155 160  
 Ala Asp Ile Leu Pro Leu Val Asn Leu Lys Lys Ser Gln Val Phe Glu  
 165 170 175  
 Leu Gly Lys Tyr Leu Asp Val Pro Lys Asn Ile Leu Asp Lys Ala Pro  
 180 185 190  
 Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val  
 195 200 205  
 Thr Tyr Gln Glu Ile Asp Asp Phe Leu Asp Gly Lys Gln Val Ser Ala  
 210 215 220  
 Lys Ala Leu Glu Arg Ile Asn Phe Trp His Asn Arg Ser His His Lys  
 225 230 235 240  
 Arg Lys Leu Ala Leu Thr Pro Asn Phe  
 245

<210> 16  
 <211> 239  
 <212> PRT  
 <213> Dichelobacter nodosus

<220>  
 <221> misc\_feature  
 <222> (1)..(239)  
 <223> CP000513.1\_translation Dichelobacter nodosus VCS1703A, Nade  
 <400> 16

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

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Arg Asp Tyr Glu Arg Met Pro Val Leu Asn Gly Asn Leu Met Ala Arg  
100 105 110

Leu Arg Met Val Met Leu Tyr Thr Val Ala Gln Ser His Arg Ser Val  
115 120 125

Val Val Gly Thr Asp Asn Ala Val Glu Tyr Tyr Leu Gly Tyr Phe Thr  
130 135 140

Lys Phe Gly Asp Gly Ala Cys Asp Ile Leu Pro Leu Ala Lys Leu Thr  
145 150 155 160

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

Ile Arg Glu Lys Ala Pro Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp  
180 185 190

Glu Asn Glu Ile Gly Val Ser Tyr Ala Asp Leu Asp Ala Phe Leu Cys  
195 200 205

Gly Lys Thr Val Asp Asp Ala Val Arg Glu Lys Ile Ala Tyr Trp His  
210 215 220

Gln Arg Ser His His Lys Arg Met Leu Pro Pro Met Pro Glu Ile  
225 230 235

<210> 17  
<211> 245  
<212> PRT  
<213> Mannheimia succiniciproducens

<220>  
<221> misc\_feature  
<222> (1)..(245)  
<223> AE016827.1\_translation Mannheimia succiniciproducens MBEL55E,  
NadE

<400> 17

Lys Arg Met Lys Thr Ala Ala Tyr Ala Asp Tyr Leu Ile Gln Trp Leu  
1 5 10 15

Glu Asn Gln Arg Thr Glu Leu Tyr Gly Met Asp Gly Tyr Thr Leu Gly  
20 25 30

Val Ser Gly Gly Ile Asp Ser Ala Val Cys Ala His Leu Ala Ala Arg  
35 40 45

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

Pro Ser Asp Val Ala Asp Ala Gln Ala Thr Leu Glu Ser Ala Gly Ile  
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65					70					75					80
Asp	Gly	Gln	Ile	Ile <sub>85</sub>	Ser	Ile	Ala	Pro	Trp <sub>90</sub>	Tyr	Asp	Leu	Ile	Met <sub>95</sub>	Gln
Gln	Leu	Ser	Pro <sub>100</sub>	Val	Leu	Asn	Ser	Glu <sub>105</sub>	Pro	Glu	Arg	Val	Asn <sub>110</sub>	Val	Leu
Lys	Gly	Asn <sub>115</sub>	Leu	Met	Ala	Arg	Leu <sub>120</sub>	Arg	Met	Ile	Ala	Leu <sub>125</sub>	Phe	Thr	Thr
Ala	Gln <sub>130</sub>	Ser	His	Arg	Ser	Ile <sub>135</sub>	Val	Leu	Gly	Thr	Asp <sub>140</sub>	Asn	Ala	Ala	Glu
Trp <sub>145</sub>	Leu	Thr	Gly	Tyr	Phe <sub>150</sub>	Thr	Lys	Phe	Gly	Asp <sub>155</sub>	Gly	Ala	Ala	Asp	Val <sub>160</sub>
Leu	Pro	Leu	Ala	Gly <sub>165</sub>	Leu	Arg	Lys	Glu	Gln <sub>170</sub>	Val	Phe	Glu	Leu	Gly <sub>175</sub>	Arg
Tyr	Leu	Gly	Val <sub>180</sub>	Pro	Gln	Ser	Val	Leu <sub>185</sub>	Asp	Lys	Lys	Pro	Ser <sub>190</sub>	Ala	Gly
Leu	Trp	Ala <sub>195</sub>	Gly	Gln	Thr	Asp	Glu <sub>200</sub>	Ala	Glu	Met	Gly	Val <sub>205</sub>	Thr	Tyr	Ala
Glu	Ile <sub>210</sub>	Asp	Ala	Tyr	Leu	Arg <sub>215</sub>	Gly	Glu	Thr	Val	Ser <sub>220</sub>	Pro	Gln	Ala	Leu
Gln <sub>225</sub>	Gln	Ile	Arg	Phe	Trp <sub>230</sub>	His	Asn	Arg	Ser	His <sub>235</sub>	His	Lys	Arg	Met	Leu <sub>240</sub>
Pro	Pro	Lys	Pro	Lys <sub>245</sub>											

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<211> 238
<212> PRT
<213> Actinobacillus succinogenes
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<220>
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<222> (1)..(238)
<223> CP000746.1_translation Actinobacillus succinogenes 130Z, NadE
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<400> 18

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1 5 10 15

Tyr Gly Met Asp Gly Tyr Thr Leu Gly Val Ser Gly Gly Ile Asp Ser  
20 25 30

Ala Val Cys Ala His Leu Ala Ala Arg Thr Gly Ala Pro Val Gln Ala  
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35

40

45

Leu Ile Leu Pro Ala Glu Val Thr Ser Pro Glu Asp Val Ala Asp Ala  
 50 55 60

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

Ala Pro Trp Tyr Asp Leu Ile Met Leu Gln Leu Thr Pro Ala Leu Asn  
 85 90 95

Ala Glu Ser Glu Arg Ile Asn Val Leu Lys Gly Asn Leu Met Ala Arg  
 100 105 110

Leu Arg Met Ile Ala Leu Phe Thr Thr Ala Gln Ser His Arg Ser Ile  
 115 120 125

Val Leu Gly Thr Asp Asn Ala Ala Glu Met Leu Thr Gly Tyr Phe Thr  
 130 135 140

Lys Phe Gly Asp Gly Ala Ala Asp Val Leu Pro Leu Ala Arg Leu Arg  
 145 150 155 160

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

Val Leu Glu Lys Lys Pro Ser Ala Gly Leu Trp Ala Gly Gln Thr Asp  
 180 185 190

Glu Gly Glu Met Gly Val Ser Tyr Ala Glu Ile Asp Ala Tyr Leu Arg  
 195 200 205

Gly Glu Thr Val Ser Pro Gln Ala Leu Lys Gln Ile Gln Phe Trp His  
 210 215 220

Asn Arg Ser His His Lys Arg Met Leu Pro Pro Thr Pro Glu  
 225 230 235

<210> 19  
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 <212> DNA  
 <213> Mannheimia succiniciproducens

<220>  
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 <223> AE016827 Mannheimia succiniciproducens MBEL55E, NadE

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 ctttacggga tggacggcta tacactgggc gtcagcggcg gtattgacag cgccgtctgc 120  
 gctcatttgg cagcgcgcac cggcgcaccg gtacaagcct taattttgcc cgccgaagta 180

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accagtccgt cagatgtggc ggatgcgcaa gccacactgg aaagcgccgg tattgacgga	240
caaataatth ccattgcacc ttggtacgat ttaattatgc aacaactttc cccggtatta	300
aattccgaac cggagcgcgt taacgtatta aagggttaatt taatggcaag actgcgatatg	360
attgcgctgt ttaccacggc acaaagccat cgttctattg tgtaggcac cgataatgcg	420
gcggaatggc tgacgggtta ttttaccaa ttcggcgacg gcgcagcgga cgtactgcct	480
ttagcgggat tgcgcaaaga gcaggtatth gaactcggac gttatcttgg cgtaccgcaa	540
agcgtgctgg ataaaaaacc gagcgccggg ttatgggcag gacaaacgga cgaagctgaa	600
atgggtgtta cttatgcgga aatcgacgct tatctgcgcg gcgaaaccgt tagcccgcat	660
gcattgcaac aaatccgtht ctggcacaac cgttctcatc acaaacgtat gttgccacct	720
aaaccgaaat caccgatga agcggagtgt taa	753

<210> 20  
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 <212> DNA  
 <213> Dichelobacter nodosus

<220>  
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 <223> CP000513 Dichelobacter nodosus VCS1703A, NadE

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ctttatgcat cagatggtha tacgttgggc gtcagcggcg gcatcgattc cgccgtthtg	120
ctgcatttac tcgcaaaaac gggaaaaccc gtgcaagcgt tagthtttgcc gatcaatgcg	180
aacgcgaacg attgtgaaga tgccgaatta gtgttaaaaa atgctaatat ttccggcaat	240
attatcgcgc tcgatgatgt ttataccgcc gcacaaaaca ccttggcgcc tgthtttaaat	300
gcgcgattatg aacgtatgcc cgtatthaac ggcaatthta tggcgcggtc gcgtatggth	360
atgctthata ccgtggcgca aagtcatcgt tcggtggtcg tgggaacgga taacgcggtg	420
gaatattatt taggttactt tacaaaatth ggcgacggcg cctgcgatat thtgccgctg	480
gcaaaactga caaatcaga agtaggacaa ttggcaaaag cgttaggcgt tccgaaaaaa	540
atccgagaaa aagcgccgag cgcaggcttg tggcaagggc aaaccgatga aaacgaaatc	600
ggcgtatcgt acgcggatth agatgcttht ttgtgcggta aaaccgttga tgatgccgtc	660
agagaaaaaa ttgcttattg gcatcaacgc tcgcatcata aaagaatgth gccgccgatg	720
ccggaaatcg gattatctth ggcgtaa	747

<210> 21  
 <211> 750  
 <212> DNA  
 <213> Actinobacillus succinogenes

<220>  
 <221> misc\_feature  
 <222> (1)..(750)

<223> CP000746 *Actinobacillus succinogenes* 130Z, NadE

<400> 21

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gcccatttag cggcacgcac cggcgccccc gtacaggcat tgattttacc cgccgaagtc      180
accagccctg aagatgtggc ggatgctcag attaccttgg aaagtgcagg tattgacggg      240
cggattatatt ctatcgctcc ttggtacgat ttaattatgc tacaacttac ccccgcatata      300
aatgcggaat ctgaacgcac taacgtattg aaaggtaact taatggcgcg cttacgtatg      360
atcgcatatg ttaccacggc gcaaagccac cgttctatcg tattgggtac ggataacgcc      420
gccgaaatgt taacgggcta tttcaccaaa ttcggcgacg gtgcggcgga cgtattgccg      480
ttagcgaggt tgcgcaaaga acaggtattc gaattagggc gttatcttgg cgtaccgaaa      540
tccgtgctgg agaaaaaacc gagtgcgggc ttatgggagg ggcaaacgga cgagggggaa      600
atgggtgtca gttatgcgga aatcgacgcc tatctgcgcg gcgaaaccgt cagtccgcag      660
gcgttaaagc agattcaatt ctggcacaac cgttctcatc acaaacgtat gctgccgccg      720
acgccagaac cgccggatga aatcgattaa                                     750

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<210> 22

<211> 750

<212> DNA

<213> *Francisella* cf. *novicida*

<220>

<221> misc\_feature

<222> (1)..(750)

<223> CP002558 *Francisella* cf. *novicida* 3523, NadE

<400> 22

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agtgatactt gtataaatta tcctgctgaa ggatttgtaa tcggcattag cggtggtata      120
gattcagctg ttgcagcttc tttagctgtc aaaactggat taccaactac agctttaata      180
ctaccttcaa aaaacaatca acaccaagat atccaagatg ctctagaact tgttgagaaa      240
cttaatatgg aacatcatat tgttacaatt caaccagcat acgaaaattt tctagcatca      300
acacaggaat ttataaatac agataataat agacaacttg tgatcaaggg aaatgctcaa      360
gcacgtttta ggatgatgta tttatatgcc tatgcccac aatataacag aatagttata      420
ggtagtgata atgcttgatg gtggtatatg ggatatttta caaaatttgg tgatggcgct      480
gctgatatat ttccgctaatt taatcttaaa aaatcacaag tttttgaatt aggtaaatac      540
ttagatgttc cgaaaaatat aattgataaa gctccgtctg ctggactatg gcaaggacaa      600
actgatgagg atgaaatggg cgtaacttat caagaaattg atgatttctt agatggtaaa      660
caaatttcag caaaagccct agaaagaata aacttctggc ataatcgtag tcatcataag      720
agaaaactag cttaactcc taatttctaa                                     750

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<210> 23  
 <211> 750  
 <212> DNA  
 <213> Francisella sp

<220>  
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 <222> (1)..(750)  
 <223> CP002872 Francisella sp. TX077308, NadE

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gattcggcag tagccgcatac ttttagcagtc aaaacaggat tacctacaac tgctctaata      180
ttgccatcga agaacaatca agaccaagat atgcgagatg gaatagaact aatcgaaaat      240
cttaatatag agtatcatac tgttttcaata caacctgctt atgacacgtt tatagagtca      300
acatttaact ttacaaactc acaaaatgat cgccaacatg ttatcaaagg aaatgcccac      360
gcgcgtctta gaatgatgta tttatatgct tatgctcagc aaaataatag aattgtttata      420
ggtacagata acgcatgtga atggtacatg ggatattttca ctaaattttgg tgatgggtgca      480
gcagatatat taccacttat taatctcaaa aaatctcaag tttttgaact aggtaaatac      540
ttaaagtgct caaaaaacat tatccaaaaa gatccttctg cgggtctatg gcaagggtcaa      600
actgatgagg atgaaatggg tgtcacatac aaagaaattg atgacttctt agacggtaaa      660
gaagtctcag aaaaagctct cgaaagaata agcttctggc ataatcgtag tcaccataaa      720
agatccatgg cttttacccc taatttttaa      750
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<210> 24  
 <211> 750  
 <212> DNA  
 <213> Francisella sp.

<220>  
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 <223> CP009574 Francisella sp. FSC1006, NadE

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aaagactctt gtttaatta tcccgctgaa ggttttgtgg taggtattag tggaggtata      120
gattcagcag tagcagtctc ttttagcagta aatactggac tacctgttac agggctaata      180
atgccatcaa aaaataatga tgataaagat accttagatg ctatagaatt agctaaaaaa      240
ttaaatatag aatatcatct cataccatt caaccagtat atgaaacatt tctagattca      300
gctgaagata tcaaaaacag tgctaatac cgtcaacatg taatcaaagg aaatgcacaa      360
gctcgtttta gaatgatata cttgtatgct tacgctcagc aaaataatag aatggtaatt      420
ggtacagata atgcttgtga atggtatatg ggctattttta caaaattttgg agatggagcc      480
gctgatatac tgcctcttat aaaattaaaa aaatcacaag tttttgaatt aggtagctat      540
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cttaatgtac ccaataacat cctcacaaaa gctccttccg caggactttg gcttggacaa	600
actgatgaag cagagatggg ggtttcatat caagaaatag atgatttcct tgatggtaaa	660
catgtctcag attatgctct taatcaaata aaattctggc ataaccgtag tcatcataaa	720
agaatcatgg ctaaggctcc agatttttaa	750

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 <212> DNA  
 <213> Francisella guangzhouensis

<220>  
 <221> misc\_feature  
 <222> (1)..(753)  
 <223> CP010427 Francisella guangzhouensis strain 08HL01032, NadE

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gattctgcag tatgtgcatc acttttatcc aaaactgac ttcctacaac agcttttata	180
ctaccatcaa aaaataactc tgatcaagat atgatcgatg cattagaact tataaataaa	240
ttaaatattc cataccatat aataccaatc cagccagttt atgaaagttt tctaaagtcc	300
acacagctat ttacaaatcc acaaaatgac agacaaaatg tcataaaagg taacgctcaa	360
gctcgtttta gaatgatgta tttatatgct tatgcacaac aaaataatcg tatagtagtt	420
ggaacagata atgcttgtga atggtatatg ggttatttca ccaaatttgg cgatggagct	480
gctgatatac taccattaat aaatcttaaa aagtcccagg tatttgagtt aggtaaatac	540
ttagatgttc caaggaatat cctaactaag gcaccctctg ctggtctttg gcaaggccaa	600
actgatgaag gtgaaatggg agttacttat caggaaatag ataattttct cgacggtaaa	660
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agaaagatgg cttaacgcc agattttaac taa	753

<210> 26  
 <211> 750  
 <212> DNA  
 <213> Francisella persica

<220>  
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 <223> CP013022 Francisella persica ATCC VR-331, NadE

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gattcggcag ttgcagcttc tttagctgtc aaaactggat tatcaactac agctttaata	180
ttaccatcaa aaaacaatca acaccaagat atacaagatg ctctagaact tgcagataaa	240
attaatatgg aacatcatac tattacaatt caaacagtat acgaaacttt tcttgcgta	300



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ataaaaaaaaa	ttacaaatac	cgaacgtgat	agacaacttg	tcattaaagg	aaatgctcaa	360
gctcgtttga	ggatgatgta	tttatatgcc	tatgctcaac	aatataatag	agtgggttatt	420
ggtactgata	atgcttgtga	atggatatatg	ggatattttta	caaagtttgg	tgatggtgct	480
gctgatattc	ttccactagt	taatctcaaa	aaatctcacg	tttttgaatt	aggtaaatac	540
ttaggtgttc	ctaaaaatat	acttgataaa	gctccatctg	ctgggctatg	gcaaggacaa	600
actgatgaag	atgaaatggg	cgtaacttat	caagaaattg	atgatttctt	agatggtaag	660
caagtttcag	cgaaagctct	agaaagaata	aatttctggc	ataatcgtag	tcatcataag	720
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<220>  
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accagtccgt	cagatgtggc ggatgcgcaa gccaccctgg aaagcgccgg tattgacggc 240
caaattatth	ccattgcacc gtggtacgat ctgattatgc aacaactgtc cccggtactg 300
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attgcgctgt	ttaccacggc acaaagccat cgttctattg tgctgggcac cgataatgcg 420
gcggaatggc	tgacgggtta ttttacaaa ttcggcgacg gcgcagcgga cgtactgccg 480
ctggcgggcc	tgcgcaaaga gcaggatattt gaactgggcc gttatctggg cgtaccgcaa 540
agcgtgctgg	ataaaaaaacc gagcgccggt ctgtgggcag gccaaacgga cgaagctgaa 600
atgggtgtta	cctatgcgga aatcgacgct tatctgcgcg gcgaaaccgt tagcccgag 660
gcactgcaac	aaatccgttt ctggcacaac cgttctcatc acaaacgtat gctgccgccg 720
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<210> 28  
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 <212> DNA  
 <213> Dichelobacter nodosus

<220>  
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 <223> Optimized\_CP000513 Dichelobacter nodosus VCS1703A, NadE

<400> 28

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aacgcgaacg attgtgaaga tgccgaactg gtgctgaaaa atgctaatat ttccggcaat	240
attatcgcgcg tggatgatgt ttataaccgcc gcacaaaaca ccctggcgcc ggttctgaat	300
cgcgattatg aacgtatgcc ggtactgaac ggcaatctga tggcgcgccct gcgtatggtt	360
atgctgtata ccgtggcgca aagtcacgt tcggtggtcg tgggcacgga taacgcggtg	420
gaatattatc tgggttactt taccaaattt ggcgacggcg cctgcgatat tctgccgctg	480
gcaaaactga ccaaatcaga agtaggcaa ctggcaaaag cgctgggctg tccgaaaaaa	540
atccgcgaaa aagcgccgag cgcgggcctg tggcaaggcc aaaccgatga aaacgaaatc	600
ggcgatctgc acgcggatct ggatgctttt ctgtgcggta aaaccgttga tgatgccgtc	660
cgcgaaaaaa ttgcttattg gcatcaacgc tcgcatcata aacgtatgct gccgccgatg	720
ccggaaatcg gcctgtctct ggcgtaa	747

<210> 29  
 <211> 750  
 <212> DNA  
 <213> Actinobacillus succinogenes

<220>  
 <221> misc\_feature  
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 <223> Optimized\_CP000746 Actinobacillus succinogenes 130Z, NadE

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ctgtacggta tggacggcta cacgctgggc gtcagcggcg gtatcgacag tgccgtttgc	120
gcccattctgg cggcacgcac cggcgccccg gtacaggcac tgattctgcc ggcggaagtc	180
accagcccgg aagatgtggc ggatgctcag attaccctgg aaagtgcagg tattgatggc	240
cgcattatct ctatcgctcc gtggtacgat ctgattatgc tgcaactgac cccggcactg	300
aatgcggaat ctgaacgcat taacgtactg aaaggtaacc tgatggcgcg cctgcgtatg	360
atcgcaactgt ttaccacggc gcaaagccac cgttctatcg tactgggtac ggataacgcc	420
gccgaaatgc tgacgggcta tttcacaaa ttcggcgacg gtgcggcgga cgtactgccg	480
ctggcgcgcc tgcgcaaaga acaggtattc gaactgggcc gttatctggg cgtaccgaaa	540
tccgtgctgg agaaaaaacc gaggcgggc ctgtgggcgg gccaaacgga cgaggcgcaa	600
atgggtgtca gttatgcgga aatcgacgcc tatctgcgcg gcgaaaccgt cagtccgcag	660
gcgctgaaac agattcaatt ctggcacaac cgttctcatc aaaaacgtat gctgccgccg	720
acgccggaac cgccggatga aattgattaa	750

<210> 30  
 <211> 750  
 <212> DNA

<213> Francisella cf. novicida

<220>

<221> misc\_feature

<222> (1)..(750)

<223> Optimized\_CP002558 Francisella cf. novicida 3523, NadE

<400> 30

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atgaaaattg ttaaagattt tagtccgaaa gaatattcac aaaatctggt taattggctg      60
agtgatacct gtattaatta tccggctgaa ggctttgtaa tcggcattag cggtggtatt      120
gattcagcgg ttgcagcttc tctggctgtc aaaaccggcc tgccgaccac cgctctgatt      180
ctgccgtcaa aaaacaatca acaccaagat attcaagatg ctctggaact ggttgagaaa      240
ctgaatattg aacatcatat tgttaccatt caaccggcat acgaaaattt tctggcatca      300
acccaggaat ttattaatac cgataataat cgccaactgg tgatcaaagg caatgctcaa      360
gcacgtctgc gcatgatgta tctgtatgcc tatgcccac aatataaccg cattgttatt      420
ggtaccgata atgcttgtga gtggtatatg ggctatttta ccaaatttgg tgatggcgct      480
gctgatattt ttccgctgat taatctgaaa aaatcacaag tttttgaact gggtaaatac      540
ctggatgttc cgaaaaatat tattgataaa gctccgtctg ctggcctgtg gcaaggccaa      600
accgatgagg atgaaatggg cgtaacctat caagaaattg atgatttcct ggatggtaaa      660
caaatttcag caaaagccct ggaacgcatt aacttctggc ataatcgtag tcatcataaa      720
cgcaaactgg ctctgacccc gaatttctaa      750

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<210> 31

<211> 750

<212> DNA

<213> Francisella sp.

<220>

<221> misc\_feature

<222> (1)..(750)

<223> Optimized\_CP002872 Francisella sp. TX077308, NadE

<400> 31

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aaagagaatt gcattaaata tccggctgaa ggttttgtga ttggtattag tggtggtatt      120
gattcggcag tagccgcata tctggcagtc aaaaccggcc tgccgaccac cgctctgatt      180
ctgccgtcga aaaacaatca agaccaagat atgcgcgatg gcattgaact gatcgaaaat      240
ctgaatattg agtatcatac cgtttcaatt caaccggctt atgacacggt tattgagtca      300
acctttaact ttaccaactc acaaaatgat cgccaacatg ttatcaaagg caatgcccaa      360
gcgcgtctgc gcatgatgta tctgtatgct tatgctcagc aaaataatcg cattgttatt      420
ggtaccgata acgcatgtga atggtacatg ggctatttca ccaaatttgg tgatggtgca      480
gcagatattc tgccgctgat taatctgaaa aaatctcaag tttttgaact gggtaaatac      540
ctgaaagtgc cgaaaaacat tatccaaaaa gatccgtctg ccggtctgtg gcaagggtcaa      600
accgatgagg atgaaatggg tgtcacctac aaagaaattg atgacttcct ggacggtaaa      660

```

32491wo\_ST25

gaagtctcag aaaaagctct ggaacgcatt agcttctggc ataatcgtag tcaccataaa 720  
cgagcatgg cttttacccc gaatttttaa 750

<210> 32  
<211> 750  
<212> DNA  
<213> Francisella sp.

<220>  
<221> misc\_feature  
<222> (1)..(750)  
<223> Optimized\_CP009574 Francisella sp. FSC1006, NadE

<400> 32  
atgagtgtag taaaaaattt taaaccgaat gaatatgcca ataaaattac cgaatggctg 60  
aaagactctt gtctgaatta tccggctgaa ggttttgtgg taggtattag tggcgggtatt 120  
gattcagcag tagcagtctc tctggcagta aataccggcc tgccgggttac cggcctgatt 180  
atgccgtcaa aaaataatga tgataaagat accctggatg ctattgaact ggctaaaaaa 240  
ctgaatattg aatatcatct gattccgatt cagccggtat atgaaacctt tctggattca 300  
gcggaagata ttaaaaacag tgctaataac cgtcaacatg taatcaaagg caatgcacaa 360  
gctcgttttc gcatgattta cctgtatgct tacgctcagc aaaataatcg catggtaatt 420  
ggtagcgata atgcttgtga atgggtatag ggctattttt ccaaatttgg cgatggcgcc 480  
gctgatattc tgccgctgat taaactgaaa aaatcacaag tttttgaact gggtagctat 540  
ctgaatgtac cgaataacat cctgaccaa gctccgagcg cgggcctgtg gctgggcca 600  
accgatgaag cagagatggg cgtttcatat caagaaattg atgatttcct ggatggtaaa 660  
catgtctcag attatgctct gaatcaaatt aaattctggc ataaccgtag tcatcataaa 720  
cgcatcatgg ctaaagctcc ggatttttaa 750

<210> 33  
<211> 753  
<212> DNA  
<213> Francisella guangzhouensis

<220>  
<221> misc\_feature  
<222> (1)..(753)  
<223> Optimized\_CP010427 Francisella guangzhouensis strain 08HL01032, NadE

<400> 33  
atgaacgtag taaaaaattt caccgccgaa aaatattcag aaaaactgat tcaatggctg 60  
accaatagct gtattaaata tccggcagaa ggtttcgtaa ttggtgtaag tgggtggtatt 120  
gattctgcgg tatgtgcatc actgctgtcc aaaaccgatc tgccgaccac cgcttttatt 180  
ctgccgtcaa aaaataactc tgatcaagat atgattgatg cactggaact gattaataaa 240  
ctgaatattc cgtaccatat tattccgatc cagccggttt atgaaagttt tctgaaatcc 300  
acccaactgt ttaccaatcc gcaaaatgac cgccaaaatg tcattaaagg taacgctcaa 360

# 32491wo\_ST25

```

gctcgttttc gcatgatgta tctgtatgct tatgcacaac aaaataatcg tattgtagtt      420
ggcaccgata atgcttgtga atggtatatg ggttattttca ccaaatttgg cgatggcgct      480
gctgatattc tgccgctgat taatctgaaa aaatcccagg tatttgagct gggtaaatac      540
ctggatgttc cgcgcaatat cctgaccaa gcaccgtctg ctgggtctgtg gcaaggccaa      600
accgatgaag gtgaaatggg cgttacctat caggaaattg ataattttct ggacggtaaa      660
gaagtatcgc cggcaacctt tgaaaaaatt agctactggc ataatcgctc tcaccacaaa      720
cgcaaaatgg ctctgacgcc ggattttaac taa                                     753

```

```

<210> 34
<211> 750
<212> DNA
<213> Francisella persica

```

```

<220>
<221> misc_feature
<222> (1)..(750)
<223> Optimized_CP013022 Francisella persica ATCC VR-331, NadE

```

```

<400> 34
atgaaaattg ttaaagattt caacatcaaa gaatattcac aaaaactgat tgattggctg      60
agtgatacct gtatgaatta cccggctgaa ggctttgtca ttgggtctgag cgggtggtatt      120
gattcggcag ttgcagcttc tctggctgtc aaaaccggcc tgtcaaccac cgctctgatt      180
ctgccgtcaa aaaacaatca acaccaagat attcaagatg ctctggaact ggcagataaa      240
attaatattg aacatcatac cattaccatt caaaccgtat acgaaacctt tctggcgctca      300
attaaaaaaaa ttaccaatac cgaacgtgat cgccaactgg tcattaaagg caatgctcaa      360
gctcgtctgc gcatgatgta tctgtatgcc tatgctcaac aatataatcg cgtgggttatt      420
ggtagccgata atgcttgtga atggtatatg ggctattttta ccaaatttgg tgatgggtgct      480
gctgatattc tgccgctggt taatctgaaa aaatctcacg tttttgaact gggtaaatac      540
ctgggtgttc cgaaaaatat tctggataaa gctccgtctg ctggcctgtg gcaaggccaa      600
accgatgaag atgaaatggg cgtaacctat caagaaattg atgatttcct ggatggtaaa      660
caagtttcag cgaaagctct ggaacgcatt aatttctggc ataatcgtag tcatcataaa      720
cgcaaaactgg ctctgattcc gaatttctaa                                     750

```

```

<210> 35
<211> 750
<212> DNA
<213> Unknown

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<220>
<223> FtNadE_star_optimized

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<220>
<221> misc_feature
<222> (1)..(750)
<223> FtNadE_star_optimized

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32491wo\_ST25

```

<400> 35
atgaaaatcg tcaaagactt ctccccgaaa gaatattccc aaaaactggt gaactggctg      60
agcgactcgt gtatgaacta tccggcagaa ggctttgtca ttggtctgag tggcgggtatc      120
gattccgctg tggcggcctc actggccggt aaaaccggcc tgccgaccac ggcactgatt      180
ctgccgtctg acaacaatca gcatcaagat atgcaggacg cgctggaact gattgaaatg      240
ctgaacatcg aacactacac catttccatc cagccggcgt atgaagcgtt tctggcgagc      300
acccaatctt tcacgaacct gcagaacaat cgtcaactgg tgatcaaagg caatgcgcag      360
gcccgtctgc gcatgatgta tctgtacgcg tatgcgcgagc aatacaaccg cattgtttatc      420
ggcaccgata atgcctgcga atggtacatg ggttattttta cgaaattcgg cgatgggtgca      480
gctgacattc tgccgctggt caacctgaaa aaatcgcagg tgtttgaact gggtaaatac      540
ctggatgttc cgaaaaatat cctggacaaa gcaccgagcg caggtctgtg gcaggggtcaa      600
accgatgaag acgaaatggg cgttacgtat caggaaattg atgacttcct ggatggtaaa      660
caagtcagcg cgaaagccct ggaacgtatc aacttctggc acaaccgctc acatcataaa      720
cgaaaactgg cactgacccc gaacttctaa      750

```

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<210> 36
<211> 750
<212> DNA
<213> Unknown

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<220>
<223> DQ682092-AL_Reverted

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```

<220>
<221> misc_feature
<222> (1)..(750)
<223> DQ682092-AL_Reverted

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```

<400> 36
atgaaaatcg tcaaagactt ctccccgaaa gaatattccc aaaaactggt gaactggctg      60
agcgactcgt gtatgaacac tccggcagaa ggctttgtca ttggtctgag tggcgggtatc      120
gattccgctg tggcggcctc actggccggt aaaaccggcc tgccgaccac ggcactgatt      180
ctgccgtctg acaacaatca gcatcaagat atgcaggacg cgctggaact gattgaaatg      240
ctgaacatcg aacactacac catttccatc cagccggcgt atgaagcgtt tctggcgagc      300
acccaatctt tcacgaacct gcagaacaat cgtcaactgg tgatcaaagg caatgcgcag      360
gcccgtctgc gcatgatgta tctgtacgcg tatgcgggtc aatacaaccg cattgtttatc      420
ggcaccgata atgcctgcga atggtacatg ggttattttta cgaaattcgg cgatgggtgca      480
gctgacattc tgccgctggt caacctgaaa aaatcgcagg tgtttgaact gggtaaatac      540
ctggatgttc cgaaaaatat cctggacaaa gcaccgagcg caggtctgtg gcaggggtcaa      600
accgatgaag acgaaatggg cgttacgtat caggaaattg atgacttcct ggatggtaaa      660
caagtcagcg cgaaagccct ggaacgtatc aacttctggc acaacgtctc acatcataaa      720
cgaaaactgg cactgacccc gaacttctaa      750

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32491wo\_ST25

<210> 37  
 <211> 753  
 <212> DNA  
 <213> Mannheimia succiniciproducens

<220>  
 <221> misc\_feature  
 <222> (1)..(753)  
 <223> Optimized\_AE016827\_Reverted Mannheimia succiniciproducens

<400> 37  
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 ctgaccggca tggacggcta taccctgggc gtcagcggcg gtattgacag cgccgtctgc 120  
 gctcatctgg cagcgcgcac cggcgcgccg gtacaagccc tgattctgcc ggcggaagta 180  
 accagtccgt cagatgtggc ggatgcgcaa gccaccctgg aaagcgccgg tattgacggc 240  
 caaattatth ccattgcacc gtggtacgat ctgattatgc aacaactgtc cccggtactg 300  
 aatagcgaac cggagcgcgt taacgtactg aaaggtaatc tgatggcacg cctgcgtatg 360  
 attgcgctgt ttaccacggc aggcagccat cgttctattg tgctgggcac cgataatgcg 420  
 gcggaatggc tgacgggtta ttttaccaa ttcggcgacg gcgcagcgga cgtactgccg 480  
 ctggcgggcc tgcgcaaaga gcaggtatth gaactgggcc gttatctggg cgtaccgcaa 540  
 agcgtgctgg ataaaaaac gagcgccggc ctgtgggcag gccaaacgga cgaagctgaa 600  
 atgggtgtta cctatgcgga aatcgacgct tatctgcgcg gcgaaaccgt tagcccgag 660  
 gcactgcaac aaatccgtht ctggcacaac gthtctatc acaaacgtat gctgccgccg 720  
 aaaccgaaat caccggatga agcggagtgt taa 753

<210> 38  
 <211> 750  
 <212> DNA  
 <213> Francisella cf. novicida

<220>  
 <221> misc\_feature  
 <222> (1)..(750)  
 <223> Optimized\_CP002558\_Reverted Francisella cf. novicida 3523

<400> 38  
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 gattcagcgg ttgcagcttc tctggctgtc aaaaccggcc tgccgaccac cgctctgatt 180  
 ctgccgtcaa aaaacaatca acaccaagat attcaagatg ctctggaact ggthgagaaa 240  
 ctgaatattg aacatcatat tgttaccatt caaccggcat acgaaaatth tctggcatca 300  
 acccaggaat ttattaatac cgataataat cgccaactgg tgatcaaagg caatgctcaa 360  
 gcacgtctgc gcatgatgta tctgtatgcc tatgccggcc aatataaccg cattgttatt 420  
 ggtaccgata atgcttgtga gtggatatat ggctatthta ccaaattthg tgatggcgct 480  
 gctgatatth ttccgctgat taatctgaaa aaatcacaag tthttgaact gggtaataac 540

32491wo\_ST25

ctggatgttc cgaaaaatat tattgataaa gtcctgtctg ctggcctgtg gcaaggccaa	600
accgatgagg atgaaatggg cgtaacctat caagaaattg atgatttcct ggatggtaaa	660
caaatttcag caaaagccct ggaacgcatt aacttctggc ataatgttag tcatcataaa	720
cgcaaactgg ctctgacccc gaatttctaa	750

<210> 39  
 <211> 750  
 <212> DNA  
 <213> Francisella sp.

<220>  
 <221> misc\_feature  
 <222> (1)..(750)  
 <223> Optimized\_CP002872\_Reverted Francisella sp. TX077308

<400> 39	
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aaagagaatt gcattaaaac tccggctgaa ggttttgtga ttggtattag tgggtggtatt	120
gattcggcag tagccgcatt tctggcagtc aaaaccggcc tgccgaccac cgctctgatt	180
ctgccgtcga aaaacaatca agaccaagat atgcgcgatg gcattgaact gatcgaaaat	240
ctgaatattg agtatcatac cgttttcaatt caaccggctt atgacacggt tattgagtca	300
acctttaact ttaccaactc acaaaatgat cgccaacatg ttatcaaagg caatgcccaa	360
gcgcgctctg gcatgatgta tctgtatgct tatgctgggc aaaataatcg cattgttatt	420
ggtaccgata acgcatgtga atggtacatg ggctattttca ccaaatttgg tgatgggtgca	480
gcagatattc tgccgctgat taatctgaaa aaatctcaag tttttgaact gggtaaatac	540
ctgaaagtgc cgaaaaacat tatccaaaaa gatccgtctg ccggtctgtg gcaagggtcaa	600
accgatgagg atgaaatggg tgtcacctac aaagaaattg atgacttcct ggacggtaaa	660
gaagtctcag aaaaagctct ggaacgcatt agcttctggc ataatgttag tcaccataaa	720
cgcgatctgg cttttacccc gaatttttaa	750

<210> 40  
 <211> 828  
 <212> DNA  
 <213> E. coli

<220>  
 <221> misc\_feature  
 <222> (1)..(828)  
 <223> E. coli NadE

<400> 40	
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gaggaaattc gtcgtagtgt cgattttctg aaaagctacc tgcaaaactta tccgttcatt	120
aaatcactgg tgctcgggat cagcggcggg caggactcca cgcttgccgg aaagctgtgc	180
cagatggcga ttaatgagct ggccttgaa accggcaacg aatcactgca atttattgcc	240



## 32491wo\_ST25

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gtacgcctgc cctatggtgt tcaggccgac gaacaagatt gccaggatgc cattgccttt      300
attcaaccgg atcgcgtatt aaccgttaat atcaagggcg cggatttggc cagcgaacag      360
gcattgcggg aagcaggcat tgaactgagc gattttgtcc gtggcaatga aaaagcgcgt      420
gagcggatga aagcacaata tagcattgcg ggtatgacca gcggtgtcgt ggtgggcacc      480
gatcatgcag cagaagccat taccggattc ttcactaaat atggtgacgg cggtagcgac      540
attaatccgc tgtatcgtct caacaaacgt cagggtaaac agttactggc ggcattagct      600
tgcccggaac acctttataa gaaagcgcca acggccgatac tggaagatga tcgcccttct      660
ctgccagatg aagtggcact cggcgtgacc tatgacaata tcgacgacta tctggaaggg      720
aaaaacgtac ctcaacaggt cgccagaaca atagagaact ggtatctgaa aaccgaacat      780
aaacgccgtc cgccaattac cgttttcgat gatttctgga aaaagtaa                    828

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<210> 41  
 <211> 540  
 <212> PRT  
 <213> Escherichia coli

<220>  
 <221> misc\_feature  
 <222> (1)..(540)  
 <223> Escherichia coli NadB >gi|260448346|gb|ACX38768.1| L-aspartate  
 oxidase [Escherichia coli DH1]

<400> 41

Met Asn Thr Leu Pro Glu His Ser Cys Asp Val Leu Ile Ile Gly Ser  
1 5 10 15

Gly Ala Ala Gly Leu Ser Leu Ala Leu Arg Leu Ala Asp Gln His Gln  
20 25 30

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

Ala Gln Gly Gly Ile Ala Ala Val Phe Asp Glu Thr Asp Ser Ile Asp  
50 55 60

Ser His Val Glu Asp Thr Leu Ile Ala Gly Ala Gly Ile Cys Asp Arg  
65 70 75 80

His Ala Val Glu Phe Val Ala Ser Asn Ala Arg Ser Cys Val Gln Trp  
85 90 95

Leu Ile Asp Gln Gly Val Leu Phe Asp Thr His Ile Gln Pro Asn Gly  
100 105 110

Glu Glu Ser Tyr His Leu Thr Arg Glu Gly Gly His Ser His Arg Arg  
115 120 125

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

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Val Ser Lys Ala Leu Asn His Pro Asn Ile Arg Val Leu Glu Arg Ser  
 145 150 155 160  
 Asn Ala Val Asp Leu Ile Val Ser Asp Lys Ile Gly Leu Pro Gly Thr  
 165 170 175  
 Arg Arg Val Val Gly Ala Trp Val Trp Asn Arg Asn Lys Glu Thr Val  
 180 185 190  
 Glu Thr Cys His Ala Lys Ala Val Val Leu Ala Thr Gly Gly Ala Ser  
 195 200 205  
 Lys Val Tyr Gln Tyr Thr Thr Asn Pro Asp Ile Ser Ser Gly Asp Gly  
 210 215 220  
 Ile Ala Met Ala Trp Arg Ala Gly Cys Arg Val Ala Asn Leu Glu Phe  
 225 230 235 240  
 Asn Gln Phe His Pro Thr Ala Leu Tyr His Pro Gln Ala Arg Asn Phe  
 245 250 255  
 Leu Leu Thr Glu Ala Leu Arg Gly Glu Gly Ala Tyr Leu Lys Arg Pro  
 260 265 270  
 Asp Gly Thr Arg Phe Met Pro Asp Phe Asp Glu Arg Gly Glu Leu Ala  
 275 280 285  
 Pro Arg Asp Ile Val Ala Arg Ala Ile Asp His Glu Met Lys Arg Leu  
 290 295 300  
 Gly Ala Asp Cys Met Phe Leu Asp Ile Ser His Lys Pro Ala Asp Phe  
 305 310 315 320  
 Ile Arg Gln His Phe Pro Met Ile Tyr Glu Lys Leu Leu Gly Leu Gly  
 325 330 335  
 Ile Asp Leu Thr Gln Glu Pro Val Pro Ile Val Pro Ala Ala His Tyr  
 340 345 350  
 Thr Cys Gly Gly Val Met Val Asp Asp His Gly Arg Thr Asp Val Glu  
 355 360 365  
 Gly Leu Tyr Ala Ile Gly Glu Val Ser Tyr Thr Gly Leu His Gly Ala  
 370 375 380  
 Asn Arg Met Ala Ser Asn Ser Leu Leu Glu Cys Leu Val Tyr Gly Trp  
 385 390 395 400  
 Ser Ala Ala Glu Asp Ile Thr Arg Arg Met Pro Tyr Ala His Asp Ile  
 405 410 415

32491wo\_ST25

Ser Thr Leu Pro Pro Trp Asp Glu Ser Arg Val Glu Asn Pro Asp Glu  
420 425 430

Arg Val Val Ile Gln His Asn Trp His Glu Leu Arg Leu Phe Met Trp  
435 440 445

Asp Tyr Val Gly Ile Val Arg Thr Thr Lys Arg Leu Glu Arg Ala Leu  
450 455 460

Arg Arg Ile Thr Met Leu Gln Gln Glu Ile Asp Glu Tyr Tyr Ala His  
465 470 475 480

Phe Arg Val Ser Asn Asn Leu Leu Glu Leu Arg Asn Leu Val Gln Val  
485 490 495

Ala Glu Leu Ile Val Arg Cys Ala Met Met Arg Lys Glu Ser Arg Gly  
500 505 510

Leu His Phe Thr Leu Asp Tyr Pro Glu Leu Leu Thr His Ser Gly Pro  
515 520 525

Ser Ile Leu Ser Pro Gly Asn His Tyr Ile Asn Arg  
530 535 540

<210> 42  
<211> 531  
<212> PRT  
<213> Bacillus subtilis

<220>  
<221> misc\_feature  
<222> (1)..(531)  
<223> Bacillus subtilis NadB >gi|16079839|ref|NP\_390665.1| L-aspartate  
oxidase [Bacillus subtilis subsp. subtilis str. 168]

<400> 42

Met Ser Lys Lys Thr Ile Ala Val Ile Gly Ser Gly Ala Ala Ala Leu  
1 5 10 15

Ser Leu Ala Ala Ala Phe Pro Pro Ser Tyr Glu Val Thr Val Ile Thr  
20 25 30

Lys Lys Ser Val Lys Asn Ser Asn Ser Val Tyr Ala Gln Gly Gly Ile  
35 40 45

Ala Ala Ala Tyr Ala Lys Asp Asp Ser Ile Glu Ala His Leu Glu Asp  
50 55 60

Thr Leu Tyr Ala Gly Cys Gly His Asn Asn Leu Ala Ile Val Ala Asp  
65 70 75 80

Val Leu His Asp Gly Lys Met Met Val Gln Ser Leu Leu Glu Arg Gly  
85 90 95

32491wo\_ST25

Phe Pro Phe Asp Arg Asn Glu Arg Gly Gly Val Cys Leu Gly Arg Glu  
 100 105 110  
 Gly Ala His Ser Tyr Asn Arg Ile Phe His Ala Gly Gly Asp Ala Thr  
 115 120 125  
 Gly Arg Leu Leu Ile Asp Tyr Leu Leu Lys Arg Ile Asn Ser Lys Ile  
 130 135 140  
 Lys Leu Ile Glu Asn Glu Thr Ala Ala Asp Leu Leu Ile Glu Asp Gly  
 145 150 155 160  
 Arg Cys Ile Gly Val Met Thr Lys Asp Ser Lys Gly Arg Leu Lys Val  
 165 170 175  
 Arg His Ala Asp Glu Val Val Leu Ala Ala Gly Gly Cys Gly Asn Leu  
 180 185 190  
 Phe Leu His His Thr Asn Asp Leu Thr Val Thr Gly Asp Gly Leu Ser  
 195 200 205  
 Leu Ala Tyr Arg Ala Gly Ala Glu Leu Thr Asp Leu Glu Phe Thr Gln  
 210 215 220  
 Phe His Pro Thr Leu Leu Val Lys Asn Gly Val Ser Tyr Gly Leu Val  
 225 230 235 240  
 Ser Glu Ala Val Arg Gly Glu Gly Gly Cys Leu Val Asp Glu Asn Gly  
 245 250 255  
 Arg Arg Ile Met Ala Glu Arg His Pro Leu Gly Asp Leu Ala Pro Arg  
 260 265 270  
 Asp Ile Val Ser Arg Val Ile His Glu Glu Met Ala Lys Gly Asn Arg  
 275 280 285  
 Val Tyr Ile Asp Phe Ser Ala Ile Ser Asp Phe Glu Thr Arg Phe Pro  
 290 295 300  
 Thr Ile Thr Ala Ile Cys Glu Lys Ala Gly Ile Asp Ile His Ser Gly  
 305 310 315 320  
 Lys Ile Pro Val Ala Pro Gly Met His Phe Leu Met Gly Gly Val Ser  
 325 330 335  
 Val Asn Arg Trp Gly Glu Thr Thr Val Pro Gly Leu Tyr Ala Ile Gly  
 340 345 350  
 Glu Thr Ala Cys Ser Gly Leu His Gly Ala Asn Arg Leu Ala Ser Asn  
 355 360 365

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Ser Leu Leu Glu Ala Leu Val Phe Gly Lys Arg Ala Ala Glu His Ile  
370 375 380

Ile Gln Lys Pro Val Tyr Asn Arg Gln Tyr Gln Ser Gly Leu Glu Thr  
385 390 395 400

Ser Val Phe Tyr Glu Val Pro Asp Ile Glu Gly His Glu Leu Gln Ser  
405 410 415

Lys Met Thr Ser His Met Ser Ile Leu Arg Glu Gln Ser Ser Leu Ile  
420 425 430

Glu Leu Ser Ile Trp Leu His Thr Leu Pro Phe Gln Glu Val Asn Val  
435 440 445

Lys Asp Ile Thr Ile Arg Gln Met Glu Leu Ser His Leu Trp Gln Thr  
450 455 460

Ala Lys Leu Met Thr Phe Ser Ala Leu Leu Arg Glu Glu Ser Arg Gly  
465 470 475 480

Ala His Phe Arg Thr Asp Phe Pro His Ala Glu Val Ser Trp Gln Gly  
485 490 495

Arg Gln Ile Val His Thr Lys Lys Gly Thr Lys Ile Arg Lys Asn Glu  
500 505 510

Gly Ile Trp Asn Asn Glu Ser Phe Thr Ala Glu Lys Ile Thr Glu Ser  
515 520 525

Leu Phe Ser  
530

<210> 43  
<211> 280  
<212> PRT  
<213> Unknown

<220>  
<223> NMN nucleotidase

<220>  
<221> misc\_feature  
<222> (1)..(280)  
<223> SC SDT1 - NMN nucleotidase

<400> 43

Met Thr Val Glu Tyr Thr Ala Ser Asp Leu Ala Thr Tyr Gln Asn Glu  
1 5 10 15

Val Asn Glu Gln Ile Ala Lys Asn Lys Ala His Leu Glu Ser Leu Thr  
20 25 30

His Pro Gly Ser Lys Val Thr Phe Pro Ile Asp Gln Asp Ile Ser Ala  
 35 40 45  
 Thr Pro Gln Asn Pro Asn Leu Lys Val Phe Phe Phe Asp Ile Asp Asn  
 50 55 60  
 Cys Leu Tyr Lys Ser Ser Thr Arg Ile His Asp Leu Met Gln Gln Ser  
 65 70 75 80  
 Ile Leu Arg Phe Phe Gln Thr His Leu Lys Leu Ser Pro Glu Asp Ala  
 85 90 95  
 His Val Leu Asn Asn Ser Tyr Tyr Lys Glu Tyr Gly Leu Ala Ile Arg  
 100 105 110  
 Gly Leu Val Met Phe His Lys Val Asn Ala Leu Glu Tyr Asn Arg Leu  
 115 120 125  
 Val Asp Asp Ser Leu Pro Leu Gln Asp Ile Leu Lys Pro Asp Ile Pro  
 130 135 140  
 Leu Arg Asn Met Leu Leu Arg Leu Arg Gln Ser Gly Lys Ile Asp Lys  
 145 150 155 160  
 Leu Trp Leu Phe Thr Asn Ala Tyr Lys Asn His Ala Ile Arg Cys Leu  
 165 170 175  
 Arg Leu Leu Gly Ile Ala Asp Leu Phe Asp Gly Leu Thr Tyr Cys Asp  
 180 185 190  
 Tyr Ser Arg Thr Asp Thr Leu Val Cys Lys Pro His Val Lys Ala Phe  
 195 200 205  
 Glu Lys Ala Met Lys Glu Ser Gly Leu Ala Arg Tyr Glu Asn Ala Tyr  
 210 215 220  
 Phe Ile Asp Asp Ser Gly Lys Asn Ile Glu Thr Gly Ile Lys Leu Gly  
 225 230 235 240  
 Met Lys Thr Cys Ile His Leu Val Glu Asn Glu Val Asn Glu Ile Leu  
 245 250 255  
 Gly Gln Thr Pro Glu Gly Ala Ile Val Ile Ser Asp Ile Leu Glu Leu  
 260 265 270  
 Pro His Val Val Ser Asp Leu Phe  
 275 280

<210> 44  
 <211> 450  
 <212> PRT  
 <213> Unknown

&lt;220&gt;

&lt;223&gt; NMN nucleotidase

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(450)

&lt;223&gt; Sc ISN1 - NMN nucleotidase

&lt;400&gt; 44

Met Ser Ser Arg Tyr Arg Val Glu Tyr His Leu Lys Ser His Arg Lys  
1 5 10 15

Asp Glu Phe Ile Asp Trp Val Lys Gly Leu Leu Ala Ser Pro Phe Val  
20 25 30

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

Thr Gln Arg Val Arg Ser Gln Tyr Ala Asp Ile Phe Lys Asp Ile Glu  
50 55 60

Gly Leu Ile Lys Asp Lys Ile Glu Phe Asp Ser Arg Asn Met Ser Gln  
65 70 75 80

Asp Glu Ile Glu Asp Gly Ala Ser Ser Gln Ser Leu Asn Ile Leu Gly  
85 90 95

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

Glu Leu Pro Leu Glu Gln Ala Phe Leu Trp Glu Asp Ser Gln Arg Ala  
115 120 125

Ile Ser Ala Arg Arg Met Val Ala Pro Ser Phe Asn Asp Ile Arg His  
130 135 140

Ile Leu Asn Thr Ala Gln Ile Phe His Phe Lys Lys Gln Glu Asn Leu  
145 150 155 160

His Asn Gly Lys Val Leu Arg Leu Val Thr Phe Asp Gly Asp Val Thr  
165 170 175

Leu Tyr Glu Asp Gly Gly Ser Leu Val Tyr Thr Asn Pro Val Ile Pro  
180 185 190

Tyr Ile Leu Lys Leu Leu Arg Cys Gly Ile Asn Val Gly Ile Val Thr  
195 200 205

Ala Ala Gly Tyr Asp Glu Ala Gly Thr Tyr Glu Asn Arg Leu Lys Gly  
210 215 220

Leu Ile Val Ala Leu His Asp Ser Thr Asp Ile Pro Val Ser Gln Lys  
225 230 235 240

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Gln Asn Leu Thr Ile Met Gly Gly Glu Ser Ser Tyr Leu Phe Arg Tyr  
245 250 255

Tyr Glu Asp Pro Glu Glu Asp Asn Phe Gly Phe Arg Gln Ile Asp Lys  
260 265 270

Glu Glu Trp Leu Leu Pro Arg Met Lys Ala Trp Ser Leu Glu Asp Val  
275 280 285

Glu Lys Thr Leu Asp Phe Ala Glu Arg Thr Leu Asn Arg Leu Arg Lys  
290 295 300

Arg Leu Asn Leu Pro Ser Glu Ile Ser Ile Ile Arg Lys Val Arg Ala  
305 310 315 320

Val Gly Ile Val Pro Gly Glu Arg Tyr Asp Glu Ala Ser Lys Arg Gln  
325 330 335

Val Pro Val Lys Leu Asp Arg Glu Gln Leu Glu Glu Ile Val Leu Thr  
340 345 350

Leu Gln Asn Thr Leu Glu Ser Phe Ala Pro Ser Arg Arg Ile Gln Phe  
355 360 365

Ser Cys Phe Asp Gly Gly Ser Asp Val Trp Cys Asp Ile Gly Gly Lys  
370 375 380

Asp Leu Gly Val Arg Ser Leu Gln Gln Phe Tyr Asn Pro Glu Ser Pro  
385 390 395 400

Ile Gln Pro Ser Glu Thr Leu His Val Gly Asp Gln Phe Ala Pro Val  
405 410 415

Gly Ser Ala Asn Asp Phe Lys Ala Arg Leu Ala Gly Cys Thr Leu Trp  
420 425 430

Ile Ala Ser Pro Gln Glu Thr Val Asn Tyr Leu His Arg Leu Leu Glu  
435 440 445

Thr Asp  
450

<210> 45  
<211> 283  
<212> PRT  
<213> Unknown

<220>  
<223> NMN nucleotidase

<220>  
<221> misc\_feature



&lt;222&gt; (1)..(283)

&lt;223&gt; CAG78734 - NMN nucleotidase

&lt;400&gt; 45

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Met Thr Gln Asp Thr Pro Lys Ala Glu Gly Ile Val Leu Phe Val Asp
 1      5      10      15

Ile Asp Asn Thr Leu Tyr Ser Lys Asp Lys Gly Val Asp Ala Leu Met
      20      25      30

Gly Glu Arg Ile Asn Asn Tyr Phe Gln Thr Lys Leu Gly Leu Asp Lys
      35      40      45

Glu His Ala Thr Glu Leu His His Arg Tyr Tyr Lys Glu Tyr Gly Ile
 50      55      60

Ala Leu Asp Gly Leu Leu Arg His His Asn Ile Asp Ile Asp Glu Tyr
65      70      75      80

Asn Arg Leu Val Asp Asp Ser Leu Pro Leu Asp Lys Ile Leu Lys Arg
      85      90      95

Asp Glu Pro Leu Arg Gln Met Phe Gln Arg Leu Asp Arg Thr Lys Val
      100      105      110

Ser Lys Leu Trp Leu Phe Thr Asn Ala Tyr Lys Thr His Gly Glu Arg
      115      120      125

Val Ala Lys Leu Val Gly Val Asp Asp Leu Ile Asp Gly Leu Thr Tyr
      130      135      140

Cys Asp Tyr Tyr His Thr Pro Leu His Cys Lys Pro Lys Pro Glu Ala
145      150      155      160

Phe Glu Lys Ala Met Lys Gln Ala Gly Val Thr Asp Lys Ser Lys Cys
      165      170      175

Trp Phe Val Asp Asp Ser Ala Leu Asn Ile Lys Ala Ser Lys Lys Phe
      180      185      190

Gly Trp Ala Glu Asn Ala Tyr Leu His Tyr Pro Gly Ala Pro Glu Ile
      195      200      205

Pro Ala Gly Thr Pro Gly Val Val Glu Ile Ser His Ile Glu Asp Leu
      210      215      220

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

Asn Gly Thr Ile Asn Gly Thr Thr Asn Gly Thr Thr Asn Gly Thr Thr
      245      250      255

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Asn Gly Ile Ile Asn Gly Thr Asn Gly Gly Ile Asn Gly Asp Gly Thr  
260 265 270

Asn Gly Ser Thr Asn Gly Gly Asn Pro Pro Ser  
275 280

<210> 46  
<211> 420  
<212> PRT  
<213> Unknown

<220>  
<223> NMN nucleotidase

<220>  
<221> misc\_feature  
<222> (1)..(420)  
<223> CAG79432 - NMN nucleotidase

<400> 46

Met Thr Ser Arg Tyr Arg Val Glu Tyr Ser Leu Lys Gln His Arg Arg  
1 5 10 15

Asp Glu Phe Ile Glu Trp Val Lys Thr Leu Leu Ala Thr Pro Phe Val  
20 25 30

Leu His Ala Gly Ser Thr Gly Asp Gly Arg Pro Gly Asp Glu Asn Arg  
35 40 45

Ser Val Val Glu Thr Arg Arg Arg Tyr Ala Glu Ile Phe Tyr Asp Val  
50 55 60

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

Glu Arg Ala Arg Leu Arg Gln Leu Val Pro Thr Ile Gly Gln Phe Phe  
85 90 95

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

Ser Ile Ser His Arg Arg Phe Val Ser Pro Ser Phe Asn Asp Val Arg  
115 120 125

Met Ile Leu Asn Thr Ala Gln Val Met Ala Leu Ala Thr Gly Arg Gln  
130 135 140

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

Gly Gly Asn Ile Asp Pro Asp Ser Pro Ile Ile Pro Val Leu Leu Gly  
165 170 175

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

180

185

190

Ser Glu Lys Asp Gly Ser Lys Tyr Gly Val Arg Leu Tyr Gly Leu Leu  
 195 200 205

Glu Ala Ile Val Lys Thr Asp Thr Leu Thr Glu Gln Gln Lys Asn His  
 210 215 220

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

Ala Glu Asn Arg Phe Glu Trp Ile Asp Pro Glu Glu Trp Thr Leu Pro  
 245 250 255

Glu Val Arg Thr Trp Ser Gln Glu Asp Ile Thr Ser Val Leu Asn Ile  
 260 265 270

Gly Glu Arg Val Phe Thr Asn Ala Leu Thr Lys Cys Ser Leu Pro Ala  
 275 280 285

Thr Ile Ile Arg Lys Val Arg Gly Val Gly Ile Val Pro Leu Pro Gly  
 290 295 300

Lys Lys Ile Met Arg Glu Gln Leu Glu Glu Met Val Leu Ala Ala Gln  
 305 310 315 320

Lys Thr Leu Glu Thr Ser Lys Ala Thr Gly Asn Val Gln Phe Cys Ala  
 325 330 335

Phe Asn Gly Gly Ser Asp Val Trp Val Asp Ile Gly Asp Lys Asp Leu  
 340 345 350

Gly Val Arg Ser Leu Gln Ala Tyr Leu Gly Asn Ile Thr Gly Thr Gln  
 355 360 365

Thr Leu His Val Gly Asp Gln Phe Ala Ala Leu Gly Ala Asn Asp Phe  
 370 375 380

Lys Ala Arg Leu Ala Ala Thr Thr Val Trp Ile Ala Asn Pro Ser Glu  
 385 390 395 400

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

Gln Cys Ser Ala  
 420

<210> 47  
 <211> 353  
 <212> PRT  
 <213> Unknown

<220>

&lt;223&gt; NMN nucleotidase

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(353)

&lt;223&gt; CAG82350 - NMN nucleotidase

&lt;400&gt; 47

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Met Lys Leu Ser Ser Leu Ile Val Pro Cys Leu Ala Ser Leu Ala Leu
1      5      10     15

Ala Gln Thr Asn Ala Thr Ala His Asn Ser Thr Val Pro His Glu Asn
      20     25     30

Ser Lys Thr Thr Ile Val Val Thr Asn Asp Asp Ser Trp Ala Ser Ala
      35     40     45

Asn Ile Arg Ala Phe Tyr Asp Ala Leu Lys Lys Glu Gly Tyr Asn Val
      50     55     60

Phe Met Phe Ala Pro Ala Val Gln Gln Ser Gly Thr Gly Gly Thr Phe
65      70     75     80

Asn Leu Pro Thr Asn Ala Thr Leu Ala Lys Gly Ala Glu Trp Gln Thr
      85     90     95

Ala Pro Ala Gly Ala Pro Ser Trp Ala His Asp Glu Lys Asp Asp His
      100    105    110

Ile Trp Tyr Phe Asp Gly Thr Pro Gly Ala Ala Val Ser Phe Gly Phe
      115    120    125

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

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

Leu Ser Gly Thr Glu Gly Ala Met Tyr Thr Ser Ile Leu Arg Gly Val
      165    170    175

Pro Ala Val Ala Phe Ser Gly Asn Asn Asp His Thr Tyr Tyr Ala Asn
      180    185    190

Ala Ser Asn Ser Glu Thr Ser Ala His Lys Ile Tyr Ala Lys Ala Ser
      195    200    205

Thr Ala Ile Val Lys Asn Leu Leu Glu Asn Ala Lys Gly Arg Pro Ser
      210    215    220

Val Leu Pro Ile Gly Val Gly Ile Ser Val Asn Leu Pro Asn Val Gly
225    230    235    240

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Asp Ile Asp Pro Thr Gly Lys Cys Val Asp Pro Lys Pro Ile Phe Thr  
245 250 255

Arg Gln Thr Gly Arg Gly Ala Ala Thr Tyr Lys Leu Ile Phe Asn Glu  
260 265 270

Thr Ser Gly Val Phe Asp Glu Asp Glu Asn Leu Lys Thr Asp Ala Leu  
275 280 285

Arg Ala Cys Phe Asn Gly Asp Cys Phe Leu Pro Asp Glu Thr Asp Val  
290 295 300

Val Thr Lys Trp Gly Cys Tyr Ser Ser Ile Ser Val Ile Thr Ala Asp  
305 310 315 320

Tyr Asp Ala Pro Gly Gly Val Ala Ala Glu Val Gln Tyr Leu Asn Arg  
325 330 335

Asn Leu Val Thr Phe Ala Pro Thr Gly Tyr Gly Ser Phe Pro Gly Arg  
340 345 350

Lys

<210> 48  
<211> 349  
<212> PRT  
<213> Unknown

<220>  
<223> NMN nucleotidase

<220>  
<221> misc\_feature  
<222> (1)..(349)  
<223> CAG83794 - NMN nucleotidase

<400> 48

Met Lys Phe Ser Asn Leu Ala Leu Pro Leu Leu Ala Ser Cys Ala Val  
1 5 10 15

Ala Gln Asn Ser Thr Asn Pro Asn Ser Asn Thr Thr Ile Ile Val Thr  
20 25 30

Asn Asp Asp Ser Trp Ala Ser Ala Asn Ile Arg Ser Leu Tyr Ser Glu  
35 40 45

Leu Lys Lys Glu Gly Tyr Asn Val Phe Met Phe Ala Pro Ala Val Gln  
50 55 60

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

Thr Lys Gly Gly Glu Phe Gly Ser Ile Pro Val Gly Ala Pro Asn Trp  
 85 90 95  
 Gly Gln Asp Asp Asn Asp Asp His Ile Trp Tyr Phe Asp Gly Thr Pro  
 100 105 110  
 Ala Ala Ala Met Ser Phe Gly Leu Asp Tyr Ala Ile Pro Arg Leu Phe  
 115 120 125  
 Asn Asn Ala Thr Val Asp Leu Val Val Ser Gly Pro Asn Glu Gly Trp  
 130 135 140  
 Asn Ile Gly Pro Asn Ile Tyr Thr Met Ser Gly Thr Asn Gly Ala Met  
 145 150 155 160  
 Tyr Met Ala Val Leu Arg Gly Ile Pro Ala Ile Ala Tyr Ser Gly Met  
 165 170 175  
 Asn Ser His Gln Tyr Tyr Ala Asn Ala Ser Thr Ser Asp Asn Ala Ala  
 180 185 190  
 His Asn Ile Tyr Ala Lys Ala Ala Thr Gly Ile Val Asn Asn Leu Val  
 195 200 205  
 Lys Asn Ala Lys Asp Arg Ala Thr Leu Leu Pro Tyr Gly Val Gly Leu  
 210 215 220  
 Ser Val Asn Leu Pro Arg Ala Gly Asp Val Asp Pro Thr Gly Gln Cys  
 225 230 235 240  
 Lys Glu Ile Lys Pro Ile Phe Thr Arg Gln Thr Gly Pro Ala Ala Ile  
 245 250 255  
 Val Leu Lys Leu Ser Tyr Asn Glu Thr Thr Asn Arg Phe Ser Pro Gly  
 260 265 270  
 Ile Thr Asn Ser Glu Ala Ser Lys Ala Cys Leu Asn Gly Asp Cys Ile  
 275 280 285  
 Leu Pro Asp Glu Ser Asp Val Val Ala Asn Trp Gly Cys Tyr Ala Ser  
 290 295 300  
 Val Ser Val Ile Thr Thr Asp Tyr Asp Ala Pro Arg Asp Val Ala Gly  
 305 310 315 320  
 Glu Val Gln Phe Leu Asn Arg Gly Glu Val Lys Phe Ala Pro Arg Val  
 325 330 335  
 Tyr Gly Ser Phe Ala Pro Val Glu Ala Ser Pro Tyr Phe  
 340 345

<211> 271  
 <212> PRT  
 <213> Unknown

<220>  
 <223> NMN nucleotidase

<220>  
 <221> misc\_feature  
 <222> (1)..(271)  
 <223> An02g02380 - NMN nucleotidase (SDT1 homolog)

<400> 49

Met Thr Thr Thr Ser Ser Pro Ala Ser Ala Pro Leu Asp Pro Arg Pro  
 1 5 10 15

Val Phe Phe Phe Asp Ile Asp Asn Cys Leu Tyr Ser Lys Gly Cys Asn  
 20 25 30

Ile His Asp Glu Met Gln Lys Leu Ile Asn Gln Phe Phe Ile Lys His  
 35 40 45

Leu Ser Leu Asn Ala Asp Asp Ala His Met Leu His Met Lys Tyr Tyr  
 50 55 60

Lys Glu Tyr Gly Leu Ala Ile Glu Gly Leu Thr Arg His His Lys Ile  
 65 70 75 80

Asp Pro Leu Glu Phe Asn Arg Glu Val Asp Asp Ala Leu Pro Leu Asp  
 85 90 95

Asp Ile Leu Lys Pro Asp Pro Lys Leu Arg Arg Leu Leu Glu Asp Ile  
 100 105 110

Asp Arg Ser Lys Val Arg Met Trp Leu Leu Thr Asn Ala Tyr Val Thr  
 115 120 125

His Ala Lys Arg Val Val Lys Leu Leu Gln Val Asp Asp Leu Phe Glu  
 130 135 140

Gly Ile Thr Tyr Cys Asp Tyr Gly Asn Ser Pro Leu Val Cys Lys Pro  
 145 150 155 160

Ser Gln Ala Met Tyr Glu Arg Ala Glu Lys Glu Ala Gly Ala Ser Ser  
 165 170 175

Thr Ser Glu Cys Tyr Phe Val Gly Lys Ser Pro Ser Gln Phe Leu Ser  
 180 185 190

His Ser Thr Tyr Pro Asp Gln Val Leu Thr Asp Arg Ser Arg Arg Leu  
 195 200 205

Arg Pro Glu Leu Tyr Ser Cys Cys Arg Pro Gly Leu Gly Cys Gly Ser  
 210 215 220

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Ser Cys Arg Ala Trp Asn Thr Pro Pro Pro Arg Ala Gly Leu Ala Ile  
225 230 235 240

Tyr Asp Thr Lys Pro Gly Gly Thr Gln Asp Leu Phe Pro His Leu Ile  
245 250 255

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

<210> 50  
<211> 411  
<212> PRT  
<213> Unknown

<220>  
<223> NMN nucleotidase

<220>  
<221> misc\_feature  
<222> (1)..(411)  
<223> An18g01690 - NMN nucleotidase (ISN1 homolog)

<400> 50

Met Thr Thr Arg Tyr Arg Val Glu Tyr Ala Leu Lys Ser His Arg Arg  
1 5 10 15

Asp Gln Leu Ile Glu Trp Ile Lys Gly Leu Leu Ala Val Pro Phe Val  
20 25 30

Leu His Ser Gln Pro Thr Ala Val Tyr Gln Glu His Ser Glu Asn Leu  
35 40 45

Ile Ala Val Ala Ala Asp Thr His Gln Arg Tyr Ala Glu Ile Phe Arg  
50 55 60

Asp Val Glu Met Leu Ile Arg Asp His Ile Thr His Gln Gln Asp Asp  
65 70 75 80

Ala Pro Gly Lys Ser Lys Leu Lys Leu Leu Val Pro Thr Val Gly Thr  
85 90 95

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

Gln Arg Phe Ile Ser Arg Arg Arg Phe Val Ala Pro Ser Phe Asn Asp  
115 120 125

Ile Arg Leu Ile Leu Asn Ser Ala Gln Leu Ile Gly Leu Ala Arg Thr  
130 135 140

Thr Gly Val Asp Leu Val Thr Phe Asp Gly Asp Val Thr Leu Tyr Asp  
145 150 155 160



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Asp Gly Ala Cys Leu Thr Asp Asp Asn Pro Val Ile Leu Arg Ile Met  
165 170 175

Arg Leu Leu Leu Gln Gly Arg Lys Val Gly Ile Val Thr Ala Ala Gly  
180 185 190

Tyr Thr Asp Ala Ala Lys Tyr Tyr Glu Arg Leu Lys Gly Leu Leu Asp  
195 200 205

Ala Met Tyr Glu Ser Ala Glu Met Thr Asp Ala Gln Arg Ala Gly Leu  
210 215 220

Val Val Met Gly Gly Glu Ser Asn Phe Leu Phe Arg Tyr Asp His Ala  
225 230 235 240

Ser Pro Ser Arg Leu Ser Tyr Val Pro Arg Glu Glu Trp Leu Leu Glu  
245 250 255

Glu Met Lys Thr Trp Gln Glu Gly Asp Ile Thr Arg Leu Leu Asp Ile  
260 265 270

Ala Glu Ser Ser Leu Arg Ala Cys Ala Ser Asn Leu Asn Leu Pro Val  
275 280 285

Ala Val Leu Arg Lys Asp Arg Ala Val Gly Val Tyr Pro Thr Glu Arg  
290 295 300

Gly Arg Ile Ser Arg Glu Gln Leu Glu Glu Thr Val Leu Val Val Gln  
305 310 315 320

Asn Thr Val Glu Arg Ser Glu Val Gly Ala Arg Leu Pro Phe Cys Ala  
325 330 335

Phe Asn Gly Gly Asn Asp Val Phe Val Asp Ile Gly Asp Lys Ser Trp  
340 345 350

Gly Val Arg Ala Cys Gln Arg Tyr Phe Gly Gly Ile Glu Pro Ala Arg  
355 360 365

Thr Leu His Val Gly Asp Gln Phe Leu Ser Ala Gly Ala Asn Asp Phe  
370 375 380

Lys Ala Arg Leu Ala Ser Thr Thr Ala Trp Ile Ala Ser Pro Ala Glu  
385 390 395 400

Thr Val Gln Leu Leu Asp Glu Leu Gln Gly Ile  
405 410

<210> 51  
<211> 401  
<212> PRT  
<213> Unknown

&lt;220&gt;

&lt;223&gt; NAMN adenytransferase

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(401)

&lt;223&gt; SC NMA1 - NAMN adenytransferase

&lt;400&gt; 51

Met Asp Pro Thr Arg Ala Pro Asp Phe Lys Pro Pro Ser Ala Asp Glu  
1 5 10 15

Glu Leu Ile Pro Pro Pro Asp Pro Glu Ser Lys Ile Pro Lys Ser Ile  
20 25 30

Pro Ile Ile Pro Tyr Val Leu Ala Asp Ala Asn Ser Ser Ile Asp Ala  
35 40 45

Pro Phe Asn Ile Lys Arg Lys Lys Lys His Pro Lys His His His His  
50 55 60

His His His Ser Arg Lys Glu Gly Asn Asp Lys Lys His Gln His Ile  
65 70 75 80

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

Glu Asp Asp Asp Ala Asp Phe Arg Ser Lys Glu Arg Tyr Gly Ser Asp  
100 105 110

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

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

Glu Asp Tyr Glu Phe Pro Ser His Arg Leu Ser Lys Lys Leu Leu Asp  
145 150 155 160

Pro Asn Lys Leu Pro Leu Val Ile Val Ala Cys Gly Ser Phe Ser Pro  
165 170 175

Ile Thr Tyr Leu His Leu Arg Met Phe Glu Met Ala Leu Asp Ala Ile  
180 185 190

Ser Glu Gln Thr Arg Phe Glu Val Ile Gly Gly Tyr Tyr Ser Pro Val  
195 200 205

Ser Asp Asn Tyr Gln Lys Gln Gly Leu Ala Pro Ser Tyr His Arg Val  
210 215 220

Arg Met Cys Glu Leu Ala Cys Glu Arg Thr Ser Ser Trp Leu Met Val  
Page 50

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

Glu

<210>	52
<211>	395
<212>	PRT
<213>	Unknown

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<220>
<221> misc_feature
<222> (1)..(395)
<223> Sc NMA2 - NAMN adenylyltransferase
```

Met Asp Pro Thr Lys Ala Pro Asp Phe Lys Pro Pro Gln Pro Asn Glu  
1 5 10 15

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Pro Ile Val<sub>35</sub> Pro Tyr Val Leu Ala<sub>40</sub> Asp Tyr Asn Ser Ser<sub>45</sub> Ile Asp Ala  
Pro Phe<sub>50</sub> Asn Leu Asp Ile Tyr<sub>55</sub> Lys Thr Leu Ser Ser<sub>60</sub> Arg Lys Lys Asn  
Ala<sub>65</sub> Asn Ser Ser Asn Arg<sub>70</sub> Met Asp His Ile Pro<sub>75</sub> Leu Asn Thr Ser Asp<sub>80</sub>  
Phe Gln Pro Leu Ser<sub>85</sub> Arg Asp Val Ser Ser<sub>90</sub> Glu Glu Glu Ser Glu<sub>95</sub> Gly  
Gln Ser Asn Gly<sub>100</sub> Ile Asp Ala Thr Leu<sub>105</sub> Gln Asp Val Thr Met<sub>110</sub> Thr Gly  
Asn Leu Gly<sub>115</sub> Val Leu Lys Ser Gln<sub>120</sub> Ile Ala Asp Leu Glu<sub>125</sub> Glu Val Pro  
His Thr<sub>130</sub> Ile Val Arg Gln Ala<sub>135</sub> Arg Thr Ile Glu Asp<sub>140</sub> Tyr Glu Phe Pro  
Val<sub>145</sub> His Arg Leu Thr Lys<sub>150</sub> Lys Leu Gln Asp Pro<sub>155</sub> Glu Lys Leu Pro Leu<sub>160</sub>  
Ile Ile Val Ala Cys<sub>165</sub> Gly Ser Phe Ser Pro<sub>170</sub> Ile Thr Tyr Leu His<sub>175</sub> Leu  
Arg Met Phe Glu<sub>180</sub> Met Ala Leu Asp Asp<sub>185</sub> Ile Asn Glu Gln Thr<sub>190</sub> Arg Phe  
Glu Val Val<sub>195</sub> Gly Gly Tyr Phe Ser<sub>200</sub> Pro Val Ser Asp Asn<sub>205</sub> Tyr Gln Lys  
Arg Gly<sub>210</sub> Leu Ala Pro Ala Tyr<sub>215</sub> His Arg Val Arg Met<sub>220</sub> Cys Glu Leu Ala  
Cys<sub>225</sub> Glu Arg Thr Ser Ser<sub>230</sub> Trp Leu Met Val Asp<sub>235</sub> Ala Trp Glu Ser Leu<sub>240</sub>  
Gln Ser Ser Tyr Thr<sub>245</sub> Arg Thr Ala Lys Val<sub>250</sub> Leu Asp His Phe Asn<sub>255</sub> His  
Glu Ile Asn Ile<sub>260</sub> Lys Arg Gly Gly Ile<sub>265</sub> Met Thr Val Asp Gly<sub>270</sub> Glu Lys  
Met Gly Val<sub>275</sub> Lys Ile Met Leu Leu<sub>280</sub> Ala Gly Gly Asp Leu<sub>285</sub> Ile Glu Ser  
Met Gly<sub>290</sub> Glu Pro His Val Trp<sub>295</sub> Ala Asp Ser Asp Leu<sub>300</sub> His His Ile Leu

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Gly Asn Tyr Gly Cys Leu Ile Val Glu Arg Thr Gly Ser Asp Val Arg  
305 310 315 320

Ser Phe Leu Leu Ser His Asp Ile Met Tyr Glu His Arg Arg Asn Ile  
325 330 335

Leu Ile Ile Lys Gln Leu Ile Tyr Asn Asp Ile Ser Ser Thr Lys Val  
340 345 350

Arg Leu Phe Ile Arg Arg Gly Met Ser Val Gln Tyr Leu Leu Pro Asn  
355 360 365

Ser Val Ile Arg Tyr Ile Gln Glu Tyr Asn Leu Tyr Ile Asn Gln Ser  
370 375 380

Glu Pro Val Lys Gln Val Leu Asp Ser Lys Glu  
385 390 395

<210> 53  
<211> 258  
<212> PRT  
<213> Unknown

<220>  
<223> NMN adenytransferase

<220>  
<221> misc\_feature  
<222> (1)..(258)  
<223> SC POF1 - NMN adenytransferase

<400> 53

Met Lys Lys Thr Phe Glu Gln Phe Arg Lys Ser Asn Leu Leu Phe Gln  
1 5 10 15

Val Leu Lys Gly Pro Gln His Leu Glu Cys Gln Lys Leu Phe Val Leu  
20 25 30

Asp Ser Ser Phe Asn Pro Pro His Leu Ala His Phe Gln Leu Leu Ser  
35 40 45

Gln Thr Ile Lys Asn Phe Lys Leu Lys Asp Thr Arg Ser His Val Leu  
50 55 60

Leu Leu Leu Ala Val Asn Asn Ala Asp Lys Leu Pro Lys Pro Ala Ser  
65 70 75 80

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

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

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

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

Ile Phe Asp Glu Lys Tyr Tyr His Pro Leu Lys Ile Ser Asp Val Met  
145 150 155 160

Glu Ser Phe Met Ser Gly Ser Gln Leu Tyr Cys Leu Ala Arg Gly Asp  
165 170 175

Cys His Leu Ser Ala Glu Ser Gln Leu Arg Tyr Ala Ser Asp Ile Leu  
180 185 190

Glu Gly Lys Phe Glu Pro Val Ile Pro Arg Glu Trp Gly Ala Arg Ile  
195 200 205

His Val Met Gln Asn Asp Tyr Pro Ala Leu Arg Asn Val Ser Ser Ser  
210 215 220

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

Glu Leu Pro Leu Cys Ile Tyr Asp Tyr Leu Ile Asn Asn Lys Thr Ile  
245 250 255

Phe Asp

<210> 54  
<211> 252  
<212> PRT  
<213> Unknown

<220>  
<223> NAMN adenylyltransferase

<220>  
<221> misc\_feature  
<222> (1)..(252)  
<223> CAG84188 - NAMN adenylyltransferase

<400> 54

Met Ser Leu Tyr Thr Leu Val Arg Ala Ala Ala Thr His Ser Arg Pro  
1 5 10 15

Pro Ala Gly Thr Asn Phe Lys Ala Glu Ile Asp Asp Phe Met Arg Gly  
20 25 30

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

Val Val Val Leu Asp Ser Ser Phe Asn Pro Pro His Tyr Ala His Leu

50

55

Glu Leu Ala Met Leu Gly Met Thr His Thr Lys Asp Asn Cys Ile Leu  
65 70 75 80

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

Phe Gln Gln Arg Leu Glu Met Met Glu Leu Phe Lys Arg Ser Ile Asp  
100 105 110

Ala Glu Val Val Leu Gly Leu Thr Lys Glu Pro Tyr Phe Val Asp Lys  
115 120 125

Tyr Lys Val Ile Lys Arg Leu Leu Ala Ser His Gly Leu Thr Pro His  
130 135 140

Leu His Phe Pro Met Gly Leu Asp Thr Leu Val Arg Leu Val Asp Gln  
145 150 155 160

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

Asp Cys His Val His Val Leu Thr Arg Asp Asp Ile His Phe Asn Met  
180 185 190

Lys Glu Leu Pro Glu Gln Trp Gln Arg His Ile His Met Ser Lys His  
195 200 205

Ser Ser Lys Thr Asp Gly Val Ser Ser Ser Asn Val Arg Ala Leu Val  
210 215 220

Lys Ser His Lys Arg His His Glu Phe Glu Arg Leu Val Pro Pro Gln  
225 230 235 240

Ile Leu Ala Tyr Ile Val Glu His Gly Leu Tyr Lys  
245 250

<210> 55  
<211> 470  
<212> PRT  
<213> Unknown

<220>  
<223> NMN adenylyltransferase

<220>  
<221> misc\_feature  
<222> (1)..(470)  
<223> CAG79991 - NMN adenylyltransferase

<400> 55

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

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

Asn Ile Ala Pro Ile Gln Pro Tyr Val Leu Glu Asp Ser Gln His Glu  
35 40 45

Ile Asp Leu Pro Gln Asp Ser Pro Arg Leu Leu Pro Ser Arg Thr Asn  
50 55 60

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

His His Ser Lys His Asn Pro Lys Asp Ser Asn Tyr His Pro Ala Pro  
85 90 95

Val Asn Ile Pro Arg Ile His Ser Glu Leu Asn Met Ser Asp Ser Ser  
100 105 110

Pro Asp Arg Cys Glu Lys Ile Asp Glu Val Asp Leu Glu Val Ser Pro  
115 120 125

Asn Glu Ile Gln Thr Asn Phe Ser Lys Phe Ser Leu Gly Asp Gln Ala  
130 135 140

Leu Pro Pro Thr Thr Val Glu Glu Ala Met Ala Pro Thr Ser Pro Lys  
145 150 155 160

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

Ser Ser Arg Thr Pro Pro Tyr Leu Leu Asp Asn Ser Gly Leu Arg Pro  
180 185 190

Ile Ile Gln Ser Ala Asp Leu Glu Glu Val Pro Ile Gly Val Ser Arg  
195 200 205

Gln Ala Arg Asp Leu Asp His Tyr Lys Phe Pro Thr His Arg Leu Ser  
210 215 220

Glu Val Met Ile Glu Glu Thr Lys Ser Pro Leu Val Ile Val Ala Cys  
225 230 235 240

Gly Ser Phe Ser Pro Ile Thr Tyr Leu His Leu Arg Met Phe Glu Met  
245 250 255

Ala Met Asp Ser Ile Arg Glu Gln Thr Arg Phe Glu Val Ile Gly Gly  
260 265 270

Tyr Tyr Ser Pro Val Ser Asp Asn Tyr Asn Lys Pro Gly Leu Ala Pro  
275 280 285



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Ala His His Arg Val Arg Met Cys Glu Leu Ala Cys Glu Arg Thr Ser  
 290 295 300

Ser Trp Leu Met Val Asp Ala Trp Glu Ser Leu Gln Pro Thr Tyr Gln  
 305 310 315 320

Arg Thr Ala Thr Val Leu Asp His Phe Asn Glu Glu Ile Asn Ile Lys  
 325 330 335

Arg Gly Gly Ile Lys Thr Val Ser Gly Lys Arg Lys Gly Val Lys Ile  
 340 345 350

Met Leu Leu Ala Gly Gly Asp Leu Ile Glu Ser Met Gly Glu Pro Asn  
 355 360 365

Val Trp Glu Glu Arg Asp Leu His His Ile Leu Gly Arg Tyr Gly Cys  
 370 375 380

Leu Ile Val Glu Arg Thr Gly Ala Asp Val Arg Ser Phe Leu Leu Ser  
 385 390 395 400

His Asp Ile Met Tyr Glu His Arg Arg Asn Val Leu Val Ile Lys Gln  
 405 410 415

Leu Ile Tyr Asn Asp Ile Ser Ser Thr Lys Val Arg Leu Phe Ile Arg  
 420 425 430

Arg Gly Met Ser Val Gln Tyr Leu Ile Pro Asn Ser Val Ile Arg Tyr  
 435 440 445

Ile Gln Glu His Arg Leu Tyr Val Gly Glu Thr Glu Pro Val Lys Gln  
 450 455 460

Val Leu Tyr Asp Arg Glu  
 465 470

<210> 56  
 <211> 285  
 <212> PRT  
 <213> Unknown

<220>  
 <223> NMN adenytransferase

<220>  
 <221> misc\_feature  
 <222> (1)..(285)  
 <223> An04g01700 - NMN adenytransferase (POF1 homolog)

<400> 56

Met Thr Ser Pro Ala Phe His Ala Leu Arg Glu Lys Tyr Ala Ala Gly  
 1 5 10 15

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Leu Arg Leu Phe Ile Ala Ser Thr Arg Ser Leu Glu Val Leu Ala Ser  
 20 25 30  
 Val Pro Ser Gly Pro Pro Asp Pro Thr Ser Ser Thr Asp Val Leu Tyr  
 35 40 45  
 Val Leu Asp Ser Ser Phe Asn Pro Pro Thr Leu Ala His Ser Arg Ile  
 50 55 60  
 Ala Thr Ser Ala Leu Leu Glu Asn Pro His Lys Pro Ser Arg Leu Leu  
 65 70 75 80  
 Leu Leu Leu Ala Thr Gln Asn Ala Asp Lys Pro Ser Lys Pro Ala Ala  
 85 90 95  
 Phe Glu Thr Arg Leu Ala Met Met Glu Leu Phe Ala Arg Asp Leu Leu  
 100 105 110  
 Ser Ser Leu Gln Thr Asn Gly Thr Ile Pro Lys Ala His Asn Leu Pro  
 115 120 125  
 Val Ile Asp Ile Gly Val Thr Lys Lys Pro Tyr Phe Val Asp Lys Ala  
 130 135 140  
 Ala Glu Ile Glu Arg Ala Gly Ile Tyr Pro Gln Ser Leu Glu Gln Val  
 145 150 155 160  
 His Leu Thr Gly Tyr Asp Thr Leu Ile Arg Ile Phe Asn Pro Lys Tyr  
 165 170 175  
 Tyr Pro Pro Glu His Thr Leu Gln Pro Leu Gly Pro Phe Leu Ser Gln  
 180 185 190  
 His Arg Leu Arg Val Thr Met Arg Pro Asp Ser Asp Trp Gly Ser Arg  
 195 200 205  
 Glu Glu Gln Glu Ala Phe Val Ala Asp Leu Ala Gln Gly Ala Met Glu  
 210 215 220  
 Arg Val Gly Gly Lys Arg Glu Trp Ala Asp Arg Ile Lys Leu Val Glu  
 225 230 235 240  
 Gly Lys Lys Pro Gly Ala Pro Ser Val Ser Ser Thr Arg Ala Arg Glu  
 245 250 255  
 Ser Ala Val Ala Asn Pro Gln Asp Leu Glu Trp Leu Val Pro Pro Ser  
 260 265 270  
 Val Arg Asp Val Ile Leu Ala Glu Lys Pro Tyr Thr Glu  
 275 280 285

&lt;210&gt; 57

<211> 281  
 <212> PRT  
 <213> Unknown

<220>  
 <223> NMN adenytransferase

<220>  
 <221> misc\_feature  
 <222> (1)..(281)  
 <223> An11g06610 - NMN adenytransferase (NMA2 homolog)

<400> 57

Met Thr Asp Thr Ile Ser Asp Asp Val His Arg Arg Ser Ser Pro Leu  
 1 5 10 15

Pro Pro Ala Pro Met Asp Asp Tyr Ala Phe Pro Glu Leu Arg Leu Lys  
 20 25 30

Arg Thr Met Asp Asp Pro Glu Lys Thr Pro Leu Leu Leu Val Ala Cys  
 35 40 45

Gly Ser Phe Ser Pro Ile Thr Tyr Leu His Leu Arg Met Phe Glu Met  
 50 55 60

Ala Ala Asp Tyr Val Lys Phe Ser Thr Asp Phe Glu Leu Val Gly Gly  
 65 70 75 80

Tyr Leu Ser Pro Val Ser Asp Ala Tyr Arg Lys Ala Gly Leu Ala Ser  
 85 90 95

Ala Glu His Arg Val Ala Met Cys Gln Leu Ala Val Asp Gln Thr Ser  
 100 105 110

Asp Trp Leu Met Val Asp Thr Trp Glu Pro Met Gln Lys Glu Tyr Gln  
 115 120 125

Pro Thr Ala Val Val Leu Asp His Phe Asp His Glu Ile Asn Thr Val  
 130 135 140

Arg Gln Gly Ile Glu Ala Gly Asn Gly Thr Arg Lys Pro Ile Gln Ile  
 145 150 155 160

Ala Leu Leu Ala Gly Ala Asp Leu Val His Thr Met Ser Thr Pro Gly  
 165 170 175

Val Trp Ser Glu Lys Asp Leu Asp His Ile Leu Gly Lys Tyr Gly Thr  
 180 185 190

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

Leu Gln Thr Trp Lys Lys Asn Ile His Val Ile Gln Gln Leu Ile Gln  
 210 215 220

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Asn Asp Val Ser Ser Thr Lys Ile Arg Leu Phe Leu Arg Arg Asp Met  
225 230 235 240

Ser Val Arg Tyr Leu Ile Pro Val Pro Val Ile His Tyr Ile Glu Gln  
245 250 255

His Asn Leu Tyr Lys Asp Asp Ser Thr Ala Ser Thr Asp Lys Gly Lys  
260 265 270

Gly Arg Gln Glu Pro Gly Ser Ser Gly  
275 280

<210> 58  
<211> 429  
<212> PRT  
<213> Unknown

<220>  
<223> Nicotinate phosphoribosyltransferase

<220>  
<221> misc\_feature  
<222> (1)..(429)  
<223> SC NPT1 - Nicotinate phosphoribosyltransferase

<400> 58

Met Ser Glu Pro Val Ile Lys Ser Leu Leu Asp Thr Asp Met Tyr Lys  
1 5 10 15

Ile Thr Met His Ala Ala Val Phe Thr Asn Phe Pro Asp Val Thr Val  
20 25 30

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

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

Phe Thr Glu Glu Glu Ile Glu Tyr Leu Lys Gln Glu Ile Pro Tyr Leu  
65 70 75 80

Pro Ser Ala Tyr Ile Lys Tyr Ile Ser Ser Ser Asn Tyr Lys Leu His  
85 90 95

Pro Glu Glu Gln Ile Ser Phe Thr Ser Glu Glu Ile Glu Gly Lys Pro  
100 105 110

Thr His Tyr Lys Leu Lys Ile Leu Val Ser Gly Ser Trp Lys Asp Thr  
115 120 125

Ile Leu Tyr Glu Ile Pro Leu Leu Ser Leu Ile Ser Glu Ala Tyr Phe  
130 135 140

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Lys Phe Val Asp Ile Asp Trp Asp Tyr Glu Asn Gln Leu Glu Gln Ala  
 145 150 155 160  
 Glu Lys Lys Ala Glu Thr Leu Phe Asp Asn Gly Ile Arg Phe Ser Glu  
 165 170 175  
 Phe Gly Thr Arg Arg Arg Arg Ser Leu Lys Ala Gln Asp Leu Ile Met  
 180 185 190  
 Gln Gly Ile Met Lys Ala Val Asn Gly Asn Pro Asp Arg Asn Lys Ser  
 195 200 205  
 Leu Leu Leu Gly Thr Ser Asn Ile Leu Phe Ala Lys Lys Tyr Gly Val  
 210 215 220  
 Lys Pro Ile Gly Thr Val Ala His Glu Trp Val Met Gly Val Ala Ser  
 225 230 235 240  
 Ile Ser Glu Asp Tyr Leu His Ala Asn Lys Asn Ala Met Asp Cys Trp  
 245 250 255  
 Ile Asn Thr Phe Gly Ala Lys Asn Ala Gly Leu Ala Leu Thr Asp Thr  
 260 265 270  
 Phe Gly Thr Asp Asp Phe Leu Lys Ser Phe Arg Pro Pro Tyr Ser Asp  
 275 280 285  
 Ala Tyr Val Gly Val Arg Gln Asp Ser Gly Asp Pro Val Glu Tyr Thr  
 290 295 300  
 Lys Lys Ile Ser His His Tyr His Asp Val Leu Lys Leu Pro Lys Phe  
 305 310 315 320  
 Ser Lys Ile Ile Cys Tyr Ser Asp Ser Leu Asn Val Glu Lys Ala Ile  
 325 330 335  
 Thr Tyr Ser His Ala Ala Lys Glu Asn Gly Met Leu Ala Thr Phe Gly  
 340 345 350  
 Ile Gly Thr Asn Phe Thr Asn Asp Phe Arg Lys Lys Ser Glu Pro Gln  
 355 360 365  
 Val Lys Ser Glu Pro Leu Asn Ile Val Ile Lys Leu Leu Glu Val Asn  
 370 375 380  
 Gly Asn His Ala Ile Lys Ile Ser Asp Asn Leu Gly Lys Asn Met Gly  
 385 390 395 400  
 Asp Pro Ala Thr Val Lys Arg Val Lys Glu Glu Leu Gly Tyr Thr Glu  
 405 410 415

32491wo\_ST25  
 Arg Ser Trp Ser Gly Asp Asn Glu Ala His Arg Trp Thr  
 420 425

<210> 59  
 <211> 298  
 <212> PRT  
 <213> Unknown

<220>  
 <223> CAG78849 - Nicotinate phosphoribosyltransferase

<220>  
 <221> misc\_feature  
 <222> (1)..(298)  
 <223> CAG78849 - Nicotinate phosphoribosyltransferase

<400> 59

Met Thr Asp Thr Phe Asp Leu Ser Leu Lys Ser Ala Asn Lys Ile Ser  
 1 5 10 15

Asp Lys Leu Pro Lys Glu Leu Gln Asn Pro Gln Ile Gly Ile Val Cys  
 20 25 30

Gly Ser Gly Leu Gly Gly Leu Ala Asn Ala Leu Lys Ala Glu Pro Gln  
 35 40 45

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

Ala Gly His Ala Gly Lys Leu Val Val Gly Leu Leu Gly Glu Lys Asn  
 65 70 75 80

Val Pro Val Val Cys Met Val Gly Arg Phe His Phe Tyr Glu Gly Tyr  
 85 90 95

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

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

Phe Lys Val Gly Asp Ile Met Leu Ile Asn Asp His Ile Asn Leu Pro  
 130 135 140

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

Gly Val Arg Phe Leu Pro Leu Ser Asp Ala Tyr Asp His Asp Leu Arg  
 165 170 175

Arg Ala Val Tyr Asp Ile Ala Lys Lys Gln Gly Val Thr Arg Gly Ile  
 180 185 190

His Glu Gly Thr Tyr Ala Phe Val Ser Gly Pro Thr Tyr Glu Ser Arg  
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195

200

205

Ala Glu Ala Arg Met Leu Ser Thr Ile Gly Ala Asp Ala Val Gly Met  
 210 215 220

Ser Thr Val Pro Glu Val Ile Val Ala Arg His Cys Gly Ile Lys Val  
 225 230 235 240

Leu Ala Leu Ser Leu Ile Thr Asn Val Val Val Leu Lys Lys Pro Asp  
 245 250 255

Ser Ala Leu Asn Asp Asn Ala Ala Lys Leu Asp Glu Gly Ile Ala Asp  
 260 265 270

His Ser Glu Val Met Glu Glu Gly Gln Arg Ala Ala Asp Asp Leu Val  
 275 280 285

Gly Ile Val Thr Asp Leu Val Asn Val Val  
 290 295

<210> 60  
 <211> 414  
 <212> PRT  
 <213> Unknown

<220>  
 <223> CAG82552 - Nicotinate phosphoribosyltransferase

<220>  
 <221> misc\_feature  
 <222> (1)..(414)  
 <223> CAG82552 - Nicotinate phosphoribosyltransferase

<400> 60

Met Ser Thr Ile Thr Ser Leu Leu Asp Thr Asp Leu Tyr Lys Leu Thr  
 1 5 10 15

Met Gln Ala Ala Val Leu Gln His Phe Pro Ala Ala Gln Ala Thr Phe  
 20 25 30

Leu Phe Lys Asn Arg Thr Pro Ser Lys Gln Leu Asn Asp Asp Ala Ile  
 35 40 45

Glu Trp Leu Lys Ser Glu Ile Ala Ala Leu Gly Glu Leu Arg Phe Thr  
 50 55 60

Glu Asp Glu Ile Val Phe Leu Gln Lys His Val Gly Phe Leu Pro Ala  
 65 70 75 80

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

Val Lys Val Thr Val Asn Thr Glu Gly His Leu Glu Ile Glu Val Asn  
 100 105 110

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Gly Pro Trp Lys Asp Thr Ile Leu Tyr Glu Ile Pro Leu Leu Ala Leu  
 115 120 125  
 Val Ser Glu Ala Tyr Phe Lys Phe Val Asp Lys Asp Trp Ser Tyr Asp  
 130 135 140  
 Gly Gln Ser Glu Leu Ala Ala Thr Lys Ala Gln Glu Leu Ile Ala Gln  
 145 150 155 160  
 Gly Cys Ala Phe Ser Glu Phe Gly Thr Arg Arg Arg Arg Ser Leu Lys  
 165 170 175  
 Thr His Asp Ile Val Ile Ala Gly Ile Leu Glu Gly Leu Lys Ser Ala  
 180 185 190  
 Gln Gly Asn Gly Ile Phe Thr Gly Thr Ser Asn Val Tyr Leu Ala Lys  
 195 200 205  
 Lys Tyr Asn Leu Lys Pro Ile Gly Thr Val Ala His Glu Trp Met Met  
 210 215 220  
 Gly Val Ala Ala Ala Thr Gly Asp Tyr Ser Thr Ala Asn Leu Arg Ala  
 225 230 235 240  
 Met Glu Leu Trp Ile Gln Thr Val Gly Asp Ala Asn Ala Gly Val Ala  
 245 250 255  
 Leu Thr Asp Thr Phe Gly Thr Glu Ser Phe Leu Leu Asp Phe Asn Lys  
 260 265 270  
 Pro Leu Thr Asp Ile Tyr Asn Gly Val Arg Gln Asp Ser Gly Asp Pro  
 275 280 285  
 Leu Glu Tyr Thr Lys Leu Leu Gly Asp His Tyr Lys Gln Leu Gly Tyr  
 290 295 300  
 Glu Pro Met Ser Lys Val Ile Val Tyr Ser Asp Ser Leu Asp Val Glu  
 305 310 315 320  
 Lys Cys Gly Lys Tyr Lys Ala Ala Ala Ala Glu Asn Gly Leu Lys Ala  
 325 330 335  
 Ala Phe Gly Val Gly Thr Phe Phe Thr Asn Asp Phe Lys Arg Leu Ser  
 340 345 350  
 Asp Gly Gln Lys Ser Thr Pro Leu Asn Ile Val Ile Lys Ile Gln Gln  
 355 360 365  
 Leu Asn Gly Gln Ser Cys Ile Lys Leu Ser Asp Asn Leu Ser Lys Asn  
 370 375 380



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Met Gly Asp Pro Glu Thr Val Glu Arg Val Lys Arg Glu Leu Gly Tyr  
385 390 395 400

Val Glu Lys Gly Asp Val Ile Asp Glu Ser Lys Arg Trp Asn  
405 410

<210> 61  
<211> 541  
<212> PRT  
<213> Unknown

<220>  
<223> An12g00760 - Nicotinate phosphoribosyltransferase (NPT1 homolog)

<220>  
<221> misc\_feature  
<222> (1)..(541)  
<223> An12g00760 - Nicotinate phosphoribosyltransferase (NPT1 homolog)

<400> 61

Met Gly Asp Phe Ser Ser Glu Tyr Phe Pro Pro Asn Ser Ser Thr Cys  
1 5 10 15

Phe Ile Leu Ile Ser His Leu Trp Ser Leu Ser Ser Gly Pro Ser Phe  
20 25 30

Gly Ile Pro Leu Cys Ala Leu Ser Phe Val Leu Arg Cys Gly Pro Asn  
35 40 45

Tyr Leu Val Met Ala Gln Asn Asn Thr Pro Pro Leu Pro Glu Gly Ile  
50 55 60

Phe Ser Leu Leu Asp Thr Asp Leu Tyr Lys Leu Thr Met Gln Cys Ala  
65 70 75 80

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

Arg Thr Pro Asp Met Lys Leu Thr Arg Gly Ala Tyr Lys Trp Leu Leu  
100 105 110

Ala Gln Leu Asp Ala Leu Ala Asn Ile Arg Val Thr Asn Glu Glu Ile  
115 120 125

Glu Phe Leu Lys Lys Trp Cys Pro Tyr Phe Asn His Ala Tyr Leu Asp  
130 135 140

Tyr Leu Thr Asn Leu Lys Leu Lys Pro Ser Glu Gln Ile Glu Val His  
145 150 155 160

Phe Thr Pro Glu Gln Asp Thr Gly Ser Glu Asp Asp Leu Gly Asn Val  
165 170 175

Asn Tyr Val Ile Lys Gly Leu Trp Val Glu Thr Ile Leu Tyr Glu Ile  
 180 185 190  
 Pro Leu Leu Ala Leu Thr Ser Gln Ala Tyr Phe Met Phe Thr Asp Lys  
 195 200 205  
 Asp Trp Asp Tyr Ser Cys Gln Glu Asp Lys Ala Phe Arg Lys Gly Cys  
 210 215 220  
 Ala Leu Leu Glu Asn Gly Cys Ile Phe Ser Glu Phe Gly Ser Arg Arg  
 225 230 235 240  
 Arg Arg Asp Tyr His Thr His Asp Leu Val Met Gln Gly Leu Met Gln  
 245 250 255  
 Ala Ala Glu Glu Gly Lys Lys Gln Gly Trp Lys Gly Val Phe Thr Gly  
 260 265 270  
 Thr Ser Asn Val His Phe Ala Met Lys Tyr Gly Val Ala Pro Val Gly  
 275 280 285  
 Thr Val Ala His Glu Trp Tyr Met Thr Ile Ala Ala Ile Thr Asp Asp  
 290 295 300  
 Tyr Glu Asn Ala Asn Glu Met Ala Leu Arg Tyr Trp Leu Gly Cys Phe  
 305 310 315 320  
 Gly Glu Gly Val Leu Gly Val Ala Leu Thr Asp Thr Phe Gly Thr Pro  
 325 330 335  
 Ala Phe Leu Asp Ala Phe Arg Lys Pro Ile Pro Ala Phe Thr Ser Ala  
 340 345 350  
 Gly Val Gly Ala Val Ser Thr Thr Ala Ser Gly Pro Gly Thr Thr Thr  
 355 360 365  
 Glu Ser Ala Val Gln Ser Glu Ala Thr Thr Lys Pro Pro Ile Ala Ala  
 370 375 380  
 Pro Leu Val Asn Asp Ala Gln Gly Glu His Ala Asn Lys Thr Tyr Ala  
 385 390 395 400  
 Gln Val Tyr Thr Gly Val Arg Gln Asp Ser Gly Asp Pro Thr Tyr Phe  
 405 410 415  
 Val Lys Met Val Arg Asp Phe Tyr Asp Arg Glu Gly Val Lys Asp Pro  
 420 425 430  
 Lys Thr Ile Val Phe Ser Asp Ser Leu Asp Ile Glu His Cys Leu Glu  
 435 440 445  
 Tyr Lys Val Ile Ala Glu Glu Ala Gly Phe Lys Pro Val Phe Gly Val

450

455

Gly Thr Phe Phe Thr Asn Asp Phe Thr Asn Lys Ser Asp Gly Ala Lys  
465 470 475 480

Ser Lys Pro Leu Asn Ile Val Ile Lys Ile Ala Thr Ala Asn Gly Arg  
485 490 495

Pro Ala Val Lys Leu Ser Asp Asn Met Gly Lys Asn Thr Gly Asp Lys  
500 505 510

Glu Thr Val Gln Ser Val Lys Lys Lys Leu Gly Tyr Val Glu His Gln  
515 520 525

Trp Glu Glu Gly Asp Glu Ser Asn Arg Trp Ala Arg Lys  
530 535 540

<210> 62  
<211> 598  
<212> PRT  
<213> Unknown

<220>  
<223> Sc NRT1 - NR transport protein

<220>  
<221> misc\_feature  
<222> (1)..(598)  
<223> Sc NRT1 - NR transport protein

<400> 62

Met Ser Phe Ser Ser Ile Val Ser Lys Phe Leu Arg Tyr Leu Glu Ile  
1 5 10 15

Pro Ala Lys Asn Arg Thr Ala Val Asn Phe Leu Arg Asn Pro Asp Leu  
20 25 30

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

Ala Tyr Trp Gly Ala Val Ser Phe Thr Ala Gly Thr Trp Met Ser Gly  
50 55 60

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

Phe Leu Leu Gly Asn Val Leu Thr Ile Ile Phe Thr Met Ala Asn Ser  
85 90 95

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

Val Phe Gly Ile Tyr Gly Ser Ala Phe Gly Ile Ile Ile Arg Ile Leu  
115 120 125

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Met Ser Ile Val Asn Tyr Gly Ser Asn Ala Trp Leu Gly Gly Leu Ser  
130 135 140

Ile Asn Met Ile Leu Asp Ser Trp Ser His His Tyr Leu His Leu Pro  
145 150 155 160

Asn Thr Leu Ser Pro Ser Val Ala Met Thr Thr Lys Gln Leu Val Gly  
165 170 175

Phe Ile Ile Phe His Val Leu Thr Ala Leu Cys Tyr Phe Met Lys Pro  
180 185 190

Tyr His Met Asn Tyr Leu Leu Ile Trp Ser Cys Val Ala Thr Cys Phe  
195 200 205

Ala Met Leu Gly Ile Val Ile Tyr Leu Thr Lys Asn Ala His Gly Val  
210 215 220

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

Ala Trp Ala Trp Val Tyr Met Ile Ser Tyr Trp Phe Gly Ser Ile Ser  
245 250 255

Pro Gly Ser Thr Asn Gln Ser Asp Tyr Ser Arg Phe Gly Ser Ser Asn  
260 265 270

Leu Ala Ile Trp Thr Gly Ser Val Cys Ala Leu Leu Ile Pro Ala Thr  
275 280 285

Leu Val Pro Ile Phe Gly Val Ile Ser Ala Ser Thr Cys Asp Lys Leu  
290 295 300

Tyr Gly Lys Gln Phe Trp Met Pro Met Asp Ile Phe Asp Tyr Trp Leu  
305 310 315 320

Thr Asn Asn Tyr Ser Ala Gly Ala Arg Ala Gly Ala Phe Phe Cys Gly  
325 330 335

Leu Cys Phe Thr Met Ser Gln Met Ser Ser Thr Ile Ser Asn Cys Gly  
340 345 350

Phe Ala Thr Gly Met Asp Met Ala Gly Leu Leu Pro Lys Tyr Val Asp  
355 360 365

Ile Lys Arg Gly Ala Leu Phe Cys Ala Cys Ile Ser Trp Ala Cys Leu  
370 375 380

Pro Trp Asn Phe Tyr Asn Ser Ser Ser Thr Phe Leu Thr Val Met Ser  
385 390 395 400

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Ser Phe Gly Val Val Met Thr Pro Ile Ile Ala Val Met Ile Cys Asp  
405 410 415

Asn Phe Leu Ile Arg Lys Arg Gln Tyr Ser Ile Thr Asn Ala Phe Ile  
420 425 430

Leu Lys Gly Glu Tyr Tyr Phe Thr Lys Gly Val Asn Trp Arg Ala Ile  
435 440 445

Val Ala Trp Val Cys Gly Met Ala Pro Gly Leu Pro Gly Ile Ala Trp  
450 455 460

Glu Val Asn Asn Asn Tyr Phe His Asp Ser Gly Ile Val Lys Phe Phe  
465 470 475 480

Tyr Gly Asp Ser Phe Phe Ser Phe Leu Ile Ser Phe Phe Val Tyr Trp  
485 490 495

Gly Leu Cys Val Phe Phe Pro Phe Lys Ile Thr Val Arg His Asp Asp  
500 505 510

Lys Asp Tyr Tyr Gly Ala Phe Thr Asp Glu Glu Ala Arg Lys Lys Gly  
515 520 525

Met Ile Pro Tyr Ser Glu Ile Ser Glu Glu Glu Ile Arg Ala Tyr Thr  
530 535 540

Leu Gly Glu Cys Tyr Thr Thr Gly His Glu Tyr Lys Pro Glu Ser Ser  
545 550 555 560

Asp Asn Glu Ser Pro Glu Leu Ile Lys Thr Ser Ser Glu Asn Thr Asn  
565 570 575

Val Phe Glu Ile Val His Gln Lys Asp Asp Glu Lys His Ser Phe Ser  
580 585 590

Thr Thr Gln Gln Val Val  
595

<210> 63  
<211> 592  
<212> PRT  
<213> Unknown

<220>  
<223> CAG80639 - NR transport protein

<220>  
<221> misc\_feature  
<222> (1)..(592)  
<223> CAG80639 - NR transport protein

<400> 63

Met Ala His Asp Ser Glu Leu Glu Leu Ser Asp Glu Lys Val Val Pro  
 1 5 10 15  
 Ser Ile Asn Gln Glu Lys His Ser Phe Phe Gln Arg His Leu Asp Asn  
 20 25 30  
 His Pro Arg Met Ala Gln Tyr Asn Ser Gln Leu Gln Arg Phe Leu Lys  
 35 40 45  
 Trp Ile Glu Val Pro Thr Lys Glu Gly Glu Ile Asn Thr Phe Leu Asn  
 50 55 60  
 Asn Glu Asp Leu Lys Pro Val Glu Val Ala Arg Gln Thr Trp Gly Trp  
 65 70 75 80  
 Lys Asn Phe Val Ser Phe Trp Ile Ala Asp Ser Phe Asn Ile Asn Thr  
 85 90 95  
 Trp Glu Ile Ala Ala Thr Gly Ile Gln Leu Gly Leu Thr Trp Trp Gln  
 100 105 110  
 Val Trp Leu Cys Val Trp Ile Gly Tyr Phe Phe Cys Gly Val Phe Val  
 115 120 125  
 Val Leu Ser Gly Arg Ile Gly Ala Ile Tyr His Val Ser Phe Pro Val  
 130 135 140  
 Ala Gly Arg Ser Thr Phe Gly Ile Phe Gly Ser Ile Trp Pro Val Ile  
 145 150 155 160  
 Asn Arg Val Val Met Ala Cys Val Trp Tyr Gly Val Gln Gly Trp Leu  
 165 170 175  
 Gly Gly Gln Cys Ile Gln Val Cys Leu Leu Ala Ile Trp Pro Ser Ala  
 180 185 190  
 Arg His Met Lys Asn Gly Ile Pro Gly Ser Gly Thr Thr Thr Phe Glu  
 195 200 205  
 Phe Leu Ser Tyr Phe Leu Phe Trp Leu Phe Ser Leu Pro Phe Ile Tyr  
 210 215 220  
 Ile Arg Pro His Asn Leu Arg His Leu Phe Met Val Lys Ala Ala Ile  
 225 230 235 240  
 Val Pro Val Ala Gly Ile Ser Phe Leu Val Trp Thr Cys Val Lys Ala  
 245 250 255  
 His Gly Ile Gly Pro Ile Met Lys Gln Pro Ala Thr Val His Gly Ser  
 260 265 270  
 Val Met Gly Trp Ala Phe Met Thr Ala Ile Met Asn Ser Leu Ser Asn

275

280

285

Phe Ala Thr Ile Ile Val Asn Ala Pro Asp Phe Thr Arg Phe Ala Lys  
 290 295 300  
 Glu Pro Asn Ala Ile Val Leu Ser Gln Leu Ile Ala Val Pro Thr Ala  
 305 310 315 320  
 Phe Ser Leu Thr Ser Phe Ile Gly Ile Ile Val Ser Ser Ser Ala Thr  
 325 330 335  
 Val Leu Tyr Asp Glu Asn Ile Trp Asn Pro Leu Asp Val Leu His Lys  
 340 345 350  
 Phe Leu Glu Gly Asn Lys Ser Gly Ser Arg Ala Gly Val Phe Phe Leu  
 355 360 365  
 Gly Phe Ala Phe Ala Val Ala Gln Leu Gly Thr Asn Ile Ala Ala Asn  
 370 375 380  
 Ser Leu Ser Ala Gly Thr Asp Met Thr Ala Leu Leu Pro Lys Tyr Ile  
 385 390 395 400  
 Asn Ile Arg Arg Gly Gly Phe Ile Cys Ala Gly Ile Ala Leu Cys Ile  
 405 410 415  
 Cys Pro Trp His Leu Leu Ser Ser Ser Asn Phe Thr Thr Tyr Leu  
 420 425 430  
 Ser Ala Tyr Ala Thr Phe Leu Ser Ala Ile Ala Gly Cys Ser Phe Ser  
 435 440 445  
 Asp Tyr Tyr Leu Val Arg Lys Gly Tyr Ile Tyr Val Gly Asp Leu Tyr  
 450 455 460  
 Asn Ala Ser Lys Gly Ser Thr Tyr Met Tyr Arg Tyr Gly Val Asn Trp  
 465 470 475 480  
 Arg Ala Phe Ala Ala Tyr Phe Cys Gly Ile Ala Ile Asn Val Val Gly  
 485 490 495  
 Phe Ala Asp Ala Val Ser Asp Gly Gly Val Asn Glu Thr Ala Arg Lys  
 500 505 510  
 Met Tyr Gln Leu Asn Phe Phe Leu Gly Phe Leu Val Ser Ala Ile Ser  
 515 520 525  
 Tyr Tyr Gly Phe Asn Trp Leu Ser Pro Val Val Gly Ala Arg Glu Thr  
 530 535 540  
 Trp Ser Glu Asp Pro Asn Ala Ser Ala Met Tyr Asp Glu Ile Thr Thr  
 545 550 555 560

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Asp Glu Leu Ser Gln Asp Ser Gln Ser Tyr Asp Pro Glu Glu Trp Asp  
565 570 575

Arg Lys Ile Ala Asn Asp Asp Pro Val Lys Thr Thr Ala Ile Ile Ser  
580 585 590

<210> 64  
<211> 445  
<212> PRT  
<213> Unknown

<220>  
<223> An04g07070 - NR transport protein

<220>  
<221> misc\_feature  
<222> (1)..(445)  
<223> An04g07070 - NR transport protein

<400> 64

Met Asp Arg Ile Arg Gly Leu Ile Ala Arg Arg Pro Thr Tyr Glu Ala  
1 5 10 15

Ile Glu Gln Pro Val Asp Ala Asp Asp Glu Ser Ile Arg Leu Thr Arg  
20 25 30

Glu Glu Glu Gln His Pro Arg Phe Ser Lys Tyr Glu Tyr Ala Val Phe  
35 40 45

Phe Leu Leu Gly Val Ser Met Leu Trp Ala Trp Asn Met Phe Leu Ala  
50 55 60

Ala Ala Pro Tyr Phe Tyr His Arg Phe His Thr Asp Asp Trp Ala Ala  
65 70 75 80

Thr His Tyr Gln Pro Ser Ile Leu Thr Val Ser Thr Val Thr Asn Leu  
85 90 95

Gly Ser Ser Phe Ile Leu Ala Lys Leu Gln Lys Gly Ala Ser Tyr Pro  
100 105 110

Lys Arg Val Thr Ile Ser Leu Leu Ile Asn Ile Val Val Phe Thr Leu  
115 120 125

Leu Ala Phe Ser Thr Ile Leu Met Lys Asp Val Ala Val Ser Thr Tyr  
130 135 140

Phe Ser Phe Leu Met Ile Met Val Phe Gly Ala Ser Leu Ala Thr Gly  
145 150 155 160

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



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Glu Tyr Thr Gln Ala Ile Met Gly Gly Gln Gly Val Ala Gly Val Leu  
180 185 190

Pro Cys Ile Val Gln Ile Leu Ser Val Val Ser Val Pro Ser Lys Lys  
195 200 205

Glu Gly Gln Lys Ala Pro Gln Glu Ser Ser Lys Ser Ala Phe Ala Tyr  
210 215 220

Phe Ile Thr Ala Thr Ala Val Ser Ser Phe Ala Leu Leu Ala Phe Leu  
225 230 235 240

Ser Leu Val Lys Arg Arg Ala Ser Ser Thr Leu Leu Asp Pro Thr Asp  
245 250 255

Asp His Ser Asp Pro Asp Val Pro Glu Asn Lys Ser Val Ser Leu Trp  
260 265 270

Thr Leu Phe Lys Lys Leu Arg Phe Met Ala Ser Ala Ile Phe Leu Cys  
275 280 285

Phe Thr Val Thr Met Thr Phe Pro Val Phe Thr Ala Glu Ile Glu Ser  
290 295 300

Val His Asp Thr Pro Gly Arg Ser Arg Leu Phe Asp Gln Ala Val Phe  
305 310 315 320

Ile Pro Leu Ala Phe Phe Phe Trp Asn Ala Gly Asp Leu Met Gly Arg  
325 330 335

Met Leu Val Leu Phe Pro Arg Leu Ser Leu Val Asn Arg Pro Phe Val  
340 345 350

Leu Phe Leu Phe Ser Ile Ala Arg Ala Ala Phe Ile Pro Leu Tyr Leu  
355 360 365

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

Tyr Leu Phe Ile Val Gln Leu Leu Phe Gly Ile Ser Asn Gly Tyr Leu  
385 390 395 400

Gly Ser Asn Cys Met Met Gly Val Gly Gln Trp Val Ser Pro Asp Glu  
405 410 415

Arg Glu Pro Ala Gly Gly Phe Met Gly Leu Met Leu Val Gly Gly Leu  
420 425 430

Thr Ala Gly Ser Leu Met Ser Phe Leu Val Ala Gly Ala  
435 440 445

<210> 65  
 <211> 340  
 <212> PRT  
 <213> Unknown

<220>  
 <223> SC URH1 - NR hydrolase

<220>  
 <221> misc\_feature  
 <222> (1)..(340)  
 <223> SC URH1 - NR hydrolase

<400> 65

Met Thr Val Ser Lys Ile Pro Ile Trp Leu Asp Cys Asp Pro Gly His  
 1 5 10 15

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

Leu Leu Gly Ile Ser Thr Cys Phe Gly Asn Ala Pro Pro Glu Asn Thr  
 35 40 45

Asp Tyr Asn Ala Arg Ser Leu Leu Thr Ala Met Gly Lys Ala Gln Ala  
 50 55 60

Ile Pro Val Tyr Lys Gly Ala Gln Arg Pro Trp Lys Arg Glu Pro His  
 65 70 75 80

Tyr Ala Pro Asp Ile His Gly Ile Ser Gly Leu Asp Gly Thr Ser Leu  
 85 90 95

Leu Pro Lys Pro Thr Phe Glu Ala Arg Thr Asp Lys Thr Tyr Ile Glu  
 100 105 110

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

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

Tyr Leu Lys Lys Ser Val Lys Tyr Ile Ser Ile Met Gly Gly Gly Leu  
 145 150 155 160

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

Trp Ile Asp Pro Asp Ala Ala Asn Tyr Ile Phe Arg Asp Pro Asp Val  
 180 185 190

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

Ala Thr Tyr Lys Val Asn Glu Met Ile Tyr Asn Glu Lys Asn Asn Ser

210

215

Lys Leu Arg Glu Leu Phe Leu Glu Leu Phe Gln Phe Phe Ala His Thr  
225 230 235 240

Tyr Lys Asp Met Gln Gly Phe Glu Ser Gly Pro Pro Ile His Asp Pro  
245 250 255

Val Ala Leu Met Pro Leu Leu Glu Phe Tyr Gly Trp Asp Pro Ser Ser  
260 265 270

Ala Val Gly Phe Arg Tyr Lys Arg Met Asp Ile Ser Cys Ile Asp Asp  
275 280 285

Val Phe Asn Glu Asn Ser Gly Lys Ile Ile Ile Glu Lys Glu Tyr Pro  
290 295 300

Asn Asp Ser Asp Val Gly Thr Ile Ile Gly Leu Asp Leu Asn Ile Gln  
305 310 315 320

Tyr Phe Trp Asp Gln Ile Phe Glu Ala Leu Asn Arg Ala Asp Lys Met  
325 330 335

Ser Thr Ile Gly  
340

<210> 66  
<211> 338  
<212> PRT  
<213> Unknown

<220>  
<223> CAG77762 - NR hydrolase

<220>  
<221> misc\_feature  
<222> (1)..(338)  
<223> CAG77762 - NR hydrolase

<400> 66

Met Ile Pro Ile Trp Leu Asp Cys Asp Pro Gly His Asp Asp Ala Val  
1 5 10 15

Ala Ile Leu Leu Ala Ala Lys Leu Pro Ala Phe Asn Leu Leu Gly Ile  
20 25 30

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

Met Ala Val Leu Lys Ala Ile Gly Gln Asp Ser Glu Ile Lys Val Tyr  
50 55 60

Pro Gly Ala Glu Arg Ile Gln Ser Arg Gly Gly Gly Gly Asp Gly Gly  
65 70 75 80

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

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<210> 67  
 <211> 435  
 <212> PRT  
 <213> Unknown

<220>  
 <223> An18g04340 - NR hydrolase (URH1 homolog)

<220>  
 <221> misc\_feature  
 <222> (1)..(435)  
 <223> An18g04340 - NR hydrolase (URH1 homolog)

<400> 67

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Met Thr Leu Cys Pro Phe Arg Ile Arg Lys Val Gly Leu Arg Ala Asp
1          5          10          15

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

Leu Gln Gln Ser Pro Gln Ser Pro Phe Arg Trp His Leu Gly Leu Pro
          35          40          45

Ser Phe Phe Ser Phe Ile Pro Ser Arg Ser Gly Phe Thr Met Asp Ser
          50          55          60

Ser Val Asp Thr Pro Ile Pro Leu Trp Leu Asp Cys Asp Pro Gly His
65          70          75          80

Asp Asp Ala Phe Ala Ile Leu Leu Ala Ala His His Pro Ser Leu Lys
          85          90          95

Leu Leu Gly Ile Thr Thr Ile His Gly Asn Ala Ser Leu Glu Asn Thr
          100          105          110

Thr Ile Asn Ala Thr Arg Val Leu Glu Ala Ile Gly Arg Pro Glu Ile
          115          120          125

Pro Val Tyr Pro Gly Ser Lys Lys Pro Phe Cys Arg Pro Ala Leu His
          130          135          140

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

Pro Lys Ala Ser Thr Ala Pro Ile Thr Asp Lys Asn Pro Ile Leu Ala
          165          170          175

Met Arg Asp Ala Leu Met Ala His Pro Lys Gly Thr Pro Trp Val Val
          180          185          190

Ala Thr Gly Thr Leu Thr Asn Val Ala Leu Leu Phe Ala Thr Phe Pro
          195          200          205
    
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Glu Val Ala Glu His Ile Ala Gly Leu Thr Ile Met Gly Gly Gly Val  
210 215 220

Gly Glu Gly Phe Thr Asp Ala Pro Met Ser Arg Leu Lys Gly Gln Glu  
225 230 235 240

Asn Arg Ile Gly Asn Val Thr Pro Leu Ala Glu Phe Asn Ile Tyr Cys  
245 250 255

Asp Pro Glu Ala Ser Gln Ala Ile Phe Ser Asp Pro Val Val Ala Ser  
260 265 270

Lys Thr Thr Leu Ile Thr Leu Asp Leu Thr His Gln Val Leu Ala Asp  
275 280 285

Gln Ser Val Arg Asn Leu Val Arg His Gly Val Asp Asp Ala Ser Val  
290 295 300

Gln Pro Thr Thr Leu Arg Gln Met Leu Tyr Glu Leu Leu Ile Phe Phe  
305 310 315 320

Ala Asn Thr Tyr Glu Thr Val Phe Gly Leu Ser Thr Gly Pro Pro Leu  
325 330 335

His Asp Pro Leu Ala Val Ala Val Ile Leu Ser Thr Leu Asn Pro Gly  
340 345 350

Tyr Ala Lys Asn His Pro Asp Gln Val Leu Lys Phe Asp Asp Arg Gly  
355 360 365

Gly Glu Arg Phe Ser Val Asn Val Ile Thr Asp Gly Leu His Gly Thr  
370 375 380

Asp Ile Ala Leu Val Gly Ser Leu Gly Arg Ser Val Val Glu Ala Asn  
385 390 395 400

Pro Asn Ala Val Cys Ile Pro Arg Gly Val Asp Leu Asp Ala Phe Trp  
405 410 415

Asn Met Ile Asn Asp Cys Ile Lys Arg Ala Asp Glu Cys Asn Ala Ala  
420 425 430

Arg Lys Ala  
435

<210> 68  
<211> 240  
<212> PRT  
<213> Unknown

<220>  
<223> SC NRK1 - NR kinase

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(240)

&lt;223&gt; Sc NRK1 - NR kinase

&lt;400&gt; 68

Met Thr Ser Lys Lys Val Ile Leu Val Ala Leu Ser Gly Cys Ser Ser  
 1 5 10 15

Ser Gly Lys Thr Thr Ile Ala Lys Leu Thr Ala Ser Leu Phe Thr Lys  
 20 25 30

Ala Thr Leu Ile His Glu Asp Asp Phe Tyr Lys His Asp Asn Glu Val  
 35 40 45

Pro Val Asp Ala Lys Tyr Asn Ile Gln Asn Trp Asp Ser Pro Glu Ala  
 50 55 60

Leu Asp Phe Lys Leu Phe Gly Lys Glu Leu Asp Val Ile Lys Gln Thr  
 65 70 75 80

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

Phe Thr Lys Phe His Ile Asp Arg Gln Val Trp Asp Glu Leu Lys Ala  
 100 105 110

Lys Tyr Asp Ser Ile Asn Asp Asp Lys Tyr Glu Val Val Ile Val Asp  
 115 120 125

Gly Phe Met Ile Phe Asn Asn Thr Gly Ile Ser Lys Lys Phe Asp Leu  
 130 135 140

Lys Ile Leu Val Arg Ala Pro Tyr Glu Val Leu Lys Lys Arg Arg Ala  
 145 150 155 160

Ser Arg Lys Gly Tyr Gln Thr Leu Asp Ser Phe Trp Val Asp Pro Pro  
 165 170 175

Tyr Tyr Phe Asp Glu Phe Val Tyr Glu Ser Tyr Arg Ala Asn His Ala  
 180 185 190

Gln Leu Phe Val Asn Gly Asp Val Glu Gly Leu Leu Asp Pro Arg Lys  
 195 200 205

Ser Lys Asn Ile Lys Glu Phe Ile Asn Asp Asp Asp Thr Pro Ile Ala  
 210 215 220

Lys Pro Leu Ser Trp Val Cys Gln Glu Ile Leu Lys Leu Cys Lys Asp  
 225 230 235 240

&lt;210&gt; 69

&lt;211&gt; 254

<212> PRT  
 <213> Unknown

<220>  
 <223> CAG83148 - NR kinase

<220>  
 <221> misc\_feature  
 <222> (1)..(254)  
 <223> CAG83148 - NR kinase

<400> 69

Met Ile Arg Arg Lys Ile Ala Glu Lys Lys Leu Ala Lys Glu Glu Asp  
 1 5 10 15

Lys Arg Glu Val Thr Leu Val Ala Leu Ser Gly Pro Ser Ser Ser Gly  
 20 25 30

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

Ile Ile His Gln Asp Asp Phe Tyr Leu Glu Asp Ser Gln Ile Pro Val  
 50 55 60

Ile Asp Gly Val Gln Asp Trp Asp Cys Pro Glu Ala Phe Asp Phe Lys  
 65 70 75 80

Leu Leu Ser Lys Val Leu Ser His Val Lys Gln Thr Gly Glu Leu Pro  
 85 90 95

Lys Asn Phe Lys Ser Lys Glu Asp Gln Asn Ser Leu Gly Pro Ala Ala  
 100 105 110

Leu Asp Glu Asn Ala Val Asp Ala Phe Lys Arg Arg Met His Pro Tyr  
 115 120 125

Met Pro Glu Phe Glu Asn Lys Leu Ile Val Ile Leu Asp Gly Ile Met  
 130 135 140

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

Val Arg Ser Ser Tyr Glu Asn Leu Lys Ser Arg Arg Glu Ala Arg Ser  
 165 170 175

Gly Tyr Val Thr Leu Glu Gly Phe Trp Lys Asp Pro Glu Gly Tyr Phe  
 180 185 190

His Asn Ile Val Trp Pro Gly Tyr Leu Lys Thr His Lys Gln Leu Phe  
 195 200 205

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



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Gly Ile Arg Ile Val Pro Thr Thr Asp Phe Asp Val Ala Glu Thr Leu  
225 230 235 240

Asp Trp Val Phe Asp Val Ile Leu Asp Tyr Tyr Asp Leu Glu  
245 250

<210> 70  
<211> 281  
<212> PRT  
<213> Unknown

<220>  
<223> NR kinase

<220>  
<221> misc\_feature  
<222> (1)..(281)  
<223> An04g05800 - NR kinase (NRK1 homolog)

<400> 70

Met Thr Lys Ser Pro Leu Ile Pro His Pro Arg Asp Pro Thr Thr Gln  
1 5 10 15

Ile Gln Asn Trp Asp Thr Leu Ser Ala Leu Asp Ile Pro Phe Leu Ser  
20 25 30

Ala Ser Leu Ser Tyr Ile His Ala His Gly His Leu Pro Pro Arg Leu  
35 40 45

Arg Ser Lys Glu Asp Leu Asn Asp Val Ala Glu Ser Gly Val Ser Glu  
50 55 60

Glu Val Val Ser Arg Met Arg Glu Val Val Arg Gly Arg Val Pro Ser  
65 70 75 80

Tyr Phe Leu Glu Asp Asn Thr Asn Ser Val Ser Gly Asp Gly Val Arg  
85 90 95

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

Glu Asp Pro Arg His Gly Leu Arg Asp Val Gln Glu Lys Met Asp Val  
115 120 125

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

Gly Arg Ser Gly Tyr Val Thr Ile Gly Pro Ala Pro Val Gln Gln Gly  
145 150 155 160

Gly Gly Gly Gly Thr Glu Leu Pro Gln Arg Gly Ser Val Glu Val Asp  
165 170 175

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Leu Glu Glu Glu Asp Asp Arg Pro Pro Gln Ser Phe Trp Glu Asp Pro  
180 185 190

Pro Gly Tyr Val Asp Asp Ile Val Trp Pro Asn Tyr Val Gln Asp His  
195 200 205

Ala Trp Leu Leu Leu Pro Glu Gly Glu Glu Gly Ser Ala Gln Thr Ala  
210 215 220

Trp Lys Asp Ala Asp Thr Gln Glu Leu Val Arg Leu Val Gly Gln Gly  
225 230 235 240

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

Lys Ala Ser Met Thr Asp Ile Leu Glu Trp Ala Val Glu Glu Val Leu  
260 265 270

Lys His Ile Ala Glu Thr Glu Gly Gln  
275 280

<210> 71  
<211> 311  
<212> PRT  
<213> Unknown

<220>  
<223> NMN/purine phosphorylase

<220>  
<221> misc\_feature  
<222> (1)..(311)  
<223> SC PNP1 - NMN/purine phosphorylase

<400> 71

Met Ser Asp Ile Leu Asn Val Ser Gln Gln Arg Glu Ala Ile Thr Lys  
1 5 10 15

Ala Ala Ala Tyr Ile Ser Ala Ile Leu Glu Pro His Phe Lys Asn Thr  
20 25 30

Thr Asn Phe Glu Pro Pro Arg Thr Leu Ile Ile Cys Gly Ser Gly Leu  
35 40 45

Gly Gly Ile Ser Thr Lys Leu Ser Arg Asp Asn Pro Pro Pro Val Thr  
50 55 60

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

His Ser Gly Thr Leu Met Phe Gly Ser Met Asn Gly Ser Pro Val Val  
85 90 95

Leu Met Asn Gly Arg Leu His Gly Tyr Glu Gly Asn Thr Leu Phe Glu  
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100

105

110

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

<210> 72  
 <211> 298  
 <212> PRT  
 <213> Unknown

<220>  
 <223> NMN/purine phosphorylase

<220>  
 <221> misc\_feature  
 <222> (1)..(298)  
 <223> CAG78849 - NMN/purine phosphorylase

&lt;400&gt; 72

Met Thr Asp Thr Phe Asp Leu Ser Leu Lys Ser Ala Asn Lys Ile Ser  
 1 5 10 15  
 Asp Lys Leu Pro Lys Glu Leu Gln Asn Pro Gln Ile Gly Ile Val Cys  
 20 25 30  
 Gly Ser Gly Leu Gly Gly Leu Ala Asn Ala Leu Lys Ala Glu Pro Gln  
 35 40 45  
 Val Thr Ile Glu Tyr Lys Asp Ile Pro Gly Phe Lys Val Ser Thr Val  
 50 55 60  
 Ala Gly His Ala Gly Lys Leu Val Val Gly Leu Leu Gly Glu Lys Asn  
 65 70 75 80  
 Val Pro Val Val Cys Met Val Gly Arg Phe His Phe Tyr Glu Gly Tyr  
 85 90 95  
 Asp Ile Gln Asp Thr Val Phe Pro Ile Arg Val Phe Ser Gln Ile Gly  
 100 105 110  
 Ile Lys Thr Val Ile Leu Thr Asn Ala Ala Gly Gly Leu Asn Gln Asp  
 115 120 125  
 Phe Lys Val Gly Asp Ile Met Leu Ile Asn Asp His Ile Asn Leu Pro  
 130 135 140  
 Gly Leu Ala Gly Asn Asn Pro Leu Arg Gly Pro Asn Asp Glu Lys Phe  
 145 150 155 160  
 Gly Val Arg Phe Leu Pro Leu Ser Asp Ala Tyr Asp His Asp Leu Arg  
 165 170 175  
 Arg Ala Val Tyr Asp Ile Ala Lys Lys Gln Gly Val Thr Arg Gly Ile  
 180 185 190  
 His Glu Gly Thr Tyr Ala Phe Val Ser Gly Pro Thr Tyr Glu Ser Arg  
 195 200 205  
 Ala Glu Ala Arg Met Leu Ser Thr Ile Gly Ala Asp Ala Val Gly Met  
 210 215 220  
 Ser Thr Val Pro Glu Val Ile Val Ala Arg His Cys Gly Ile Lys Val  
 225 230 235 240  
 Leu Ala Leu Ser Leu Ile Thr Asn Val Val Val Leu Lys Lys Pro Asp  
 245 250 255  
 Ser Ala Leu Asn Asp Asn Ala Ala Lys Leu Asp Glu Gly Ile Ala Asp  
 260 265 270

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His Ser Glu Val Met Glu Glu Gly Gln Arg Ala Ala Asp Asp Leu Val  
275 280 285

Gly Ile Val Thr Asp Leu Val Asn Val Val  
290 295

<210> 73  
<211> 550  
<212> PRT  
<213> Escherichia coli

<220>  
<221> misc\_feature  
<222> (1)..(550)  
<223> Escherichia coli UshA (nucleotide  
hydrolase)>gi|16128464|ref|NP\_415013.1| bifunctional UDP-sugar  
hydrolase/5'-nucleotidase [Escherichia coli str. K-12 substr.  
MG1655]

<400> 73

Met Lys Leu Leu Gln Arg Gly Val Ala Leu Ala Leu Leu Thr Thr Phe  
1 5 10 15

Thr Leu Ala Ser Glu Thr Ala Leu Ala Tyr Glu Gln Asp Lys Thr Tyr  
20 25 30

Lys Ile Thr Val Leu His Thr Asn Asp His His Gly His Phe Trp Arg  
35 40 45

Asn Glu Tyr Gly Glu Tyr Gly Leu Ala Ala Gln Lys Thr Leu Val Asp  
50 55 60

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

Ser Gly Gly Asp Ile Asn Thr Gly Val Pro Glu Ser Asp Leu Gln Asp  
85 90 95

Ala Glu Pro Asp Phe Arg Gly Met Asn Leu Val Gly Tyr Asp Ala Met  
100 105 110

Ala Ile Gly Asn His Glu Phe Asp Asn Pro Leu Thr Val Leu Arg Gln  
115 120 125

Gln Glu Lys Trp Ala Lys Phe Pro Leu Leu Ser Ala Asn Ile Tyr Gln  
130 135 140

Lys Ser Thr Gly Glu Arg Leu Phe Lys Pro Trp Ala Leu Phe Lys Arg  
145 150 155 160

Gln Asp Leu Lys Ile Ala Val Ile Gly Leu Thr Thr Asp Asp Thr Ala  
165 170 175

Lys Ile Gly Asn<sub>180</sub> Pro Glu Tyr Phe Thr<sub>185</sub> Asp Ile Glu Phe Arg<sub>190</sub> Lys Pro  
 Ala Asp Glu<sub>195</sub> Ala Lys Leu Val Ile<sub>200</sub> Gln Glu Leu Gln<sub>205</sub> Thr Glu Lys  
 Pro Asp<sub>210</sub> Ile Ile Ile Ala Ala<sub>215</sub> Thr His Met Gly His<sub>220</sub> Tyr Asp Asn Gly  
 Glu<sub>225</sub> His Gly Ser Asn Ala<sub>230</sub> Pro Gly Asp Val Glu<sub>235</sub> Met Ala Arg Ala Leu<sub>240</sub>  
 Pro Ala Gly Ser Leu<sub>245</sub> Ala Met Ile Val Gly<sub>250</sub> Gly His Ser Gln Asp<sub>255</sub> Pro  
 Val Cys Met Ala<sub>260</sub> Ala Glu Asn Lys Lys<sub>265</sub> Gln Val Asp Tyr Val<sub>270</sub> Pro Gly  
 Thr Pro Cys<sub>275</sub> Lys Pro Asp Gln Gln<sub>280</sub> Asn Gly Ile Trp Ile<sub>285</sub> Val Gln Ala  
 His Glu<sub>290</sub> Trp Gly Lys Tyr Val<sub>295</sub> Gly Arg Ala Asp Phe<sub>300</sub> Glu Phe Arg Asn  
 Gly<sub>305</sub> Glu Met Lys Met Val<sub>310</sub> Asn Tyr Gln Leu Ile<sub>315</sub> Pro Val Asn Leu Lys<sub>320</sub>  
 Lys Lys Val Thr Trp<sub>325</sub> Glu Asp Gly Lys Ser<sub>330</sub> Glu Arg Val Leu Tyr<sub>335</sub> Thr  
 Pro Glu Ile Ala<sub>340</sub> Glu Asn Gln Gln<sub>345</sub> Met Ile Ser Leu Leu Ser<sub>350</sub> Pro Phe  
 Gln Asn Lys<sub>355</sub> Gly Lys Ala Gln Leu<sub>360</sub> Glu Val Lys Ile Gly<sub>365</sub> Glu Thr Asn  
 Gly<sub>370</sub> Arg Leu Glu Gly Asp Arg<sub>375</sub> Asp Lys Val Arg Phe<sub>380</sub> Val Gln Thr Asn  
 Met<sub>385</sub> Gly Arg Leu Ile Leu<sub>390</sub> Ala Ala Gln Met Asp<sub>395</sub> Arg Thr Gly Ala Asp<sub>400</sub>  
 Phe Ala Val Met Ser<sub>405</sub> Gly Gly Gly Ile Arg<sub>410</sub> Asp Ser Ile Glu Ala Gly<sub>415</sub>  
 Asp Ile Ser Tyr<sub>420</sub> Lys Asn Val Leu Lys<sub>425</sub> Val Gln Pro Phe Gly<sub>430</sub> Asn Val  
 Val Val Tyr<sub>435</sub> Ala Asp Met Thr Gly<sub>440</sub> Lys Glu Val Ile Asp<sub>445</sub> Tyr Leu Thr  
 Ala Val Ala Gln Met Lys Pro Asp Ser Gly Ala Tyr Pro Gln Phe Ala

450

455

460

Asn Val Ser Phe Val Ala Lys Asp Gly Lys Leu Asn Asp Leu Lys Ile  
 465 470 475 480

Lys Gly Glu Pro Val Asp Pro Ala Lys Thr Tyr Arg Met Ala Thr Leu  
 485 490 495

Asn Phe Asn Ala Thr Gly Gly Asp Gly Tyr Pro Arg Leu Asp Asn Lys  
 500 505 510

Pro Gly Tyr Val Asn Thr Gly Phe Ile Asp Ala Glu Val Leu Lys Ala  
 515 520 525

Tyr Ile Gln Lys Ser Ser Pro Leu Asp Val Ser Val Tyr Glu Pro Lys  
 530 535 540

Gly Glu Val Ser Trp Gln  
 545 550

<210> 74  
 <211> 1462  
 <212> PRT  
 <213> Bacillus subtilis

<220>  
 <221> misc\_feature  
 <222> (1)..(1462)  
 <223> Bacillus subtilis Yfkn (nucleotide hydrolase)  
 >gi|16077851|ref|NP\_388665.1| nucleotide phosphoesterase  
 [Bacillus subtilis subsp. subtilis str. 168]

<400> 74

Met Arg Ile Gln Lys Arg Arg Thr His Val Glu Asn Ile Leu Arg Ile  
 1 5 10 15

Leu Leu Pro Pro Ile Met Ile Leu Ser Leu Ile Leu Pro Thr Pro Pro  
 20 25 30

Ile His Ala Glu Glu Ser Ala Ala Pro Gln Val His Leu Ser Ile Leu  
 35 40 45

Ala Thr Thr Asp Ile His Ala Asn Met Met Asp Tyr Asp Tyr Tyr Ser  
 50 55 60

Asp Lys Glu Thr Ala Asp Phe Gly Leu Ala Arg Thr Ala Gln Leu Ile  
 65 70 75 80

Gln Lys His Arg Glu Gln Asn Pro Asn Thr Leu Leu Val Asp Asn Gly  
 85 90 95

Asp Leu Ile Gln Gly Asn Pro Leu Gly Glu Tyr Ala Val Lys Tyr Gln  
 100 105 110

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Lys Asp Asp Ile Ile Ser Gly Thr Lys Thr His Pro Ile Ile Ser Val  
 115 120 125  
 Met Asn Ala Leu Lys Tyr Asp Ala Gly Thr Leu Gly Asn His Glu Phe  
 130 135 140  
 Asn Tyr Gly Leu Asp Phe Leu Asp Gly Thr Ile Lys Gly Ala Asp Phe  
 145 150 155 160  
 Pro Ile Val Asn Ala Asn Val Lys Thr Thr Ser Gly Glu Asn Arg Tyr  
 165 170 175  
 Thr Pro Tyr Val Ile Asn Glu Lys Thr Leu Ile Asp Glu Asn Gly Asn  
 180 185 190  
 Glu Gln Lys Val Lys Val Gly Tyr Ile Gly Phe Val Pro Pro Gln Ile  
 195 200 205  
 Met Thr Trp Asp Lys Lys Asn Leu Glu Gly Gln Val Gln Val Gln Asp  
 210 215 220  
 Ile Val Glu Ser Ala Asn Glu Thr Ile Pro Lys Met Lys Ala Glu Gly  
 225 230 235 240  
 Ala Asp Val Ile Ile Ala Leu Ala His Thr Gly Ile Glu Lys Gln Ala  
 245 250 255  
 Gln Ser Ser Gly Ala Glu Asn Ala Val Phe Asp Leu Ala Thr Lys Thr  
 260 265 270  
 Lys Gly Ile Asp Ala Ile Ile Ser Gly His Gln His Gly Leu Phe Pro  
 275 280 285  
 Ser Ala Glu Tyr Ala Gly Val Ala Gln Phe Asn Val Glu Lys Gly Thr  
 290 295 300  
 Ile Asn Gly Ile Pro Val Val Met Pro Ser Ser Trp Gly Lys Tyr Leu  
 305 310 315 320  
 Gly Val Ile Asp Leu Lys Leu Glu Lys Ala Asp Gly Ser Trp Lys Val  
 325 330 335  
 Ala Asp Ser Lys Gly Ser Ile Glu Ser Ile Ala Gly Asn Val Thr Ser  
 340 345 350  
 Arg Asn Glu Thr Val Thr Asn Thr Ile Gln Gln Thr His Gln Asn Thr  
 355 360 365  
 Leu Glu Tyr Val Arg Lys Pro Val Gly Lys Thr Glu Ala Asp Ile Asn  
 370 375 380



Ser Phe Phe Ala Gln Val Lys Asp Asp Pro Ser Ile Gln Ile Val Thr  
 385 390 395 400  
 Asp Ala Gln Lys Trp Tyr Ala Glu Lys Glu Met Lys Asp Thr Glu Tyr  
 405 410 415  
 Lys Asn Leu Pro Ile Leu Ser Ala Gly Ala Pro Phe Lys Ala Gly Gly  
 420 425 430  
 Arg Asn Gly Ala Asn Tyr Tyr Thr Asn Ile Pro Ala Gly Asp Leu Ala  
 435 440 445  
 Ile Lys Asn Val Gly Asp Leu Tyr Leu Tyr Asp Asn Thr Val Gln Ile  
 450 455 460  
 Val Lys Leu Thr Gly Ser Glu Val Lys Asp Trp Leu Glu Met Ser Ala  
 465 470 475 480  
 Gly Gln Phe Asn Gln Ile Asp Pro Ala Lys Gly Gly Asp Gln Ala Leu  
 485 490 495  
 Leu Asn Glu Asn Phe Arg Ser Tyr Asn Phe Asp Val Ile Asp Gly Val  
 500 505 510  
 Thr Tyr Gln Val Asp Val Thr Lys Pro Ala Lys Tyr Asn Glu Asn Gly  
 515 520 525  
 Lys Val Ile Asn Ala Asp Ser Ser Arg Ile Ile Asn Leu Ser Tyr Glu  
 530 535 540  
 Gly Lys Pro Ile Ser Pro Ser Gln Glu Phe Leu Val Val Thr Asn Asn  
 545 550 555 560  
 Tyr Arg Ala Ser Gly Gly Gly Gly Phe Pro His Leu Thr Ser Asp Lys  
 565 570 575  
 Ile Val His Gly Ser Ala Val Glu Asn Arg Gln Val Leu Met Asp Tyr  
 580 585 590  
 Ile Ile Glu Gln Lys Thr Val Asn Pro Lys Ala Asp Asn Asn Trp Ser  
 595 600 605  
 Ile Ala Pro Val Ser Gly Thr Asn Leu Thr Phe Glu Ser Ser Leu Leu  
 610 615 620  
 Ala Lys Pro Phe Ala Asp Lys Ala Asp Asp Val Ala Tyr Val Gly Lys  
 625 630 635 640  
 Ser Ala Asn Glu Gly Tyr Gly Val Tyr Lys Leu Gln Phe Asp Asp Asp  
 645 650 655  
 Ser Asn Pro Asp Pro Pro Lys Asp Gly Leu Trp Asp Leu Thr Val Met  
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660

665

670

His Thr Asn Asp Thr His Ala His Leu Asp Asp Ala Ala Arg Arg Met  
 675 680 685

Thr Lys Ile Asn Glu Val Arg Ser Glu Thr Asn His Asn Ile Leu Leu  
 690 695 700

Asp Ala Gly Asp Val Phe Ser Gly Asp Leu Tyr Phe Thr Lys Trp Asn  
 705 710 715 720

Gly Leu Ala Asp Leu Lys Met Met Asn Met Met Gly Tyr Asp Ala Met  
 725 730 735

Thr Phe Gly Asn His Glu Phe Asp Lys Gly Pro Thr Val Leu Ser Asp  
 740 745 750

Phe Leu Ser Gly Asn Ser Ala Thr Val Asp Pro Ala Asn Arg Tyr His  
 755 760 765

Phe Glu Ala Pro Glu Phe Pro Ile Val Ser Ala Asn Val Asp Val Ser  
 770 775 780

Asn Glu Pro Lys Leu Lys Ser Phe Val Lys Lys Pro Gln Thr Phe Thr  
 785 790 795 800

Ala Gly Glu Lys Lys Glu Ala Gly Ile His Pro Tyr Ile Leu Leu Asp  
 805 810 815

Val Asp Gly Glu Lys Val Ala Val Phe Gly Leu Thr Thr Glu Asp Thr  
 820 825 830

Ala Thr Thr Ser Ser Pro Gly Lys Ser Ile Val Phe Asn Asp Ala Phe  
 835 840 845

Glu Thr Ala Gln Asn Thr Val Lys Ala Ile Gln Glu Glu Glu Lys Val  
 850 855 860

Asn Lys Ile Ile Ala Leu Thr His Ile Gly His Asn Arg Asp Leu Glu  
 865 870 875 880

Leu Ala Lys Lys Val Lys Gly Ile Asp Leu Ile Ile Gly Gly His Thr  
 885 890 895

His Thr Leu Val Asp Lys Met Glu Val Val Asn Asn Glu Glu Pro Thr  
 900 905 910

Ile Val Ala Gln Ala Lys Glu Tyr Gly Gln Phe Leu Gly Arg Val Asp  
 915 920 925

Val Ala Phe Asp Glu Lys Gly Val Val Gln Thr Asp Lys Ser Asn Leu  
 930 935 940

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Ser Val Leu Pro Ile Asp Glu His Thr Glu Glu Asn Pro Glu Ala Lys  
945 950 955 960

Gln Glu Leu Asp Gln Phe Lys Asn Glu Leu Glu Asp Val Lys Asn Glu  
965 970 975

Lys Val Gly Tyr Thr Asp Val Ala Leu Asp Gly Gln Arg Glu His Val  
980 985 990

Arg Thr Lys Glu Thr Asn Leu Gly Asn Phe Ile Ala Asp Gly Met Leu  
995 1000 1005

Ala Lys Ala Lys Glu Ala Ala Gly Ala Arg Ile Ala Ile Thr Asn  
1010 1015 1020

Gly Gly Gly Ile Arg Ala Gly Ile Asp Lys Gly Asp Ile Thr Leu  
1025 1030 1035

Gly Glu Val Leu Asn Val Met Pro Phe Gly Asn Thr Leu Tyr Val  
1040 1045 1050

Ala Asp Leu Thr Gly Lys Gln Ile Lys Glu Ala Leu Glu Gln Gly  
1055 1060 1065

Leu Ser Asn Val Glu Asn Gly Gly Gly Ala Phe Pro Gln Val Ala  
1070 1075 1080

Gly Ile Glu Tyr Thr Phe Thr Leu Asn Asn Lys Pro Gly His Arg  
1085 1090 1095

Val Leu Glu Val Lys Ile Glu Ser Pro Asn Gly Asp Lys Val Ala  
1100 1105 1110

Ile Asn Thr Asp Asp Thr Tyr Arg Val Ala Thr Asn Asn Phe Val  
1115 1120 1125

Gly Ala Gly Gly Asp Gly Tyr Ser Val Phe Thr Glu Ala Ser His  
1130 1135 1140

Gly Glu Asp Leu Gly Tyr Val Asp Tyr Glu Ile Phe Thr Glu Gln  
1145 1150 1155

Leu Lys Lys Leu Gly Asn Lys Val Ser Pro Lys Val Glu Gly Arg  
1160 1165 1170

Ile Lys Glu Val Phe Leu Pro Thr Lys Gln Lys Asp Gly Ser Trp  
1175 1180 1185

Thr Leu Asp Glu Asp Lys Phe Ala Ile Tyr Ala Lys Asn Ala Asn  
1190 1195 1200

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Thr	Pro 1205	Phe	Val	Tyr	Tyr	Gly 1210	Ile	His	Glu	Gly	Ser 1215	Gln	Glu	Lys
Pro	Ile 1220	Asn	Leu	Lys	Val	Lys 1225	Lys	Asp	Gln	Val	Lys 1230	Leu	Leu	Lys
Glu	Arg 1235	Glu	Ser	Asp	Pro	Ser 1240	Leu	Thr	Met	Phe	Asn 1245	Tyr	Trp	Tyr
Ser	Met 1250	Lys	Met	Pro	Met	Ala 1255	Asn	Leu	Lys	Thr	Ala 1260	Asp	Thr	Ala
Ile	Gly 1265	Ile	Lys	Ser	Thr	Gly 1270	Glu	Leu	Asp	Val	Ser 1275	Leu	Ser	Asp
Val	Tyr 1280	Asp	Phe	Thr	Val	Lys 1285	Gln	Lys	Gly	Lys	Glu 1290	Ile	Lys	Ser
Phe	Lys 1295	Glu	Pro	Val	Gln	Leu 1300	Ser	Leu	Arg	Met	Phe 1305	Asp	Ile	Glu
Glu	Ala 1310	His	Asn	Pro	Ala	Ile 1315	Tyr	His	Val	Asp	Arg 1320	Lys	Lys	Lys
Ala	Phe 1325	Thr	Lys	Thr	Gly	His 1330	Gly	Ser	Val	Asp	Asp 1335	Asp	Met	Val
Thr	Gly 1340	Tyr	Thr	Asn	His	Phe 1345	Ser	Glu	Tyr	Thr	Ile 1350	Leu	Asn	Ser
Gly	Ser 1355	Asn	Asn	Lys	Pro	Pro 1360	Ala	Phe	Pro	Ser	Asp 1365	Gln	Pro	Thr
Gly	Gly 1370	Asp	Asp	Gly	Asn	His 1375	Gly	Gly	Gly	Ser	Asp 1380	Lys	Pro	Gly
Gly	Lys 1385	Gln	Pro	Thr	Asp	Gly 1390	Asn	Gly	Gly	Asn	Asp 1395	Thr	Pro	Pro
Gly	Thr 1400	Gln	Pro	Thr	Asn	Gly 1405	Ser	Gly	Gly	Asn	Gly 1410	Ser	Gly	Gly
Ser	Gly 1415	Thr	Asp	Gly	Pro	Ala 1420	Gly	Gly	Leu	Leu	Pro 1425	Asp	Thr	Ala
Thr	Ser 1430	Met	Tyr	Ser	Ile	Leu 1435	Leu	Ala	Gly	Phe	Leu 1440	Ile	Ser	Ala
Leu	Gly 1445	Thr	Ala	Met	Tyr	Leu 1450	His	Gln	Arg	Arg	Lys 1455	Gln	Asn	Arg

Ala Asn Gln Ala  
1460

<210> 75  
<211> 694  
<212> PRT  
<213> Corynebacterium glutamicum

<220>  
<221> misc\_feature  
<222> (1)..(694)  
<223> Corynebacterium glutamicum Cg0397 (nucleotide hydrolase)  
>gi|41324559|emb|CAF18899.1| PROBABLE 5'-NUCLEOTIDASE PRECURSOR  
[Corynebacterium glutamicum ATCC 13032]

<400> 75

Met Lys Arg Leu Ser Arg Ala Ala Leu Ala Val Val Ala Thr Thr Ala  
1 5 10 15

Val Ser Phe Ser Ala Leu Ala Val Pro Ala Phe Ala Asp Glu Ala Ser  
20 25 30

Asn Val Glu Leu Asn Ile Leu Gly Val Thr Asp Phe His Gly His Ile  
35 40 45

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

Glu Met Gly Ala Ser Gly Val Ala Cys Tyr Val Asp Ala Glu Arg Ala  
65 70 75 80

Asp Asn Pro Asn Thr Arg Phe Ile Thr Val Gly Asp Asn Ile Gly Gly  
85 90 95

Ser Pro Phe Val Ser Ser Ile Leu Lys Asp Glu Pro Thr Leu Gln Ala  
100 105 110

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

Asp Gln Gly Tyr Ser Asp Leu Val Asn Arg Val Ser Leu Asp Gly Ser  
130 135 140

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

Pro Ala Pro Ala Lys Ser Glu Ile Ile Glu Met Asp Gly Val Lys Ile  
165 170 175

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

Ala Gly Ile Glu Gly Ile Thr Phe Thr Gly Asp Ile Asp Ala Ile Asn  
195 200 205

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Ala Glu Ala Asp Arg Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile  
210 215 220

Ala Leu Ile His Ala Glu Ala Ala Pro Thr Asp Leu Phe Ser Asn Asn  
225 230 235 240

Val Asp Val Val Phe Ser Gly His Thr His Phe Asp Tyr Val Ala Glu  
245 250 255

Gly Glu Ala Arg Gly Asp Lys Gln Pro Leu Val Val Ile Gln Gly His  
260 265 270

Glu Tyr Gly Lys Val Ile Ser Asp Val Glu Ile Ser Tyr Asp Arg Glu  
275 280 285

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

Val Val Glu Asn Cys Glu Thr Pro Asn Thr Ala Val Asp Ala Ile Val  
305 310 315 320

Ala Ala Ala Val Glu Ala Ala Glu Glu Ala Gly Asn Glu Val Val Ala  
325 330 335

Thr Ile Asp Asn Gly Phe Tyr Arg Gly Ala Asp Glu Glu Gly Thr Thr  
340 345 350

Gly Ser Asn Arg Gly Val Glu Ser Ser Leu Ser Asn Leu Ile Ala Glu  
355 360 365

Ala Gly Leu Trp Ala Val Asn Asp Ala Thr Ile Leu Asn Ala Asp Ile  
370 375 380

Gly Ile Met Asn Ala Gly Gly Val Arg Ala Asp Leu Glu Ala Gly Glu  
385 390 395 400

Val Thr Phe Ala Asp Ala Tyr Ala Thr Gln Asn Phe Ser Asn Thr Tyr  
405 410 415

Gly Val Arg Glu Val Ser Gly Ala Gln Phe Lys Glu Ala Leu Glu Gln  
420 425 430

Gln Trp Lys Glu Thr Gly Asp Arg Pro Arg Leu Ala Leu Gly Leu Ser  
435 440 445

Ser Asn Val Gln Tyr Ser Tyr Asp Glu Thr Arg Glu Tyr Gly Asp Arg  
450 455 460

Ile Thr His Ile Thr Phe Asn Gly Glu Pro Met Asp Met Lys Glu Thr  
465 470 475 480

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Tyr Arg Val Thr Gly Ser Ser Phe Leu Leu Ala Gly Gly Asp Ser Phe  
485 490 495

Thr Ala Phe Ala Glu Gly Gly Pro Ile Ala Glu Thr Gly Met Val Asp  
500 505 510

Ile Asp Leu Phe Asn Asn Tyr Ile Ala Ala His Pro Asp Ala Pro Ile  
515 520 525

Arg Ala Asn Gln Ser Ser Val Gly Ile Ala Leu Ser Gly Pro Ala Val  
530 535 540

Ala Glu Asp Gly Thr Leu Val Pro Gly Glu Glu Leu Thr Val Asp Leu  
545 550 555 560

Ser Ser Leu Ser Tyr Thr Gly Pro Glu Ala Lys Pro Thr Thr Val Glu  
565 570 575

Val Thr Val Gly Thr Glu Lys Lys Thr Ala Asp Val Asp Asn Thr Ile  
580 585 590

Val Pro Gln Phe Asp Ser Thr Gly Lys Ala Thr Val Thr Leu Thr Val  
595 600 605

Pro Glu Gly Ala Thr Ser Val Lys Ile Ala Thr Asp Asn Gly Thr Thr  
610 615 620

Phe Glu Leu Pro Val Thr Val Asn Gly Glu Gly Asn Asn Asp Asp Asp  
625 630 635 640

Asp Asp Lys Glu Gln Gln Ser Ser Gly Ser Ser Asp Ala Gly Ser Leu  
645 650 655

Val Ala Val Leu Gly Val Leu Gly Ala Leu Gly Gly Leu Val Ala Phe  
660 665 670

Phe Leu Asn Ser Ala Gln Gly Ala Pro Phe Leu Ala Gln Leu Gln Ala  
675 680 685

Met Phe Ala Gln Phe Met  
690

<210> 76  
<211> 347  
<212> PRT  
<213> Escherichia coli

<220>  
<221> misc\_feature  
<222> (1)..(347)  
<223> Escherichia coli NadA >gi|260450103|gb|ACX40525.1| quinolinate  
synthetase complex, A subunit [Escherichia coli DH1]

&lt;400&gt; 76

Met Ser Val Met Phe Asp Pro Asp Thr Ala Ile Tyr Pro Phe Pro Pro  
 1 5 10 15  
 Lys Pro Thr Pro Leu Ser Ile Asp Glu Lys Ala Tyr Tyr Arg Glu Lys  
 20 25 30  
 Ile Lys Arg Leu Leu Lys Glu Arg Asn Ala Val Met Val Ala His Tyr  
 35 40 45  
 Tyr Thr Asp Pro Glu Ile Gln Gln Leu Ala Glu Glu Thr Gly Gly Cys  
 50 55 60  
 Ile Ser Asp Ser Leu Glu Met Ala Arg Phe Gly Ala Lys His Pro Ala  
 65 70 75 80  
 Ser Thr Leu Leu Val Ala Gly Val Arg Phe Met Gly Glu Thr Ala Lys  
 85 90 95  
 Ile Leu Ser Pro Glu Lys Thr Ile Leu Met Pro Thr Leu Gln Ala Glu  
 100 105 110  
 Cys Ser Leu Asp Leu Gly Cys Pro Val Glu Glu Phe Asn Ala Phe Cys  
 115 120 125  
 Asp Ala His Pro Asp Arg Thr Val Val Val Tyr Ala Asn Thr Ser Ala  
 130 135 140  
 Ala Val Lys Ala Arg Ala Asp Trp Val Val Thr Ser Ser Ile Ala Val  
 145 150 155 160  
 Glu Leu Ile Asp His Leu Asp Ser Leu Gly Glu Lys Ile Ile Trp Ala  
 165 170 175  
 Pro Asp Lys His Leu Gly Arg Tyr Val Gln Lys Gln Thr Gly Gly Asp  
 180 185 190  
 Ile Leu Cys Trp Gln Gly Ala Cys Ile Val His Asp Glu Phe Lys Thr  
 195 200 205  
 Gln Ala Leu Thr Arg Leu Gln Glu Glu Tyr Pro Asp Ala Ala Ile Leu  
 210 215 220  
 Val His Pro Glu Ser Pro Gln Ala Ile Val Asp Met Ala Asp Ala Val  
 225 230 235 240  
 Gly Ser Thr Ser Gln Leu Ile Ala Ala Ala Lys Thr Leu Pro His Gln  
 245 250 255  
 Arg Leu Ile Val Ala Thr Asp Arg Gly Ile Phe Tyr Lys Met Gln Gln  
 260 265 270



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Ala Val Pro Asp Lys Glu Leu Leu Glu Ala Pro Thr Ala Gly Glu Gly  
275 280 285

Ala Thr Cys Arg Ser Cys Ala His Cys Pro Trp Met Ala Met Asn Gly  
290 295 300

Leu Gln Ala Ile Ala Glu Ala Leu Glu Gln Glu Gly Ser Asn His Glu  
305 310 315 320

Val His Val Asp Glu Arg Leu Arg Glu Arg Ala Leu Val Pro Leu Asn  
325 330 335

Arg Met Leu Asp Phe Ala Ala Thr Leu Arg Gly  
340 345

<210> 77  
<211> 368  
<212> PRT  
<213> Bacillus subtilis

<220>  
<221> misc\_feature  
<222> (1)..(368)  
<223> Bacillus subtilis NadA >gi|16079837|ref|NP\_390663.1| quinolinate  
synthase A [Bacillus subtilis subsp. subtilis str. 168]

<400> 77

Met Ser Ile Leu Asp Val Ile Lys Gln Ser Asn Asp Met Met Pro Glu  
1 5 10 15

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

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

Gln Lys Asp Glu Val Ile Gln Phe Ala Asp Gln Thr Gly Asp Ser Leu  
50 55 60

Gln Leu Ala Gln Val Ala Glu Lys Asn Lys Glu Ala Asp Tyr Ile Val  
65 70 75 80

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

Glu Gln Gln Thr Val Val Leu Pro Asp Met Arg Ala Gly Cys Ser Met  
100 105 110

Ala Asp Met Ala Asp Met Gln Gln Thr Asn Arg Ala Trp Lys Lys Leu  
115 120 125

Gln His Ile Phe Gly Asp Thr Ile Ile Pro Leu Thr Tyr Val Asn Ser  
130 135 140

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Thr Ala Glu Ile Lys Ala Phe Val Gly Lys His Gly Gly Ala Thr Val  
145 150 155 160

Thr Ser Ser Asn Ala Lys Lys Val Leu Glu Trp Ala Phe Thr Gln Lys  
165 170 175

Lys Arg Ile Leu Phe Leu Pro Asp Gln His Leu Gly Arg Asn Thr Ala  
180 185 190

Tyr Asp Leu Gly Ile Ala Leu Glu Asp Met Ala Val Trp Asp Pro Met  
195 200 205

Lys Asp Glu Leu Val Ala Glu Ser Gly His Thr Asn Val Lys Val Ile  
210 215 220

Leu Trp Lys Gly His Cys Ser Val His Glu Lys Phe Thr Thr Lys Asn  
225 230 235 240

Ile His Asp Met Arg Glu Arg Asp Pro Asp Ile Gln Ile Ile Val His  
245 250 255

Pro Glu Cys Ser His Glu Val Val Thr Leu Ser Asp Asp Asn Gly Ser  
260 265 270

Thr Lys Tyr Ile Ile Asp Thr Ile Asn Gln Ala Pro Ala Gly Ser Lys  
275 280 285

Trp Ala Ile Gly Thr Glu Met Asn Leu Val Gln Arg Ile Ile His Glu  
290 295 300

His Pro Asp Lys Gln Ile Glu Ser Leu Asn Pro Asp Met Cys Pro Cys  
305 310 315 320

Leu Thr Met Asn Arg Ile Asp Leu Pro His Leu Leu Trp Ser Leu Glu  
325 330 335

Gln Ile Glu Lys Gly Glu Pro Ser Gly Val Ile Lys Val Pro Lys Ala  
340 345 350

Ile Gln Glu Asp Ala Leu Leu Ala Leu Asn Arg Met Leu Ser Ile Thr  
355 360 365

<210> 78  
<211> 428  
<212> PRT  
<213> Corynebacterium glutamicum

<220>  
<221> misc\_feature  
<222> (1)..(428)  
<223> Corynebacterium glutamicum NadA >gi|41325294|emb|CAF19774.1|  
QUINOLINATE SYNTHETASE [Corynebacterium glutamicum ATCC 13032]

&lt;400&gt; 78

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala  
 1 5 10 15  
 Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln  
 20 25 30  
 Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro  
 35 40 45  
 Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln  
 50 55 60  
 Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp  
 65 70 75 80  
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp  
 85 90 95  
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala  
 100 105 110  
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly  
 115 120 125  
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln  
 130 135 140  
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met  
 145 150 155 160  
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile  
 165 170 175  
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala  
 180 185 190  
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser  
 195 200 205  
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg  
 210 215 220  
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala  
 225 230 235 240  
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro  
 245 250 255  
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu  
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Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile  
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Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro  
 290 295 300

Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr  
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Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe  
 325 330 335

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