

32492wo_ST25
SEQUENCE LISTING

<110> DSM IP Assets B.V.
<120> MICROBIAL PRODUCTION OF NICOTINAMIDE RIBOSIDE
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<213> Francisella tularensis

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<222> (1)..(249)
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Met Lys Ile Val Lys Asp Phe Ser Pro Lys Glu Tyr Ser Gln Lys Leu
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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 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
245

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<213> Francisella tularensis

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gattcagcag ttgcggcttc tttagctgtc aaaactggat taccaactac agctttaata 180
ctaccttcag ataataatca acaccaagat atgcaagatg ctctagagct tattgaaatg 240
cttaatatg aacattatac catttcgatt caaccagctt atgaggcttt tcttgcttca 300
acgcaaagct ttacaaatct acaaaacaat agacaacttg tgatcaaggg aaatgctcaa 360
gcacgtttta ggatgatgta tttgtatgcc tatgcgcaac aatataacag aatagttata 420
ggtactgata atgcttgtga gtggtatatg ggatatttta caaaattcgg tgatggggct 480
gccgatatac ttccactagt taatctcaaa aaatctcaag tttttgaatt agggcaatac 540
ctagatgtcc ctaaaaacat acttgataaa gctccatctg caggactatg gcaaggacaa 600
actgatgagg atgaaatggg tgtaacttat caagaaattg atgatttctt agatggtaaa 660
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<213> Francisella sp.

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Met Ser Val Val Lys Asn Phe Lys Pro Asn Glu Tyr Ala Asn Lys Ile
 1 5 10 15
 Thr Glu Trp Leu Lys Asp Ser Cys Leu Asn Tyr Pro Ala Glu Gly Phe
 20 25 30
 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
 225 230 235 240
 Arg Ile Met Ala Lys Ala Pro Asp Phe
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<212> PRT
 <213> Francisella Guangzhouensis

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 <223> CP010427.1_translation Francisella Guangzhouensis strain
 08HL01032, NadE

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Met Asn Val Val Lys Asn Phe Thr Pro Glu Lys Tyr Ser Glu Lys Leu
 1 5 10 15

Ile Gln Trp Leu Thr Asn Ser Cys Ile Lys Tyr Pro Ala Glu Gly Phe
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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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230

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Arg Lys Met Ala Leu Thr Pro Asp Phe
245

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

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

Ser Ala Gly Leu Trp Gln Gly Gln Thr Asp Glu Asp Glu Met Gly Val
Page 5

195

200

205

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

Lys Ala Leu Glu Arg Ile Ser 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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 philomiragia ATCC 25017, Nade

<400> 6

Met Lys Ile Ile Lys Asn Phe Ile Ala Glu Glu Tyr Ser Lys Lys Leu
 1 5 10 15

Ile Glu Trp Leu Lys Lys Ile Cys Ile Asn 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 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
245

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[FSC 153], NadE

<400> 7

Met Lys Ile Ile Lys Asn Phe Ile Ala Glu Glu Tyr Ser Lys Lys Leu
1 5 10 15

Ile Glu Trp Leu Lys Lys Ile Cys Ile Asn 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 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
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
245

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<223> CP003402.1_translation Francisella noatunensis subsp. orientalis
str. Toba 04, NadE

<400> 8

Met Lys Ile Ile Lys Asn Phe Ile Ala Lys Glu Tyr Ser Lys Lys Leu
1 5 10 15

Ile Glu Trp Leu Lys Lys Ile Cys Ile Asn 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 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
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
225 230 235 240

Arg Ser Ile Ala Phe Thr Pro Asp Phe
245

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NadE

<400> 9

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

Ile Glu Trp Leu Lys Lys Ile Cys Ile Asn 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

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
225 230 235 240

Arg Ser Ile Ala Phe Thr Pro Asp Phe
245

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<213> Francisella persica

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<400> 10

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

Ile Asp Trp Leu Ser Asp Thr Cys Met Asn Tyr Pro Ala Glu Gly Phe
Page 10

Val Ile Gly₃₅ Leu Ser Gly Gly Ile₄₀ Asp Ser Ala Val Ala₄₅ Ala Ser Leu
 Ala Val₅₀ Lys Thr Gly Leu Ser₅₅ Thr Thr Ala Leu Ile₆₀ Leu Pro Ser Lys
 Asn₆₅ Asn Gln His Gln₇₀ Asp Ile Gln Asp Ala₇₅ Leu Glu Leu Ala Asp₈₀ Lys
 Ile Asn Ile Glu His₈₅ His Thr Ile Thr Ile₉₀ Gln Thr Val Tyr Glu₉₅ Thr
 Phe Leu Ala Ser₁₀₀ Ile Lys Lys Ile Thr₁₀₅ Asn Thr Glu Arg Asp₁₁₀ Arg Gln
 Leu Val Ile₁₁₅ Lys Gly Asn Ala Gln₁₂₀ Ala Arg Leu Arg Met₁₂₅ Met Tyr Leu
 Tyr Ala₁₃₀ Tyr Ala Gln Gln Tyr₁₃₅ Asn Arg Val Val Ile₁₄₀ Gly Thr Asp Asn
 Ala₁₄₅ Cys Glu Trp Tyr Met₁₅₀ Gly Tyr Phe Thr Lys₁₅₅ Phe Gly Asp Gly Ala₁₆₀
 Ala Asp Ile Leu Pro₁₆₅ Leu Val Asn Leu Lys₁₇₀ Lys Ser His Val Phe₁₇₅ Glu
 Leu Gly Lys Tyr₁₈₀ Leu Gly Val Pro Lys₁₈₅ Asn Ile Leu Asp Lys₁₉₀ Ala Pro
 Ser Ala Gly₁₉₅ Leu Trp Gln Gly Gln₂₀₀ Thr Asp Glu Asp Glu₂₀₅ Met Gly Val
 Thr Tyr₂₁₀ Gln Glu Ile Asp Asp₂₁₅ Phe Leu Asp Gly Lys₂₂₀ Gln Val Ser Ala
 Lys₂₂₅ Ala Leu Glu Arg Ile₂₃₀ Asn Phe Trp His Asn₂₃₅ Arg Ser His His Lys₂₄₀
 Arg Lys Leu Ala Leu₂₄₅ Ile Pro Asn Phe

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 <213> Francisella cf.

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<400> 11

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 Val Asn Trp Leu Ser Asp Thr Cys Ile Asn 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 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
 225 230 235 240
 Arg Lys Leu Ala Leu Thr Pro Asn Phe
 245

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<212> PRT
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 D9876, NadE

<400> 12

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 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
 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

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

32492wo_ST25
 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

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 strain NIH B-38, NadE

<400> 14

Met Lys Ile Val Lys Asp Phe Ser Pro Lys Glu Tyr Ser Gln Lys Leu
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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 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
 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

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
225 230 235 240

Arg Lys Leu Ala Leu Thr Pro Asn Phe
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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> Unknown

<220>
<223> 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

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

Asp Gly Gln Ile Ile Ser Ile Ala Pro Trp Tyr Asp Leu Ile Met Gln
85 90 95

Gln Leu Ser Pro Val Leu Asn Ser Glu Pro Glu Arg Val Asn Val Leu
100 105 110

Lys Gly Asn Leu Met Ala Arg Leu Arg Met Ile Ala Leu Phe Thr Thr
115 120 125

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

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

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

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

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

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

Gln Gln Ile Arg Phe Trp His Asn Arg Ser His His Lys Arg Met Leu
225 230 235 240

Pro Pro Lys Pro Lys
245

<210> 18
<211> 238
<212> PRT
<213> Actinobacillus succinogenes

<220>
<221> misc_feature
<222> (1)..(238)
<223> CP000746.1_translation Actinobacillus succinogenes 130Z, NadE
<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

32492wo_ST25

Ala Val Cys Ala His Leu Ala Ala Arg Thr Gly Ala Pro Val Gln Ala
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
<211> 753
<212> DNA
<213> Unknown

<220>
<223> Mannheimia succiniciproducens

<220>
<221> misc_feature
<222> (1)..(753)
<223> AE016827 Mannheimia succiniciproducens MBEL55E, Nade

<400> 19

32492wo_ST25

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ctttacggga tggacggcta tacactgggc gtcagcggcg gtattgacag cgccgtctgc      120
gctcatttgg cagcgcgcac cggcgcaccg gtacaagcct taattttgcc cgccgaagta      180
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 gcgagcgga cgtactgcct      480
ttagcgggat tgcgcaaaga gcaggtatth gaactcggac gttatcttgg cgtaccgcaa      540
agcgtgctgg ataaaaaac gagcgccggg ttatgggcag gacaaacgga cgaagctgaa      600
atgggtgtta cttatgcgga aatcgacgct tatctgcgcg gcgaaaccgt tagcccgacg      660
gcattgcaac aaatccgtth ctggcacaac cgthctcatc acaaacgtat gttgccacct      720
aaaccgaaat caccgatga agcggagtgt taa                                     753

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<210> 20
<211> 747
<212> DNA
<213> Dichelobacter nodosus

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<220>
<221> misc_feature
<222> (1)..(747)
<223> CP000513 Dichelobacter nodosus VCS1703A, NadE

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<400> 20
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ctgcatttac tcgcaaaac gggaaaaccc gtgcaagcgt tagttttgcc gatcaatgcg      180
aacgcgaacg attgtgaaga tgccgaatta gtgttaaaaa atgctaatat ttccggcaat      240
attatcgcg ctcgatgatgt ttataccgcc gcacaaaaca ccttggcgcc tgthtttaaat      300
cgcgattatg aacgtatgcc cgtattaaac ggcaatttaa tggcgcggtc gcgtatggth      360
atgctttata ccgtggcgca aagtcacgtt tcggtggtcg tgggaacgga taacgcggtg      420
gaatattatt taggttactt tacaaaatth ggcgacggcg cctgcgatat tttgccgctg      480
gcaaaactga caaatcaga agtaggacaa ttggcaaaag cgtaggcgt 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

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<210> 21
<211> 750
<212> DNA

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<213> *Actinobacillus succinogenes*

<220>

<221> misc_feature

<222> (1)..(750)

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

<400> 21

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ttatacggta tggacggcta cacgctggg gtcagcggcg gtatcgacag tgccgtttgc      120
gcccatttag cggcacgcac cggcgcccc gtacaggcat tgattttacc cgccgaagtc      180
accagccctg aagatgtggc ggatgctcag attaccttg aaagtgcagg tattgacggg      240
cggattattt ctatcgctcc ttggtacgat ttaattatgc tacaacttac cccgcatta      300
aatgcggaat ctgaacgcac taacgtattg aaaggtaact taatggcgcg cttacgtatg      360
atgcgattat ttaccacggc gcaaagccac cgttctatcg tattgggtac ggataacgcc      420
gccgaaatgt taacgggcta tttcaccaa ttcggcgacg gtgcggcgga cgtattgccg      480
ttagcgaggt tgcgcaaaga acaggtattc gaattagggc gttatcttgg cgtaccgaaa      540
tccgtgctgg agaaaaaacc gagtgcgggc ttatggcgcg ggcaaacgga cgagggggaa      600
atgggtgtca gttatgcgga aatcgacgcc tatctgcgcg gcgaaaccgt cagtccgcag      660
gcgttaaagc agattcaatt ctggcacaac cgttctcatc acaaacttat gctgccgccg      720
acgccagaac cgccggatga aatcgattaa                                     750

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<210> 22

<211> 750

<212> DNA

<213> *Francisella* cf.

<220>

<221> misc_feature

<222> (1)..(750)

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

<400> 22

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gattcagctg ttgcagcttc tttagctgtc aaaactggat taccaactac agctttaata      180
ctaccttcaa aaaacaatca acaccaagat atccaagatg ctctagaact tgttgagaaa      240
cttaatattg aacatcatat tgttacaatt caaccagcat acgaaaattt tctagcatca      300
acacaggaat ttataaatac agataataat agacaacttg tgatcaaggg aaatgctcaa      360
gcacgtttaa ggatgatgta tttatatgcc tatgcccaac aatataacag aatagttata      420
ggtactgata 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

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32492wo_ST25

caaatttcag caaaagccct agaaagaata aacttctggc ataatcgtag tcatcataag 720
agaaaactag cttaaactcc taattttctaa 750

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

<220>
<221> misc_feature
<222> (1)..(750)
<223> CP002872 Francisella sp. TX077308, NadE

<400> 23
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aaagagaatt gcataaaata tcctgctgaa ggttttgtga ttggtattag tgggtggatc 120
gattcggcag tagccgcac ttttagcagtc aaaacaggat tacctacaac tgctctaata 180
ttgccatcga agaacaatca agaccaagat atgcgagatg gaatagaact aatcgaaaat 240
cttaatatag agtatcatc tgtttcaata caacctgctt atgacacggt tatagagtca 300
acatttaact ttacaaactc acaaaatgat cgccaacatg ttatcaaagg aaatgcccaa 360
gcgcgtctta gaatgatgta tttatatgct tatgctcagc aaaataatag aattgttata 420
ggtacagata acgcatgtga atgggtacatg ggatatttca ctaaatttgg tgatgggtgca 480
gcagatatat taccacttat taatctcaaa aaatctcaag tttttgaact aggtaaatac 540
ttaaagtgc caaaaaacat tatccaaaaa gatccttctg ccggtctatg gcaagggtcaa 600
actgatgagg atgaaatggg tgtcacatac aaagaaattg atgacttctt agacggtaaa 660
gaagtctcag aaaaagctct cgaaagaata agcttctggc ataatcgtag tcaccataaa 720
agatccatgg cttttacccc taatttttaa 750

<210> 24
<211> 750
<212> DNA
<213> Francisella sp.

<220>
<221> misc_feature
<222> (1)..(750)
<223> CP009574 Francisella sp. FSC1006, NadE

<400> 24
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aaagactctt gtttaaatta tcccgtgaa 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

32492wo_ST25

gctcgtttta gaatgatata cttgtatgct tacgctcagc aaaataatag aatggtaatt	420
ggtagacagata atgcttgtga atggtatatg ggctatttta caaaatttgg agatggagcc	480
gctgatatac tgcctcttat aaaattaaaa aaatcacaaag tttttgaatt aggtagctat	540
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

<210> 25
 <211> 753
 <212> DNA
 <213> Francisella guangzhouensis

<220>
 <221> misc_feature
 <222> (1)..(753)
 <223> Francisella guangzhouensis strain 08HL01032, NadE

<400> 25	
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gattctgcag tatgtgcatc actttttatcc aaaactgatc ttcctacaac agctttttata	180
ctaccatcaa aaaataactc tgatcaagat atgatcgatg cattagaact tataaataaa	240
ttaaataattc cataccatat aataccaatc cagccagttt atgaaagttt tctaaagtcc	300
acacagctat ttacaaatcc acaaaatgac agacaaaatg tcataaaagg taacgctcaa	360
gctcgtttta gaatgatgta tttatatgct tatgcacaac aaaataatcg tatagtagtt	420
ggaacagata atgcttgtga atggtatatg ggttattttca ccaaatttgg cgatggagct	480
gctgatatac taccattaat aaatcttaaa agtcccagg tatttgagtt aggtaaatac	540
ttagatgttc caaggaatat cctaactaag gcaccctctg ctgggtctttg gcaaggccaa	600
actgatgaag gtgaaatggg agttacttat caggaaatag ataattttct cgacggtaaa	660
gaagtatcgc cagcaacttt tgaaaaaata agctactggc ataatcgctc tcaccacaaa	720
agaaagatgg cttaacgcc agattttaac taa	753

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

<220>
 <221> misc_feature
 <222> (1)..(750)
 <223> CP013022 Francisella persica ATCC VR-331, NadE

<400> 26	
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agtgatactt gtatgaatta ccctgctgaa ggatttgtca ttggtcttag cggtgggtata	120

32492wo_ST25

gattcggcag	ttgcagcttc	tttagctgtc	aaaactggat	tatcaactac	agctttaata	180
ttaccatcaa	aaaacaatca	acaccaagat	atacaagatg	ctctagaact	tgagataaaa	240
attaatattg	aacatcatac	tattacaatt	caaacagtat	acgaaacttt	tcttgcgta	300
ataaaaaaaaa	ttacaaatac	cgaacgtgat	agacaacttg	tcattaaagg	aaatgctcaa	360
gctcgtttga	ggatgatgta	tttatatgcc	tatgctcaac	aatataatag	agtgggttatt	420
ggtactgata	atgcttgtga	atgggtatatg	ggatatttta	caaagtttgg	tgatgggtgct	480
gctgatattc	ttccactagt	taatctcaaa	aaatctcacg	tttttgaatt	aggtaaatac	540
ttagggtgtc	ctaaaaatat	acttgataaa	gctccatctg	ctgggctatg	gcaaggacaa	600
actgatgaag	atgaaatggg	cgtaacttat	caagaaattg	atgatttctt	agatggtaag	660
caagtttcag	cgaaagctct	agaaagaata	aatttctggc	ataatcgtag	tcatacataag	720
agaaaactag	ctttaattcc	taatttctaa				750

<210> 27
 <211> 753
 <212> DNA
 <213> Unknown

<220>
 <223> Mannheimia succiniciproducens

<220>
 <221> misc_feature
 <222> (1)..(753)
 <223> Optimized_AE016827 Mannheimia succiniciproducens MBEL55E, NadE

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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 acaaagccat cgttctattg tgctgggcac cgataatgcg 420
gcggaatggc	tgacgggtta ttttacaaa ttcggcgacg gcgcagcgga cgtactgccg 480
ctggcggggc	tgcgcaaaga gcaggtatth gaactgggcc gttatctggg cgtaccgcaa 540
agcgtgctgg	ataaaaaacc gagcgccggt ctgtgggcag gccaaacgga cgaagctgaa 600
atgggtgtta	cctatgcgga aatcgacgct tatctgcgcg gcgaaaccgt tagcccgag 660
gcactgcaac	aaatccgtth ctggcacaac cgttctcatc acaaacgtat gctgccgccg 720
aaaccgaaat	caccggatga agcggagtgt taa 753

<210> 28
 <211> 747
 <212> DNA

<213> Dichelobacter nodosus

<220>

<221> misc_feature

<222> (1)..(747)

<223> Optimized_CP000513 Dichelobacter nodosus VCS1703A, NadE

<400> 28

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ctgcatctgc tggccaaaac gggcaaacca gtgcaagcgc tggttctgcc gatcaatgcg      180
aacgcgaacg attgtgaaga tgccgaactg gtgctgaaaa atgctaatat ttccggcaat      240
attatcgcgc tggatgatgt ttataccgcc gcacaaaaca ccctggcgcc ggttctgaat      300
cgcgattatg aacgtatgcc ggtactgaac ggcaatctga tggcgcgccct gcgtatggtt      360
atgctgtata ccgtggcgca aagtcacgtc tcggtgggtc tgggcacgga taacgcggtg      420
gaatattatc tgggttactt taccaaattt ggcgacggcg cctgcgatat tctgccgctg      480
gcaaaactga ccaaatcaga agtaggccaa ctggcaaaag cgctgggctg tccgaaaaaa      540
atccgcgaaa aagcgccgag cgcgggcctg tggcaaggcc aaaccgatga aaacgaaatc      600
ggcgtatcgt acgcggatct ggatgctttt ctgtgcggta aaaccgttga tgatgccgtc      660
cgcgaaaaaa ttgcttattg gcatcaacgc tcgcatcata aacgtatgct gccgccgatg      720
ccggaaatcg gcctgtctct ggcgtaa                                     747

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<210> 29

<211> 750

<212> DNA

<213> Actinobacillus succinogenes

<220>

<221> misc_feature

<222> (1)..(750)

<223> Optimized_CP000746 Actinobacillus succinogenes 130Z, NadE

<400> 29

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ctgtacggta tggacggcta cacgctgggc gtcagcggcg gtatcgacag tgccgtttgc      120
gcccattctg cggcacgcac cggcgccccg gtacaggcac tgattctgcc ggcggaagtc      180
accagcccgg aagatgtggc ggatgctcag attaccctgg aaagtgcagg tattgatggc      240
cgcattattt ctatcgctcc gtggtacgat ctgattatgc tgcaactgac cccggcactg      300
aatgcggaat ctgaacgcat taacgtactg aaaggtaacc tgatggcgcg cctgcgtatg      360
atcgcactgt ttaccacggc gcaaagccac cgttctatcg tactgggtac ggataacgcc      420
gccgaaatgc tgacgggcta tttaccaaaa ttcggcgacg gtgcggcgga cgtactgccg      480
ctggcgcgcc tgcgcaaaga acaggtattc gaactgggcc gttatctggg cgtaccgaaa      540
tccgtgctgg agaaaaaacc gagtgcgggc ctgtgggcgg gccaaacgga cgagggcgaa      600
atgggtgtca gttatgcgga aatcgacgcc tatctgcgcg gcgaaaccgt cagtccgcag      660

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32492wo_ST25

gcgctgaaac agattcaatt ctggcacaac cgttctcatc acaaacgtat gctgccgccg 720
acgccggaac cgccggatga aattgattaa 750

<210> 30
<211> 750
<212> DNA
<213> Francisella cf.

<220>
<221> misc_feature
<222> (1)..(750)
<223> Optimized_CP002558 Francisella cf. novicida 3523, NadE

<400> 30
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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
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gcacgtctgc gcatgatgta tctgtatgcc tatgcccac aatataaccg cattgttatt 420
ggtagcgata atgcttgtga gtggtatatg ggctatttta ccaaatttgg tgatggcgct 480
gctgatattt ttccgctgat taatctgaaa aaatcacaag tttttgaact gggtaaatac 540
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accgatgagg atgaaatggg cgtaacctat caagaaattg atgatttcct ggatggtaaa 660
caaatttcag caaaagccct ggaacgcatt aacttctggc ataatcgtag tcatcataaa 720
cgcaaactgg ctctgacccc gaatttctaa 750

<210> 31
<211> 750
<212> DNA
<213> Francisella sp.

<220>
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<223> Optimized_CP002872 Francisella sp. TX077308, NadE

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gattcggcag tagccgcac tctggcagtc aaaaccggcc tgccgaccac cgctctgatt 180
ctgccgtcga aaaacaatca agaccaagat atgcgcgatg gcattgaact gatcgaaaat 240
ctgaatattg agtatcatat cgtttcaatt caaccggctt atgacacggt tattgagtca 300
acctttaact ttaccaactc acaaaatgat cgccaacatg ttatcaaagg caatgcccaa 360

32492wo_ST25

gcgcgctctgc 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
gaagtctcag aaaaagctct ggaacgcatt agcttctggc ataatcgtag tcaccataaa	720
cgcatcatgg 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

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gattcagcag tagcagtctc tctggcagta aataccggcc tgccgggttac cggcctgatt	180
atgccgtcaa aaaataatga tgataaagat accctggatg ctattgaact ggctaaaaaa	240
ctgaatattg aatatcatct gattccgatt cagccgggtat atgaaacctt tctggattca	300
gcggaagata ttaaaaacag tgctaattgac cgtcaacatg taatcaaagg caatgcacaa	360
gctcgttttc gcatgattta cctgtatgct tacgctcagc aaaataatcg catggtaatt	420
ggtaccgata atgcttgtga atggtatatg ggctatttta ccaaatttgg cgatggcgcc	480
gctgatattc tgccgctgat taaactgaaa aaatcacaag tttttgaact gggtagctat	540
ctgaatgtac cgaataacat cctgaccaa gctccgagcg cgggcctgtg gctgggccaa	600
accgatgaag cagagatggg cgtttcatat caagaaattg atgatttcct ggatggtaaa	660
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<210> 33
 <211> 753
 <212> DNA
 <213> Francisella guangzhouensis

<220>
 <221> misc_feature
 <222> (1)..(753)
 <223> Optimized_CP010427 Francisella guangzhouensis strain 08HL01032, NadE

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32492wo_ST25

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ggcaccgata atgcttgtga atggtatatg ggttatttca ccaaatttgg cgatggcgct	480
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ctggatgttc cgcgcaatat cctgaccaa gcaccgtctg ctggtctgtg gcaaggccaa	600
accgatgaag gtgaaatggg cgttacctat caggaaattg ataattttct ggacggtaaa	660
gaagtatcgc cggcaacctt tgaaaaaatt agctactggc ataatcgctc tcaccacaaa	720
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<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

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gattcggcag ttgcagcttc tctggctgtc aaaaccggcc tgtcaaccac cgctctgatt	180
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attaaaaaaa ttaccaatac cgaacgtgat cgccaactgg tcattaaagg caatgctcaa	360
gctcgtctgc gcatgatgta tctgtatgcc tatgctcaac aatataatcg cgtgggttatt	420
ggtaccgata atgcttgtga atggtatatg ggctatttta ccaaatttgg tgatggtgct	480
gctgatattc tgccgctggt taatctgaaa aaatctcacg tttttgaact gggtaaatac	540
ctgggtgttc cgaaaaatat tctggataaa gctccgtctg ctggcctgtg gcaaggccaa	600
accgatgaag atgaaatggg cgtaacctat caagaaattg atgatttcct ggatggtaaa	660
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<210> 35
 <211> 750
 <212> DNA
 <213> Unknown

<220>
 <223> FtNadE_star_optimized

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

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 acccaatctt tcacgaacct gcagaacaat cgtcaactgg tgatcaaagg caatgcgcag 360
 gcccgtctgc gcatgatgta tctgtacgcg tatgcbgagc aatacaaccg cattgtttatc 420
 ggcaccgata atgcctgcga atggtacatg gggtattttta cgaaattcgg cgatgggtgca 480
 gctgacattc tgccgctggg caacctgaaa aaatcgcagg tgtttgaaact gggtaaatac 540
 ctggatgttc cgaaaaatat cctggacaaa gcaccgagcg cagggtctgtg gcaggggtcaa 600
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 caagtcagcg cgaaagccct ggaacgtatc aacttctggc acaaccgctc acatcataaa 720
 cgcaaaactgg cactgacccc gaacttctaa 750

<210> 36
 <211> 782
 <212> DNA
 <213> Bacillus

<220>
 <221> misc_feature
 <222> (1)..(782)
 <223> Optimized_FtNadE_star_Bacillus

<400> 36
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 attcggcgat ggtgctgctg acattcttcc gcttggttaac cttaaaaaat ctcagggtgtt 540
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32492wo_ST25

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gc	782

<210> 37
 <211> 785
 <212> DNA
 <213> *Bacillus Mannheimia succiniciproducens*

<220>
 <221> misc_feature
 <222> (1)..(785)
 <223> Optimized_AE016827_ *Bacillus Mannheimia succiniciproducens*
 MBEL55E, complete genome

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actttctccg gtacttaata gcgaaccgga acgcgttaac gtacttaaag gtaatcttat	360
ggcacgcctt cgtatgattg cgctttttac aacagcacia agccatcggt ctattgtgct	420
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tcttggcgta ccgcaaagcg tgcttgataa aaaaccgagc gctgggtcttt gggcaggcca	600
aacagacgaa gctgaaatgg gtgttacata cgcggaaatc gacgcttatc ttcgcggcga	660
aacagttagc ccgcaggcac ttcaacaaat ccgtttcttg cacaaccggt ctcatacacia	720
acgtatgctt ccgccgaaac cgaaatcacc ggatgaagcg gaatgttaag catgcagtaa	780
gtagc	785

<210> 38
 <211> 782
 <212> DNA
 <213> *Bacillus Francisella*

<220>
 <221> misc_feature
 <222> (1)..(782)
 <223> Optimized_CP002558_ *Bacillus Francisella* cf. *novicida* 3523,
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cattagcggg ggtattgatt cagcgggtgc agcttctctt gctgttaaaa caggccttcc	180

32492wo_ST25

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aaattttctt gcatcaacac aggaatttat taatacagat aataatcgcc aacttgatgat	360
caaaggcaat gctcaagcac gtcttcgcat gatgtatctt tatgcttatg ctcaacaata	420
taaccgcatt gttattggta cagataatgc ttgtgaatgg tatatgggct attttacaaa	480
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tgaacttggt aaataccttg atgttccgaa aaatattatt gataaagctc cgtctgctgg	600
cctttggcaa ggccaaacag atgaagatga aatgggcgta acatatcaag aaattgatga	660
tttccttgat ggtaaacaaa tttcagcaaa agctcttgaa cgcattaact tctggcataa	720
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gc	782

<210> 39
 <211> 782
 <212> DNA
 <213> Francisella sp.

<220>
 <221> misc_feature
 <222> (1)..(782)
 <223> Optimized_CP002872_Bacillus Francisella sp. TX077308, complete genome

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caaaggcaat gctcaagcgc gtcttcgcat gatgtatctt tatgcttatg ctcaacaaaa	420
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tgaacttggt aaatacctta aagtgccgaa aaacattatc caaaaagatc cgtctgctgg	600
tctttggcaa ggtcaaacag atgaagatga aatgggtggt acatacaaag aaattgatga	660
cttccttgac ggtaaagaag tttcagaaaa agctcttgaa cgcattagct tctggcataa	720
tcgttctcac cataaacgca gcatggcttt tacaccgaat ttttaagcat gcagtaagta	780
gc	782

<210> 40
 <211> 750
 <212> DNA

<213> Unknown

<220>

<223> DQ682092-AL_Reverted

<220>

<221> misc_feature

<222> (1)..(750)

<223> DQ682092-AL_Reverted

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accgatgaag acgaaatggg cgttacgtat caggaaattg atgacttcct ggatggtaaa    660
caagtcagcg cgaaagccct ggaacgtatc aacttctggc acaacgtctc acatcataaa    720
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<210> 41

<211> 540

<212> PRT

<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)..(540)

<223> Escherichia coli NadB

<400> 41

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1           5           10          15

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

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32492wo_ST25

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

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
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Leu His Phe Thr Leu Asp Tyr Pro Glu Leu Leu Thr His Ser Gly Pro
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Ser Ile Leu Ser Pro Gly Asn His Tyr Ile Asn Arg
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<210> 42
<211> 531
<212> PRT
<213> Bacillus subtilis

<220>
<221> misc_feature
<222> (1)..(531)
<223> Bacillus subtilis NadB

<400> 42

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

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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
 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

32492wo_ST25

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

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
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<210> 43
<211> 750
<212> DNA
<213> Francisella sp.

<220>
<221> misc_feature

32492wo_ST25

<222> (1)..(750)

<223> Optimized_CP002872_Reverted Francisella sp. TX077308

<400> 43

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accgatgagg atgaaatggg tgtcacctac aaagaaattg atgacttcct ggacggtaaa    660
gaagtctcag aaaaagctct ggaacgcatt agcttctggc ataatgttag tcaccataaa    720
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<210> 44

<211> 828

<212> DNA

<213> E. coli

<220>

<221> misc_feature

<222> (1)..(828)

<223> E. coli NadE

<400> 44

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gaggaaattc gtcgtagtgt cgattttctg aaaagctacc tgcaaaactta tccgttcatt    120
aatcactggt tgctcgggat cagcggcggg caggactcca cgcttgccgg aaagctgtgc    180
cagatggcga ttaatgagct ggcctggaa accggcaacg aatcactgca atttattgcc    240
gtacgcctgc cctatggtgt tcaggccgac gaacaagatt gccaggatgc cattgccttt    300
attcaaccgg atcgcgtatt aaccgttaat atcaagggcg cggatttggc cagcgaacag    360
gcattgcggg aagcaggcat tgaactgagc gattttgtcc gtggcaatga aaaagcgcgt    420
gagcggatga aagcacaata tagcattgct ggtatgacca gcggtgtcgt ggtgggcacc    480
gatcatgcag cagaagccat taccggattc ttcactaaat atggtgacgg cggtagcgac    540
attaatccgc tgtatcgtct caacaaacgt cagggtaaac agttactggc ggcattagct    600
tgcccggaac acctttataa gaaagcgcca acggccgatc tggaagatga tcgcccttct    660
ctgccgatg aagtggcact cggcgtgacc tatgacaata tcgacgacta tctggaaggg    720
aaaaacgtac ctcaacaggt cgccagaaca atagagaact ggtatctgaa aaccgaacat    780

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aaacgccgtc cgccaattac cgttttcgat gatttctgga aaaagtaa

828

<210> 45
<211> 750
<212> DNA
<213> Unknown

<220>
<223> C. glutamicum

<220>
<221> misc_feature
<222> (1)..(750)
<223> FnNadE optimized for C. glutamicum

<400> 45
atgaaaattg tgaaagattt ttccccaaaa gaatattccc aaaatctggt gaattggctg 60
tccgatacct gtattaatta tccagcagaa ggctttgtga tcggcatttc cgggtggtatt 120
gattccgcag tggcagcatc cctggcagtg aaaaccggcc tgccaaccac cgcactgatt 180
ctgccatcca aaaacaatca acaccaagat attcaagatg cactggaact ggtggaaaaa 240
ctgaatattg aacatcatat tgtgaccatt caaccagcat acgaaaattt tctggcatcc 300
accaggaat ttattaatac cgataataat cgccaactgg tgatcaaagg caatgcacaa 360
gcacgcctgc gcatgatgta tctgtatgca tatgcacaac aatataaccg cattgtgatt 420
ggtagcgata atgcatgtga atggatatat ggctatttta ccaaatttgg tgatggcgca 480
gcagatattt ttccactgat taatctgaaa aaatcccaag tgtttgaact gggtaaatac 540
ctggatgtgc caaaaaatat tattgataaa gcaccatccg caggcctgtg gcaaggccaa 600
accgatgaag atgaaatggg cgtgacctat caagaaattg atgatttcct ggatggtaaa 660
caaatttccg caaaagcact ggaacgcatt aacttctggc ataatcgctc ccatcataaa 720
cgcaaactgg cactgacccc aaatttctaa 750

<210> 46
<211> 828
<212> DNA
<213> E. coli

<220>
<221> misc_feature
<222> (1)..(828)
<223> E. coli NadE enzyme (EcNadE)

<400> 46
atgacattgc aacaacaaat aataaaggcg ctgggcgcaa aaccgcagat taatgctgaa 60
gaggaaattc gtcgtagtgt cgattttctg aaaagctacc tgcaaaactta tccgttcatt 120
aaatcactgg tgctcgggat cagcggcggc caggactcca cgcttgccgg aaagctgtgc 180
cagatggcga ttaatgagct ggcctggaa accggcaacg aatcactgca atttattgcc 240
gtacgcctgc cctatgggtg tcaggccgac gaacaagatt gccaggatgc cattgccttt 300
attcaaccgg atcgcgtatt aaccgttaat atcaagggcg cggatttggc cagcgaacag 360

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gcattgcggg aagcaggcat tgaactgagc gattttgtcc gtggcaatga aaaagcgcgt      420
gagcggatga aagcacaata tagcattgcg ggtatgacca gcggtgtcgt ggtgggcacc      480
gatcatgcag cagaagccat taccggattc ttcactaaat atggtgacgg cggtacggac      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

```

```

<210> 47
<211> 750
<212> DNA
<213> Francisella

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```

<220>
<221> misc_feature
<222> (1)..(750)
<223> Optimized_CP002558_Reverted Francisella cf. novicida 3523

```

```

<400> 47
atgaaaattg ttaaagattt tagtccgaaa gaatattcac aaaatctggt taattggctg      60
agtgatacct gtattaatac tccggctgaa ggctttgtaa tcggcattag cgggtggtatt      120
gattcagcgg ttgcagcttc tctggctgtc aaaaccggcc tgccgaccac cgctctgatt      180
ctgccgtcaa aaaacaatca acaccaagat attcaagatg ctctggaact ggttgagaaa      240
ctgaatattg aacatcatat tgttaccatt caaccggcat acgaaaattt tctggcatca      300
accaggaat ttattaatac cgataataat cgccaactgg tgatcaaagg caatgctcaa      360
gcacgtctgc gcatgatgta tctgtatgcc tatgccggcc aatataaccg cattgttatt      420
ggtaccgata atgcttgtga gtgggtatat 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 ataatgttag tcatcataaa      720
cgcaaactgg ctctgacccc gaatttctaa      750

```

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

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<220>
<223> CAG83794 - 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

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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

<210> 49
<211> 271
<212> PRT
<213> Unknown

<220>
<223> An02g02380 - NMN nucleotidase (SDT1 homolog)

<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

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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

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> An02g02380 - NMN nucleotidase (SDT1 homolog)

<220>
<221> misc_feature
<222> (1)..(411)
<223> An02g02380 - NMN nucleotidase (SDT1 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
 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 32492wo_ST25 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> 410
<212> PRT
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)..(410)
<223> Escherichia coli NadR (NMN synthetase, NR kinase, negative
regulator of NAD biosynthesis) >gi|90111746|ref|NP_418807.4|
trifunctional protein: nicotinamide mononucleotide
adenylyltransferase, ribosylnicotinamide kinase, transcriptional

<400> 51

Met Ser Ser Phe Asp Tyr Leu Lys Thr Ala Ile Lys Gln Gln Gly Cys
1 5 10 15

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

Ser Gln Leu Leu Asn Ala Lys Ile Lys Ser Pro Ser Ala Gln Lys Leu
35 40 45

Glu Ala Leu His Arg Phe Leu Gly Leu Glu Phe Pro Arg Gln Lys Lys
50 55 60

Thr Ile Gly Val Val Phe Gly Lys Phe Tyr Pro Leu His Thr Gly His
65 70 75 80

Ile Tyr Leu Ile Gln Arg Ala Cys Ser Gln Val Asp Glu Leu His Ile
85 90 95

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

Ala Met Ser Gln Gln Pro Thr Val Pro Asp Arg Leu Arg Trp Leu Leu
115 120 125

Gln Thr Phe Lys Tyr Gln Lys Asn Ile Arg Ile His Ala Phe Asn Glu
Page 45

130 135 140
 Glu Gly Met Glu Pro Tyr Pro His Gly Trp Asp Val Trp Ser Asn Gly
 145 150 155 160
 Ile Lys Lys Phe Met Ala Glu Lys Gly Ile Gln Pro Asp Leu Ile Tyr
 165 170 175
 Thr Ser Glu Glu Ala Asp Ala Pro Gln Tyr Met Glu His Leu Gly Ile
 180 185 190
 Glu Thr Val Leu Val Asp Pro Lys Arg Thr Phe Met Ser Ile Ser Gly
 195 200 205
 Ala Gln Ile Arg Glu Asn Pro Phe Arg Tyr Trp Glu Tyr Ile Pro Thr
 210 215 220
 Glu Val Lys Pro Phe Phe Val Arg Thr Val Ala Ile Leu Gly Gly Glu
 225 230 235 240
 Ser Ser Gly Lys Ser Thr Leu Val Asn Lys Leu Ala Asn Ile Phe Asn
 245 250 255
 Thr Thr Ser Ala Trp Glu Tyr Gly Arg Asp Tyr Val Phe Ser His Leu
 260 265 270
 Gly Gly Asp Glu Ile Ala Leu Gln Tyr Ser Asp Tyr Asp Lys Ile Ala
 275 280 285
 Leu Gly His Ala Gln Tyr Ile Asp Phe Ala Val Lys Tyr Ala Asn Lys
 290 295 300
 Val Ala Phe Ile Asp Thr Asp Phe Val Thr Thr Gln Ala Phe Cys Lys
 305 310 315 320
 Lys Tyr Glu Gly Arg Glu His Pro Phe Val Gln Ala Leu Ile Asp Glu
 325 330 335
 Tyr Arg Phe Asp Leu Val Ile Leu Leu Glu Asn Asn Thr Pro Trp Val
 340 345 350
 Ala Asp Gly Leu Arg Ser Leu Gly Ser Ser Val Asp Arg Lys Glu Phe
 355 360 365
 Gln Asn Leu Leu Val Glu Met Leu Glu Glu Asn Asn Ile Glu Phe Val
 370 375 380
 Arg Val Glu Glu Glu Asp Tyr Asp Ser Arg Phe Leu Arg Cys Val Glu
 385 390 395 400
 Leu Val Arg Glu Met Met Gly Glu Gln Arg
 405 410

<210> 52
 <211> 180
 <212> PRT
 <213> Bacillus subtilis

<220>
 <221> misc_feature
 <222> (1)..(180)
 <223> Bacillus subtilis YxrA (repressor protein)
 >gi|251757401|sp|P39667.2|NADR_BACSU RecName: Full=Transcription
 repressor NadR; AltName: Full=ORF1

<400> 52

Met Thr Glu Glu Leu Lys Leu Met Gly Ala Asn Arg Arg Asp Gln Leu
 1 5 10 15

Leu Leu Trp Leu Lys Glu Ser Lys Ser Pro Leu Thr Gly Gly Glu Leu
 20 25 30

Ala Lys Lys Ala Asn Val Ser Arg Gln Val Ile Val Gln Asp Ile Ser
 35 40 45

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

Val Tyr Met Asp Ala Ala Ala Gln Gln His Gln Gln Ala Glu Arg Ile
 65 70 75 80

Ile Ala Cys Leu His Gly Pro Glu Arg Thr Glu Glu Glu Leu Gln Leu
 85 90 95

Ile Val Asp Glu Gly Val Thr Val Lys Asp Val Lys Ile Glu His Pro
 100 105 110

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

Val Ser His Phe Ile Lys Lys Ile Asn Ser Thr Asn Ala Ala Tyr Leu
 130 135 140

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

Glu His Arg Ile Asp Gln Ala Cys Gln Ala Leu Glu Glu Ala Gly Ile
 165 170 175

Leu Ile Lys Asp
 180

<210> 53
 <211> 214
 <212> PRT
 <213> Corynebacterium glutamicum

<220>
 <221> misc_feature
 <222> (1)..(214)
 <223> Corynebacterium glutamicum CgR_1153 (repressor protein)
 >gi|140845132|dbj|BAF54131.1| hypothetical protein cgR_1153
 [Corynebacterium glutamicum R]

<400> 53

Met Pro Ala Ser Pro Glu Ile Gln Met Ala Val Ser Thr Ile Ile Phe
 1 5 10 15

Ala Leu Arg Pro Gly Pro Gln Asp Leu Pro Ser Leu Trp Ala Pro Phe
 20 25 30

Val Pro Arg Thr Arg Glu Pro His Leu Asn Lys Trp Ala Leu Pro Gly
 35 40 45

Gly Trp Leu Pro Pro His Glu Glu Leu Glu Asp Ala Ala Ala Arg Thr
 50 55 60

Leu Ala Glu Thr Thr Gly Leu His Pro Ser Tyr Leu Glu Gln Leu Tyr
 65 70 75 80

Thr Phe Gly Lys Val Asp Arg Ser Pro Thr Gly Arg Val Ile Ser Val
 85 90 95

Val Tyr Trp Ala Leu Val Arg Ala Asp Glu Ala Leu Lys Ala Ile Pro
 100 105 110

Gly Glu Asn Val Gln Trp Phe Pro Ala Asp His Leu Pro Glu Leu Ala
 115 120 125

Phe Asp His Asn Asp Ile Val Lys Tyr Ala Leu Glu Arg Leu Arg Thr
 130 135 140

Lys Val Glu Tyr Ser Glu Ile Ala His Ser Phe Leu Gly Glu Thr Phe
 145 150 155 160

Thr Ile Ala Gln Leu Arg Ser Val His Glu Ala Val Leu Gly His Lys
 165 170 175

Leu Asp Ala Ala Asn Phe Arg Arg Ser Val Ala Thr Ser Pro Asp Leu
 180 185 190

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

Leu Phe Arg Phe Gln Arg
 210

<210> 54
 <211> 191

<212> PRT
 <213> Acinetobacter baylyi

<220>
 <221> misc_feature
 <222> (1)..(191)
 <223> Acinetobacter baylyi PnuC (NR transporter protein)
 >gi|49530211|emb|CAG67923.1| putative
 nucleoside/purine/pyrimidine transport protein (NMN family)
 (PnuC) [Acinetobacter sp. ADP1]

<400> 54

Met Ser Pro Leu Glu Ile Phe Ala Val Ile Ile Ser Val Ile Gly Val
 1 5 10 15

Ala Leu Thr Ile Lys Arg Asn Met Trp Cys Trp Gly Phe Asn Phe Leu
 20 25 30

Ala Phe Ile Leu Tyr Gly Tyr Leu Phe Phe Ser Phe Lys Leu Tyr Gly
 35 40 45

Glu Thr Ile Leu Gln Gly Phe Phe Ile Ile Ile Asn Phe Tyr Gly Phe
 50 55 60

Tyr Tyr Trp Leu Lys Gly Lys Gln Thr Glu His Glu Ile Arg Ile Val
 65 70 75 80

Ala Ile Pro Ala Lys Thr Val Ile Ile Gln Met Leu Leu Ala Ala Leu
 85 90 95

Gly Gly Leu Ile Phe Gly Leu Ser Leu Lys His Phe Thr Asp Ala Ala
 100 105 110

Val Pro Met Leu Asp Ser Gln Leu Ala Ala Phe Ser Leu Leu Ala Thr
 115 120 125

Tyr Trp Thr Ser Arg Lys His Ile Ala Thr Trp Val Leu Trp Val Phe
 130 135 140

Val Asp Ile Val Tyr Val Gly Met Phe Ile Tyr Lys Asp Leu Tyr Leu
 145 150 155 160

Thr Ala Gly Leu Tyr Ala Ala Phe Val Val Met Ala Ala Phe Gly Trp
 165 170 175

Trp Gln Trp Glu Gln Val Lys Arg Lys Gln Arg Ser Gly Leu Ile
 180 185 190

<210> 55
 <211> 230
 <212> PRT
 <213> Corynebacterium glutamicum

<220>

<221> misc_feature
 <222> (1)..(230)
 <223> Corynebacterium glutamicum NR transporter protein
 >gi|19551314|ref|NP_599316.1| nicotinamide mononucleotide
 transporter [Corynebacterium glutamicum ATCC 13032]

<400> 55

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

Val Pro Ile Leu Trp Arg Glu Ile Ile Gly Asn Val Phe Gly Leu Phe
 20 25 30

Ser Ala Trp Ala Gly Met Arg Arg Ile Val Trp Ala Trp Pro Ile Gly
 35 40 45

Ile Ile Gly Asn Ala Leu Leu Phe Thr Val Phe Met Gly Gly Leu Phe
 50 55 60

His Thr Pro Gln Asn Leu Asp Leu Tyr Gly Gln Ala Gly Arg Gln Ile
 65 70 75 80

Met Phe Ile Ile Val Ser Gly Tyr Gly Trp Tyr Gln Trp Ser Ala Ala
 85 90 95

Lys Arg Arg Ala Leu Thr Pro Glu Asn Ala Val Ala Val Val Pro Arg
 100 105 110

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

Gly Thr Leu Ser Phe Ala Trp Ile Phe Gln Ala Leu Gly Ser Trp Gly
 130 135 140

Pro Trp Ala Asp Ala Trp Ile Phe Val Gly Ser Ile Leu Ala Thr Tyr
 145 150 155 160

Gly Met Ala Arg Gly Trp Thr Glu Phe Trp Leu Ile Trp Ile Ala Val
 165 170 175

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

Ala Val Leu Tyr Leu Val Tyr Gly Ala Phe Val Ser Trp Gly Phe Val
 195 200 205

Val Trp Leu Arg Val Gln Lys Ala Asp Lys Ala Arg Ala Leu Glu Ala
 210 215 220

Gln Glu Ser Val Thr Val
 225 230

<210> 56

<211> 239
 <212> PRT
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)..(239)
 <223> Escherichia coli PnuC (NR transporter protein)
 >gi|16128719|ref|NP_415272.1| nicotinamide riboside transporter
 [Escherichia coli str. K-12 substr. MG1655]

<400> 56

Met Asp Phe Phe Ser Val Gln Asn Ile Leu Val His Ile Pro Ile Gly
 1 5 10 15

Ala Gly Gly Tyr Asp Leu Ser Trp Ile Glu Ala Val Gly Thr Ile Ala
 20 25 30

Gly Leu Leu Cys Ile Gly Leu Ala Ser Leu Glu Lys Ile Ser Asn Tyr
 35 40 45

Phe Phe Gly Leu Ile Asn Val Thr Leu Phe Gly Ile Ile Phe Phe Gln
 50 55 60

Ile Gln Leu Tyr Ala Ser Leu Leu Leu Gln Val Phe Phe Phe Ala Ala
 65 70 75 80

Asn Ile Tyr Gly Trp Tyr Ala Trp Ser Arg Gln Thr Ser Gln Asn Glu
 85 90 95

Ala Glu Leu Lys Ile Arg Trp Leu Pro Leu Pro Lys Ala Leu Ser Trp
 100 105 110

Leu Ala Val Cys Val Val Ser Ile Gly Leu Met Thr Val Phe Ile Asn
 115 120 125

Pro Val Phe Ala Phe Leu Thr Arg Val Ala Val Met Ile Met Gln Ala
 130 135 140

Leu Gly Leu Gln Val Val Met Pro Glu Leu Gln Pro Asp Ala Phe Pro
 145 150 155 160

Phe Trp Asp Ser Cys Met Met Val Leu Ser Ile Val Ala Met Ile Leu
 165 170 175

Met Thr Arg Lys Tyr Val Glu Asn Trp Leu Leu Trp Val Ile Ile Asn
 180 185 190

Val Ile Ser Val Val Ile Phe Ala Leu Gln Gly Val Tyr Ala Met Ser
 195 200 205

Leu Glu Tyr Ile Ile Leu Thr Phe Ile Ala Leu Asn Gly Ser Arg Met
 210 215 220

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Trp Ile Asn Ser Ala Arg Glu Arg Gly Ser Arg Ala Leu Ser His
225 230 235

<210> 57
<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> 57

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 Pro Glu Tyr Phe Thr Asp Ile Glu Phe Arg Lys Pro
180 185 190

Ala Asp Glu₁₉₅ Ala Lys Leu Val Ile₂₀₀ Gln Glu Leu Gln₂₀₅ Gln Thr Glu Lys
 Pro Asp₂₁₀ Ile Ile Ile Ala Ala₂₁₅ Thr His Met Gly His₂₂₀ Tyr Asp Asn Gly
 Glu₂₂₅ His Gly Ser Asn Ala₂₃₀ Pro Gly Asp Val Glu₂₃₅ Met Ala Arg Ala Leu₂₄₀
 Pro Ala Gly Ser Leu₂₄₅ Ala Met Ile Val Gly₂₅₀ Gly His Ser Gln Asp₂₅₅ Pro
 Val Cys Met Ala₂₆₀ Ala Glu Asn Lys Lys₂₆₅ Gln Val Asp Tyr Val₂₇₀ Pro Gly
 Thr Pro Cys₂₇₅ Lys Pro Asp Gln Gln₂₈₀ Asn Gly Ile Trp Ile₂₈₅ Val Gln Ala
 His Glu₂₉₀ Trp Gly Lys Tyr Val₂₉₅ Gly Arg Ala Asp Phe₃₀₀ Glu Phe Arg Asn
 Gly₃₀₅ Glu Met Lys Met Val₃₁₀ Asn Tyr Gln Leu Ile₃₁₅ Pro Val Asn Leu Lys₃₂₀
 Lys Lys Val Thr Trp₃₂₅ Glu Asp Gly Lys Ser₃₃₀ Glu Arg Val Leu Tyr₃₃₅ Thr
 Pro Glu Ile Ala₃₄₀ Glu Asn Gln Gln₃₄₅ Met Ile Ser Leu Leu Ser₃₅₀ Pro Phe
 Gln Asn Lys₃₅₅ Gly Lys Ala Gln Leu₃₆₀ Glu Val Lys Ile Gly₃₆₅ Glu Thr Asn
 Gly Arg₃₇₀ Leu Glu Gly Asp Arg₃₇₅ Asp Lys Val Arg Phe₃₈₀ Val Gln Thr Asn
 Met₃₈₅ Gly Arg Leu Ile Leu₃₉₀ Ala Ala Gln Met Asp₃₉₅ Arg Thr Gly Ala Asp₄₀₀
 Phe Ala Val Met Ser₄₀₅ Gly Gly Gly Ile Arg₄₁₀ Asp Ser Ile Glu Ala₄₁₅ Gly
 Asp Ile Ser Tyr₄₂₀ Lys Asn Val Leu Lys₄₂₅ Val Gln Pro Phe Gly₄₃₀ Asn Val
 Val Val Tyr₄₃₅ Ala Asp Met Thr Gly₄₄₀ Lys Glu Val Ile Asp₄₄₅ Tyr Leu Thr
 Ala Val₄₅₀ Ala Gln Met Lys Pro₄₅₅ Asp Ser Gly Ala Tyr₄₆₀ Pro Gln Phe Ala
 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> 58
<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> 58

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

Lys Asp Asp Ile Ile Ser Gly Thr Lys Thr His Pro Ile Ile Ser Val
115 120 125

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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
 660 665 670
 His Thr Asn Asp Thr His Ala His Leu Asp Asp Ala Ala Arg Arg Met
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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
 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

Thr Pro Phe Val Tyr Tyr Gly Ile His Glu Gly Ser Gln Glu Lys
 1205 1210 1215

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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 1460	Gln	Ala											

<210> 59
 <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> 59

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

Ala Glu Ala Asp Arg Val Ile Glu Ala Gly Glu Ala Asp Val Val Ile
 210 215 220

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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
 Tyr Arg Val Thr Gly Ser Ser Phe Leu Leu Ala Gly Gly Asp Ser Phe
 485 490 495

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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> 60
<211> 165
<212> PRT
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)..(165)
<223> Escherichia coli PncC (nicotinamide mononucleotide
amidohydrolase) >gi|16130607|ref|NP_417180.1|
nicotinamide-nucleotide amidohydrolase; NMN amidohydrolase
[Escherichia coli str. K-12 substr. MG1655]

<400> 60

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

<210> 61
 <211> 416
 <212> PRT
 <213> Bacillus subtilis

<220>
 <221> misc_feature
 <222> (1)..(416)
 <223> Bacillus subtilis ClnA (nicotinamide mononucleotide
 amidohydrolase) >gi|1314847|gb|AAB00568.1| ClnA [Bacillus
 subtilis subsp. subtilis str. 168]

<400> 61

Met Glu Phe Pro Lys Lys Ala Glu Ile Ile Ala Val Gly Ser Glu Leu
 1 5 10 15
 Leu Leu Gly Gln Ile Ala Asn Thr Asn Ala Gln Phe Ile Ser Lys Gln
 20 25 30
 Leu Ala Glu Ile Gly Val His Val Phe Tyr His Thr Ala Val Gly Asp
 35 40 45

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Asn Pro Glu Arg Leu Lys Gln Val Ile Arg Ile Ala Glu Glu Arg Ser
 50 55 60
 Asp Phe Ile Ile Phe Ser Gly Gly Leu Gly Pro Thr Lys Asp Asp Leu
 65 70 75 80
 Thr Lys Glu Thr Ile Ala Asn Thr Leu Gly Arg Pro Leu Val Leu Asn
 85 90 95
 Asp Glu Ala Phe Gln Ser Ile Glu Asp Tyr Pro Lys Arg Thr Lys Arg
 100 105 110
 Thr Met Ser Pro Asn Asn Arg Lys Gln Ala Leu Val Ile Glu Gly Ser
 115 120 125
 Asp Val Leu Ala Asn His Phe Gly Met Ala Pro Gly Met Leu Thr Glu
 130 135 140
 His Glu Ser Arg Tyr Tyr Met Leu Leu Pro Gly Pro Pro Ser Glu Leu
 145 150 155 160
 Arg Pro Met Phe Glu Asn Glu Ala Lys Pro Leu Leu Leu Lys Lys Met
 165 170 175
 Gly Ser Asn Glu Lys Ile Val Ser Thr Val Leu Arg Phe Phe Gly Ile
 180 185 190
 Gly Glu Ser Gln Leu Glu Pro Asp Leu Glu Asp Ile Ile Asp Ala Gln
 195 200 205
 Thr Asn Pro Thr Ile Ala Pro Leu Ala Ala Asp Gly Glu Val Thr Leu
 210 215 220
 Arg Leu Thr Ala Lys His Ala Asp Glu Lys Glu Thr Glu Arg Leu Leu
 225 230 235 240
 Lys Glu Thr Glu Ala Val Ile Leu Glu Arg Val Gly Glu Phe Phe Tyr
 245 250 255
 Gly Tyr Asp Asp Thr Ser Leu Val Lys Glu Leu Ser Ile Ala Cys Lys
 260 265 270
 Glu Lys Gly Ile Thr Ile Ser Ala Ala Glu Ser Phe Thr Gly Gly Leu
 275 280 285
 Phe Ser Glu Trp Leu Thr Asp His Ser Gly Ala Ser Lys Leu Phe Ala
 290 295 300
 Gly Gly Val Val Cys Tyr Thr Asn Asp Val Lys Gln Asn Val Leu Gly
 305 310 315 320

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Val Lys Lys Glu Thr Leu Asp Arg Phe Gly Ala Val Ser Lys Glu Cys
325 330 335

Ala Ser Glu Leu Ala Lys Gly Val Gln Lys Leu Thr Gly Ser Asp Ile
340 345 350

Gly Ile Ser Phe Thr Gly Val Ala Gly Pro Asp Ala Gln Glu Gly His
355 360 365

Glu Pro Gly His Val Phe Ile Gly Ile Ser Ala Asn Gly Lys Glu Glu
370 375 380

Val His Glu Phe His Phe Ala Gly Ser Arg Thr Gly Ile Arg Lys Arg
385 390 395 400

Gly Ala Lys Tyr Gly Cys His Leu Ile Leu Lys Leu Leu Glu Gln Lys
405 410 415

<210> 62
<211> 172
<212> PRT
<213> Corynebacterium glutamicum

<220>
<221> misc_feature
<222> (1)..(172)
<223> Corynebacterium glutamicum Cg2153 (nicotinamide mononucleotide
amidohydrolase) >gi|41326141|emb|CAF20304.1| similar to
competence-and mitomycin-induced protein [Corynebacterium
glutamicum ATCC 13032]

<400> 62

Met Ser Glu Asn Leu Ala Gly Arg Val Val Glu Leu Leu Lys Ser Arg
1 5 10 15

Gly Glu Thr Leu Ala Phe Cys Glu Ser Leu Thr Ala Gly Leu Ala Ser
20 25 30

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

Leu Val Thr Tyr Ala Thr Glu Leu Lys Val Ala Leu Ala Gly Val Pro
50 55 60

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

Ala Met Ala Thr Gly Ala Ala His Arg Cys Gln Ala Asp Trp Ala Val
85 90 95

Ser Leu Thr Gly Val Ala Gly Pro Ser Lys Gln Asp Gly His Pro Val
100 105 110

Gly Glu Val Trp Ile Gly Val Ala Gly Pro Ala His Phe Gly Ala Ser
 115 120 125

Gly Thr Ile Asp Ala Tyr Arg Ala Phe Glu Ser Glu Gln Gln Val Ile
 130 135 140

Leu Ala Glu Leu Gly Arg His His Ile Arg Glu Ser Ala Val Gln Gln
 145 150 155 160

Ser Phe Arg Leu Leu Ile Asp His Ile Glu Ser Gln
 165 170

<210> 63
 <211> 213
 <212> PRT
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)..(213)
 <223> Escherichia coli NadD (nicotinic acid mononucleotide
 adenylyltransferase) >gi|16128622|ref|NP_415172.1| nicotinic acid
 mononucleotide adenylyltransferase, NAD(P)-dependent [Escherichia
 coli str. K-12 substr. MG1655]

<400> 63

Met Lys Ser Leu Gln Ala Leu Phe Gly Gly Thr Phe Asp Pro Val His
 1 5 10 15

Tyr Gly His Leu Lys Pro Val Glu Thr Leu Ala Asn Leu Ile Gly Leu
 20 25 30

Thr Arg Val Thr Ile Ile Pro Asn Asn Val Pro Pro His Arg Pro Gln
 35 40 45

Pro Glu Ala Asn Ser Val Gln Arg Lys His Met Leu Glu Leu Ala Ile
 50 55 60

Ala Asp Lys Pro Leu Phe Thr Leu Asp Glu Arg Glu Leu Lys Arg Asn
 65 70 75 80

Ala Pro Ser Tyr Thr Ala Gln Thr Leu Lys Glu Trp Arg Gln Glu Gln
 85 90 95

Gly Pro Asp Val Pro Leu Ala Phe Ile Ile Gly Gln Asp Ser Leu Leu
 100 105 110

Thr Phe Pro Thr Trp Tyr Glu Tyr Glu Thr Ile Leu Asp Asn Ala His
 115 120 125

Leu Ile Val Cys Arg Arg Pro Gly Tyr Pro Leu Glu Met Ala Gln Pro
 130 135 140

Gln Tyr Gln Gln Trp Leu Glu Asp His Leu Thr His Asn Pro Glu Asp
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145 150 160

Leu His Leu Gln Pro Ala Gly Lys Ile Tyr Leu Ala Glu Thr Pro Trp
165 170 175Phe Asn Ile Ser Ala Thr Ile Ile Arg Glu Arg Leu Gln Asn Gly Glu
180 185 190Ser Cys Glu Asp Leu Leu Pro Glu Pro Val Leu Thr Tyr Ile Asn Gln
195 200 205Gln Gly Leu Tyr Arg
210<210> 64
<211> 189
<212> PRT
<213> Bacillus subtilis<220>
<221> misc_feature
<222> (1)..(189)
<223> Bacillus subtilis NadD (nicotinic acid mononucleotide
adenyltransferase) >gi|16079618|ref|NP_390442.1|
nicotinate-nucleotide adenyltransferase [Bacillus subtilis
subsp. subtilis str. 168]

<400> 64

Met Lys Lys Ile Gly Ile Phe Gly Gly Thr Phe Asp Pro Pro His Asn
1 5 10 15Gly His Leu Leu Met Ala Asn Glu Val Leu Tyr Gln Ala Gly Leu Asp
20 25 30Glu Ile Trp Phe Met Pro Asn Gln Ile Pro Pro His Lys Gln Asn Glu
35 40 45Asp Tyr Thr Asp Ser Phe His Arg Val Glu Met Leu Lys Leu Ala Ile
50 55 60Gln Ser Asn Pro Ser Phe Lys Leu Glu Leu Val Glu Met Glu Arg Glu
65 70 75 80Gly Pro Ser Tyr Thr Phe Asp Thr Val Ser Leu Leu Lys Gln Arg Tyr
85 90 95Pro Asn Asp Gln Leu Phe Phe Ile Ile Gly Ala Asp Met Ile Glu Tyr
100 105 110Leu Pro Lys Trp Tyr Lys Leu Asp Glu Leu Leu Asn Leu Ile Gln Phe
115 120 125Ile Gly Val Lys Arg Pro Gly Phe His Val Glu Thr Pro Tyr Pro Leu
130 135 140

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Leu Phe Ala Asp Val Pro Glu Phe Glu Val Ser Ser Thr Met Ile Arg
145 150 155 160

Glu Arg Phe Lys Ser Lys Lys Pro Thr Asp Tyr Leu Ile Pro Asp Lys
165 170 175

Val Lys Lys Tyr Val Glu Glu Asn Gly Leu Tyr Glu Ser
180 185

<210> 65
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<220>
<221> misc_feature
<222> (1)..(226)
<223> Corynebacterium glutamicum Cg2584 (nicotinic acid mononucleotide
adenyltransferase) >gi|41326535|emb|CAF21017.1| PUTATIVE
NICOTINIC ACID MONONUCLEOTIDE ADENYLYLTRANSFERASE
[Corynebacterium glutamicum ATCC 13032]

<400> 65

Met Arg Thr Leu Tyr Cys Pro Leu Met Thr Thr Thr Val Lys Arg Arg
1 5 10 15

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

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

Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala Asn Lys Lys
50 55 60

Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile Ala Thr Ala
65 70 75 80

Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp Arg Gly Gly
85 90 95

Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys Gln Tyr Pro
100 105 110

Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu Ala Gln Ile
115 120 125

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

Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile Ile Pro Glu
145 150 155 160

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Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala Met Ala Ile
165 170 175

Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg Pro Val Trp
180 185 190

Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys Arg Gln Leu
195 200 205

Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys Gly Gln Asn
210 215 220

Gln Ala
225

<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

Ser His Asp Gln Ser Asn Gln Ser His Ser Pro Ser Ser Cys Ser Arg
85 90 95

Gly His Tyr Glu Thr Ala Pro Ser Thr Phe Ala Pro Ser Ile His Gly
100 105 110

Glu Ser Gly Leu Asp Gly Thr Ser Leu Leu Pro Glu Ile Thr Cys Thr
115 120 125

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

Arg Asn Asn Pro Gly Thr Cys Leu Val Ala Thr Gly Ser Leu Thr Asn
145 150 155 160

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

Thr Val Ser Ile Met Gly Gly Gly Phe Gly Met Gly Asn Trp Thr Pro
180 185 190

Tyr Ala Glu Phe Asn Ile Trp Cys Asp Ala Glu Ser Ala Ser Gln Val
195 200 205

Leu Gly Asp Pro Ile Val Ala Ala Lys Val Val Leu Cys Pro Leu Asn
210 215 220

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

Ser Val Gly Gly Asn Val Ser Gln Met Phe Phe Glu Leu Met Thr Phe
245 250 255

Phe Lys Glu Thr Tyr Glu Ser Glu Phe Gly Phe Lys Asp Gly Pro Pro
260 265 270

Val His Asp Pro Leu Ser Val Ala Val Leu Leu Asn Gly Ile Val Thr
275 280 285

Lys Glu Arg Arg Val Thr Val Asp Val Thr Val Gly Gly Glu Gln Arg
290 295 300

Gly Met Leu Thr Glu Gln Val Gly Gly His Leu Thr Val Val Glu Glu
305 310 315 320

Val Asp Leu Asn Lys Phe Trp Ala Leu Val Val Thr Cys Leu Glu Ala
325 330 335

Cys Lys

<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

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

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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

<220>
<221> misc_feature
<222> (1)..(240)
<223> Sc NRK1 - NR kinase

<400> 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

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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

<210> 69
<211> 254
<212> PRT
<213> Unknown

<220>
<223> CAG83148 - NR kinase

<220>
<221> misc_feature
<222> (1)..(254)
<223> CAG83148 - NR kinase

<400> 69

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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
 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> An04g05800 - NR kinase (NRK1 homolog)

<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

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

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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> SC PNP1 - 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
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

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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> CAG78849 - NMN/purine phosphorylase

<220>
<221> misc_feature
<222> (1)..(298)
<223> CAG78849 - NMN/purine phosphorylase

<400> 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
 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> 433
 <212> PRT
 <213> Bacillus subtilis

<220>
 <221> misc_feature
 <222> (1)..(433)
 <223> Bacillus subtilis Pdp (nucleoside phosphorylase)
 >gi|50812307|ref|NP_391819.2| pyrimidine-nucleoside phosphorylase
 [Bacillus subtilis subsp. subtilis str. 168]

<400> 73

Met Arg Met Val Asp Ile Ile Ile Lys Lys Gln Asn Gly Lys Glu Leu
 1 5 10 15

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

Ile Pro Asp Tyr Gln Ala Ser Ala Leu Ala Met Ala Ile Phe Phe Gln
 35 40 45

Asp Met Ser Asp Arg Glu Arg Ala Asp Leu Thr Met Ala Met Val Asn
 50 55 60

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

Lys His Ser Thr Gly Gly Val Gly Asp Thr Thr Thr Leu Val Leu Ala
 85 90 95

Pro Leu Val Ala Ala Leu Asp Val Pro Val Ala Lys Met Ser Gly Arg
 100 105 110

Gly Leu Gly His Thr Gly Gly Thr Ile Asp Lys Leu Glu Ala Ile Met
 115 120 125

Gly Phe His Val Glu Leu Thr Lys Asp Glu Phe Ile Lys Leu Val Asn
 130 135 140

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

Asp Lys Lys Leu Tyr Ala Leu Arg Asp Val Thr Gly Thr Val Asn Ser
 165 170 175

Ile Pro Leu Ile Ala Ser Ser Ile Met Ser Lys Lys Ile Ala Ala Gly
 180 185 190

Ala Asp Ala Ile Val Leu Asp Val Lys Thr Gly Ala Gly Ala Phe Met
 195 200 205

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

Gly Asn Asn Val Gly Arg Gln Thr Met Ala Val Ile Ser Asp Met Ser
 225 230 235 240

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Gln Pro Leu Gly Phe Ala Ile Gly Asn Ala Leu Glu Val Lys Glu Ala
245 250 255

Ile Asp Thr Leu Lys Gly Glu Gly Pro Glu Asp Leu His Glu Leu Val
260 265 270

Leu Thr Leu Gly Ser Gln Met Val Val Leu Ala Lys Lys Ala Asp Thr
275 280 285

Leu Asp Glu Ala Arg Ala Lys Leu Glu Glu Val Met Lys Asn Gly Lys
290 295 300

Ala Leu Glu Lys Phe Lys Asp Phe Leu Lys Asn Gln Gly Gly Asp Ser
305 310 315 320

Ser Ile Val Asp Asp Pro Ser Lys Leu Pro Gln Ala Ala Tyr Gln Ile
325 330 335

Asp Val Pro Ala Lys Glu Ala Gly Val Val Ser Glu Ile Val Ala Asp
340 345 350

Glu Ile Gly Val Ala Ala Met Leu Leu Gly Ala Gly Arg Ala Thr Lys
355 360 365

Glu Asp Glu Ile Asp Leu Ala Val Gly Ile Met Leu Arg Lys Lys Val
370 375 380

Gly Asp Lys Val Glu Lys Gly Glu Pro Leu Val Thr Leu Tyr Ala Asn
385 390 395 400

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

Ile Ala Ala Glu Ala Lys Ala Pro Lys Leu Ile His Thr Leu Ile Thr
420 425 430

Glu

<210> 74
<211> 271
<212> PRT
<213> Bacillus subtilis

<220>
<221> misc_feature
<222> (1)..(271)
<223> Bacillus subtilis PupG (nucleoside phosphorylase)
>gi|16079406|ref|NP_390230.1| purine nucleoside phosphorylase 1
[Bacillus subtilis subsp. subtilis str. 168]

<400> 74

Met Lys Asp Arg Ile Glu Arg Ala Ala Ala Phe Ile Lys Gln Asn Leu

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

$\langle 210 \rangle$	75
$\langle 211 \rangle$	694

<212> PRT
 <213> Corynebacterium glutamicum

<220>
 <221> misc_feature
 <222> (1)..(694)
 <223> Corynebacterium glutamicum Cg0397 (nucleotide hydrolase)

<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

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 Phe₂₄₅ Ser Gly His Thr His₂₅₀ Phe Asp Tyr Val Ala₂₅₅ Glu
 Gly Glu Ala Arg₂₆₀ Gly Asp Lys Gln₂₆₅ Leu Val Val Ile Gln₂₇₀ Gly His
 Glu Tyr Gly₂₇₅ Lys Val Ile Ser Asp₂₈₀ Val Glu Ile Ser Tyr₂₈₅ Asp Arg Glu
 Ala Gly₂₉₀ Lys Ile Thr Asn Ile₂₉₅ Glu Ala Lys Asn Val₃₀₀ Ser Ala Thr Asp
 Val₃₀₅ Val Glu Asn Cys Glu₃₁₀ Thr Pro Asn Thr Ala₃₁₅ Val Asp Ala Ile Val₃₂₀
 Ala Ala Ala Val Glu₃₂₅ Ala Ala Glu Glu Ala₃₃₀ Gly Asn Glu Val Val₃₃₅ Ala
 Thr Ile Asp Asn₃₄₀ Gly Phe Tyr Arg Gly₃₄₅ Ala Asp Glu Glu Gly₃₅₀ Thr Thr
 Gly Ser Asn₃₅₅ Arg Gly Val Glu Ser₃₆₀ Ser Leu Ser Asn Leu₃₆₅ Ile Ala Glu
 Ala Gly₃₇₀ Leu Trp Ala Val Asn₃₇₅ Asp Ala Thr Ile Leu₃₈₀ Asn Ala Asp Ile
 Gly₃₈₅ Ile Met Asn Ala Gly₃₉₀ Gly Val Arg Ala Asp₃₉₅ Leu Glu Ala Gly Glu₄₀₀
 Val Thr Phe Ala Asp₄₀₅ Ala Tyr Ala Thr Gln₄₁₀ Asn Phe Ser Asn Thr₄₁₅ Tyr
 Gly Val Arg Glu₄₂₀ Val Ser Gly Ala Gln₄₂₅ Phe Lys Glu Ala Leu₄₃₀ Glu Gln
 Gln Trp Lys₄₃₅ Glu Thr Gly Asp Arg₄₄₀ Pro Arg Leu Ala Leu₄₄₅ Gly Leu Ser
 Ser Asn₄₅₀ Val Gln Tyr Ser Tyr₄₅₅ Asp Glu Thr Arg Glu₄₆₀ Tyr Gly Asp Arg
 Ile Thr His Ile Thr Phe₄₇₀ Asn Gly Glu Pro Met₄₇₅ Asp Met Lys Glu Thr₄₈₀
 Tyr Arg Val Thr Gly₄₈₅ Ser Ser Phe Leu Leu₄₉₀ Ala Gly Gly Asp Ser₄₉₅ Phe
 Thr Ala Phe Ala₅₀₀ Glu Gly Gly Pro Ile₅₀₅ Ala Glu Thr Gly Met₅₁₀ Val Asp

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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]

<400> 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
 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

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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

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

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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]

<400> 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
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20

25

30

Pro Gly Met₃₅ Pro Asp Val Tyr Gly₄₀ Pro Gly Ala Ser Gln₄₅ Asn Asp Pro
 Ile Pro Ala His Ala Pro Arg₅₅ Gln Gln Val Leu Pro₆₀ Glu Glu Tyr Gln
 Arg Ala Ser Asp Asp Glu₇₀ Leu His Arg Arg Ile₇₅ Arg Glu Ala Lys Asp₈₀
 Thr Leu Gly Asp Lys₈₅ Val Val Ile Leu Gly₉₀ His Phe Tyr Gln Arg₉₅ Asp
 Glu Val Ile Gln₁₀₀ His Ala Asp Phe Val₁₀₅ Gly Asp Ser Phe Gln₁₁₀ Leu Ala
 Arg Ala Ala₁₁₅ Lys Thr Arg Pro Glu₁₂₀ Ala Glu Ala Ile Val₁₂₅ Phe Cys Gly
 Val His₁₃₀ Phe Met Ala Glu Thr₁₃₅ Ala Asp Leu Leu Ser₁₄₀ Thr Asp Glu Gln
 Ser Val Ile Leu Pro Asn₁₅₀ Leu Ala Ala Gly Cys₁₅₅ Ser Met Ala Asp Met₁₆₀
 Ala Asp Leu Asp Ser₁₆₅ Val Glu Asp Cys Trp₁₇₀ Glu Gln Leu Thr Ser₁₇₅ Ile
 Tyr Gly Asp Asp₁₈₀ Thr Leu Ile Pro Val₁₈₅ Thr Tyr Met Asn Ser₁₉₀ Ser Ala
 Ala Leu Lys₁₉₅ Gly Phe Val Gly Glu₂₀₀ His Gly Gly Ile Val₂₀₅ Cys Thr Ser
 Ser Asn₂₁₀ Ala Arg Ser Val Leu₂₁₅ Glu Trp Ala Phe Glu₂₂₀ Arg Gly Gln Arg
 Val Leu Phe Phe Pro Asp₂₃₀ Gln His Leu Gly Arg₂₃₅ Asn Thr Ala Lys Ala₂₄₀
 Met Gly Ile Gly Ile₂₄₅ Asp Gln Met Pro Leu₂₅₀ Trp Asn Pro Asn Lys₂₅₅ Pro
 Leu Gly Gly Asn Thr Val Ser Glu Leu₂₆₅ Glu Asn Ala Lys Val₂₇₀ Leu Leu
 Trp His Gly₂₇₅ Phe Cys Ser Val His₂₈₀ Lys Arg Phe Thr Val₂₈₅ Glu Gln Ile
 Asn Lys₂₉₀ Ala Arg Ala Glu Tyr₂₉₅ Pro Asp Val His Val₃₀₀ Ile Val His Pro

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Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
305 310 315 320

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
340 345 350

Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
355 360 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
370 375 380

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

Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro
405 410 415

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala
420 425

<210> 79
<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> 79

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

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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

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

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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

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> 80
<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> 80

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
 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

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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

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> 81
<211> 297
<212> PRT
<213> Escherichia coli

<220>

<221> misc_feature

<222> (1)..(297)

<223> Escherichia coli NadC

>gi|260450686|gb|ACX41108.1| nicotinate-nucleotide
pyrophosphorylase [Escherichia coli DH1]

<400> 81

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

Glu Gln Met Arg Glu Ala Val Lys Arg Thr Asn Gly Lys Ala Leu Leu
 245 250 255

Glu Val Ser Gly Asn Val Thr Asp Lys Thr Leu Arg Glu Phe Ala Glu
 260 265 270

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

Ala Leu Asp Leu Ser Met Arg Phe Arg
 290 295

<210> 82
 <211> 289
 <212> PRT
 <213> Bacillus subtilis

<220>
 <221> misc_feature
 <222> (1)..(289)
 <223> Bacillus subtilis NadC

>gi|16079838|ref|NP_390664.1| nicotinate-nucleotide
 pyrophosphorylase [Bacillus subtilis subsp. subtilis str. 168]

<400> 82

Met Asn His Leu Gln Leu Lys Lys Leu Leu Asn His Phe Phe Leu Glu
 1 5 10 15

Asp Ile Gly Thr Gly Asp Leu Thr Ser Gln Ser Ile Phe Gly Glu Gln
 20 25 30

Ser Cys Glu Ala Glu Ile Val Ala Lys Ser Glu Gly Ile Phe Ala Gly
 35 40 45

Ala Ala Ile Ile Lys Glu Gly Phe Ser Leu Leu Asp Glu Asn Val Gln
 50 55 60

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

Ile Ala Glu Leu His Gly Pro Ala Ala Ala Leu Leu Ser Gly Glu Arg
 85 90 95

Val Val Leu Asn Leu Ile Gln Arg Leu Ser Gly Ile Ala Thr Met Thr
 100 105 110

Arg Glu Ala Val Arg Cys Leu Asp Asp Glu Gln Ile Lys Ile Cys Asp
 115 120 125

Thr Arg Lys Thr Thr Pro Gly Leu Arg Met Leu Glu Lys Tyr Ala Val
 130 135 140

Arg Ala Gly Gly Gly Tyr Asn His Arg Phe Gly Leu Tyr Asp Gly Ile
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145 150 155 160
 Met Ile Lys Asp Asn His Ile Ala Ala Cys Gly Ser Ile Leu Glu Ala
 165 170 175
 Cys Lys Lys Ala Arg Gln Ala Ala Gly His Met Val Asn Ile Glu Val
 180 185 190
 Glu Ile Glu Thr Glu Glu Gln Leu Arg Glu Ala Ile Ala Ala Gly Ala
 195 200 205
 Asp Val Ile Met Phe Asp Asn Cys Pro Pro Asp Thr Val Arg His Phe
 210 215 220
 Ala Lys Leu Thr Pro Ala Asn Ile Lys Thr Glu Ala Ser Gly Gly Ile
 225 230 235 240
 Thr Leu Glu Ser Leu Pro Ala Phe Lys Gly Thr Gly Val Asn Tyr Ile
 245 250 255
 Ser Leu Gly Phe Leu Thr His Ser Val Lys Ser Leu Asp Ile Ser Met
 260 265 270
 Asp Val Thr Leu Ser Asn Glu Ser Val Glu Glu Cys Cys Tyr Val Asn
 275 280 285

Ser

<210> 83
 <211> 279
 <212> PRT
 <213> Corynebacterium glutamicum

<220>
 <221> misc_feature
 <222> (1)..(279)
 <223> Corynebacterium glutamicum NadC

>gi|41325293|emb|CAF19773.1| PUTATIVE NICOTINATE-NUCLEOTIDE
 PYROPHOSPHORYLASE [Corynebacterium glutamicum ATCC 13032]

<400> 83

Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp
 1 5 10 15
 Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala
 20 25 30
 Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly
 35 40 45
 Gln Ala Leu Phe Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
 50 55 60

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

Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
85 90 95

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

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

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

Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val
145 150 155 160

Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser
165 170 175

Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr
180 185 190

His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu
195 200 205

Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln
210 215 220

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

Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly
245 250 255

Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu
260 265 270

Asp Leu Gly Leu Asp Ile Phe
275

<210> 84
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 10444

<400> 84
cggtaagtcc cgtctagcct

<210> 85
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 10447

<400> 85
 atgtttgcaa aacgattcaa aacct 25

<210> 86
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 11222

<400> 86
 ttacaccgaa tttctaataa taaccgggca ggccatg 37

<210> 87
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 11223

<400> 87
 ggctgcccg gttattatta gaaattcggg gtaagag 37

<210> 88
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 11226

<400> 88
 cttttacacc gaatttttaa taataaccgg gcaggccatg 40

<210> 89
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 11227

<400> 89
 ggctgcccg gttattatta aaaattcggg gtaaaag 37

<210> 90
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer 11230

<400> 90
cggaatgaagc ggaatgttaa taataaccgg gcaggccatg 40

<210> 91
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 11230

<400> 91
ggcctgcccg gttattatta acattccgct tcattccg 37

<210> 92
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 11232

<400> 92
gaaaggtggt gaactactat gaaaacagca gcatacgc 38

<210> 93
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer11233

<400> 93
gcgtatgctg ctgttttcat agtagttcac cacctttctc 40

<210> 94
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 11234

<400> 94
cacttacacc gaacttctaa taataaccgg gcaggccatg 40

<210> 95
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 11235

<400> 95
ggcctgcccg gttattatta gaagttcggg gtaagtg 37

<210> 96
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
 <223> primer 11341
 <400> 96
 aaggagggtt tcatatgaaa attgttaaag att 33
 <210> 97
 <211> 37
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer 11342
 <400> 97
 tttaacaatt ttcatatgaa acctccctta attctcg 37
 <210> 98
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer 11352
 <400> 98
 gtgaactact atgaaaattg taaaaaactt tattg 35
 <210> 99
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer 11352
 <400> 99
 ttacaatttt catagtagtt caccaccttt ctcta 35
 <210> 100
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer 11353
 <400> 100
 aaggagggtt tcatatgaaa atcgttaaag acttc 35
 <210> 101
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> primer 11354
 <400> 101
 taacgatttt catatgaaac ctcccttaat tctcg 35
 <210> 102
 <211> 36

<212> DNA
<213> Artificial Sequence

<220>
<223> primer 11159

<400> 102
gctacttact ctcgagttac tttttccaga aatcat

36

<210> 103
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer 11160

<400> 103
gctaacttag catatgatga cattgcaaca aca

33