

SEQUENCE LISTING

<110> Bayer Technology Services GmbH

<120> Neuartige Varianten PQQ-abhängiger Glukosedehydrogenase mit verbesserter Substratspezifität

<130> AFR

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 3

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 1

Ala Tyr Gln

1

<210> 2

<211> 3

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 2

Ala Trp Leu

1

<210> 3

<211> 3

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 3

Ala Phe Val

1

<210> 4

<211> 3

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 4

Gly Tyr Ile

1

<210> 5

<211> 3

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 5

Ala Tyr Val

1

<210> 6

<211> 3

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 6

Ala Phe Gln

1

<210> 7
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Insertion

<400> 7

Ala Gly Arg Met
1

<210> 8
<211> 4
<212> PRT
<213> Artificial

<220>
<223> Insertion

<400> 8

Gly Leu Ala Val
1

<210> 9
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Insertion

<400> 9

Met Gly Arg Phe Leu
1 5

<210> 10
<211> 5
<212> PRT
<213> Artificial

<220>

<223> Insertion

<400> 10

Val Ser Thr Phe Phe
1 5

<210> 11

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 11

Val Ser Lys Asn His
1 5

<210> 12

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 12

Ser Ser Arg Asn His
1 5

<210> 13

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 13

Ser Gly Arg Ile Leu

1 5

<210> 14
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Insertion

<400> 14

Val Gly Arg Leu Thr
1 5

<210> 15
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Insertion

<400> 15

Ala Glu Arg Asn Tyr
1 5

<210> 16
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Insertion

<400> 16

Met Glu Ser His Asn
1 5

<210> 17
<211> 5
<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 17

Val Gly His Val Thr
1 5

<210> 18

<211> 5

<212> PRT

<213> Artificial

<220>

<223> Insertion

<400> 18

Val Gly Arg Tyr Gln
1 5

<210> 19

<211> 42

<212> DNA

<213> Artificial

<220>

<223> Synthetic Oligonucleotide

<400> 19

tggtaggtct caaatgaata aacatttatt ggctaaaatt ac

42

<210> 20

<211> 32

<212> DNA

<213> Artificial

<220>

<223> Synthetic Oligonucleotide

<400> 20

ttcagctctg agctttatat gtaaactctaa tc

32

<210> 21
 <211> 4560
 <212> DNA
 <213> Artificial

<220>
 <223> Expression plasmid

<220>
 <221> CDS
 <222> (139)..(1581)

<220>
 <221> sig_peptide
 <222> (139)..(213)

<220>
 <221> mat_peptide
 <222> (214)..(1581)

<400> 21
 ccatcgaatg gccagatgat taattcctaa ttttgttga cactctatca ttgatagagt 60
 tattttacca ctccctatca gtgatagaga aaagtgaaat gaatagttcg acaaaaatct 120
 agataacgag ggcaaaaa atg aat aaa cat tta ttg gct aaa att act tta 171
 Met Asn Lys His Leu Leu Ala Lys Ile Thr Leu
 -25 -20 -15
 tta ggt gct gct cag cta ctt acg ctc aat tca gca ttt gct gat gtc 219
 Leu Gly Ala Ala Gln Leu Leu Thr Leu Asn Ser Ala Phe Ala Asp Val
 -10 -5 -1 1
 cct ctt aca cca tct caa ttt gct aaa gcg aaa aca gaa agc ttt gat 267
 Pro Leu Thr Pro Ser Gln Phe Ala Lys Ala Lys Thr Glu Ser Phe Asp
 5 10 15
 aag aaa gtt ctt cta tct aat tta aat aag cca cat gct ttg ttg tgg 315
 Lys Lys Val Leu Leu Ser Asn Leu Asn Lys Pro His Ala Leu Leu Trp
 20 25 30
 gga ccg gat aat caa att tgg tta acg gag cgg gca aca ggt aag att 363
 Gly Pro Asp Asn Gln Ile Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile
 35 40 45 50
 cta aga gtt aat cca gag tcg ggc agt gta aaa aca gtt ttt cag gtt 411

Leu Arg Val Asn Pro Glu Ser Gly Ser Val Lys Thr Val Phe Gln Val
 55 60 65

cct gag att gta aat gat gct gat gga caa aac ggt tta ttg ggt ttt 459
 Pro Glu Ile Val Asn Asp Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe
 70 75 80

gcc ttt cat cct gac ttt aaa aat aat cct tat atc tat gtt tca ggt 507
 Ala Phe His Pro Asp Phe Lys Asn Asn Pro Tyr Ile Tyr Val Ser Gly
 85 90 95

aca ttt aaa aat ccg aaa tct aca gat aaa gaa tta ccg aat caa act 555
 Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr
 100 105 110

att atc cgt cga tat acc tat aac aag gca aca gat acc ctt gag aaa 603
 Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Ala Thr Asp Thr Leu Glu Lys
 115 120 125 130

cca gta gat tta ttg gca gga tta cct tca tcg aaa gac cat cag tcg 651
 Pro Val Asp Leu Leu Ala Gly Leu Pro Ser Ser Lys Asp His Gln Ser
 135 140 145

ggc cgt ctt gtg att ggt cca gac caa aag att tac tat acg att ggt 699
 Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly
 150 155 160

gat cag gga cgt aac cag ctg gct tat tta ttc tta cca aat caa gca 747
 Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn Gln Ala
 165 170 175

cag cat acg ccg act caa cag gaa ctg agc ggc aaa gac tat cat acc 795
 Gln His Thr Pro Thr Gln Gln Gly Leu Ser Gly Lys Asp Tyr His Thr
 180 185 190

tat atg ggt aaa gta ttg cgc tta aat ctg gat gga agt att cca aaa 843
 Tyr Met Gly Lys Val Leu Arg Leu Asn Leu Asp Gly Ser Ile Pro Lys
 195 200 205 210

gat aat cca agc ttt aac ggt gta att agc cat att tat acg ctc ggt 891
 Asp Asn Pro Ser Phe Asn Gly Val Ile Ser His Ile Tyr Thr Leu Gly
 215 220 225

cat cgt aac cca cag ggc ttg gca ttt act cca aat ggt aaa ctg ttg 939
 His Arg Asn Pro Gln Gly Leu Ala Phe Thr Pro Asn Gly Lys Leu Leu
 230 235 240

caa tct gaa cag ggt cca aac tct gat gat gaa att aac ctc att gtc 987

Gln Ser Glu Gln Gly Pro Asn Ser Asp Asp Glu Ile Asn Leu Ile Val
 245 250 255

aaa ggt ggt aac tat ggc tgg cca aat gta gcg ggt tat aaa gat gat 1035
 Lys Gly Gly Asn Tyr Gly Trp Pro Asn Val Ala Gly Tyr Lys Asp Asp
 260 265 270

agt ggt tat gcc tat gca aat tat tcg gca gca agc aat aaa gca caa 1083
 Ser Gly Tyr Ala Tyr Ala Asn Tyr Ser Ala Ala Ser Asn Lys Ala Gln
 275 280 285 290

att aaa gat tta gga caa aat ggt tta aaa gtg gcg gca ggt gta cct 1131
 Ile Lys Asp Leu Gly Gln Asn Gly Leu Lys Val Ala Ala Gly Val Pro
 295 300 305

gtg atg aaa gag tct gaa tgg act ggt aaa aac ttt gta ccg ccg tta 1179
 Val Met Lys Glu Ser Glu Trp Thr Gly Lys Asn Phe Val Pro Pro Leu
 310 315 320

aaa act tta tat acc gtc caa gat acc tat aac tat aat gac cca act 1227
 Lys Thr Leu Tyr Thr Val Gln Asp Thr Tyr Asn Tyr Asn Asp Pro Thr
 325 330 335

tgt ggg gat atg acc tac att tgc tgg cca acg gtt gcg ccg tca tct 1275
 Cys Gly Asp Met Thr Tyr Ile Cys Trp Pro Thr Val Ala Pro Ser Ser
 340 345 350

gct tat gtc tat aag gga ggc aaa aaa gca att tct ggt tgg gaa aat 1323
 Ala Tyr Val Tyr Lys Gly Gly Lys Lys Ala Ile Ser Gly Trp Glu Asn
 355 360 365 370

aca tta ttg gtt cca tct tta aag cgc ggt gtt att ttc cgt att aag 1371
 Thr Leu Leu Val Pro Ser Leu Lys Arg Gly Val Ile Phe Arg Ile Lys
 375 380 385

cta gat cca act tac agt act act tat gat gat gct gtg ccg atg ttt 1419
 Leu Asp Pro Thr Tyr Ser Thr Thr Tyr Asp Asp Ala Val Pro Met Phe
 390 395 400

aag agc aac aat cgt tat cgt gac gtg att gca agt cca gat ggg aat 1467
 Lys Ser Asn Asn Arg Tyr Arg Asp Val Ile Ala Ser Pro Asp Gly Asn
 405 410 415

gtt tta tat gta ttg act gat act tcc gga aat gtc caa aaa gat gat 1515
 Val Leu Tyr Val Leu Thr Asp Thr Ser Gly Asn Val Gln Lys Asp Asp
 420 425 430

ggt tct gta acg aat aca tta gaa aac cca gga tct ctg att aga ttt 1563

Gly Ser Val Thr Asn Thr Leu Glu Asn Pro Gly Ser Leu Ile Arg Phe
 435 440 445 450

aca tat aaa gct cag agc tgaaagcttg acctgtgaag tgaaaaatgg 1611
 Thr Tyr Lys Ala Gln Ser
 455

cgcacattgt gcgacatttt tttgtctgc cgttaccgc tactgcgtca cggatctcca 1671

cgcgccctgt agcggcgcgt taagcgcggc ggggtgtggtg gttacgcgca gcgtgaccgc 1731

tacactgcc agcgcctag cgcccgctcc ttccgttcc ttcccttctc ttctgccac 1791

gttcgccggc tttcccgctc aagctctaaa tcgggggctc ccttaggggt tccgatttag 1851

tgctttacgg cacctcgacc ccaaaaaact tgattagggt gatggttcac gtagtgggcc 1911

atgccctga tagacgggtt ttgcccttt gacgttgag tccacgttct ttaatagtgg 1971

actctgttc caaactggaa caacactcaa ccctatctcg gtctattctt ttgattata 2031

agggatttg cggatttcgg cctattggtt aaaaaatgag ctgatttaac aaaaatttaa 2091

cgcgaaattht acaaaaatat taacgcttac aatttcaggt ggcacttttc ggggaaatgt 2151

gcgcggaacc cctatttgtt tatttttcta aatacatcca aatatgtatc cgctcatgag 2211

acaataacc tgataaatgc ttcaataata tgaaaaagg aagagtatga gtattcaaca 2271

ttccgtgtc gcccttattc cttttttgc ggcattttgc cttctgttt ttgtcaccc 2331

agaaacgctg gtgaaagtaa aagatgctga agatcagtg ggtgcacgag tgggttacat 2391

cgaactggat ctcaacagcg gtaagatcct tgagagtttt cgccccgaag aacgttttcc 2451

aatgatgagc acttttaaag ttctgctatg tggcgcggta ttatcccgtg ttgacgccgg 2511

gcaagagcaa ctgggtgcc gcataccta ttctcagaat gacttggtg agtactcacc 2571

agtcacagaa aagcatctta cggatggcat gacagtaaga gaattatgca gtgctgccat 2631

aaccatgagt gataaactg cggccaactt acttctgaca acgatcggag gaccgaagga 2691

gctaaccgtt tttttgcaca acatggggga tcatgtaact cgccttgatc gttgggaacc 2751

ggagctgaat gaagccatac caaacgacga gcgtgacacc acgatgcctg tagcaatggc 2811

aacaacgttg cgcaaactat taactggcga actacttact ctacttccc ggcaacaatt 2871

gatagactgg atggaggcgg ataaagttgc aggaccactt ctgcgctcgg cccctccggc 2931
tggctggttt attgctgata aatctggagc cggtagagcgt ggctctcgcg gtatcattgc 2991
agcactgggg ccagatggta agccctcccg tatcgtagtt atctacacga cggggagtca 3051
ggcaactatg gatgaacgaa atagacagat cgctgagata ggtgcctcac tgattaagca 3111
ttggtaggaa ttaatgatgt ctgttttaga taaaagtaaa gtgattaaca ggcattaga 3171
gctgcttaat gaggtcggaa tcgaagggtt aacaaccgt aaactcgccc agaagctagg 3231
ttagagcag cctacattgt attggcatgt aaaaaataag cgggctttgc tcgacgcctt 3291
agccattgag atgtagata ggcaccatac tcacttttgc ctttagaag gggaaagctg 3351
gcaagatttt ttacgtaata acgctaaaag ttttagatgt gctttactaa gtcacgcga 3411
tggagcaaaa gtacatttag gtacacggcc tacagaaaaa cagtatgaaa ctctcgaaaa 3471
tcaattagcc ttttatgcc aacaagggtt ttcactagag aatgcattat atgcactcag 3531
cgcagtgggg cattttactt taggttgcgt attggaagat caagagcatc aagtcgctaa 3591
agaagaaagg gaaacaccta ctactgatag tatgccgcca ttattacgac aagctatoga 3651
attatttgat caccaagggtg cagagccagc ctcttattc ggccttgaat tgatcatatg 3711
cggattagaa aaacaactta aatgtgaaag tgggtcttaa aagcagcata acccttttcc 3771
gtgatggtaa cttcactagt taaaaggat ctagggtgaag atccttttg ataatctcat 3831
gacaaaaatc ccttaacgtg agttttcgtt cactgagcg tcagacccc tagaaaagat 3891
caaaggatct tcttgagatc cttttttct ggcgtaatc tgctgcttgc aaacaaaaaa 3951
accaccgcta ccagcgggtg ttgtttgcc ggatcaagag ctaccaactc ttttccgaa 4011
ggtaactggc ttacgagag cgcagatacc aaatactgtc ctctagtgt agccgtagt 4071
aggccaccac ttaagaact ctgtagcacc gctacatac ctgcctctgc taatcctgtt 4131
accagtggct gctgccagt gcgataagtc gtgtcttacc gggttggact caagacgata 4191
gttaccggat aaggcgcagc ggtcgggctg aacggggggt tcgtgcacac agcccagctt 4251
ggagcgaacg acctacaccg aactgagata cctacagcgt gagctatgag aaagcggccac 4311

gcttcccgaa gggagaaagg cggacaggta tccggttaagc ggcaggggtcg gaacaggaga 4371

gcgcacgagg gagcttcag ggggaaacgc ctggtatctt tatagtcctg tcgggttcg 4431

ccacctctga cttgagcgtc gattttgtg atgctcgtca ggggggcgga gcctatggaa 4491

aaacgccagc aacgcggcct tttacggtt cctggcctt tgctggcctt ttgtcacat 4551

gacccgaca 4560

<210> 22

<211> 481

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 22

Met Asn Lys His Leu Leu Ala Lys Ile Thr Leu Leu Gly Ala Ala Gln
-25 -20 -15 -10

Leu Leu Thr Leu Asn Ser Ala Phe Ala Asp Val Pro Leu Thr Pro Ser
-5 -1 1 5

Gln Phe Ala Lys Ala Lys Thr Glu Ser Phe Asp Lys Lys Val Leu Leu
10 15 20

Ser Asn Leu Asn Lys Pro His Ala Leu Leu Trp Gly Pro Asp Asn Gln
25 30 35

Ile Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile Leu Arg Val Asn Pro
40 45 50 55

Glu Ser Gly Ser Val Lys Thr Val Phe Gln Val Pro Glu Ile Val Asn
60 65 70

Asp Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe Ala Phe His Pro Asp
75 80 85

Phe Lys Asn Asn Pro Tyr Ile Tyr Val Ser Gly Thr Phe Lys Asn Pro
90 95 100

Lys Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr Ile Ile Arg Arg Tyr
105 110 115

Thr Tyr Asn Lys Ala Thr Asp Thr Leu Glu Lys Pro Val Asp Leu Leu
120 125 130 135

Ala Gly Leu Pro Ser Ser Lys Asp His Gln Ser Gly Arg Leu Val Ile
140 145 150

Gly Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly Asp Gln Gly Arg Asn
155 160 165

Gln Leu Ala Tyr Leu Phe Leu Pro Asn Gln Ala Gln His Thr Pro Thr
170 175 180

Gln Gln Glu Leu Ser Gly Lys Asp Tyr His Thr Tyr Met Gly Lys Val
185 190 195

Leu Arg Leu Asn Leu Asp Gly Ser Ile Pro Lys Asp Asn Pro Ser Phe
200 205 210 215

Asn Gly Val Ile Ser His Ile Tyr Thr Leu Gly His Arg Asn Pro Gln
220 225 230

Gly Leu Ala Phe Thr Pro Asn Gly Lys Leu Leu Gln Ser Glu Gln Gly
235 240 245

Pro Asn Ser Asp Asp Glu Ile Asn Leu Ile Val Lys Gly Gly Asn Tyr
250 255 260

Gly Trp Pro Asn Val Ala Gly Tyr Lys Asp Asp Ser Gly Tyr Ala Tyr
265 270 275

Ala Asn Tyr Ser Ala Ala Ser Asn Lys Ala Gln Ile Lys Asp Leu Gly
280 285 290 295

Gln Asn Gly Leu Lys Val Ala Ala Gly Val Pro Val Met Lys Glu Ser
300 305 310

Glu Trp Thr Gly Lys Asn Phe Val Pro Pro Leu Lys Thr Leu Tyr Thr
315 320 325

Val Gln Asp Thr Tyr Asn Tyr Asn Asp Pro Thr Cys Gly Asp Met Thr
330 335 340

Tyr Ile Cys Trp Pro Thr Val Ala Pro Ser Ser Ala Tyr Val Tyr Lys
345 350 355

Gly Gly Lys Lys Ala Ile Ser Gly Trp Glu Asn Thr Leu Leu Val Pro
360 365 370 375

Ser Leu Lys Arg Gly Val Ile Phe Arg Ile Lys Leu Asp Pro Thr Tyr
380 385 390

Ser Thr Thr Tyr Asp Asp Ala Val Pro Met Phe Lys Ser Asn Asn Arg
395 400 405

Tyr Arg Asp Val Ile Ala Ser Pro Asp Gly Asn Val Leu Tyr Val Leu
410 415 420

Thr Asp Thr Ser Gly Asn Val Gln Lys Asp Asp Gly Ser Val Thr Asn
425 430 435

Thr Leu Glu Asn Pro Gly Ser Leu Ile Arg Phe Thr Tyr Lys Ala Gln
440 445 450 455

Ser

<210> 23
<211> 22
<212> DNA
<213> Artificial

<220>
<223> PCR-primer

<400> 23
tagagttatt ttaccactcc ct 22

<210> 24
<211> 24
<212> DNA
<213> Artificial

<220>
<223> PCR-primer

<400> 24
ggtaggtcc ctgacacca atcg 24

<210> 25
<211> 22
<212> DNA
<213> Artificial

<220>
<223> PCR-primer

<400> 25
cacaggtaca cctgccgcca ct 22

<210> 26
<211> 25
<212> DNA
<213> Artificial

<220>
<223> PCR-primer

<400> 26
tacgaggacc caacaggaac tgagc 25

<210> 27
 <211> 4508
 <212> DNA
 <213> Artificial

<220>
 <223> Expression vector

<220>
 <221> CDS
 <222> (139)..(720)

<220>
 <221> sig_peptide
 <222> (139)..(213)

<220>
 <221> mat_peptide
 <222> (214)..(720)

<400> 27
 ccacgaatg gccagatgat taattcctaa tttttgttga cactctatca ttgatagagt 60
 tattttacca ctccctatca gtgatagaga aaagtgaaat gaatagttcg acaaaaatct 120
 agataacgag ggcaaaaa atg aat aaa cat tta ttg gct aaa att act tta 171
 Met Asn Lys His Leu Leu Ala Lys Ile Thr Leu
 -25 -20 -15
 tta ggt gct gct cag cta ctt acg ctc aat tca gca ttt gct gat gtc 219
 Leu Gly Ala Ala Gln Leu Leu Thr Leu Asn Ser Ala Phe Ala Asp Val
 -10 -5 -1 1
 cct ctt aca cca tct caa ttt gct aaa gcg aaa aca gaa agc ttt gat 267
 Pro Leu Thr Pro Ser Gln Phe Ala Lys Ala Lys Thr Glu Ser Phe Asp
 5 10 15
 aag aaa gtt ctt cta tct aat tta aat aag cca cat gct ttg ttg tgg 315
 Lys Lys Val Leu Leu Ser Asn Leu Asn Lys Pro His Ala Leu Leu Trp
 20 25 30
 gga ccg gat aat caa att tgg tta acg gag cgg gca aca ggt aag att 363
 Gly Pro Asp Asn Gln Ile Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile
 35 40 45 50

cta aga gtt aat cca gag tcg ggc agt gta aaa aca gtt ttt cag gtt 411
 Leu Arg Val Asn Pro Glu Ser Gly Ser Val Lys Thr Val Phe Gln Val
 55 60 65

cct gag att gta aat gat gct gat gga caa aac ggt tta ttg ggt ttt 459
 Pro Glu Ile Val Asn Asp Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe
 70 75 80

gcc ttt cat cct gag ttt aaa aat aat cct tat atc tat gtt tca ggt 507
 Ala Phe His Pro Asp Phe Lys Asn Asn Pro Tyr Ile Tyr Val Ser Gly
 85 90 95

aca ttt aaa aat ccg aaa tct aca gat aaa gaa tta ccg aat caa act 555
 Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr
 100 105 110

att atc cgt cga tat acc tat aac aag gca aca gat acc ctt gag aaa 603
 Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Ala Thr Asp Thr Leu Glu Lys
 115 120 125 130

cca gta gat tta ttg gca gga tta cct tca tcg aaa gac cat cag tcg 651
 Pro Val Asp Leu Leu Ala Gly Leu Pro Ser Ser Lys Asp His Gln Ser
 135 140 145

ggt cgt ctt gtg att ggt cca gac caa aag att tac tat acg att ggt 699
 Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly
 150 155 160

gat cag gga ccc aac agg aac tgagcggcaa agactatcat acctatatgg 750
 Asp Gln Gly Pro Asn Arg Asn
 165

gtaaagtatt gcgcttaaatt ctggatggaa gtattccaaa agataatcca agctttaacg 810

gtgtaattag ccatatttat acgctcggtc atcgtaaccc acagggettgc gcatttactc 870

caaatggtaa actgttgcaa tctgaacagg gtccaaactc tgatgatgaa attaacctca 930

ttgtcaaagg tggttaactat ggctggccaa atgtagcggg ttataaagat gatagtgggt 990

atgcctatgc aaattattcg gcagcaagca ataaagcaca aattaaagat ttaggacaaa 1050

atgggttaaa agtggcggca ggtgtacctg tgatgaaaga gtctgaatgg actggtaaaa 1110

actttgtacc gccgttaaaa actttatata ccgtccaaga tacctataac tataatgacc 1170

caacttgggg ggatatgacc tacatttgct ggccaacggg tgcgccgtca tctgcttatg 1230

tctataaggg aggcaaaaa gcaatttctg gttgggaaaa tacattattg gttccatctt 1290
taaagcgcgg tgtattttc cgtattaagc tagatccaac ttacagtact acttatgatg 1350
atgctgtgcc gatgtttaag agcaacaatc gttatcgtga cgtgattgca agtccagatg 1410
ggaatgtttt atatgtattg actgatactt ccggaaatgt ccaaaaagat gatggttctg 1470
taacgaatac attagaaaac ccaggatctc tgattagatt tacatataaa gtcagagct 1530
gaaagcttga cctgtgaagt gaaaaatggc gcacatttg cgacattttt ttgtctgcc 1590
gtttaccgct actgcgtcac ggatctccac gcgccctgta gcggcgcatt aagcgcggcg 1650
ggtgtggtgg ttacgcgcag cgtgaccgct acacttgcca gcgccctagc gcccgctcct 1710
ttcgctttct tcccttctt tctcgccacg ttgcgcggct ttccccgta agctctaaat 1770
cgggggctcc cttaggggt ccgatttagt gctttacggc acctcgacc caaaaaactt 1830
gattaggggtg atgggtcacg tagtgggcca tcgccctgat agacggttt tcgcccttg 1890
acgttggagt ccacgttctt taatagtga ctctgttcc aaactggaac aacactcaac 1950
cctatctcgg tctattctt tgattataa gggattttgc cgatttcggc ctattggta 2010
aaaaatgagc tgatttaaca aaaattaac gcgaatttta acaaaatatt aacgcttaca 2070
attcaggtg gcactttcg gggaaatgt gcgcgaacct ctattgttt attttctaa 2130
atacattcaa atatgtatcc gtcgatgaga caataaccct gataaatgct tcaataatat 2190
tgaaaaagga agagtatgag tattcaacat ttccgtgtcg ccttattcc ctttttgcg 2250
gcattttgcc ttctgtttt tgctcaccca gaaacgctgg tgaaagtaaa agatgctgaa 2310
gatcagttgg gtgcacgagt gggttacatc gaactggatc tcaacagcgg taagatcctt 2370
gagagtttc gcccgaaga acgtttcca atgatgagca cttttaaagt tctgctatgt 2430
ggcgcgggtat tatcccgat tgacgccggg caagagcaac tcggtcgccg catacactat 2490
tctcagaatg acttgggtga gtactacca gtcacagaaa agcatcttac ggatggcatg 2550
acagtaagag aattatgcag tgctgccata accatgagtg ataactgc ggccaactta 2610
cttctgacaa cgatcggagg accgaaggag ctaaccgctt tttgcacaa catgggggat 2670

catgtaactc gccttgatcg ttgggaaccg gagctgaatg aagccatacc aaacgacgag 2730
cgtgacacca cgatgcctgt agcaatggca acaacgttgc gcaaactatt aactggcgaa 2790
ctacttactc tagcttcccc gcaacaattg atagactgga tggaggcgga taaagttgca 2850
ggaccacttc tgcgctcggc ccttccggct ggctggttta ttgctgataa atctggagcc 2910
ggtgagcgtg gctctcgcg tatcattgca gcaactgggc cagatggtaa gccctccgt 2970
atcgtagtta tctacacgac ggggagtcag gcaactatgg atgaacgaaa tagacagatc 3030
gctgagatag gtgcctcact gattaagcat tggtaggaat taatgatgtc tcgtttagat 3090
aaaagtaaag tgattaacag cgcatlagag ctgcttaatg aggtcggaat cgaaggttta 3150
acaacccgta aactcgccca gaagctaggt gtagagcagc ctacattgta ttggcatgta 3210
aaaaataagc gggctttgct cgacgcctta gccattgaga tgtagatag gcaccatact 3270
cacttttgcc ctttagaagg ggaaagctgg caagattttt tacgtaataa cgctaaaagt 3330
tttagatgtg ctttactaag tcatcgcat ggagcaaaag tacatttagg tacacggcct 3390
acagaaaaac agtatgaac tctcgaaaat caattagcct ttttatgcca acaaggtttt 3450
tcactagaga atgcattata tgcactcagc gcagtggggc attttacttt aggttgcgta 3510
ttggaagatc aagagcatca agtcgctaaa gaagaaagg aaacacctac tactgatagt 3570
atgccgccat tattacgaca agctatcgaa ttatttgatc accaagggtgc agagccagcc 3630
ttcttattcg gccttgaatt gatcatatgc ggattagaaa aacaacttaa atgtgaaagt 3690
gggtcttaaa agcagcataa cctttttccg tgatggtaac ttactagtt taaaaggatc 3750
taggtgaaga tccttttga taatctcatg accaaaatcc cttaacgtga gtttcgttc 3810
cactgagcgt cagaccccg agaaaagatc aaaggatctt ctgagatcc tttttctg 3870
cgcgtaatct gctgcttgca aacaaaaaaa ccaccgctac cagcgggtgt ttgttgccg 3930
gatcaagagc taccaactct tttccgaag gtaactggct tcagcagagc gcagatacca 3990
aatactgtcc ttctagtga gccgtagtta ggccaccact tcaagaactc ttagcaccg 4050
cctacatacc tcgctctgct aatcctgta ccagtggctg ctgccagtgg cgataagtcg 4110

tgtcttaccg ggttgactc aagacgatag ttaccggata aggcgcagcg gtcgggctga 4170
 acgggggggtt cgtgcacaca gcccagcttg gagcgaacga cctacaccga actgagatac 4230
 ctacagcgtg agctatgaga aagcgccacg cttcccgaag ggagaaaggc ggacaggtat 4290
 ccggtaaagc gcagggtcgg aacaggagag cgcacgaggg agcttcagg gggaacgcc 4350
 tggatatctt atagtctgt cgggtttcgc cacctctgac ttgagcgtcg atttttgtga 4410
 tgctcgtcag gggggcggag cctatggaaa aacgccagca acgcggcctt ttacgggtc 4470
 ctggcctttt gctggccttt tgctcacatg acccgaca 4508

<210> 28
 <211> 194
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 28

Met Asn Lys His Leu Leu Ala Lys Ile Thr Leu Leu Gly Ala Ala Gln
 -25 -20 -15 -10

Leu Leu Thr Leu Asn Ser Ala Phe Ala Asp Val Pro Leu Thr Pro Ser
 -5 -1 1 5

Gln Phe Ala Lys Ala Lys Thr Glu Ser Phe Asp Lys Lys Val Leu Leu
 10 15 20

Ser Asn Leu Asn Lys Pro His Ala Leu Leu Trp Gly Pro Asp Asn Gln
 25 30 35

Ile Trp Leu Thr Glu Arg Ala Thr Gly Lys Ile Leu Arg Val Asn Pro
 40 45 50 55

Glu Ser Gly Ser Val Lys Thr Val Phe Gln Val Pro Glu Ile Val Asn
 60 65 70

Asp Ala Asp Gly Gln Asn Gly Leu Leu Gly Phe Ala Phe His Pro Asp
 75 80 85

Phe Lys Asn Asn Pro Tyr Ile Tyr Val Ser Gly Thr Phe Lys Asn Pro
 90 95 100

Lys Ser Thr Asp Lys Glu Leu Pro Asn Gln Thr Ile Ile Arg Arg Tyr
 105 110 115

Thr Tyr Asn Lys Ala Thr Asp Thr Leu Glu Lys Pro Val Asp Leu Leu
 120 125 130 135

Ala Gly Leu Pro Ser Ser Lys Asp His Gln Ser Gly Arg Leu Val Ile
 140 145 150

Gly Pro Asp Gln Lys Ile Tyr Tyr Thr Ile Gly Asp Gln Gly Pro Asn
 155 160 165

Arg Asn

<210> 29
 <211> 36
 <212> DNA
 <213> Artificial

<220>
 <223> PCR-primer

<220>
 <221> misc_feature
 <222> (13)..(24)
 <223> n corresponds to a, c, g, or t; k corresponds to g or t

<400> 29
 cgacgtaacc agnnknknkn knnktggct tacctg 36

<210> 30

<211> 38
<212> DNA
<213> Artificial

<220>
<223> PCR-primer

<400> 30
gtgtgctgtg cctggtcgg caggaacagg taagccag 38

<210> 31
<211> 29
<212> DNA
<213> Artificial

<220>
<223> PCR-primer

<400> 31
cctacctacg actcttccga cgtaaccag 29

<210> 32
<211> 30
<212> DNA
<213> Artificial

<220>
<223> PCR-primer

<400> 32
ccatgctctt cagtcggagt gtgctgtgcc 30

<210> 33
<211> 64
<212> DNA
<213> Artificial

<220>
<223> Insertion fragment with four randomized positions

<220>
<221> misc_feature
<222> (12)..(23)
<223> n is a, c, g, or t

<400> 33

gacgtaacca gnnnnnnnnnn nnnctggctt acctgttct gccgaaccag gcacagcaca 60

ctcc

64

<210> 34

<211> 22

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 34

cacggtaaa gcttgatta tc

22

<210> 35

<211> 21

<212> DNA

<213> Artificial

<220>

<223> sequencing primer

<400> 35

ccttcacga aagaccatca g

21