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SEQUENCE LISTING

<110> Merial Limited
University of Georgia
Bublout, Michel
Mundt, Egbert
Mebatsion, Teshome
Pritchard, Joyce

<120> RECOMBINANT AVIAN PARAMYXOVIRUS VACCINE AND METHOD FOR MAKING AND
USING THEREOF

<130> MER 09-133

<150> US 61/235,912

<151> 2009-08-21

<160> 88

<170> PatentIn version 3.5

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Sequence

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caaagaaaat tgggtgcctgt aatattcttc ttgccaaatg attgtgaagt gtctagccta	15240
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 <211> 1386
 <212> DNA
 <213> artificial sequence

<220>
 <223> APMV8 NP gene

<400> 2
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 agtgattcat caaccacacc aatgaagcaa ggagcaatat tgtcactgct gagtctacat 240
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<210> 3
 <211> 461
 <212> PRT
 <213> artificial sequence

<220>
 <223> APMV8 NP protein

<400> 3

Sequence

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20 25 30

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

Trp Ser Leu Ala Cys Leu Asn Ile Arg Trp Leu Ala Ser Asp Ser Ser
50 55 60

Thr Thr Pro Met Lys Gln Gly Ala Ile Leu Ser Leu Leu Ser Leu His
65 70 75 80

Ser Asp Asn Met Arg Ala His Ala Thr Leu Ala Ala Arg Ser Ala Asp
85 90 95

Ala Ser Leu Thr Ile Leu Glu Val Asp Glu Val Asp Ile Ser Asn Ser
100 105 110

Leu Ile Lys Phe Asn Ala Arg Ser Gly Val Ser Asp Lys Arg Ser Asn
115 120 125

Gln Leu Leu Ala Ile Ala Asp Asp Ile Pro Lys Ser Cys Ser Asn Gly
130 135 140

His Pro Phe Leu Asp Thr Asp Ile Glu Thr Arg Asp Pro Leu Asp Leu
145 150 155 160

Ser Glu Thr Ile Asp Arg Leu Gln Gly Ile Ala Ala Gln Ile Trp Val
165 170 175

Ser Ala Ile Lys Ser Met Thr Ala Pro Asp Thr Ala Ser Glu Ser Glu
180 185 190

Ser Lys Arg Leu Ala Lys Tyr Gln Gln Gln Gly Arg Leu Val Lys Gln
195 200 205

Val Leu Leu His Ser Val Val Arg Thr Glu Phe Met Arg Val Ile Arg
210 215 220

Gly Ser Leu Val Leu Arg Gln Phe Met Val Ser Glu Cys Lys Arg Ala
225 230 235 240

Ser Ala Met Gly Gly Asp Thr Ser Arg Tyr Tyr Ala Met Val Gly Asp
245 250 255

Ile Ser Leu Tyr Ile Lys Asn Ala Gly Leu Thr Ala Phe Phe Leu Thr
260 265 270

Sequence

Leu Lys Phe Gly Val Gly Thr Gln Tyr Pro Thr Leu Ala Met Ser Val
275 280 285

Phe Ser Ser Asp Leu Lys Arg Leu Ala Ala Leu Ile Arg Leu Tyr Lys
290 295 300

Thr Lys Gly Asp Asn Ala Pro Tyr Met Ala Phe Leu Glu Asp Ser Asp
305 310 315 320

Met Gly Asn Phe Ala Pro Ala Asn Tyr Ser Thr Met Tyr Ser Tyr Ala
325 330 335

Met Gly Ile Gly Thr Ile Leu Glu Ala Ser Val Ser Arg Tyr Gln Tyr
340 345 350

Ala Arg Asp Phe Thr Ser Glu Asn Tyr Phe Arg Leu Gly Val Glu Thr
355 360 365

Ala Gln Ser Gln Gln Gly Ala Phe Asp Glu Arg Thr Ala Arg Glu Met
370 375 380

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

Val Asp Met Gly Pro Ser Ser Ile His Glu Pro Ser Arg Pro Ala Phe
405 410 415

Ile Ser Gln Glu Glu Asn Arg Gln Pro Ala Gln Asn Leu Ser Asp Thr
420 425 430

Gln Gly Gln Thr Lys Pro Val Pro Lys Gln Pro Ala Pro Arg Ala Asp
435 440 445

Ser Asp Asp Ile Asp Pro Tyr Glu Asn Gly Leu Glu Trp
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<211> 1218
<212> DNA
<213> artificial sequence

<220>
<223> APMV8 P gene

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caaggggaaca caagaaatct aactgatcta tgggaaaagg agactgcaag tcagaccaag 180
acaccggccc aatctacaca aaccacacaa gttcagtctg atgaaaatga ggagggagaa 240
atcaagtccg agtcaactga tggccacatc agaggaactg ttaatcaatc agagcaagtc 300
ccagaacaaa accagagcag atcttcacca ggtgatgatc tcgacagagc tctcaacaag 360

Sequence

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gacaccccga acatgcaagc acagacaaaa gccctggcga agccacatca agaggcaatc      540
aatcctggca accaggacac aggagagagt attcatttac caccttccat ggcaccacca      600
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gttgtgaaca ctacccccct tattaggaat gatattaacc aacttaaggc cacaaccgca      840
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gaaatagaag gattgattgc attggtggaa acattagttg acaatgacaa gaaggcagca     1140
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<210> 5
 <211> 405
 <212> PRT
 <213> artificial sequence

<220>
 <223> APMV8 P protein

<400> 5

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Thr Asn Val Ile Lys Glu Ile Gln Lys Ser Glu Leu Lys Pro Pro Gln
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Thr Thr Gly Arg Pro Pro Val Ser Gln Gly Asn Thr Arg Asn Leu Thr
 35 40 45

Asp Leu Trp Glu Lys Glu Thr Ala Ser Gln Thr Lys Thr Pro Ala Gln
 50 55 60

Ser Thr Gln Thr Thr Gln Val Gln Ser Asp Glu Asn Glu Glu Gly Glu
 65 70 75 80

Ile Lys Ser Glu Ser Thr Asp Gly His Ile Arg Gly Thr Val Asn Gln
 85 90 95

Ser Glu Gln Val Pro Glu Gln Asn Gln Ser Arg Ser Ser Pro Gly Asp
 100 105 110

Sequence

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

Sequence

Met Ile Asp Gln Val Lys Ser His Ala Asp Tyr Ala Arg Val Lys Gln
385 390 395 400

Ala Ile Tyr Asn Ala
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<210> 6
<211> 1110
<212> DNA
<213> artificial sequence

<220>
<223> APMV8 M gene

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tatggtttca tccaagcaat taaggagagt tcagatcgat cgaaattctt ccatccaaaa 240
gatgacttca aacctgagac agtcactgca ggactggtag tggtaggtgc gatccgaatg 300
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<210> 7
<211> 369
<212> PRT
<213> artificial sequence

<220>
<223> APMV8 M protein

<400> 7

Sequence

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

Thr Lys Glu Leu Gln Pro Gln Val Arg Val Asp Ser Ile Gly Asp Val
35 40 45

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

Gln Ala Ile Lys Glu Ser Ser Asp Arg Ser Lys Phe Phe His Pro Lys
65 70 75 80

Asp Asp Phe Lys Pro Glu Thr Val Thr Ala Gly Leu Val Val Val Gly
85 90 95

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

Ala Leu Glu Ile Thr Val Lys Lys Ser Ala Thr Ser Gln Glu Lys Met
115 120 125

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

Ile Arg Ala Gly Gly Phe Ile Ser Asn Ala Asp Glu Asn Ile Lys Cys
145 150 155 160

Ala Ser Lys Leu Thr Ala Gly Val Gln Tyr Ile Phe Arg Pro Met Phe
165 170 175

Val Ser Ile Thr Lys Leu His Asn Gly Lys Leu Tyr Arg Val Pro Lys
180 185 190

Ser Ile His Ser Ile Ser Ser Thr Leu Leu Tyr Ser Val Met Leu Glu
195 200 205

Val Gly Phe Lys Val Asp Ile Gly Lys Asp His Pro Gln Ala Lys Met
210 215 220

Leu Lys Lys Val Thr Ile Gly Asp Ala Asp Thr Tyr Trp Gly Phe Ala
225 230 235 240

Trp Phe His Leu Cys Asn Phe Lys Lys Thr Ser Ser Lys Gly Lys Pro
245 250 255

Arg Thr Leu Asp Glu Leu Lys Thr Lys Val Lys Asn Met Gly Leu Lys
260 265 270

Sequence

Leu Glu Leu His Asp Leu Trp Gly Pro Thr Ile Val Val Gln Ile Thr
275 280 285

Gly Lys Ser Ser Lys Tyr Ala Gln Gly Phe Phe Ser Ser Asn Gly Thr
290 295 300

Cys Cys Leu Pro Ile Ser Arg Ser Ala Pro Glu Leu Gly Lys Leu Leu
305 310 315 320

Trp Ser Cys Ser Ala Thr Ile Gly Asp Ala Thr Val Val Ile Gln Ser
325 330 335

Ser Glu Lys Gly Glu Leu Leu Arg Ser Asp Asp Leu Glu Ile Arg Gly
340 345 350

Ala Val Ala Ser Lys Lys Gly Arg Leu Gly Ser Phe His Pro Phe Lys
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Lys

<210> 8
<211> 1632
<212> DNA
<213> artificial sequence

<220>
<223> APMV8 F gene

<400> 8
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aacatcttag gcccaactcaa atccaatctg gatgcactgc tctcatctga gacttatccc 300
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Sequence

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acagagattg gagcattatc atccccggtat ataacactag atggggggggt cttagttaat      1140
tgcaagtcaa ttgtttgtag gtgccttaat ccaagtaaga tcattctctca aaatacaaac      1200
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gtgaatcgtg tggaggattt aattcaccaa tcagaggaat ggctggcaaa ggtaaccca      1440
cacattgtta ataatacaac actaattgta ctctgtgtgt taagtgcgct tgctgtgatc      1500
tggctggcag tattaacggc tattataata tacttgagaa caaagttgaa gactatatcg      1560
gcattagctg taaccaatac aatacagtct aaccctatg ttaaccaaac gaaacatgaa      1620
tctaagtttt ga                                                                1632

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<210> 9
<211> 543
<212> PRT
<213> artificial sequence

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<220>
<223> APMV8 F protein

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<400> 9

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

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

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```

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

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```

Thr Thr Cys Leu Lys Glu Thr Ile Thr Thr Tyr Asn Asn Thr Val Asn
65          70          75          80

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

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Glu Thr Tyr Pro Gln Thr Arg Leu Ile Gly Ala Val Ile Gly Ser Ile
100         105         110

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165 170 175

Ile Leu Pro Ser Ile Asn Gln Leu Ser Cys Glu Val Thr Ala Asn Lys
180 185 190

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

Leu Tyr Asn Leu Cys Gly Gly Asn Met Ala Met Leu Thr Gln Lys Ile
225 230 235 240

Gly Ile Lys Gln Gln Asp Val Asn Ser Leu Tyr Glu Ala Gly Leu Ile
245 250 255

Thr Gly Gln Val Ile Gly Tyr Asp Ser His Tyr Gln Leu Leu Val Ile
260 265 270

Gln Val Asn Tyr Pro Ser Ile Ser Glu Val Thr Gly Val Arg Ala Thr
275 280 285

Glu Leu Val Thr Val Ser Val Thr Thr Asp Lys Gly Glu Gly Lys Ala
290 295 300

Ile Val Pro Gln Phe Val Ala Glu Ser Arg Val Thr Ile Glu Glu Leu
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Asp Val Ala Ser Cys Lys Phe Ser Ser Thr Thr Leu Tyr Cys Arg Gln
325 330 335

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

Asn Tyr Asp Asp Cys Gln Tyr Thr Thr Glu Ile Gly Ala Leu Ser Ser
355 360 365

Arg Tyr Ile Thr Leu Asp Gly Gly Val Leu Val Asn Cys Lys Ser Ile
370 375 380

Val Cys Arg Cys Leu Asn Pro Ser Lys Ile Ile Ser Gln Asn Thr Asn
385 390 395 400

Sequence

Ala Ala Val Thr Tyr Val Asp Ala Thr Ile Cys Lys Thr Ile Gln Leu
405 410 415

Asp Asp Ile Gln Leu Gln Leu Glu Gly Ser Leu Ser Ser Val Tyr Ala
420 425 430

Arg Asn Ile Ser Ile Glu Ile Ser Gln Val Thr Thr Ser Gly Ser Leu
435 440 445

Asp Ile Ser Ser Glu Ile Gly Asn Ile Asn Asn Thr Val Asn Arg Val
450 455 460

Glu Asp Leu Ile His Gln Ser Glu Glu Trp Leu Ala Lys Val Asn Pro
465 470 475 480

His Ile Val Asn Asn Thr Thr Leu Ile Val Leu Cys Val Leu Ser Ala
485 490 495

Leu Ala Val Ile Trp Leu Ala Val Leu Thr Ala Ile Ile Ile Tyr Leu
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Arg Thr Lys Leu Lys Thr Ile Ser Ala Leu Ala Val Thr Asn Thr Ile
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Sequence

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Thr Thr Gly Cys Leu Ala Leu Ser Ile Val Ser Ile Val Gln Ile Gly
 35 40 45

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

Pro Leu Lys Thr Thr Leu Ser Asp Thr Leu Arg Asn Pro Ile Asn Gln
 65 70 75 80

Ile Asn Asp Ile Phe Arg Ile Val Ala Leu Asp Ile Pro Leu Gln Val
 85 90 95

Sequence

Thr Ser Ile Gln Lys Asp Leu Ala Ser Gln Phe Asn Met Leu Ile Asp
100 105 110

Ser Leu Asn Ala Ile Lys Leu Gly Asn Gly Thr Asn Leu Ile Ile Pro
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Thr Ser Asp Lys Glu Tyr Ala Gly Gly Ile Gly Asn Pro Val Phe Thr
130 135 140

Val Asp Ala Gly Gly Ser Ile Gly Phe Lys Gln Phe Ser Leu Ile Glu
145 150 155 160

His Pro Ser Phe Ile Ala Gly Pro Thr Thr Thr Arg Gly Cys Thr Arg
165 170 175

Ile Pro Thr Phe His Met Ser Glu Ser His Trp Cys Tyr Ser His Asn
180 185 190

Ile Ile Ala Ala Gly Cys Gln Asp Ala Ser Ala Ser Ser Met Tyr Ile
195 200 205

Ser Met Gly Val Leu His Val Ser Ser Ser Gly Thr Pro Ile Phe Leu
210 215 220

Thr Thr Ala Ser Glu Leu Ile Asp Asp Gly Val Asn Arg Lys Ser Cys
225 230 235 240

Ser Ile Val Ala Thr Gln Phe Gly Cys Asp Ile Leu Cys Ser Ile Val
245 250 255

Thr Glu Lys Glu Gly Asp Asp Tyr Trp Ser Asp Thr Pro Thr Pro Met
260 265 270

Arg His Gly Arg Phe Ser Phe Asn Gly Ser Phe Val Glu Ala Glu Leu
275 280 285

Pro Val Ser Ser Met Phe Ser Ser Phe Ser Ala Asn Tyr Pro Ala Val
290 295 300

Gly Ser Gly Glu Ile Val Lys Asp Arg Ile Leu Phe Pro Ile Tyr Gly
305 310 315 320

Gly Ile Lys Gln Thr Ser Pro Glu Phe Thr Glu Leu Val Lys Tyr Gly
325 330 335

Leu Phe Val Ser Thr Pro Thr Thr Val Cys Gln Ser Ser Trp Thr Tyr
340 345 350

Asp Gln Val Lys Ala Ala Tyr Arg Pro Asp Tyr Ile Ser Gly Arg Phe
355 360 365

Sequence

Trp Ala Gln Val Ile Leu Ser Cys Ala Leu Asp Ala Val Asp Leu Ser
370 375 380

Ser Cys Ile Val Lys Ile Met Asn Ser Ser Thr Val Met Met Ala Ala
385 390 395 400

Glu Gly Arg Ile Met Lys Ile Gly Ile Asp Tyr Phe Tyr Tyr Gln Arg
405 410 415

Ser Ser Ser Trp Trp Pro Leu Ala Phe Val Thr Lys Leu Asp Pro Gln
420 425 430

Glu Leu Ala Asp Thr Asn Ser Ile Trp Leu Thr Asn Ser Ile Pro Ile
435 440 445

Pro Gln Ser Lys Phe Pro Arg Pro Ser Tyr Ser Glu Asn Tyr Cys Thr
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Lys Pro Ala Val Cys Pro Ala Thr Cys Val Thr Gly Val Tyr Ser Asp
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Ile Trp Pro Leu Thr Ser Ser Ser Ser Leu Pro Ser Ile Ile Trp Ile
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Gly Gln Tyr Leu Asp Ala Pro Val Gly Arg Thr Tyr Pro Arg Phe Gly
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Ile Ala Asn Gln Ser His Trp Tyr Leu Gln Glu Asp Ile Leu Pro Thr
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Ser Thr Ala Ser Ala Tyr Ser Thr Thr Thr Cys Phe Lys Asn Thr Ala
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Arg Asn Arg Val Phe Cys Val Thr Ile Ala Glu Phe Ala Asp Gly Leu
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Phe Gly Glu Tyr Arg Ile Thr Pro Gln Leu Tyr Glu Leu Val Arg Asn
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<223> APMV8 L gene

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Page 22

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Sequence

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Sequence

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 35 40 45

Arg Gln Lys Ser Val Val Met His Ile Pro Asp His Ile Leu Glu Lys
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Ser Glu Tyr Arg Ile Lys His Arg Leu Gly Lys Ile Lys Ser Asp Ile
 65 70 75 80

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Ile Thr His Pro Lys Ser Leu Tyr Trp Leu Ser Arg Leu Thr Ile Ala
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Ser Ala Gly Thr Phe Arg His Met Lys Asp Arg Ile Leu Cys Thr Val
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Gly Ser Glu Phe Gly His Lys Ile Gln Asp Leu Phe Ser Leu Leu Ser
 130 135 140

Sequence

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 195 200 205

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 210 215 220

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 260 265 270

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 305 310 315 320

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 385 390 395 400

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

Sequence

Ile Ile Ile Asn Gly Tyr Arg Arg Ser His Ser Gly Leu Trp Pro Asn
420 425 430

Val Glu Pro Ser Ser Ile Tyr Asp Asp Asp Leu Arg Gln Leu Tyr Leu
435 440 445

Glu Ser Ala Glu Ile Ser His His Phe Met Leu Lys Asn Tyr Lys Ser
450 455 460

Leu Ser Met Ile Glu Phe Lys Lys Ser Ile Asp Tyr Asp Leu His Asp
465 470 475 480

Asp Leu Ser Thr Phe Leu Lys Asp Arg Ala Ile Cys Arg Pro Lys Ser
485 490 495

Gln Trp Asp Val Ile Phe Arg Lys Ser Leu Arg Arg Ser His Thr Gln
500 505 510

Ser Gln Tyr Leu Asp Glu Ile Lys Ser Asn Arg Leu Leu Ile Asp Phe
515 520 525

Leu Asp Ser Ala Glu Phe Asp Pro Gly Lys Glu Phe Ala Tyr Val Thr
530 535 540

Thr Met Asp Tyr Leu His Asp Asn Glu Phe Cys Ala Ser Tyr Ser Leu
545 550 555 560

Lys Glu Lys Glu Ile Lys Thr Thr Gly Arg Ile Phe Ala Lys Met Thr
565 570 575

Arg Asn Met Arg Ser Cys Gln Val Ile Leu Glu Ser Leu Leu Ser Lys
580 585 590

His Ile Cys Lys Phe Phe Lys Glu Asn Gly Val Ser Met Glu Gln Leu
595 600 605

Ser Leu Thr Lys Ser Leu Leu Ala Met Ser Gln Leu Ser Pro Lys Val
610 615 620

Ser Thr Leu Gln Asp Thr Ala Ser Arg His Val Gly Asn Ser Lys Ser
625 630 635 640

Gln Ile Ala Thr Ser Asn Pro Ser Arg His His Ser Thr Pro Asn Gln
645 650 655

Met Ser Leu Ser Asn Arg Lys Thr Val Val Ala Thr Phe Leu Thr Thr
660 665 670

Asp Leu Glu Lys Tyr Cys Leu Gln Trp Arg Tyr Ser Thr Ile Lys Leu
675 680 685

Sequence

Phe Ala Gln Ala Leu Asn Gln Leu Phe Gly Ile Asp His Gly Phe Glu
690 695 700

Trp Ile His Leu Arg Leu Met Asn Ser Thr Leu Phe Val Gly Asp Pro
705 710 715 720

Tyr Ser Pro Pro Glu Asp Pro Thr Leu Glu Asp Ile Asp Lys Ala Pro
725 730 735

Asn Asp Asp Ile Phe Ile Val Ser Pro Arg Gly Gly Ile Glu Gly Leu
740 745 750

Cys Gln Lys Met Trp Thr Met Ile Ser Ile Ser Ala Ile His Cys Val
755 760 765

Ala Glu Lys Ile Gly Ala Arg Val Ala Ala Met Val Gln Gly Asp Asn
770 775 780

Gln Val Ile Ala Ile Thr Lys Glu Leu Phe Arg Gly Glu Lys Ala Cys
785 790 795 800

Asp Val Arg Asp Glu Leu Asp Glu Leu Gly Gln Val Phe Phe Asp Glu
805 810 815

Phe Lys Arg His Asn Tyr Ala Ile Gly His Asn Leu Lys Leu Asn Glu
820 825 830

Thr Ile Gln Ser Gln Ser Phe Phe Val Tyr Ser Lys Arg Ile Phe Phe
835 840 845

Glu Gly Arg Leu Leu Ser Gln Val Leu Lys Asn Ala Ala Lys Leu Cys
850 855 860

Met Val Ala Asp His Leu Gly Glu Asn Thr Val Ser Ser Cys Ser Asn
865 870 875 880

Leu Ser Ser Thr Ile Ala Arg Leu Val Glu Asn Gly Phe Glu Lys Asp
885 890 895

Thr Ala Phe Val Leu Asn Leu Val Tyr Ile Met Thr Gln Ile Leu Phe
900 905 910

Asp Glu His Tyr Ser Ile Val Cys Asp His His Ser Val Lys Ser Leu
915 920 925

Ile Gly Ser Lys Asn His Arg Asn Leu Leu Tyr Ser Ser Leu Ile Pro
930 935 940

Gly Gln Leu Gly Gly Phe Asn Phe Leu Asn Ile Ser Arg Leu Phe Thr
945 950 955 960

Sequence

Arg Asn Ile Gly Asp Pro Val Thr Cys Ser Leu Ser Asp Leu Lys Cys
 965 970 975
 Phe Ile Ala Ala Gly Leu Leu Pro Pro Tyr Val Leu Lys Asn Val Val
 980 985 990
 Leu Arg Glu Pro Gly Pro Gly Thr Trp Leu Thr Leu Cys Ser Asp Pro
 995 1000 1005
 Tyr Thr Leu Asn Ile Pro Tyr Thr Gln Leu Pro Thr Thr Tyr Leu
 1010 1015 1020
 Lys Lys His Thr Gln Arg Ser Leu Leu Ser Arg Ala Val Asn Pro
 1025 1030 1035
 Leu Leu Ala Gly Val Gln Val Pro Asn Gln His Glu Glu Glu Glu
 1040 1045 1050
 Met Leu Ala Arg Phe Leu Leu Asp Arg Glu Tyr Val Met Pro Arg
 1055 1060 1065
 Val Ala His Val Ile Leu Glu Ser Ser Val Leu Gly Lys Arg Lys
 1070 1075 1080
 Gln Ile Gln Gly Leu Ile Asp Thr Thr Pro Thr Ile Ile Arg Thr
 1085 1090 1095
 Ser Leu Val Asn Leu Pro Val Ser Arg Lys Lys Cys Glu Lys Ile
 1100 1105 1110
 Ile Asn Tyr Ser Leu Asn Tyr Ile Ala Glu Cys His Asp Ser Leu
 1115 1120 1125
 Leu Ser Gln Val Cys Phe Ser Asp Asn Lys Glu Tyr Leu Trp Ser
 1130 1135 1140
 Thr Ser Leu Ile Ser Val Glu Thr Cys Ser Val Thr Ile Ala Asp
 1145 1150 1155
 Tyr Leu Arg Ala Val Ser Trp Ser Asn Ile Leu Gly Gly Arg Asn
 1160 1165 1170
 Ile Ser Gly Val Thr Thr Pro Asp Thr Ile Glu Leu Ile Gln Gly
 1175 1180 1185
 Cys Leu Ile Gly Glu Asn Ser Ser Cys Thr Leu Cys Glu Ser His
 1190 1195 1200
 Asp Asp Ala Phe Thr Trp Met His Leu Pro Gly Pro Leu Tyr Ile
 1205 1210 1215

Sequence														
Pro	Glu	Pro	Ser	Val	Thr	Asn	Ser	Lys	Met	Arg	Val	Pro	Tyr	Leu
	1220					1225					1230			
Gly	Ser	Lys	Thr	Glu	Glu	Arg	Lys	Thr	Ala	Ser	Met	Ala	Ala	Ile
	1235					1240					1245			
Lys	Gly	Met	Ser	His	His	Leu	Arg	Ala	Val	Leu	Arg	Gly	Thr	Ser
	1250					1255					1260			
Val	Phe	Ile	Trp	Ala	Phe	Gly	Asp	Thr	Asp	Ile	Asn	Trp	Asp	Asn
	1265					1270					1275			
Ala	Leu	Gln	Ile	Ala	Gln	Ser	Arg	Cys	Asn	Ile	Thr	Leu	Asp	Gln
	1280					1285					1290			
Met	Arg	Leu	Leu	Thr	Pro	Ile	Pro	Ser	Ser	Ser	Asn	Ile	Gln	His
	1295					1300					1305			
Arg	Leu	Asp	Asp	Gly	Ile	Ser	Thr	Gln	Lys	Phe	Thr	Pro	Ala	Ser
	1310					1315					1320			
Leu	Ala	Arg	Ile	Thr	Ser	Phe	Val	His	Ile	Cys	Asn	Asp	Ser	Gln
	1325					1330					1335			
Arg	Leu	Glu	Lys	Asp	Gly	Ser	Ser	Val	Asp	Ser	Asn	Leu	Ile	Tyr
	1340					1345					1350			
Gln	Gln	Ile	Met	Leu	Leu	Gly	Leu	Ser	Ile	Phe	Glu	Thr	Met	Tyr
	1355					1360					1365			
Ser	Met	Asp	Gln	Lys	Trp	Val	Phe	Asn	Asn	His	Thr	Leu	His	Leu
	1370					1375					1380			
His	Thr	Gly	His	Ser	Cys	Cys	Pro	Arg	Glu	Leu	Asp	Ile	Ser	Leu
	1385					1390					1395			
Val	Asn	Pro	Pro	Arg	His	Gln	Thr	Pro	Glu	Leu	Thr	Ser	Thr	Thr
	1400					1405					1410			
Thr	Asn	Pro	Phe	Leu	Tyr	Asp	Gln	Leu	Pro	Leu	Asn	Gln	Glu	Asn
	1415					1420					1425			
Leu	Thr	Thr	Leu	Glu	Ile	Lys	Thr	Phe	Lys	Phe	Asn	Glu	Leu	Asn
	1430					1435					1440			
Ile	Asp	Gly	Leu	Asp	Phe	Gly	Glu	Gly	Ile	Gln	Leu	Leu	Ser	Arg
	1445					1450					1455			
Cys	Thr	Ala	Arg	Leu	Met	Ala	Glu	Cys	Ile	Leu	Glu	Glu	Gly	Ile
	1460					1465					1470			

Sequence														
Gly	Ser	Ser	Val	Lys	Asn	Glu	Ala	Ile	Val	Asn	Phe	Asp	Asn	Ser
	1475					1480					1485			
Val	Asn	Trp	Ile	Ser	Glu	Cys	Leu	Met	Cys	Asp	Ile	Arg	Ser	Leu
	1490					1495					1500			
Cys	Val	Asn	Leu	Gly	Gln	Glu	Ile	Leu	Cys	Ser	Leu	Ala	Tyr	Gln
	1505					1510					1515			
Met	Tyr	Tyr	Leu	Arg	Ile	Arg	Gly	Arg	Arg	Ala	Ile	Leu	Asn	Tyr
	1520					1525					1530			
Leu	Asp	Thr	Thr	Leu	Gln	Arg	Ile	Pro	Val	Ile	Gln	Leu	Ala	Asn
	1535					1540					1545			
Ile	Ala	Leu	Thr	Ile	Ser	His	Pro	Glu	Ile	Phe	Arg	Arg	Ile	Val
	1550					1555					1560			
Asn	Thr	Gly	Ile	His	Asn	Gln	Ile	Lys	Gly	Pro	Tyr	Val	Ala	Thr
	1565					1570					1575			
Thr	Asp	Phe	Ile	Ala	Ala	Ser	Arg	Asp	Ile	Ile	Leu	Ser	Gly	Ala
	1580					1585					1590			
Arg	Glu	Tyr	Leu	Ser	Tyr	Leu	Ser	Ser	Gly	Gln	Glu	Asp	Cys	Tyr
	1595					1600					1605			
Thr	Phe	Phe	Asn	Cys	Gln	Asp	Gly	Asp	Leu	Thr	Pro	Lys	Met	Glu
	1610					1615					1620			
Gln	Tyr	Leu	Ala	Arg	Arg	Ala	Cys	Leu	Leu	Thr	Leu	Leu	Tyr	Asn
	1625					1630					1635			
Thr	Gly	His	Gln	Ile	Pro	Val	Ile	Arg	Ser	Leu	Thr	Pro	Ile	Glu
	1640					1645					1650			
Lys	Cys	Lys	Val	Leu	Thr	Glu	Tyr	Asn	Gln	Gln	Ile	Glu	Tyr	Ala
	1655					1660					1665			
Asp	Gln	Glu	Phe	Ser	Ser	Val	Leu	Lys	Val	Val	Asn	Ala	Leu	Leu
	1670					1675					1680			
Gln	Asn	Pro	Lys	Ile	Asp	Ala	Leu	Val	Ser	Asn	Leu	Tyr	Phe	Thr
	1685					1690					1695			
Thr	Arg	Arg	Val	Leu	Ser	Asn	Leu	Arg	Ser	Cys	Asp	Lys	Ala	Arg
	1700					1705					1710			
Ser	Tyr	Ile	Glu	Tyr	Leu	Tyr	Thr	Glu	Asp	Phe	Gly	Glu	Lys	Glu
	1715					1720					1725			

Sequence

Asp	Thr	Val	Gln	Tyr	Asp	Ile	Met	Thr	Thr	Asn	Asp	Ile	Ile	Leu
1730						1735					1740			
Thr	His	Gly	Leu	Phe	Thr	Gln	Ile	Glu	Ile	Ser	Tyr	Gln	Gly	Asn
1745						1750					1755			
Ser	Leu	His	Lys	Phe	Leu	Thr	Pro	Asp	Asn	Ala	Pro	Gly	Ser	Leu
1760						1765					1770			
Ile	Pro	Phe	Ser	Ile	Ser	Pro	Asn	Ser	Leu	Ala	Cys	Asp	Pro	Leu
1775						1780					1785			
His	His	Leu	Leu	Lys	Ser	Val	Gly	Thr	Ser	Ser	Thr	Ser	Trp	Tyr
1790						1795					1800			
Lys	Tyr	Ala	Ile	Ala	Tyr	Ala	Val	Ser	Glu	Lys	Arg	Ser	Ala	Arg
1805						1810					1815			
Leu	Gly	Gly	Ser	Leu	Tyr	Ile	Gly	Glu	Gly	Ser	Gly	Ser	Val	Met
1820						1825					1830			
Thr	Leu	Leu	Glu	Tyr	Leu	Glu	Pro	Ser	Val	Asp	Ile	Phe	Tyr	Asn
1835						1840					1845			
Ser	Leu	Phe	Ser	Asn	Gly	Met	Asn	Pro	Pro	Gln	Arg	Asn	Tyr	Gly
1850						1855					1860			
Leu	Met	Pro	Leu	Gln	Phe	Val	Asn	Ser	Val	Val	Tyr	Lys	Asn	Leu
1865						1870					1875			
Thr	Ala	Lys	Ser	Glu	Cys	Lys	Leu	Gly	Phe	Val	Gln	Gln	Phe	Lys
1880						1885					1890			
Pro	Leu	Trp	Arg	Asp	Ile	Asp	Ile	Glu	Thr	Asn	Val	Thr	Asp	Pro
1895						1900					1905			
Ser	Phe	Ile	Asn	Phe	Ala	Leu	Asn	Glu	Ile	Pro	Met	Gln	Ser	Leu
1910						1915					1920			
Lys	Arg	Val	Asn	Cys	Asp	Val	Glu	Phe	Asp	Arg	Gly	Met	Pro	Ile
1925						1930					1935			
Glu	Arg	Val	Ile	Gln	Gly	Tyr	Thr	His	Ile	Leu	Leu	Val	Ala	Thr
1940						1945					1950			
Tyr	Gly	Leu	Gln	Gln	Asp	Ser	Ile	Leu	Trp	Val	Lys	Val	Tyr	Arg
1955						1960					1965			
Thr	Ser	Glu	Lys	Val	Phe	Gln	Phe	Leu	Leu	Ser	Ala	Met	Ile	Met
1970						1975					1980			

Sequence														
Ile	Phe	Gly	Tyr	Val	Lys	Ile	His	Arg	Asn	Gly	Tyr	Met	Ser	Thr
	1985					1990					1995			
Lys	Asp	Glu	Glu	Tyr	Ile	Leu	Met	Ser	Asp	Cys	Lys	Glu	Pro	Val
	2000					2005					2010			
Asn	Tyr	Thr	Ala	Val	Pro	Asn	Ile	Leu	Thr	Arg	Val	Ser	Asp	Leu
	2015					2020					2025			
Val	Ser	Lys	Asn	Leu	Ser	Leu	Ile	His	Pro	Glu	Asp	Leu	Arg	Lys
	2030					2035					2040			
Val	Arg	Cys	Glu	Thr	Asp	Ser	Leu	Asn	Leu	Lys	Cys	Asn	His	Ile
	2045					2050					2055			
Tyr	Glu	Lys	Ile	Ile	Ala	Arg	Lys	Ile	Pro	Leu	Gln	Val	Ser	Ser
	2060					2065					2070			
Thr	Asp	Ser	Leu	Leu	Leu	Gln	Leu	Gly	Gly	Val	Ile	Asn	Ser	Val
	2075					2080					2085			
Gly	Ser	Thr	Asp	Pro	Arg	Glu	Val	Ala	Thr	Leu	Ser	Ser	Ile	Glu
	2090					2095					2100			
Cys	Met	Asp	Tyr	Val	Val	Ser	Ser	Ile	Asp	Leu	Ala	Ile	Leu	Glu
	2105					2110					2115			
Ala	Asn	Ile	Val	Ile	Ser	Glu	Ser	Ala	Gly	Leu	Asp	Leu	Ala	Leu
	2120					2125					2130			
Met	Leu	Gly	Pro	Phe	Asn	Leu	Asn	Lys	Leu	Lys	Lys	Ile	Asp	Thr
	2135					2140					2145			
Ile	Leu	Lys	Ser	Ser	Thr	Tyr	Gln	Leu	Ile	Pro	Tyr	Trp	Leu	Arg
	2150					2155					2160			
Tyr	Glu	Tyr	Ser	Ile	Asn	Pro	Arg	Ser	Leu	Ser	Phe	Leu	Ile	Thr
	2165					2170					2175			
Lys	Leu	Gln	Gln	Cys	Arg	Ile	Ser	Trp	Ser	Asp	Met	Ile	Thr	Ile
	2180					2185					2190			
Ser	Glu	Phe	Arg	Lys	Lys	Ser	Lys	Arg	Pro	Ile	Phe	Ile	Lys	Arg
	2195					2200					2205			
Val	Ile	Gly	Asn	Gln	Gln	Leu	Lys	Ser	Phe	Phe	Asn	Glu	Ser	Ser
	2210					2215					2220			
Ser	Ile	Val	Leu	Thr	Arg	Ala	Glu	Val	Lys	Val	Cys	Ile	Lys	Phe
	2225					2230					2235			

Sequence

Leu Gly Ala Ile Ile Lys Leu Lys
2240 2245

<210> 14
<211> 2238
<212> PRT
<213> artificial sequence

<220>
<223> APMV8 L protein2

<400> 14

Met Asp Ile Lys Gln Val Asp Leu Ile Ile Gln Pro Glu Val His Leu
1 5 10 15

Asp Ser Pro Ile Ile Leu Asn Lys Leu Ala Leu Leu Trp Arg Leu Ser
20 25 30

Gly Leu Pro Met Pro Ala Asp Leu Arg Gln Lys Ser Val Val Met His
35 40 45

Ile Pro Asp His Ile Leu Glu Lys Ser Glu Tyr Arg Ile Lys His Arg
50 55 60

Leu Gly Lys Ile Lys Ser Asp Ile Thr His Tyr Cys Gln Tyr Phe Asn
65 70 75 80

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

Trp Leu Ser Arg Leu Thr Ile Ala Ser Ala Gly Thr Phe Arg His Met
100 105 110

Lys Asp Arg Ile Leu Cys Thr Val Gly Ser Glu Phe Gly His Lys Ile
115 120 125

Gln Asp Leu Phe Ser Leu Leu Ser His Lys Leu Val Gly Asn Gly Asp
130 135 140

Leu Phe Asn Gln Ser Leu Ser Gly Thr Arg Leu Thr Ala Ser Pro Leu
145 150 155 160

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

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

Met Arg Tyr Leu Ile Lys Gln Ser Arg Thr Thr Asn Ser Ala His Leu
195 200 205

Thr Glu Ile Ile Lys Glu Glu Trp Gly Leu Val Gly Ile Thr Pro Asp
210 215 220

Sequence

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

Phe Glu Met Val Leu Met Tyr Ser Asp Val Leu Glu Ser Arg Asp Asn
245 250 255

Ile Val Leu Val Gly Arg Leu Ser Thr Phe Leu Gln Pro Val Val Ser
260 265 270

Arg Leu Glu Val Leu Phe Asp Leu Val Asp Ser Leu Ala Lys Ile Leu
275 280 285

Gly Asp Thr Ile Tyr Glu Ile Ile Ala Val Leu Glu Ser Leu Ser Tyr
290 295 300

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

Phe Ser Phe Asn Met Asn Glu Leu Asp Asn Thr Leu Ser Lys Arg Val
325 330 335

Asp Pro Lys His Lys Asn Thr Ile Met Ser Ile Ile Arg Gln Cys Phe
340 345 350

Ser Asn Leu Asp Val Asp Gln Ala Ala Glu Met Leu Cys Leu Met Arg
355 360 365

Leu Phe Gly His Pro Met Leu Thr Ala Pro Asp Ala Ala Ala Lys Val
370 375 380

Arg Lys Ala Met Cys Ala Pro Lys Leu Val Glu His Asp Thr Ile Leu
385 390 395 400

Gln Thr Leu Ser Phe Phe Lys Gly Ile Ile Ile Asn Gly Tyr Arg Arg
405 410 415

Ser His Ser Gly Leu Trp Pro Asn Val Glu Pro Ser Ser Ile Tyr Asp
420 425 430

Asp Asp Leu Arg Gln Leu Tyr Leu Glu Ser Ala Glu Ile Ser His His
435 440 445

Phe Met Leu Lys Asn Tyr Lys Ser Leu Ser Met Ile Glu Phe Lys Lys
450 455 460

Ser Ile Asp Tyr Asp Leu His Asp Asp Leu Ser Thr Phe Leu Lys Asp
465 470 475 480

Arg Ala Ile Cys Arg Pro Lys Ser Gln Trp Asp Val Ile Phe Arg Lys
485 490 495

Sequence

Ser Leu Arg Arg Ser His Thr Gln Ser Gln Tyr Leu Asp Glu Ile Lys
 500 505 510
 Ser Asn Arg Leu Leu Ile Asp Phe Leu Asp Ser Ala Glu Phe Asp Pro
 515 520 525
 Gly Lys Glu Phe Ala Tyr Val Thr Thr Met Asp Tyr Leu His Asp Asn
 530 535 540
 Glu Phe Cys Ala Ser Tyr Ser Leu Lys Glu Lys Glu Ile Lys Thr Thr
 545 550 555 560
 Gly Arg Ile Phe Ala Lys Met Thr Arg Asn Met Arg Ser Cys Gln Val
 565 570 575
 Ile Leu Glu Ser Leu Leu Ser Lys His Ile Cys Lys Phe Phe Lys Glu
 580 585 590
 Asn Gly Val Ser Met Glu Gln Leu Ser Leu Thr Lys Ser Leu Leu Ala
 595 600 605
 Met Ser Gln Leu Ser Pro Lys Val Ser Thr Leu Gln Asp Thr Ala Ser
 610 615 620
 Arg His Val Gly Asn Ser Lys Ser Gln Ile Ala Thr Ser Asn Pro Ser
 625 630 635 640
 Arg His His Ser Thr Pro Asn Gln Met Ser Leu Ser Asn Arg Lys Thr
 645 650 655
 Val Val Ala Thr Phe Leu Thr Thr Asp Leu Glu Lys Tyr Cys Leu Gln
 660 665 670
 Trp Arg Tyr Ser Thr Ile Lys Leu Phe Ala Gln Ala Leu Asn Gln Leu
 675 680 685
 Phe Gly Ile Asp His Gly Phe Glu Trp Ile His Leu Arg Leu Met Asn
 690 695 700
 Ser Thr Leu Phe Val Gly Asp Pro Tyr Ser Pro Pro Glu Asp Pro Thr
 705 710 715 720
 Leu Glu Asp Ile Asp Lys Ala Pro Asn Asp Asp Ile Phe Ile Val Ser
 725 730 735
 Pro Arg Gly Gly Ile Glu Gly Leu Cys Gln Lys Met Trp Thr Met Ile
 740 745 750
 Ser Ile Ser Ala Ile His Cys Val Ala Glu Lys Ile Gly Ala Arg Val
 755 760 765

Sequence

Ala Ala Met Val Gln Gly Asp Asn Gln Val Ile Ala Ile Thr Lys Glu
770 775 780

Leu Phe Arg Gly Glu Lys Ala Cys Asp Val Arg Asp Glu Leu Asp Glu
785 790 795 800

Leu Gly Gln Val Phe Phe Asp Glu Phe Lys Arg His Asn Tyr Ala Ile
805 810 815

Gly His Asn Leu Lys Leu Asn Glu Thr Ile Gln Ser Gln Ser Phe Phe
820 825 830

Val Tyr Ser Lys Arg Ile Phe Phe Glu Gly Arg Leu Leu Ser Gln Val
835 840 845

Leu Lys Asn Ala Ala Lys Leu Cys Met Val Ala Asp His Leu Gly Glu
850 855 860

Asn Thr Val Ser Ser Cys Ser Asn Leu Ser Ser Thr Ile Ala Arg Leu
865 870 875 880

Val Glu Asn Gly Phe Glu Lys Asp Thr Ala Phe Val Leu Asn Leu Val
885 890 895

Tyr Ile Met Thr Gln Ile Leu Phe Asp Glu His Tyr Ser Ile Val Cys
900 905 910

Asp His His Ser Val Lys Ser Leu Ile Gly Ser Lys Asn His Arg Asn
915 920 925

Leu Leu Tyr Ser Ser Leu Ile Pro Gly Gln Leu Gly Gly Phe Asn Phe
930 935 940

Leu Asn Ile Ser Arg Leu Phe Thr Arg Asn Ile Gly Asp Pro Val Thr
945 950 955 960

Cys Ser Leu Ser Asp Leu Lys Cys Phe Ile Ala Ala Gly Leu Leu Pro
965 970 975

Pro Tyr Val Leu Lys Asn Val Val Leu Arg Glu Pro Gly Pro Gly Thr
980 985 990

Trp Leu Thr Leu Cys Ser Asp Pro Tyr Thr Leu Asn Ile Pro Tyr Thr
995 1000 1005

Gln Leu Pro Thr Thr Tyr Leu Lys Lys His Thr Gln Arg Ser Leu
1010 1015 1020

Leu Ser Arg Ala Val Asn Pro Leu Leu Ala Gly Val Gln Val Pro
1025 1030 1035

Sequence

Asn	Gln	His	Glu	Glu	Glu	Glu	Met	Leu	Ala	Arg	Phe	Leu	Leu	Asp
1040						1045					1050			
Arg	Glu	Tyr	Val	Met	Pro	Arg	Val	Ala	His	Val	Ile	Leu	Glu	Ser
1055						1060					1065			
Ser	Val	Leu	Gly	Lys	Arg	Lys	Gln	Ile	Gln	Gly	Leu	Ile	Asp	Thr
1070						1075					1080			
Thr	Pro	Thr	Ile	Ile	Arg	Thr	Ser	Leu	Val	Asn	Leu	Pro	Val	Ser
1085						1090					1095			
Arg	Lys	Lys	Cys	Glu	Lys	Ile	Ile	Asn	Tyr	Ser	Leu	Asn	Tyr	Ile
1100						1105					1110			
Ala	Glu	Cys	His	Asp	Ser	Leu	Leu	Ser	Gln	Val	Cys	Phe	Ser	Asp
1115						1120					1125			
Asn	Lys	Glu	Tyr	Leu	Trp	Ser	Thr	Ser	Leu	Ile	Ser	Val	Glu	Thr
1130						1135					1140			
Cys	Ser	Val	Thr	Ile	Ala	Asp	Tyr	Leu	Arg	Ala	Val	Ser	Trp	Ser
1145						1150					1155			
Asn	Ile	Leu	Gly	Gly	Arg	Asn	Ile	Ser	Gly	Val	Thr	Thr	Pro	Asp
1160						1165					1170			
Thr	Ile	Glu	Leu	Ile	Gln	Gly	Cys	Leu	Ile	Gly	Glu	Asn	Ser	Ser
1175						1180					1185			
Cys	Thr	Leu	Cys	Glu	Ser	His	Asp	Asp	Ala	Phe	Thr	Trp	Met	His
1190						1195					1200			
Leu	Pro	Gly	Pro	Leu	Tyr	Ile	Pro	Glu	Pro	Ser	Val	Thr	Asn	Ser
1205						1210					1215			
Lys	Met	Arg	Val	Pro	Tyr	Leu	Gly	Ser	Lys	Thr	Glu	Glu	Arg	Lys
1220						1225					1230			
Thr	Ala	Ser	Met	Ala	Ala	Ile	Lys	Gly	Met	Ser	His	His	Leu	Arg
1235						1240					1245			
Ala	Val	Leu	Arg	Gly	Thr	Ser	Val	Phe	Ile	Trp	Ala	Phe	Gly	Asp
1250						1255					1260			
Thr	Asp	Ile	Asn	Trp	Asp	Asn	Ala	Leu	Gln	Ile	Ala	Gln	Ser	Arg
1265						1270					1275			
Cys	Asn	Ile	Thr	Leu	Asp	Gln	Met	Arg	Leu	Leu	Thr	Pro	Ile	Pro
1280						1285					1290			

Sequence

Ser Ser Ser Asn Ile Gln His Arg Leu Asp Asp Gly Ile Ser Thr
 1295 1300 1305
 Gln Lys Phe Thr Pro Ala Ser Leu Ala Arg Ile Thr Ser Phe Val
 1310 1315 1320
 His Ile Cys Asn Asp Ser Gln Arg Leu Glu Lys Asp Gly Ser Ser
 1325 1330 1335
 Val Asp Ser Asn Leu Ile Tyr Gln Gln Ile Met Leu Leu Gly Leu
 1340 1345 1350
 Ser Ile Phe Glu Thr Met Tyr Ser Met Asp Gln Lys Trp Val Phe
 1355 1360 1365
 Asn Asn His Thr Leu His Leu His Thr Gly His Ser Cys Cys Pro
 1370 1375 1380
 Arg Glu Leu Asp Ile Ser Leu Val Asn Pro Pro Arg His Gln Thr
 1385 1390 1395
 Pro Glu Leu Thr Ser Thr Thr Thr Asn Pro Phe Leu Tyr Asp Gln
 1400 1405 1410
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Sequence

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 Thr Thr Asn Asp Ile Ile Leu Thr His Gly Leu Phe Thr Gln Ile
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Sequence

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

Ile Pro Leu Gln Val Ser Ser Thr Asp Ser Leu Leu Leu Gln Leu
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Sequence

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Sequence

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Sequence

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Sequence

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Sequence

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32

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35

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<220>
 <223> APMV8 minigenome

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Sequence

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Sequence

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

Sequence

Leu Lys Phe Gly Val Gly Thr Gln Tyr Pro Thr Leu Ala Met Ser Val
275 285

Phe Ser Ser Asp Leu Lys Arg Leu Ala Ala Leu Ile Arg Leu Tyr Lys
290 295 300

Thr Lys Gly Asp Asn Ala Pro Tyr Met Ala Phe Leu Glu Asp Ser Asp
305 310 315 320

Met Gly Asn Phe Ala Pro Ala Asn Tyr Ser Thr Met Tyr Ser Tyr Ala
325 330 335

Met Gly Ile Gly Thr Ile Leu Glu Ala Ser Val Ser Arg Tyr Gln Tyr
340 345 350

Ala Arg Asp Phe Thr Ser Glu Asn Tyr Phe Arg Leu Gly Val Glu Thr
355 360 365

Ala Gln Ser Gln Gln Gly Ala Phe Asp Glu Arg Thr Ala Arg Glu Met
370 375 380

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

Val Asp Met Gly Pro Ser Ser Val His Glu Pro Ser Arg Pro Ala Phe
405 410 415

Ile Ser Gln Glu Glu Asn Arg Gln Pro Ala Gln Asn Ser Ser Asp Thr
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Gln Gly Gln Thr Lys Pro Val Pro Lys Gln Pro Ala Pro Arg Ala Asp
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acaccggccc aatctccaca aaccacacaa gttcagtctg atgaaaatga ggagggagaa 240
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Sequence

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<220>
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Thr Thr Gly Arg Pro Pro Val Ser Gln Gly Asn Thr Arg Asn Leu Thr
 35 40 45

Asp Leu Trp Glu Lys Glu Thr Ala Ser Gln Thr Lys Thr Pro Ala Gln
 50 55 60

Ser Pro Gln Thr Thr Gln Val Gln Ser Asp Glu Asn Glu Glu Gly Glu
 65 70 75 80

Ile Lys Ser Glu Ser Ile Asp Gly His Ile Arg Gly Thr Val Asn Gln
 85 90 95

Sequence

Ser Glu Gln Val Pro Glu Gln Asn Gln Ser Arg Ser Ser Pro Gly Asp
100 105 110

Asp Leu Asp Arg Ala Leu Asn Lys Leu Glu Gly Arg Ile Asn Ser Ile
115 120 125

Ser Ser Met Asp Lys Glu Ile Lys Lys Gly Pro Arg Ile Gln Asn Leu
130 135 140

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

Asp Thr Pro Asn Met Gln Ala Gln Thr Lys Ala Leu Ala Lys Pro His
165 170 175

Gln Glu Ala Ile Asn Pro Gly Asn Gln Asp Thr Gly Glu Ser Ile His
180 185 190

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

Asn Ala Pro Gln Phe Val Pro Asp Gln Ser Met Thr Asn Val Asp Ala
210 215 220

Gly Ser Val Gln Leu His Ala Ser Cys Ala Glu Met Ile Ser Arg Met
225 230 235 240

Phe Val Glu Val Ile Ser Lys Leu Asp Lys Leu Glu Ser Arg Leu Asn
245 250 255

Asp Ile Ala Lys Val Val Asn Thr Thr Pro Leu Ile Arg Asn Asp Ile
260 265 270

Asn Gln Leu Lys Ala Thr Thr Ala Leu Met Ser Asn Gln Ile Ala Ser
275 280 285

Ile Gln Ile Leu Asp Pro Gly Asn Ala Gly Val Arg Ser Leu Ser Glu
290 295 300

Met Lys Ser Val Thr Lys Lys Ala Ala Val Val Ile Ala Gly Phe Gly
305 310 315 320

Asp Asp Pro Thr Gln Ile Ile Glu Glu Gly Ile Met Ala Lys Asp Ala
325 330 335

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

Thr Ser Ser Gly Val Ser Lys Gly Glu Ile Glu Gly Leu Ile Ala Leu
355 360 365

Sequence

Val Glu Thr Leu Val Asp Asn Asp Lys Lys Ala Ala Lys Leu Ile Lys
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Ala Ile Tyr Asn Ala
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<210> 58
 <211> 369
 <212> PRT
 <213> artificial sequence

<220>
 <223> M protein of AC048299

Sequence

<400> 58

Met Ala Tyr Thr Thr Leu Lys Leu Trp Val Asp Glu Gly Asp Met Ser
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Ser Ser Leu Leu Ser Phe Pro Leu Val Leu Lys Glu Thr Asp Arg Gly
20 25 30

Thr Lys Glu Leu Gln Pro Gln Val Arg Val Asp Ser Ile Gly Asp Val
35 40 45

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

Gln Ala Ile Lys Glu Ser Thr Asp Arg Ser Lys Phe Phe His Pro Lys
65 70 75 80

Asp Asp Phe Lys Pro Glu Thr Val Thr Ala Gly Leu Val Val Val Gly
85 90 95

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

Ala Leu Glu Ile Thr Val Lys Lys Ser Ala Thr Ser Gln Glu Lys Met
115 120 125

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

Ile Arg Ala Gly Gly Phe Ile Ser Asn Ala Asp Glu Asn Ile Lys Cys
145 150 155 160

Ala Ser Lys Leu Thr Ala Gly Val Gln Tyr Ile Phe Arg Pro Met Phe
165 170 175

Val Ser Ile Thr Lys Leu His Asn Gly Lys Leu Tyr Arg Val Pro Lys
180 185 190

Ser Ile His Ser Ile Ser Ser Thr Leu Leu Tyr Ser Val Met Leu Glu
195 200 205

Val Gly Phe Lys Val Asp Ile Gly Lys Asp His Pro Gln Ala Lys Met
210 215 220

Leu Lys Lys Val Thr Ile Gly Asp Ala Asp Thr Tyr Trp Gly Phe Ala
225 230 235 240

Trp Phe His Leu Cys Asn Phe Lys Lys Thr Ser Ser Lys Gly Lys Pro
245 250 255

Arg Thr Leu Asp Glu Leu Lys Thr Lys Val Lys Asn Met Gly Leu Lys
260 265 270

Sequence

Leu Glu Leu His Asp Leu Trp Gly Pro Thr Ile Val Val Gln Ile Thr
275 280 285

Gly Lys Ser Ser Lys Tyr Ala Gln Gly Phe Phe Ser Ser Asn Gly Thr
290 295 300

Cys Cys Leu Pro Ile Ser Arg Ser Ala Pro Gly Leu Gly Lys Leu Leu
305 310 315 320

Trp Ser Cys Ser Ala Thr Ile Gly Asp Ala Thr Val Val Ile Gln Ser
325 330 335

Ser Glu Lys Gly Glu Leu Leu Arg Ser Asp Asp Leu Glu Ile Arg Gly
340 345 350

Ala Val Ala Ser Lys Lys Gly Arg Leu Ser Ser Phe His Pro Phe Lys
355 360 365

Lys

<210> 59
<211> 1632
<212> DNA
<213> artificial sequence

<220>
<223> F gene of FJ215863

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cttgctgcat atacaacatc actttcaggg acaattgccg tgcgattcct acctgtgctc 180
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aacatcttag gccactcaa atccaatctg gatgcactgc tctcatctga gacttatccc 300
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caaacagcta ttgcacttgg taagatacag agttttgtga atgaggaaat tctgccatct 540
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tcatatcaag cgctgtacia cctgtgtggt ggcaacatgg caatgcttac tcagaagatt 720
ggaattaaac aacaagacgt taattcgcta tatgaagccg gactaatcac aggacaagtc 780
attggttatg actctcagta ccagctgctg gtcattccagg tcaattatcc aagcatttct 840
gaggtcactg gtgtacgtgc aacagaatta gtcactgtta gtgtaacaac agacaagggg 900

Sequence

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gaagggaaag caattgtacc ccaatttgta gctgaaagtc gggtgactat tgaagagctt      960
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gcacttcccc cgctagtagc tagctgtctt cgaggtaact atgatgattg tcaatataacc      1080
acagagattg gagcattatc atccccggtat ataacactag atgggggggt cttagttaat      1140
tgtaagtcaa ttgtttgtag gtgccttaat ccaagtaaga tcattctctca aaatacaaac      1200
gctgcagtaa catatgttga tgccacaatc tgcaaaacaa ttcaattgga tgatatacaa      1260
ctccagctgg aagggtcact atcatcagtt tatgcaagaa acatctcaat tgagatcagt      1320
caggtgacca cctccgggtc tttagatatc agcagtgaga taggaaacat caataatacg      1380
gtgaatcgtg tggaggattt aattcaccaa tcagaggaat ggctggcaaa ggttaaccga      1440
cacattgtta ataatacaac actaatcgta ctctgtgtgt taagtgcgct tgctgtgatc      1500
tggtctggcag tattaacggc tattataata tacttgagaa caaagttgaa gactatatcg      1560
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 <212> PRT
 <213> artificial sequence

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 <223> F protein of AC048300
 <400> 60

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

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

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

Thr Thr Cys Leu Arg Glu Thr Ile Thr Thr Tyr Asn Asn Thr Val Asn
 65 70 75 80

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

Glu Thr Tyr Pro Gln Thr Arg Leu Ile Gly Ala Val Ile Gly Ser Ile
 100 105 110

Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu
 115 120 125

Sequence

Lys Gln Ala Gln Asp Asn Ala Arg Asn Ile Leu Ala Leu Lys Glu Ala
130 135 140

Leu Ser Lys Thr Asn Glu Ala Val Lys Glu Leu Ser Ser Gly Leu Gln
145 150 155 160

Gln Thr Ala Ile Ala Leu Gly Lys Ile Gln Ser Phe Val Asn Glu Glu
165 170 175

Ile Leu Pro Ser Ile Asn Gln Leu Ser Cys Glu Val Thr Ala Asn Lys
180 185 190

Leu Gly Val Tyr Leu Ser Leu Tyr Leu Thr Glu Leu Thr Thr Ile Phe
195 200 205

Gly Ala Gln Leu Thr Asn Pro Ala Leu Thr Ser Leu Ser Tyr Gln Ala
210 215 220

Leu Tyr Asn Leu Cys Gly Gly Asn Met Ala Met Leu Thr Gln Lys Ile
225 230 235 240

Gly Ile Lys Gln Gln Asp Val Asn Ser Leu Tyr Glu Ala Gly Leu Ile
245 250 255

Thr Gly Gln Val Ile Gly Tyr Asp Ser Gln Tyr Gln Leu Leu Val Ile
260 265 270

Gln Val Asp Tyr Pro Ser Ile Ser Glu Val Thr Gly Val Arg Ala Thr
275 280 285

Glu Leu Val Thr Val Ser Val Thr Thr Asp Lys Gly Glu Gly Lys Ala
290 295 300

Ile Val Pro Gln Phe Val Ala Glu Ser Arg Val Thr Ile Glu Glu Leu
305 310 315 320

Asp Val Ala Ser Cys Lys Phe Ser Ser Thr Thr Leu Tyr Cys Arg Gln
325 330 335

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

Asn Tyr Asp Asp Cys Gln Tyr Thr Thr Glu Ile Gly Ala Leu Ser Ser
355 360 365

Arg Tyr Ile Thr Leu Asp Gly Gly Val Leu Val Asn Cys Lys Ser Ile
370 375 380

Val Cys Arg Cys Leu Asn Pro Ser Lys Ile Ile Ser Gln Asn Thr Asn
385 390 395 400

Sequence

Ala Ala Val Thr Tyr Val Asp Ala Thr Ile Cys Lys Thr Ile Gln Leu
405 410 415

Asp Asp Ile Gln Leu Gln Leu Glu Gly Ser Leu Ser Ser Val Tyr Ala
420 425 430

Arg Asn Ile Ser Ile Glu Ile Ser Gln Val Thr Thr Ser Gly Ser Leu
435 440 445

Asp Ile Ser Ser Glu Ile Gly Asn Ile Asn Asn Thr Val Asn Arg Val
450 455 460

Glu Asp Leu Ile His Gln Ser Glu Glu Trp Leu Ala Lys Val Asn Pro
465 470 475 480

His Ile Val Asn Asn Thr Thr Leu Ile Val Leu Cys Val Leu Ser Ala
485 490 495

Leu Ala Val Ile Trp Leu Ala Val Leu Thr Ala Ile Ile Ile Tyr Leu
500 505 510

Arg Thr Lys Leu Lys Thr Ile Ser Ala Leu Ala Val Thr Asn Thr Ile
515 520 525

Gln Ser Asn Pro Tyr Val Asn Gln Thr Lys Arg Glu Ser Lys Phe
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<211> 1734

<212> DNA

<213> artificial sequence

<220>

<223> HN gene of FJ215863

<400> 61

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gaagtgggtga cacccttgaa aaccactctg tctgatacac tcaggaatcc aattaaccag	240
ataaatgaca tatttaggat tgttgccctt gatattccat tgcaagtgac caatatccaa	300
aaagaccttg caagtcaatt taacatgttg atagatagtt taaatgctat caaattaggc	360
aacgggacca accttatcat acctacatca gacaaggagt atgcaggagg aattggaaac	420
cctgtattta ctgtcgatgc tggaggttct ataggattca aacagtttag cttaatagaa	480
catccgagct ttattgctgg acctacaacg acccgaggct gtacaagaat acccactttt	540
cacatgtcag aaagtcattg gtgctactca cacaacatca tcgctgctgg ctgtcaagat	600
gccagtgcac ccagtatgta tatctcaatg ggagttctcc atgtgtcctc atctggcact	660

Sequence

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cccatTTTTtC ttactactgc aagtGagctg atagacgatg gagttaaccg taagtcatgc      720
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taccctgctg tgggatcagg cgaaattgta aaagatagaa tattattccc aatttacgga      960
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acacctacaa ctgtgtgcca gagtagctgg acttatgacc aggtaaaagc agcgtatagg     1080
ccagattaca tatcaggccg gttctgggca caagtgatac tcagctgcgc tcttgatgca     1140
gtcgacttat caagttgtat tgtaaagatt atgaatagca gcacagtgat gatggcagcg     1200
gaaggaagga taatgaagat agggattgat tacttttact atcagcggtc atcttcttgg     1260
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aagaatactg ccaggaatag agtgttctgc gtcaccattg ccgaatttgc agatggggtg     1680
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<210> 62
 <211> 577
 <212> PRT
 <213> artificial sequence

<220>
 <223> HN protein of AC048301

<400> 62

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Arg Lys Thr Thr Trp Arg Ala Ile Phe Arg Trp Ser Val Leu Leu Ile
 20 25 30

Thr Thr Gly Cys Leu Ala Leu Ser Ile Ile Ser Ile Val Gln Ile Gly
 35 40 45

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

Pro Leu Lys Thr Thr Leu Ser Asp Thr Leu Arg Asn Pro Ile Asn Gln
 65 70 75 80

Sequence

Ile Asn Asp Ile Phe Arg Ile Val Ala Leu Asp Ile Pro Leu Gln Val
85 90 95

Thr Asn Ile Gln Lys Asp Leu Ala Ser Gln Phe Asn Met Leu Ile Asp
100 105 110

Ser Leu Asn Ala Ile Lys Leu Gly Asn Gly Thr Asn Leu Ile Ile Pro
115 120 125

Thr Ser Asp Lys Glu Tyr Ala Gly Gly Ile Gly Asn Pro Val Phe Thr
130 135 140

Val Asp Ala Gly Gly Ser Ile Gly Phe Lys Gln Phe Ser Leu Ile Glu
145 150 155 160

His Pro Ser Phe Ile Ala Gly Pro Thr Thr Thr Arg Gly Cys Thr Arg
165 170 175

Ile Pro Thr Phe His Met Ser Glu Ser His Trp Cys Tyr Ser His Asn
180 185 190

Ile Ile Ala Ala Gly Cys Gln Asp Ala Ser Ala Ser Ser Met Tyr Ile
195 200 205

Ser Met Gly Val Leu His Val Ser Ser Ser Gly Thr Pro Ile Phe Leu
210 215 220

Thr Thr Ala Ser Glu Leu Ile Asp Asp Gly Val Asn Arg Lys Ser Cys
225 230 235 240

Ser Ile Val Ala Thr Arg Phe Gly Cys Asp Ile Leu Cys Ser Ile Val
245 250 255

Thr Glu Lys Glu Gly Asp Asp Tyr Trp Ser Asp Thr Pro Thr Pro Met
260 265 270

Arg His Gly Arg Phe Ser Phe Asn Gly Ser Phe Val Glu Ala Glu Leu
275 280 285

Pro Val Ser Ser Met Phe Ser Ser Phe Ser Ala Asn Tyr Pro Ala Val
290 295 300

Gly Ser Gly Glu Ile Val Lys Asp Arg Ile Leu Phe Pro Ile Tyr Gly
305 310 315 320

Gly Ile Lys Gln Thr Ser Pro Glu Phe Thr Glu Leu Val Lys Tyr Gly
325 330 335

Leu Phe Val Ser Thr Pro Thr Thr Val Cys Gln Ser Ser Trp Thr Tyr
340 345 350

Sequence

Asp Gln Val Lys Ala Ala Tyr Arg Pro Asp Tyr Ile Ser Gly Arg Phe
 355 360 365

Trp Ala Gln Val Ile Leu Ser Cys Ala Leu Asp Ala Val Asp Leu Ser
 370 375 380

Ser Cys Ile Val Lys Ile Met Asn Ser Ser Thr Val Met Met Ala Ala
 385 390 395 400

Glu Gly Arg Ile Met Lys Ile Gly Ile Asp Tyr Phe Tyr Tyr Gln Arg
 405 410 415

Ser Ser Ser Trp Trp Pro Leu Ala Phe Val Thr Lys Leu Asp Pro Gln
 420 425 430

Glu Leu Ala Asp Thr Asn Ser Ile Trp Leu Thr Asn Ser Ile Pro Ile
 435 440 445

Pro Gln Ser Lys Phe Pro Arg Pro Ser Tyr Ser Glu Asn Tyr Cys Thr
 450 455 460

Lys Pro Ala Val Cys Pro Ala Thr Cys Val Thr Gly Val Tyr Ser Asp
 465 470 475 480

Ile Trp Pro Leu Thr Ser Ser Ser Ser Leu Pro Ser Ile Ile Trp Ile
 485 490 495

Gly Gln Tyr Leu Asp Ala Pro Val Arg Arg Thr Tyr Pro Arg Phe Gly
 500 505 510

Ile Ala Asn Gln Ser His Trp Tyr Leu Gln Glu Asp Ile Leu Pro Thr
 515 520 525

Ser Thr Ala Ser Ala Tyr Ser Thr Thr Thr Cys Phe Lys Asn Thr Ala
 530 535 540

Arg Asn Arg Val Phe Cys Val Thr Ile Ala Glu Phe Ala Asp Gly Leu
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Phe Gly Glu Tyr Arg Ile Thr Pro Gln Leu Tyr Glu Leu Val Arg Asn
 565 570 575

Asn

<210> 63
 <211> 6717
 <212> DNA
 <213> artificial sequence

<220>
 <223> L gene of FJ215863

Sequence

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atcaagcacc gtctagggaa aatcaagagt gacataacac attactgcca gtattttaat 240
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Sequence

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Sequence

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gatgcattag	tttcaaatct	ctacttcacc	accagacgtg	ttctatcaaa	cctcagatca	5100
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tcatttgtca	attttgcatt	gaatgaaatc	ccaatgcaat	cattaaaacg	agtaaattgt	5760
gatgtggaat	ttgaccgtgg	tatgccgatt	gaacgggtta	ttcagggtta	tacccatatac	5820
ttacttgttg	ctacttacgg	attacagcaa	gattcaatac	tgtgggtgaa	ggtatatagg	5880
acatctgaaa	aagtatttca	attcttactg	agtgccatga	tcatgatctt	tggttatgtc	5940
aaaatccaca	ggaatgggtta	tatgtcgaca	aaggatgaag	agtacatatt	gatgtctgac	6000
tgcaaggaac	ctgtaaaacta	tacagctgtc	cctaacattc	ttacacgtgt	aagtgattta	6060
gtgtcgaaga	atctgagtct	tatccatcca	gaagacctca	gaaaagtaag	gtgtgaaaca	6120

Sequence

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gattccctga atttgaagtg caatcatatt tatgagaaaa taattgccag aaaaattcca 6180
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gtaataggga atcaacagct aaaatcattc tttaatgaaa gctcaagtat tgttttgact 6660
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<211> 2238
<212> PRT
<213> artificial sequence

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<400> 64

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Asp Ser Pro Ile Ile Leu Asn Lys Leu Ala Leu Leu Trp Arg Leu Ser
20          25          30

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Gly Leu Pro Met Pro Ala Asp Leu Arg Gln Lys Ser Val Val Met His
35          40          45

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Ile Pro Asp His Ile Leu Glu Lys Ser Glu Tyr Arg Ile Lys His Arg
50          55          60

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Leu Gly Lys Ile Lys Ser Asp Ile Thr His Tyr Cys Gln Tyr Phe Asn
65          70          75          80

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```

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

```

```

Trp Leu Ser Arg Leu Thr Ile Ala Ser Ala Gly Thr Phe Arg His Met
100          105          110

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```

Lys Asp Arg Ile Leu Cys Thr Val Gly Ser Glu Phe Gly His Lys Ile
115          120          125

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Gln Asp Leu Phe Ser Leu Leu Ser His Lys Leu Val Gly Asn Gly Asp
130          135          140

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Sequence

Leu Phe Asn Gln Ser Leu Ser Gly Thr Arg Leu Thr Ala Ser Pro Leu
 145 150 155 160

Ser Pro Leu Cys Asp Gln Phe Val Ser Asp Ile Lys Ser Ala Val Thr
 165 170 175

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

Met Arg Tyr Leu Ile Lys Gln Ser Cys Thr Thr Asn Ser Ala His Leu
 195 200 205

Thr Glu Ile Ile Lys Glu Glu Trp Gly Leu Val Gly Ile Thr Pro Asp
 210 215 220

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

Phe Glu Met Val Leu Met Tyr Ser Asp Val Leu Glu Ser Arg Asp Asn
 245 250 255

Ile Val Leu Val Gly Arg Leu Ser Thr Phe Leu Gln Pro Val Val Ser
 260 265 270

Arg Leu Glu Val Leu Phe Asp Leu Val Asp Ser Leu Ala Lys Ile Leu
 275 280 285

Gly Asp Thr Ile Tyr Glu Ile Ile Ala Val Leu Glu Ser Leu Ser Tyr
 290 295 300

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

Phe Ser Phe Asn Met Asn Glu Leu Asp Asn Thr Leu Ser Lys Arg Val
 325 330 335

Asp Pro Lys His Lys Asn Thr Ile Met Ser Ile Ile Arg Gln Cys Phe
 340 345 350

Ser Asn Leu Asp Val Asp Gln Ala Ala Glu Met Leu Cys Leu Met Arg
 355 360 365

Leu Phe Gly His Pro Met Leu Thr Ala Pro Asp Ala Ala Ala Lys Val
 370 375 380

Arg Lys Ala Met Cys Ala Pro Lys Leu Val Glu His Asp Thr Ile Leu
 385 390 395 400

Gln Thr Leu Ser Phe Phe Lys Gly Ile Ile Ile Asn Gly Tyr Arg Arg
 405 410 415

Sequence

Ser His Ser Gly Leu Trp Pro Asn Val Glu Pro Ser Ser Ile Tyr Asp
420 425 430

Asp Asp Leu Arg Gln Leu Tyr Leu Glu Ser Ala Glu Ile Ser His His
435 440 445

Phe Met Leu Lys Asn Tyr Lys Ser Leu Ser Met Ile Glu Phe Lys Lys
450 455 460

Ser Ile Asp Tyr Asp Leu His Asp Asp Leu Ser Thr Phe Leu Lys Asp
465 470 475 480

Arg Ala Ile Cys Arg Pro Lys Ser Gln Trp Asp Val Ile Phe Arg Lys
485 490 495

Ser Leu Arg Arg Ser His Thr Gln Ser Gln Tyr Leu Asp Glu Ile Lys
500 505 510

Ser Asn Arg Leu Leu Ile Asp Phe Leu Asp Ser Ala Glu Phe Asp Pro
515 520 525

Glu Lys Glu Phe Ala Tyr Val Thr Thr Met Asp Tyr Leu His Asp Asn
530 535 540

Glu Phe Cys Ala Ser Tyr Ser Leu Lys Glu Lys Glu Ile Lys Thr Thr
545 550 555 560

Gly Arg Ile Phe Ala Lys Met Thr Arg Asn Met Arg Ser Cys Gln Val
565 570 575

Ile Leu Glu Ser Leu Leu Ser Lys His Ile Cys Lys Phe Phe Lys Glu
580 585 590

Asn Gly Val Ser Met Glu Gln Leu Ser Leu Thr Lys Ser Leu Leu Ala
595 600 605

Met Ser Gln Leu Ser Pro Lys Val Ser Thr Leu Gln Asp Thr Ala Ser
610 615 620

Arg His Val Gly Asn Ser Lys Ser Gln Ile Ala Thr Ser Asn Pro Ser
625 630 635 640

Arg His His Ser Thr Ala Asn Gln Met Ser Leu Ser Asn Arg Lys Thr
645 650 655

Val Val Ala Thr Phe Leu Thr Thr Asp Leu Glu Lys Tyr Cys Leu Gln
660 665 670

Trp Arg Tyr Ser Thr Ile Lys Leu Phe Ala Gln Ala Leu Asn Gln Leu
675 680 685

Sequence

Phe Gly Ile Asp His Gly Phe Glu Trp Ile His Leu Arg Leu Met Asn
 690 695 700

Ser Thr Leu Phe Val Gly Asp Pro Tyr Ser Pro Pro Glu Asp Pro Thr
 705 710 715 720

Leu Glu Asp Ile Asp Lys Ala Pro Asn Asp Asp Ile Phe Ile Val Ser
 725 730 735

Pro Arg Gly Gly Ile Glu Gly Leu Cys Gln Lys Met Trp Thr Met Ile
 740 745 750

Ser Ile Ser Ala Ile His Cys Val Ala Glu Lys Ile Gly Ala Arg Val
 755 760 765

Ala Ala Met Val Gln Gly Asp Asn Gln Val Ile Ala Ile Thr Lys Glu
 770 775 780

Leu Phe Arg Gly Glu Lys Ala Cys Asp Val Arg Asp Glu Leu Asp Glu
 785 790 795 800

Leu Gly Gln Val Phe Phe Asp Glu Phe Lys Arg His Asn Tyr Ala Ile
 805 810 815

Gly His Asn Leu Lys Leu Asn Glu Thr Ile Gln Ser Gln Ser Phe Phe
 820 825 830

Val Tyr Ser Lys Arg Ile Phe Phe Glu Gly Arg Leu Leu Ser Gln Val
 835 840 845

Leu Lys Asn Ala Ala Lys Leu Cys Met Val Ala Asp His Leu Gly Glu
 850 855 860

Asn Thr Val Ser Ser Cys Ser Asn Leu Ser Ser Thr Ile Ala Arg Leu
 865 870 875 880

Val Glu Asn Gly Phe Glu Lys Asp Thr Ala Phe Val Leu Asn Leu Val
 885 890 895

Tyr Ile Met Thr Gln Ile Leu Phe Asp Glu His Tyr Ser Ile Val Cys
 900 905 910

Asp His His Ser Val Lys Ser Leu Ile Gly Ser Lys Asn His Arg Asn
 915 920 925

Leu Leu Tyr Ser Ser Leu Ile Pro Gly Gln Leu Gly Gly Phe Asn Phe
 930 935 940

Leu Asn Ile Ser Arg Leu Phe Thr Arg Asn Ile Gly Asp Pro Val Thr
 945 950 955 960

Sequence

Cys Ser Leu Ser Asp Leu Lys Cys Phe Ile Ala Ala Gly Leu Leu Pro
965 970 975

Pro Tyr Val Leu Lys Asn Val Val Leu Arg Glu Pro Gly Pro Gly Thr
980 985 990

Trp Leu Thr Leu Cys Ser Asp Pro Tyr Thr Leu Asn Ile Pro Tyr Thr
995 1000 1005

Gln Leu Pro Thr Thr Tyr Leu Lys Lys His Thr Gln Arg Ser Leu
1010 1015 1020

Leu Ser Arg Ala Val Asn Pro Leu Leu Ala Gly Val Gln Val Pro
1025 1030 1035

Asn Gln His Glu Glu Glu Glu Val Leu Ala Arg Phe Leu Leu Asp
1040 1045 1050

Arg Glu Tyr Val Met Pro Arg Val Ala His Val Ile Leu Glu Thr
1055 1060 1065

Ser Val Leu Gly Lys Arg Lys Gln Ile Gln Gly Leu Ile Asp Thr
1070 1075 1080

Thr Pro Thr Ile Ile Arg Thr Ser Leu Val Asn Leu Pro Val Ser
1085 1090 1095

Arg Lys Lys Cys Glu Lys Ile Ile Asn Tyr Ser Leu Asn Tyr Ile
1100 1105 1110

Ala Glu Cys His Asp Ser Leu Leu Ser Gln Val Cys Phe Ser Asp
1115 1120 1125

Asn Lys Glu Tyr Leu Trp Ser Thr Ser Leu Ile Ser Val Glu Thr
1130 1135 1140

Cys Ser Val Thr Ile Ala Asp Tyr Leu Arg Ala Val Ser Trp Ser
1145 1150 1155

Asn Ile Leu Gly Gly Arg Asn Ile Ser Gly Val Thr Thr Pro Asp
1160 1165 1170

Thr Ile Glu Leu Ile Gln Gly Cys Leu Ile Gly Glu Asn Ser Ser
1175 1180 1185

Cys Thr Leu Cys Glu Ser His Asp Asp Ala Phe Thr Trp Met His
1190 1195 1200

Leu Pro Gly Pro Leu Tyr Ile Pro Glu Pro Ser Val Thr Asn Ser
1205 1210 1215

Sequence												
Lys	Met	Arg	Val	Pro	Tyr	Leu	Gly	Ser	Lys	Thr	Glu	Glu Arg Lys
	1220					1225					1230	
Thr	Ala	Ser	Met	Ala	Ala	Ile	Lys	Gly	Met	Ser	His	His Leu Arg
	1235					1240					1245	
Ala	Val	Leu	Arg	Gly	Thr	Ser	Val	Phe	Ile	Trp	Ala	Phe Gly Asp
	1250					1255					1260	
Thr	Asp	Ile	Asn	Trp	Asp	Asn	Ala	Leu	Gln	Ile	Ala	Gln Ser Arg
	1265					1270					1275	
Cys	Asn	Ile	Thr	Leu	Asp	Gln	Met	Arg	Leu	Leu	Thr	Pro Ile Pro
	1280					1285					1290	
Ser	Ser	Ser	Asn	Ile	Gln	His	Arg	Leu	Asp	Asp	Gly	Ile Ser Thr
	1295					1300					1305	
Gln	Lys	Phe	Thr	Pro	Ala	Ser	Leu	Ala	Arg	Ile	Thr	Ser Phe Val
	1310					1315					1320	
His	Ile	Cys	Asn	Asp	Ser	Gln	Arg	Leu	Glu	Lys	Asp	Gly Ser Ser
	1325					1330					1335	
Val	Asp	Ser	Asn	Leu	Ile	Tyr	Gln	Gln	Ile	Met	Leu	Leu Gly Leu
	1340					1345					1350	
Ser	Ile	Phe	Glu	Thr	Met	Tyr	Ser	Met	Asp	Gln	Lys	Trp Val Phe
	1355					1360					1365	
Asn	Asn	His	Thr	Leu	His	Leu	His	Thr	Gly	His	Ser	Cys Cys Pro
	1370					1375					1380	
Arg	Glu	Leu	Asp	Ile	Ser	Leu	Val	Asn	Pro	Pro	Arg	His Gln Thr
	1385					1390					1395	
Pro	Glu	Leu	Thr	Ser	Thr	Thr	Thr	Asn	Pro	Phe	Leu	Tyr Asp Gln
	1400					1405					1410	
Leu	Pro	Leu	Asn	Gln	Glu	Asn	Leu	Thr	Thr	Leu	Glu	Ile Lys Thr
	1415					1420					1425	
Phe	Lys	Phe	Asn	Glu	Leu	Asn	Ile	Asp	Gly	Leu	Asp	Phe Gly Glu
	1430					1435					1440	
Gly	Ile	Gln	Leu	Leu	Ser	Arg	Cys	Thr	Ala	Arg	Leu	Met Ala Glu
	1445					1450					1455	
Cys	Ile	Leu	Glu	Glu	Gly	Ile	Gly	Ser	Ser	Val	Lys	Asn Glu Ala
	1460					1465					1470	

Sequence														
Ile	Val	Asn	Phe	Asp	Asn	Ser	Val	Asn	Trp	Ile	Ser	Glu	Cys	Leu
1475						1480					1485			
Met	Cys	Asp	Ile	Arg	Ser	Leu	Cys	Val	Asn	Leu	Gly	Gln	Glu	Ile
1490						1495					1500			
Leu	Cys	Ser	Leu	Ala	Tyr	Gln	Met	Tyr	Tyr	Leu	Arg	Ile	Arg	Gly
1505						1510					1515			
Arg	Arg	Ala	Ile	Leu	Asn	Tyr	Leu	Asp	Thr	Thr	Leu	Gln	Arg	Ile
1520						1525					1530			
Pro	Val	Ile	Gln	Leu	Ala	Asn	Ile	Ala	Leu	Thr	Ile	Ser	His	Pro
1535						1540					1545			
Glu	Ile	Phe	Arg	Arg	Ile	Val	Asn	Thr	Gly	Ile	His	Asn	Gln	Ile
1550						1555					1560			
Lys	Gly	Pro	Tyr	Val	Ala	Thr	Thr	Asp	Phe	Ile	Ala	Ala	Ser	Arg
1565						1570					1575			
Asp	Ile	Ile	Leu	Ser	Gly	Ala	Arg	Glu	Tyr	Leu	Ser	Tyr	Leu	Ser
1580						1585					1590			
Ser	Gly	Gln	Glu	Asp	Cys	Tyr	Thr	Phe	Phe	Asn	Cys	Gln	Asp	Gly
1595						1600					1605			
Asp	Leu	Thr	Pro	Lys	Met	Glu	Gln	Tyr	Leu	Ala	Arg	Arg	Ala	Cys
1610						1615					1620			
Leu	Leu	Thr	Leu	Leu	Tyr	Asn	Thr	Gly	His	Gln	Ile	Pro	Val	Ile
1625						1630					1635			
Arg	Ser	Leu	Thr	Pro	Ile	Glu	Lys	Cys	Lys	Val	Leu	Thr	Glu	Tyr
1640						1645					1650			
Asn	Gln	Gln	Ile	Glu	Tyr	Ala	Asp	Gln	Glu	Phe	Ser	Ser	Val	Leu
1655						1660					1665			
Lys	Val	Val	Asn	Ala	Leu	Leu	Gln	Asn	Pro	Lys	Ile	Asp	Ala	Leu
1670						1675					1680			
Val	Ser	Asn	Leu	Tyr	Phe	Thr	Thr	Arg	Arg	Val	Leu	Ser	Asn	Leu
1685						1690					1695			
Arg	Ser	Cys	Asp	Lys	Ala	Arg	Ser	Tyr	Ile	Glu	Tyr	Leu	Tyr	Thr
1700						1705					1710			
Glu	Asp	Phe	Gly	Glu	Lys	Glu	Asp	Thr	Val	Gln	Tyr	Asp	Ile	Met
1715						1720					1725			

Sequence

Thr Thr Asn Asp Ile Ile Leu Thr His Gly Leu Phe Thr Gln Ile
 1730 1735 1740
 Glu Ile Ser Tyr Gln Gly Asn Ser Leu His Lys Phe Leu Thr Pro
 1745 1750 1755
 Asp Asn Ala Pro Gly Ser Leu Ile Pro Phe Ser Ile Ser Pro Asn
 1760 1765 1770
 Ser Leu Ala Cys Asp Pro Leu His His Leu Leu Lys Ser Val Gly
 1775 1780 1785
 Thr Ser Ser Thr Ser Trp Tyr Lys Tyr Ala Ile Ala Tyr Ala Val
 1790 1795 1800
 Ser Glu Lys Arg Ser Ala Arg Leu Gly Gly Ser Leu Tyr Ile Gly
 1805 1810 1815
 Glu Gly Ser Gly Ser Val Met Thr Leu Leu Glu Tyr Leu Glu Pro
 1820 1825 1830
 Ser Val Asp Ile Phe Tyr Asn Ser Leu Phe Ser Asn Gly Met Asn
 1835 1840 1845
 Pro Pro Gln Arg Asn Tyr Gly Leu Met Pro Leu Gln Phe Val Asn
 1850 1855 1860
 Ser Val Val Tyr Lys Asn Leu Thr Ala Lys Ser Glu Cys Lys Leu
 1865 1870 1875
 Gly Phe Val Gln Gln Phe Lys Pro Leu Trp Arg Asp Ile Asp Ile
 1880 1885 1890
 Glu Thr Asn Val Thr Asp Pro Ser Phe Val Asn Phe Ala Leu Asn
 1895 1900 1905
 Glu Ile Pro Met Gln Ser Leu Lys Arg Val Asn Cys Asp Val Glu
 1910 1915 1920
 Phe Asp Arg Gly Met Pro Ile Glu Arg Val Ile Gln Gly Tyr Thr
 1925 1930 1935
 His Ile Leu Leu Val Ala Thr Tyr Gly Leu Gln Gln Asp Ser Ile
 1940 1945 1950
 Leu Trp Val Lys Val Tyr Arg Thr Ser Glu Lys Val Phe Gln Phe
 1955 1960 1965
 Leu Leu Ser Ala Met Ile Met Ile Phe Gly Tyr Val Lys Ile His
 1970 1975 1980

Sequence														
Arg	Asn	Gly	Tyr	Met	Ser	Thr	Lys	Asp	Glu	Glu	Tyr	Ile	Leu	Met
1985						1990					1995			
Ser	Asp	Cys	Lys	Glu	Pro	Val	Asn	Iyr	Thr	Ala	Val	Pro	Asn	Ile
2000						2005					2010			
Leu	Thr	Arg	Val	Ser	Asp	Leu	Val	Ser	Lys	Asn	Leu	Ser	Leu	Ile
2015						2020					2025			
His	Pro	Glu	Asp	Leu	Arg	Lys	Val	Arg	Cys	Glu	Thr	Asp	Ser	Leu
2030						2035					2040			
Asn	Leu	Lys	Cys	Asn	His	Ile	Tyr	Glu	Lys	Ile	Ile	Ala	Arg	Lys
2045						2050					2055			
Ile	Pro	Leu	Gln	Val	Ser	Ser	Thr	Asp	Ser	Leu	Leu	Leu	Gln	Leu
2060						2065					2070			
Gly	Gly	Val	Ile	Asn	Ser	Val	Gly	Ser	Thr	Asp	Pro	Arg	Glu	Val
2075						2080					2085			
Ala	Thr	Leu	Ser	Ser	Ile	Glu	Cys	Met	Asp	Tyr	Val	Val	Ser	Ser
2090						2095					2100			
Ile	Asp	Leu	Ala	Ile	Leu	Glu	Ala	Asn	Ile	Val	Ile	Ser	Glu	Ser
2105						2110					2115			
Ala	Gly	Leu	Asp	Leu	Ala	Leu	Met	Leu	Gly	Pro	Phe	Asn	Leu	Asn
2120						2125					2130			
Lys	Leu	Lys	Lys	Ile	Asp	Thr	Ile	Leu	Lys	Ser	Ser	Thr	Tyr	Gln
2135						2140					2145			
Leu	Ile	Pro	Tyr	Trp	Leu	Arg	Tyr	Glu	Tyr	Ser	Ile	Asn	Pro	Arg
2150						2155					2160			
Ser	Leu	Ser	Phe	Leu	Ile	Thr	Lys	Leu	Gln	Gln	Cys	Arg	Ile	Ser
2165						2170					2175			
Trp	Ser	Asp	Met	Ile	Thr	Ile	Ser	Glu	Phe	Arg	Lys	Lys	Ser	Lys
2180						2185					2190			
Arg	Pro	Ile	Phe	Ile	Lys	Arg	Val	Ile	Gly	Asn	Gln	Gln	Leu	Lys
2195						2200					2205			
Ser	Phe	Phe	Asn	Glu	Ser	Ser	Ser	Ile	Val	Leu	Thr	Arg	Ala	Glu
2210						2215					2220			
Val	Lys	Val	Cys	Ile	Lys	Phe	Leu	Gly	Ala	Ile	Ile	Lys	Leu	Lys
2225						2230					2235			

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 <211> 1386
 <212> DNA
 <213> artificial sequence

<220>
 <223> NP gene of FJ215864

<400> 65
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 ttgtctcaag accccgggtga gagatggagc cttgcttgcc ttaatatccg atggcttgtg 180
 agtgattcat caaccacacc aatgaagcag ggagcaatat tgtcactgct gagtctacat 240
 tcagacaata tgcgagctca cgcaacatta gcagcaagggt ctgcagatgc ttcactcacc 300
 atacttgagg tagatgaagt agatattggc aactccctaa tcaaattcaa cgctagaagt 360
 ggtgtatctg ataaacgatc aaatcaattg cttgcaattg cggatgacat ccccaaaagt 420
 tgcagtaatg ggcattccatt tcttgacaca gacattgaga ccagagaccc gctcgatcta 480
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 caacaaggcc gactgggttaa gcaagtactt ttgcattctg tagtcaggac agaatttatg 660
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 tcagccatgg gcggagacac atctaggtac tatgctatgg tgggtgacat cagtctgtac 780
 atcaagaatg caggattgac tgcatttttc ctcaccctga agttcggggg tggtagccag 840
 tatccaacct tagcaatgag tgttttctcc agtgacctta aaagacttgc tgcactcatc 900
 aggctgtaca aaaccaaggg agacaatgca ccatacatgg cattcctgga ggactccgat 960
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 gcccagagaga tgggcttgac tgaggaatcc aaacagcagg ttagatcact gctaattgtca 1200
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 gaaaataggc agcctgcca gaattcttca gatactcagg gtcagaccaa gccagtcccg 1320
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 tggtaa 1386

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 <211> 461
 <212> PRT
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 <223> NP protein of ACO48303

<400> 66

Sequence

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

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

Trp Ser Leu Ala Cys Leu Asn Ile Arg Trp Leu Val Ser Asp Ser Ser
50 55 60

Thr Thr Pro Met Lys Gln Gly Ala Ile Leu Ser Leu Leu Ser Leu His
65 70 75 80

Ser Asp Asn Met Arg Ala His Ala Thr Leu Ala Ala Arg Ser Ala Asp
85 90 95

Ala Ser Leu Thr Ile Leu Glu Val Asp Glu Val Asp Ile Gly Asn Ser
100 105 110

Leu Ile Lys Phe Asn Ala Arg Ser Gly Val Ser Asp Lys Arg Ser Asn
115 120 125

Gln Leu Leu Ala Ile Ala Asp Asp Ile Pro Lys Ser Cys Ser Asn Gly
130 135 140

His Pro Phe Leu Asp Thr Asp Ile Glu Thr Arg Asp Pro Leu Asp Leu
145 150 155 160

Ser Glu Thr Ile Asp Arg Leu Gln Gly Ile Ala Ala Gln Ile Trp Val
165 170 175

Ser Ala Ile Lys Ser Met Thr Ala Pro Asp Thr Ala Ser Glu Ser Glu
180 185 190

Ser Lys Arg Leu Ala Lys Tyr Gln Gln Gln Gly Arg Leu Val Lys Gln
195 200 205

Val Leu Leu His Ser Val Val Arg Thr Glu Phe Met Arg Val Ile Arg
210 215 220

Gly Ser Leu Val Leu Arg Gln Phe Met Val Ser Glu Cys Lys Arg Ala
225 230 235 240

Ser Ala Met Gly Gly Asp Thr Ser Arg Tyr Tyr Ala Met Val Gly Asp
245 250 255

Ile Ser Leu Tyr Ile Lys Asn Ala Gly Leu Thr Ala Phe Phe Leu Thr
260 265 270

Sequence

Leu Lys Phe Gly Val Gly Thr Gln Tyr Pro Thr Leu Ala Met Ser Val
275 280 285

Phe Ser Ser Asp Leu Lys Arg Leu Ala Ala Leu Ile Arg Leu Tyr Lys
290 295 300

Thr Lys Gly Asp Asn Ala Pro Tyr Met Ala Phe Leu Glu Asp Ser Asp
305 310 315 320

Met Gly Asn Phe Ala Pro Ala Asn Tyr Ser Thr Met Tyr Ser Tyr Ala
325 330 335

Met Gly Ile Gly Thr Ile Leu Glu Ala Ser Val Ser Arg Tyr Gln Tyr
340 345 350

Ala Arg Asp Phe Thr Ser Glu Asn Tyr Phe Arg Leu Gly Val Glu Thr
355 360 365

Ala Gln Ser Gln Gln Gly Ala Phe Asp Glu Arg Thr Ala Arg Glu Met
370 375 380

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

Val Asp Met Gly Pro Ser Ser Val Arg Glu Pro Ser Arg Pro Ala Phe
405 410 415

Ile Ser Gln Glu Glu Asn Arg Gln Pro Ala Gln Asn Ser Ser Asp Thr
420 425 430

Gln Gly Gln Thr Lys Pro Val Pro Asn Gln Pro Ala Pro Arg Ala Asp
435 440 445

Pro Asp Asp Ile Asp Pro Tyr Glu Asn Gly Leu Glu Trp
450 455 460

<210> 67
<211> 1218
<212> DNA
<213> artificial sequence

<220>
<223> P gene of FJ215864

<400> 67
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caagggaaca caagaaatct aactgatcta tgggaaaagg agactgcaag tcagaacaag 180
acatcggtc aatctccaca aaccacacaa gttcagtctg atggaaatga ggaggaagaa 240
atcaaatcag agtcaattga tggccacatc agtggaactg ttaatcaatt agagcaagtc 300
ccagaacaaa accagagcag atcttcacca ggtgatgatc tcgacagagc tctcaacaag 360

Sequence

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cttgaagggga gaatcaactc aatcagctca atggataaag aaattaaaaa gggccctcgc      420
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aatcctggca accaggacac aggagagaat attcatttac caccttccat ggcaccacca      600
gagtcattag ttggtgcaat ccgcaatgta cccaattcg tgccagacca atctatgacg      660
aatgtagatg cggggagtgt ccaactacat gcatcatgtg cagagatgat aagtagaatg      720
tttgtagaag ttatatctaa gcttgataaa ctcgagtcga gactgaatga tatagcaaaa      780
gttgtaaaca ccacccccct tatcaggaat gatattaacc aacttaaggc cacaactgca      840
ctgatgtcca accaaattgc ttccatacaa attcttgacc caggggaatgc aggggtgagg      900
tccctctctg aaatgagatc tgtgacgaag aaagctgctg ttgtaattgc aggatttgga      960
gacgacccaa ctcaaattat tgaagaaggc atcatggcca aagatgctct tggaaaacct     1020
gtgcctccaa catctgttat cgcagccaaa gctcagactt cttccggtgt gagtaagggc     1080
gaaatagaag gattgattgc attggtggaa acattagttg acaatgacaa gaaggcagcg     1140
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gcaatatata atgcataa                                     1218

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<210> 68
<211> 405
<212> PRT
<213> artificial sequence

<220>
<223> P protein of AC048304

<400> 68

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Met Asp Phe Ala Asn Asp Glu Glu Ile Ala Glu Leu Leu Asn Leu Ser
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20          25          30

Thr Thr Gly Arg Pro Pro Val Ser Gln Gly Asn Thr Arg Asn Leu Thr
35          40          45

Asp Leu Trp Glu Lys Glu Thr Ala Ser Gln Asn Lys Thr Ser Ala Gln
50          55          60

Ser Pro Gln Thr Thr Gln Val Gln Ser Asp Gly Asn Glu Glu Glu Glu
65          70          75          80

Ile Lys Ser Glu Ser Ile Asp Gly His Ile Ser Gly Thr Val Asn Gln
85          90          95

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

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Sequence

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

Sequence

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385 390 395 400

Ala Ile Tyr Asn Ala
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<212> DNA
<213> artificial sequence

<220>
<223> M gene of FJ215864

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agggtagatt caattggcga tgtgcagaat gccaaagagt cctcgatatt cgtgactcta 180
tatggtttca tccaagcaat taaggagaat tcagatcgat cgaaattctt ccatccaaaa 240
gatgacttca aacctgagac agtcactgca ggactggtag tagtgggtgc aatccgaatg 300
atggctgatg tcaataccat ctctaatagat gactagcgc tggagatcac tgtaagaaa 360
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actgcaataa ctatccgagc agggaggtttc atctcgaatg cagacgaaaa tataaaatgt 480
gccagcaagt tgactgcagg agtgcagtag atattccgtc caatgtttgt ttcaatcact 540
aaattacaca atggcaaaact atataggggtg cccaaaagta tccacagcat ctcgtctacc 600
ctactgtata gtgtgatgtt ggaggtagga ttcaaagtgg acatcgggaa ggatcatccc 660
caggcaaaaa tgctgaagag ggtcacaatt ggcgatgcag acacatactg gggatttgca 720
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gaactgaaga caaaagtcaa aaatatgggg ttgaaattgg agttacatga cctatgggggt 840
ccgactattg tgggtccaaat cactggcaag agcagcaaat atgctcaagg atttttttct 900
tccaatggta cttgttgctt cccaatcagc agatctgcac cagagcttgg gaagcttctg 960
tggtcctgct cagcaactat tgggtgacgca acagttgtta tccaatcaag cgagaagggg 1020
gaactcctaa ggtctgatga tctcgagata cgagggtgctg tggcctcaa gaaaggtaga 1080
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<210> 70
<211> 369
<212> PRT
<213> artificial sequence

<220>
<223> M protein of AC048305

<400> 70

Sequence

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

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

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

Gln Ala Ile Lys Glu Asn Ser Asp Arg Ser Lys Phe Phe His Pro Lys
65 70 75 80

Asp Asp Phe Lys Pro Glu Thr Val Thr Ala Gly Leu Val Val Val Gly
85 90 95

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

Ala Leu Glu Ile Thr Val Lys Lys Ser Ala Thr Ser Gln Glu Lys Met
115 120 125

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

Ile Arg Ala Gly Gly Phe Ile Ser Asn Ala Asp Glu Asn Ile Lys Cys
145 150 155 160

Ala Ser Lys Leu Thr Ala Gly Val Gln Tyr Ile Phe Arg Pro Met Phe
165 170 175

Val Ser Ile Thr Lys Leu His Asn Gly Lys Leu Tyr Arg Val Pro Lys
180 185 190

Ser Ile His Ser Ile Ser Ser Thr Leu Leu Tyr Ser Val Met Leu Glu
195 200 205

Val Gly Phe Lys Val Asp Ile Gly Lys Asp His Pro Gln Ala Lys Met
210 215 220

Leu Lys Arg Val Thr Ile Gly Asp Ala Asp Thr Tyr Trp Gly Phe Ala
225 230 235 240

Trp Phe His Leu Cys Asn Phe Lys Lys Thr Ser Ser Lys Gly Lys Pro
245 250 255

Arg Thr Leu Asp Glu Leu Lys Thr Lys Val Lys Asn Met Gly Leu Lys
260 265 270

Sequence

Leu Glu Leu His Asp Leu Trp Gly Pro Thr Ile Val Val Gln Ile Thr
 275 280 285

Gly Lys Ser Ser Lys Tyr Ala Gln Gly Phe Phe Ser Ser Asn Gly Thr
 290 295 300

Cys Cys Leu Pro Ile Ser Arg Ser Ala Pro Glu Leu Gly Lys Leu Leu
 305 310 315 320

Trp Ser Cys Ser Ala Thr Ile Gly Asp Ala Thr Val Val Ile Gln Ser
 325 330 335

Ser Glu Lys Gly Glu Leu Leu Arg Ser Asp Asp Leu Glu Ile Arg Gly
 340 345 350

Ala Val Ala Ser Lys Lys Gly Arg Leu Ser Ser Phe His Pro Phe Lys
 355 360 365

Lys

<210> 71
 <211> 1632
 <212> DNA
 <213> artificial sequence

<220>
 <223> F gene of FJ215864

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 aacatcttag gccactcaa atccaatctg gatgcactgc tctcatctga gacttatccc 300
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 gaggttaactg gtgtgcgtgc gacagaatta gtcactgtta gtgtaacaac agacaagggg 900
 gaagggaaaag caattgtacc ccaatttcta gctgaaagtc ggggtgactat tgaggagctt 960

Sequence

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gatgtagcat cttgtaaatt cagcagcaca accctatact gcaggcaggt caacacaagg 1020
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acagagattg gagcattatc atcccggtat ataacactag atggaggggt cttagtcaat 1140
tgtaagtcaa ttgtttgtag gtgccttaat ccaagtaaga tcatctctca aaatacaaat 1200
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caggtgacta cctccggttc tttggatatc agcagtgaga tagggaacat caataatacg 1380
gtgaatcgtg tggaggattt aatccaccaa tcggaggaat ggctggcaaa agttaacca 1440
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tggctggcag tattaacggc tattataata tacttgagaa caaagttgaa gactatatcg 1560
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tctaagtttt ga 1632

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<210> 72
 <211> 543
 <212> PRT
 <213> artificial sequence

<220>
 <223> F protein of AC048306

<400> 72

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20 25 30

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

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

Thr Thr Cys Leu Arg Glu Thr Ile Thr Thr Tyr Asn Asn Thr Val Asn
65 70 75 80

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

Glu Thr Tyr Pro Gln Thr Arg Leu Ile Gly Ala Val Ile Gly Ser Ile
100 105 110

Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu
115 120 125

Sequence

Lys Gln Ala Gln Asp Asn Ala Arg Asn Ile Leu Ala Leu Lys Glu Ala
130 135 140

Leu Ser Lys Thr Asn Glu Ala Val Lys Glu Leu Ser Ser Gly Leu Gln
145 150 155 160

Gln Thr Ala Ile Ala Leu Gly Lys Ile Gln Ser Phe Val Asn Glu Glu
165 170 175

Ile Leu Pro Ser Ile Asn Gln Leu Ser Cys Glu Val Thr Ala Asn Lys
180 185 190

Leu Gly Val Tyr Leu Ser Leu Tyr Leu Thr Glu Leu Thr Thr Ile Phe
195 200 205

Gly Ala Gln Leu Thr Asn Pro Ala Leu Thr Ser Leu Ser Tyr Gln Ala
210 215 220

Leu Tyr Asn Leu Cys Gly Gly Asn Met Ala Met Leu Thr Gln Lys Ile
225 230 235 240

Gly Ile Lys Gln Gln Asp Val Asn Ser Leu Tyr Glu Ala Gly Leu Ile
245 250 255

Thr Gly Gln Val Ile Gly Tyr Asp Ser Gln Tyr Gln Leu Leu Val Ile
260 265 270

Gln Val Asn Tyr Pro Ser Ile Ser Glu Val Thr Gly Val Arg Ala Thr
275 280 285

Glu Leu Val Thr Val Ser Val Thr Thr Asp Lys Gly Glu Gly Lys Ala
290 295 300

Ile Val Pro Gln Phe Val Ala Glu Ser Arg Val Thr Ile Glu Glu Leu
305 310 315 320

Asp Val Ala Ser Cys Lys Phe Ser Ser Thr Thr Leu Tyr Cys Arg Gln
325 330 335

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

Asn Tyr Asp Asp Cys Gln Tyr Thr Thr Glu Ile Gly Ala Leu Ser Ser
355 360 365

Arg Tyr Ile Thr Leu Asp Gly Gly Val Leu Val Asn Cys Lys Ser Ile
370 375 380

Val Cys Arg Cys Leu Asn Pro Ser Lys Ile Ile Ser Gln Asn Thr Asn
385 390 395 400

Sequence

Ala Ala Val Thr Tyr Val Asp Ala Thr Ile Cys Lys Thr Ile Gln Leu
405 410 415

Asp Asp Ile Gln Leu Gln Leu Glu Gly Ser Leu Ser Ser Val Tyr Ala
420 425 430

Arg Asn Ile Ser Ile Glu Ile Ser Gln Val Thr Thr Ser Gly Ser Leu
435 440 445

Asp Ile Ser Ser Glu Ile Gly Asn Ile Asn Asn Thr Val Asn Arg Val
450 455 460

Glu Asp Leu Ile His Gln Ser Glu Glu Trp Leu Ala Lys Val Asn Pro
465 470 475 480

His Ile Val Asn Asn Thr Thr Leu Ile Val Leu Cys Val Leu Ser Ala
485 490 495

Leu Ala Val Ile Trp Leu Ala Val Leu Thr Ala Ile Ile Ile Tyr Leu
500 505 510

Arg Thr Lys Leu Lys Thr Ile Ser Ala Leu Ala Val Thr Asn Thr Ile
515 520 525

Gln Ser Asn Pro Tyr Val Asn Gln Thr Lys Arg Glu Ser Lys Phe
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<211> 1734
<212> DNA
<213> artificial sequence

<220>
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attgttagca tagttcaaat tgggaatttg aaaattcctt ctgtagggga tctggcggac 180
gaggtggtaa cacctttgaa aaccactctg tctgatacac tcaggaatcc aattaaccag 240
ataaatgaca tattcaggat tgttgccctt gatattccat tgcaagtaac tagtatccaa 300
aaagacctcg caagtcaatt tagcatgttg atagatagtt taaatgctat caaattgggc 360
aacgggacca accttatcat acctacatca gataaggagt atgcaggagg aattggaaac 420
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catccgagct ttattgctgg acctacaacg acccgaggct gtacaagaat acccactttt 540
cacatgtcag aaagtcattg gtgctactca cacaacatca tcgctgctgg ctgtcaagat 600
gccagtgcac ctagtatgta tatctcaatg ggggttctcc atgtgtcttc atctggcact 660
cctatctttc ttactactgc aagtgaactg atagacgatg gagttaatcg taagtcatgc 720

Sequence

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agtattgtag caaccaatt cggctgtgac attttgtgca gtattgtcat agagaaggag      780
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gggagttttg tagaaaccga actaccctgtg tccagtatgt tctcgtcatt ctctgccaac      900
taccctgctg tgggatcagg cgaaattgta aaagatagaa tattattccc aatttacgga      960
ggtataaagc agacttcacc agagtttacc gaattagtga aatatggact ctttgtgtca     1020
acacctacaa ctgtatgtca gagtagctgg acttatgacc aggtaaaagc agcgtatagg     1080
ccagattaca tatcaggccg gttctgggca caagtgatac tcagctgcgc tcttgatgca     1140
gtcgaacttat caagttgtat tgtaaagatt atgaatagca gcacagtgat gatggcagca     1200
gaaggaagga taataaagat agggattgat tacttttact atcagcggtc atcttcttgg     1260
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aattattgca caaagccagc agtttgccct gctacttggtg tcaactggtgt atactctgat     1440
atttggccct tgacctcatc ttcatcactc ccgagcataa tttggatcgg ccagtacctt     1500
gatgcccctg ttggaaggac ttatcccaga tttggaattg caaatcaatc aactggttac     1560
cttcaagaag atattctacc cacctccact gcaagtgcgt attcaaccac tacatgtttt     1620
aagaatactg ccaggaatag agtgttctgc gtcaccattg ctgaatttgc agatggggtg     1680
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<210> 74
 <211> 577
 <212> PRT
 <213> artificial sequence

<220>
 <223> HN protein of AC048307

<400> 74

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Thr Thr Gly Cys Leu Ala Leu Ser Ile Val Ser Ile Val Gln Ile Gly
 35 40 45

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

Pro Leu Lys Thr Thr Leu Ser Asp Thr Leu Arg Asn Pro Ile Asn Gln
 65 70 75 80

Ile Asn Asp Ile Phe Arg Ile Val Ala Leu Asp Ile Pro Leu Gln Val
 85 90 95

Sequence

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

Sequence

Trp Ala Gln Val Ile Leu Ser Cys Ala Leu Asp Ala Val Asp Leu Ser
370 375 380

Ser Cys Ile Val Lys Ile Met Asn Ser Ser Thr Val Met Met Ala Ala
385 390 395 400

Glu Gly Arg Ile Ile Lys Ile Gly Ile Asp Tyr Phe Tyr Tyr Gln Arg
405 410 415

Ser Ser Ser Trp Trp Pro Leu Ala Phe Val Thr Lys Leu Asp Pro Gln
420 425 430

Glu Leu Ala Asp Thr Asn Ser Ile Trp Leu Thr Asn Ser Ile Pro Ile
435 440 445

Pro Gln Ser Lys Phe Pro Arg Pro Ser Tyr Ser Glu Asn Tyr Cys Thr
450 455 460

Lys Pro Ala Val Cys Pro Ala Thr Cys Val Thr Gly Val Tyr Ser Asp
465 470 475 480

Ile Trp Pro Leu Thr Ser Ser Ser Ser Leu Pro Ser Ile Ile Trp Ile
485 490 495

Gly Gln Tyr Leu Asp Ala Pro Val Gly Arg Thr Tyr Pro Arg Phe Gly
500 505 510

Ile Ala Asn Gln Ser His Trp Tyr Leu Gln Glu Asp Ile Leu Pro Thr
515 520 525

Ser Thr Ala Ser Ala Tyr Ser Thr Thr Thr Cys Phe Lys Asn Thr Ala
530 535 540

Arg Asn Arg Val Phe Cys Val Thr Ile Ala Glu Phe Ala Asp Gly Leu
545 550 555 560

Phe Gly Glu Tyr Arg Ile Thr Pro Gln Leu Tyr Glu Leu Val Arg Asn
565 570 575

Asn

<210> 75
<211> 6717
<212> DNA
<213> artificial sequence

<220>
<223> L gene of FJ215864

<400> 75
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Page 175

Sequence

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cgacaaaaat ccgtagtgat gcacatccca gaccacatct tagaaaaatc agaatatcgg	180
atcaagcacc gtctagggaa aatcaagagt gacatagcac attactgtca gtattttta	240
attaatttgg caaatcttga tccgataacc caccctcaaaa gtttgtattg gttatccaga	300
ctaacaatag ctagtgctgg aacctttaga catatgaaag atagaatctt atgtacagtt	360
ggctccgaat tcggacacaa aattcaagat ttatttttcac tgctgagcca taaattagta	420
ggtaacggtg atttatttta tcaaagtctc tcaggtacac gtttgactgc gagtccgtta	480
tcccccttat gcaatcaatt tgtctctgac atcaagtctg cagtcacgac accctgggtca	540
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cgcactacaa attcagctca tttaacagaa attataaaag aggaatgggg tttagtaggt	660
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Sequence

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Sequence

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Sequence

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<213> artificial sequence

<220>
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<400> 76

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      20     25     30

Gly Leu Pro Met Pro Ala Asp Leu Arg Gln Lys Ser Val Val Met His
      35     40     45

Ile Pro Asp His Ile Leu Glu Lys Ser Glu Tyr Arg Ile Lys His Arg
      50     55     60

Leu Gly Lys Ile Lys Ser Asp Ile Ala His Tyr Cys Gln Tyr Phe Asn
65     70     75     80

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

Trp Leu Ser Arg Leu Thr Ile Ala Ser Ala Gly Thr Phe Arg His Met
      100    105    110

Lys Asp Arg Ile Leu Cys Thr Val Gly Ser Glu Phe Gly His Lys Ile
      115    120    125

Gln Asp Leu Phe Ser Leu Leu Ser His Lys Leu Val Gly Asn Gly Asp
      130    135    140

Leu Phe Asn Gln Ser Leu Ser Gly Thr Arg Leu Thr Ala Ser Pro Leu
145    150    155    160

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Sequence

Ser Pro Leu Cys Asn Gln Phe Val Ser Asp Ile Lys Ser Ala Val Thr
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Thr Pro Trp Ser Glu Ala Arg Trp Ser Trp Leu His Ile Lys Gln Thr
180 185 190

Met Arg Tyr Leu Ile Lys Gln Ser Arg Thr Thr Asn Ser Ala His Leu
195 200 205

Thr Glu Ile Ile Lys Glu Glu Trp Gly Leu Val Gly Ile Thr Pro Asp
210 215 220

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

Phe Glu Met Val Leu Met Tyr Ser Asp Val Leu Glu Ser Arg Asp Asn
245 250 255

Ile Val Leu Val Gly Arg Leu Ser Thr Phe Leu Gln Pro Val Val Ser
260 265 270

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

Gly Asp Thr Ile Tyr Glu Ile Ile Ala Val Leu Glu Ser Leu Ser Tyr
290 295 300

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

Phe Ser Phe Asn Met Asn Glu Leu Asp Asn Thr Leu Ser Lys Arg Val
325 330 335

Asp Pro Lys His Lys Asn Thr Ile Met Ser Ile Ile Arg Gln Cys Phe
340 345 350

Ser Asn Leu Asp Val Asp Gln Ala Ala Glu Met Leu Cys Leu Met Arg
355 360 365

Leu Phe Gly His Pro Met Leu Thr Ala Pro Asp Ala Ala Ala Lys Val
370 375 380

Arg Lys Ala Met Cys Ala Pro Lys Leu Val Glu His Asp Thr Ile Leu
385 390 395 400

Gln Thr Leu Ser Phe Phe Lys Gly Ile Ile Ile Asn Gly Tyr Arg Arg
405 410 415

Ser His Ser Gly Leu Trp Pro Asn Val Glu Pro Ser Ser Ile Tyr Asp
420 425 430

Sequence

Asp Asp Leu Arg Gln Leu Tyr Leu Glu Ser Ala Glu Ile Ser His His
435 440 445

Phe Met Leu Lys Asn Tyr Lys Ser Leu Ser Met Ile Glu Phe Lys Lys
450 455 460

Ser Ile Asp Tyr Asp Leu His Asp Asp Leu Ser Thr Phe Leu Lys Asp
465 470 475 480

Arg Ala Ile Cys Arg Pro Lys Ser Gln Trp Asp Val Ile Phe Arg Lys
485 490 495

Ser Leu Arg Arg Ser His Thr Arg Ser Gln Tyr Met Asp Glu Ile Lys
500 505 510

Ser Asn Arg Leu Leu Ile Asp Phe Leu Asp Ser Ala Asp Phe Asp Pro
515 520 525

Glu Lys Glu Phe Ala Tyr Val Thr Thr Met Asp Tyr Leu His Asp Asn
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Glu Phe Cys Ala Ser Tyr Ser Leu Lys Glu Lys Glu Ile Lys Thr Thr
545 550 555 560

Gly Arg Ile Phe Ala Lys Met Thr Arg Asn Met Arg Ser Cys Gln Val
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Ile Leu Glu Ser Leu Leu Ser Lys His Ile Cys Lys Phe Phe Lys Glu
580 585 590

Asn Gly Val Ser Met Glu Gln Leu Ser Leu Thr Lys Ser Leu Leu Ala
595 600 605

Met Ser Gln Leu Ser Pro Lys Val Ser Thr Leu Gln Asp Thr Ala Ser
610 615 620

Arg His Val Gly Asn Ser Lys Ser Gln Ile Ala Thr Ser Asn Pro Ser
625 630 635 640

Arg His His Ser Thr Thr Asn Gln Met Ser Leu Ser Asn Arg Lys Thr
645 650 655

Val Val Ala Thr Phe Leu Thr Thr Asp Leu Glu Lys Tyr Cys Leu Gln
660 665 670

Trp Arg Tyr Ser Thr Ile Lys Leu Phe Ala Gln Ala Leu Asn Gln Leu
675 680 685

Phe Gly Ile Asp His Gly Phe Glu Trp Ile His Leu Arg Leu Met Asn
690 695 700

Sequence

Ser Thr Leu Phe Val Gly Asp Pro Tyr Ser Pro Pro Glu Asp Pro Thr
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 Leu Glu Asp Ile Asp Lys Ala Pro Asn Asp Asp Ile Phe Ile Val Ser
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 Pro Arg Gly Gly Ile Glu Gly Leu Cys Gln Lys Met Trp Thr Met Ile
 740 745 750
 Ser Ile Ser Ala Ile His Cys Val Ala Glu Lys Ile Gly Ala Arg Val
 755 760 765
 Ala Ala Met Val Gln Gly Asp Asn Gln Val Ile Ala Ile Thr Lys Glu
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 Gly His Asn Leu Lys Leu Asn Glu Thr Ile Gln Ser Gln Ser Phe Phe
 820 825 830
 Val Tyr Ser Lys Arg Ile Phe Phe Glu Gly Arg Leu Leu Ser Gln Val
 835 840 845
 Leu Lys Asn Ala Ala Lys Leu Cys Met Val Ala Asp His Leu Gly Glu
 850 855 860
 Asn Thr Val Ser Ser Cys Ser Asn Leu Ser Ser Thr Ile Ala Arg Leu
 865 870 875 880
 Val Glu Asn Gly Phe Glu Lys Asp Thr Ala Phe Val Leu Asn Leu Val
 885 890 895
 Tyr Ile Met Thr Gln Ile Leu Phe Asp Glu His Tyr Ser Ile Val Cys
 900 905 910
 Asp His Asn Ser Val Lys Ser Leu Ile Gly Ser Lys Asn Tyr Arg Asn
 915 920 925
 Leu Leu Tyr Ser Ser Leu Ile Pro Gly Gln Leu Gly Gly Phe Asn Phe
 930 935 940
 Leu Asn Ile Ser Arg Leu Phe Thr Arg Asn Ile Gly Asp Pro Val Thr
 945 950 955 960
 Cys Ser Leu Ser Asp Leu Lys Cys Phe Ile Ala Ala Gly Leu Leu Pro
 965 970 975

Sequence

Pro Tyr Val Leu Lys Asn Val Val Leu Arg Glu Pro Gly Pro Gly Thr
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Trp Leu Thr Leu Cys Ser Asp Pro Tyr Thr Leu Asn Ile Pro Tyr Thr
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Gln Leu Pro Thr Thr Tyr Leu Lys Lys His Thr Gln Arg Ser Leu
1010 1015 1020

Leu Ser Arg Ala Val Asn Pro Leu Leu Ala Gly Val Gln Val Pro
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Asn Gln His Glu Glu Glu Glu Met Leu Ala Arg Phe Leu Leu Asp
1040 1045 1050

Arg Glu Tyr Val Met Pro Arg Val Ala His Val Ile Leu Glu Thr
1055 1060 1065

Ser Val Leu Gly Lys Arg Lys Gln Ile Gln Gly Leu Ile Asp Thr
1070 1075 1080

Thr Pro Thr Ile Ile Arg Thr Ser Leu Val Asn Leu Pro Val Ser
1085 1090 1095

Arg Lys Lys Cys Glu Lys Ile Ile Asn Tyr Ser Leu Asn Tyr Ile
1100 1105 1110

Ala Glu Cys His Asp Ser Leu Leu Ser Gln Ile Cys Phe Ser Asp
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Asn Lys Glu Tyr Leu Trp Ser Thr Ser Leu Ile Ser Val Glu Thr
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Cys Ser Val Thr Ile Ala Asp Tyr Leu Arg Ala Val Ser Trp Ser
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Asn Ile Leu Gly Gly Arg Asn Ile Ser Gly Val Thr Thr Pro Asp
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Cys Thr Leu Cys Glu Ser His Asp Asp Ala Phe Thr Trp Met His
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Leu Pro Gly Pro Leu Tyr Ile Pro Glu Pro Ser Val Thr Asn Ser
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Lys Met Arg Val Pro Tyr Leu Gly Ser Lys Thr Glu Glu Arg Lys
1220 1225 1230

Sequence

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Cys	Asn	Ile	Thr	Leu	Asp	Gln	Met	Arg	Leu	Leu	Thr	Pro	Ile	Pro
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Gln	Lys	Phe	Thr	Pro	Ala	Ser	Leu	Ala	Arg	Ile	Thr	Ser	Phe	Val
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His	Ile	Cys	Asn	Asp	Ser	Gln	Arg	Leu	Glu	Lys	Asp	Gly	Ser	Ser
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Val	Asp	Ser	Asn	Leu	Ile	Tyr	Gln	Gln	Ile	Met	Leu	Leu	Gly	Leu
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Ser	Ile	Phe	Glu	Thr	Met	Tyr	Ser	Met	Asp	Gln	Lys	Trp	Val	Phe
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Asn	Asn	His	Thr	Leu	His	Leu	His	Thr	Gly	His	Ser	Cys	Cys	Pro
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Arg	Glu	Leu	Asp	Ile	Ser	Leu	Val	Asn	Pro	Pro	Arg	His	Gln	Thr
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Pro	Glu	Leu	Thr	Ser	Thr	Thr	Thr	Asn	Pro	Phe	Leu	Tyr	Asp	Gln
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Leu	Pro	Leu	Asn	Gln	Asp	Asn	Leu	Thr	Thr	Leu	Glu	Ile	Lys	Thr
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Phe	Lys	Phe	Asn	Glu	Leu	Asn	Ile	Asp	Gly	Leu	Asp	Phe	Gly	Glu
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Gly	Ile	Gln	Leu	Leu	Ser	Arg	Cys	Thr	Ala	Arg	Leu	Met	Ala	Glu
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	1475					1480					1485			

Sequence

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Sequence

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Pro	Pro	Gln	Arg	Asn	Tyr	Gly	Leu	Met	Pro	Leu	Gln	Phe	Val	Asn
	1850					1855					1860			
Ser	Val	Val	Tyr	Lys	Asn	Leu	Thr	Ala	Lys	Ser	Glu	Cys	Lys	Leu
	1865					1870					1875			
Gly	Phe	Val	Gln	Gln	Phe	Lys	Pro	Leu	Trp	Arg	Asp	Ile	Asp	Ile
	1880					1885					1890			
Glu	Thr	Asn	Val	Thr	Asp	Pro	Ser	Phe	Val	Asn	Phe	Ala	Leu	Asn
	1895					1900					1905			
Glu	Ile	Pro	Met	Gln	Ser	Leu	Lys	Arg	Val	Asn	Cys	Asp	Val	Glu
	1910					1915					1920			
Phe	Asp	Arg	Gly	Met	Pro	Ile	Glu	Arg	Val	Ile	Gln	Gly	Tyr	Thr
	1925					1930					1935			
His	Ile	Leu	Leu	Val	Ala	Thr	Tyr	Gly	Leu	Gln	Gln	Asp	Ser	Ile
	1940					1945					1950			
Leu	Trp	Val	Lys	Val	Tyr	Arg	Thr	Ser	Glu	Lys	Val	Phe	Gln	Phe
	1955					1960					1965			
Leu	Leu	Ser	Ala	Met	Ile	Met	Ile	Phe	Gly	Tyr	Val	Lys	Ile	His
	1970					1975					1980			
Arg	Asn	Gly	Tyr	Met	Ser	Ala	Lys	Asp	Glu	Glu	Tyr	Ile	Leu	Met
	1985					1990					1995			

Sequence

Ser Asp Cys Lys Glu Pro Val Asn Tyr Thr Ala Val Pro Asn Ile
2000 2005 2010

Leu Thr Arg Val Ser Asp Leu Val Ser Lys Asn Leu Ser Leu Ile
2015 2020 2025

His Pro Glu Asp Leu Arg Lys Val Arg Cys Glu Thr Asp Ser Leu
2030 2035 2040

Asn Leu Lys Cys Asn His Ile Tyr Glu Lys Ile Ile Ala Arg Lys
2045 2050 2055

Ile Pro Leu Gln Val Ser Ser Thr Asp Ser Leu Leu Leu Gln Leu
2060 2065 2070

Gly Gly Val Ile Asn Ser Val Gly Ser Thr Asp Pro Arg Glu Val
2075 2080 2085

Ala Thr Leu Ser Ser Ile Glu Cys Met Asp Tyr Val Val Ser Ser
2090 2095 2100

Ile Asp Leu Ala Ile Leu Glu Ala Asn Ile Val Ile Ser Glu Ser
2105 2110 2115

Ala Gly Leu Asp Leu Ala Leu Met Leu Gly Pro Phe Asn Leu Asn
2120 2125 2130

Lys Leu Lys Lys Ile Asp Thr Ile Leu Lys Ser Ser Thr Tyr Gln
2135 2140 2145

Leu Ile Pro Tyr Trp Leu Arg Tyr Glu Tyr Ser Ile Asn Pro Arg
2150 2155 2160

Ser Leu Ser Phe Leu Ile Thr Lys Leu Gln Gln Cys Arg Ile Ser
2165 2170 2175

Trp Ser Asp Met Ile Thr Ile Ser Glu Phe Cys Lys Lys Ser Lys
2180 2185 2190

Arg Pro Ile Phe Ile Lys Arg Val Ile Gly Asn Gln Gln Leu Lys
2195 2200 2205

Ser Phe Phe Asn Glu Ser Ser Ser Ile Val Leu Thr Arg Ala Glu
2210 2215 2220

Val Lys Val Cys Ile Lys Phe Leu Gly Ala Ile Ile Lys Leu Lys
2225 2230 2235

<210> 77
<211> 1570

Sequence

<212> DNA
<213> artificial sequence

<220>
<223> NP gene of FJ619036

<400> 77
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 agaacaactt gtaaagccgg ctgtcaggag acctgatgtt gcctcaacag gtttactcag 180
 ggcggaaata cctgtctgtg ttacattgtc tcaagacccc ggtgagagat ggagccttgc 240
 ttgccttaat atccgatggc ttgtgagtga ttcacaaacc acaccaatga agcagggagc 300
 aatattgtca ctgctgagtc tacattcaga caatatgcga gctcacgcaa cattagcagc 360
 aaggtctgca gatgcttcac tcaccatact tgaggtagat gaagtagata ttggcaactc 420
 cctaataaaa ttcaacgcta gaagtgggtg atctgataaa cgatcaaata aattgcttgc 480
 aattgcggtg gacatcccca aaagttagcag taatgggcat ccatttcttg acacagacat 540
 tgagaccaga gaccgctcg atctatcaga gaccatagac cgcctgcagg gtattgcagc 600
 tcagatatgg gtgtcagcca taaagagcat gacagcgctt gacaccgcat cagagtcaga 660
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 ttctgtagtc aggacagaat ttatgagagt tattcggggc agcttggtac tgcgccagtt 780
 tatggttagc gaggcgaaga gggcttcagc catgggcgga gacacatcta ggtactatgc 840
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 gcagggagcg ttgacgaga gaacagcccg agagatgggc ttgactgagg aatccaaaca 1260
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 ccgccctgca ttcacagtc aagaagaaaa taggcagcct gccagaatt cttcagatac 1380
 tcagggtcag accaagccag tcccgaatca acccgacca agggccgacc cagatgacat 1440
 tgatccatac gagaacgggc tagaatggta attcaatcac ctgcacacat ccacctatac 1500
 accaattctg tgacatatta acctaatcaa acatttcata aactatagta gtcattgatt 1560
 taagaaaaaa 1570

<210> 78
 <211> 461
 <212> PRT
 <213> artificial sequence

<220>

Sequence

<223> NP protein of ACN88139

<400> 78

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

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

Trp Ser Leu Ala Cys Leu Asn Ile Arg Trp Leu Val Ser Asp Ser Ser
 50 55 60

Thr Thr Pro Met Lys Gln Gly Ala Ile Leu Ser Leu Leu Ser Leu His
 65 70 75 80

Ser Asp Asn Met Arg Ala His Ala Thr Leu Ala Ala Arg Ser Ala Asp
 85 90 95

Ala Ser Leu Thr Ile Leu Glu Val Asp Glu Val Asp Ile Gly Asn Ser
 100 105 110

Leu Ile Lys Phe Asn Ala Arg Ser Gly Val Ser Asp Lys Arg Ser Asn
 115 120 125

Gln Leu Leu Ala Ile Ala Asp Asp Ile Pro Lys Ser Cys Ser Asn Gly
 130 135 140

His Pro Phe Leu Asp Thr Asp Ile Glu Thr Arg Asp Pro Leu Asp Leu
 145 150 155 160

Ser Glu Thr Ile Asp Arg Leu Gln Gly Ile Ala Ala Gln Ile Trp Val
 165 170 175

Ser Ala Ile Lys Ser Met Thr Ala Pro Asp Thr Ala Ser Glu Ser Glu
 180 185 190

Ser Lys Arg Leu Ala Lys Tyr Gln Gln Gln Gly Arg Leu Val Lys Gln
 195 200 205

Val Leu Leu His Ser Val Val Arg Thr Glu Phe Met Arg Val Ile Arg
 210 215 220

Gly Ser Leu Val Leu Arg Gln Phe Met Val Ser Glu Cys Lys Arg Ala
 225 230 235 240

Ser Ala Met Gly Gly Asp Thr Ser Arg Tyr Tyr Ala Met Val Gly Asp
 245 250 255

Sequence

Ile Ser Leu Tyr Ile Lys Asn Ala Gly Leu Thr Ala Phe Phe Leu Thr
260 265 270

Leu Lys Phe Gly Val Gly Thr Gln Tyr Pro Thr Leu Ala Met Ser Val
275 280 285

Phe Ser Ser Asp Leu Lys Arg Leu Ala Ala Leu Ile Arg Leu Tyr Lys
290 295 300

Thr Lys Gly Asp Asn Ala Pro Tyr Met Ala Phe Leu Glu Asp Ser Asp
305 310 315 320

Met Gly Asn Phe Ala Pro Ala Asn Tyr Ser Thr Met Tyr Ser Tyr Ala
325 330 335

Met Gly Ile Gly Thr Ile Leu Glu Ala Ser Val Ser Arg Tyr Gln Tyr
340 345 350

Ala Arg Asp Phe Thr Ser Glu Asn Tyr Phe Arg Leu Gly Val Glu Thr
355 360 365

Ala Gln Ser Gln Gln Gly Ala Phe Asp Glu Arg Thr Ala Arg Glu Met
370 375 380

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

Val Asp Met Gly Pro Ser Ser Val Arg Glu Pro Ser Arg Pro Ala Phe
405 410 415

Ile Ser Gln Glu Glu Asn Arg Gln Pro Ala Gln Asn Ser Ser Asp Thr
420 425 430

Gln Gly Gln Thr Lys Pro Val Pro Asn Gln Pro Ala Pro Arg Ala Asp
435 440 445

Pro Asp Asp Ile Asp Pro Tyr Glu Asn Gly Leu Glu Trp
450 455 460

<210> 79
<211> 1374
<212> DNA
<213> artificial sequence

<220>
<223> P gene of FJ619036

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acaagatgga cttcgccaat gatgaagaaa ttgcagaact tctgaacctc agcaccactg 120
taatcaagga gattcagaaa tctgaactca agcctcccca aaccactggg cgaccacctg 180
tcagtcaagg gaacacaaga aatctaactg atctatggga aaaggagact gcaagtcaga 240

Sequence

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acaagacatc ggctcaatct ccacaaacca cacaagttca gtctgatgga aatgaggagg      300
aagaaatcaa atcagagtca attgatggcc acatcagtgg aactgttaat caattagagc      360
aagtcccaga acaaaaccag agcagatctt caccagggtga tgatctcgac agagctctca      420
acaagcttga agggagaatc aactcaatca gctcaatgga taaagaaatt aaaaagggcc      480
ctcgcattca gaatctccct ggggtcccaag cagcaactca acaggcgacc caccattgg      540
cagggggacac cccgaacatg caggcacgga caaaacccct gaccaagcca catcaagagg      600
caatcaatcc tggcaaccag gacacaggag agaatattca tttaccacct tccatggcac      660
caccagagtc attagttggg gcaatccgca atgtacccca attcgtgcca gaccaatcta      720
tgacgaatgt agatgcgggg agtgtccaac tacatgcatt atgtgcagag atgataagta      780
gaatgcttgt agaagttata tctaagcttg ataaactcga gtcgagactg aatgatatag      840
caaaagttgt aaacaccacc ccccttatca ggaatgatat taaccaactt aaggccacaa      900
ctgcactgat gtccaaccaa attgcttcca tacaaattct tgacccaggg aatgcagggg      960
tgagggtccct ctctgaaatg agatctgtga cgaagaaagc tgctgttgta attgcaggat     1020
ttggagacga cccaactcaa attattgaag aaggatcat ggccaaagat gctcttgaa      1080
aacctgtgcc tccaacatct gttatcgag ccaaagctca gacttcttcc ggtgtgagta     1140
aggggtgaaat agaaggattg attgcattgg tggaaacatt agttgacaat gacaagaagg     1200
cagcgaaaact gattaaaatg attgatcaag ttaaattcca cgccgattac gcccgagtca     1260
agcaggcaat atataatgca taatattgta attatacaaa caatcaatac tgctgtcggg     1320
tgcaccacc ttagcaaatc aataatcttt taaaattgat tgattaagaa aaaa           1374

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<210> 80
 <211> 405
 <212> PRT
 <213> artificial sequence

<220>
 <223> P protein of ACN88140
 <400> 80

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Met Asp Phe Ala Asn Asp Glu Glu Ile Ala Glu Leu Leu Asn Leu Ser
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Thr Thr Val Ile Lys Glu Ile Gln Lys Ser Glu Leu Lys Pro Pro Gln
20        25        30

Thr Thr Gly Arg Pro Pro Val Ser Gln Gly Asn Thr Arg Asn Leu Thr
35        40        45

Asp Leu Trp Glu Lys Glu Thr Ala Ser Gln Asn Lys Thr Ser Ala Gln
50        55        60

Ser Pro Gln Thr Thr Gln Val Gln Ser Asp Gly Asn Glu Glu Glu Glu
65        70        75        80

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Sequence

Ile Lys Ser Glu Ser Ile Asp Gly His Ile Ser Gly Thr Val Asn Gln
85 90 95

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

Asp Leu Asp Arg Ala Leu Asn Lys Leu Glu Gly Arg Ile Asn Ser Ile
115 120 125

Ser Ser Met Asp Lys Glu Ile Lys Lys Gly Pro Arg Ile Gln Asn Leu
130 135 140

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

Asp Thr Pro Asn Met Gln Ala Arg Thr Lys Pro Leu Thr Lys Pro His
165 170 175

Gln Glu Ala Ile Asn Pro Gly Asn Gln Asp Thr Gly Glu Asn Ile His
180 185 190

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

Asn Val Pro Gln Phe Val Pro Asp Gln Ser Met Thr Asn Val Asp Ala
210 215 220

Gly Ser Val Gln Leu His Ala Ser Cys Ala Glu Met Ile Ser Arg Met
225 230 235 240

Leu Val Glu Val Ile Ser Lys Leu Asp Lys Leu Glu Ser Arg Leu Asn
245 250 255

Asp Ile Ala Lys Val Val Asn Thr Thr Pro Leu Ile Arg Asn Asp Ile
260 265 270

Asn Gln Leu Lys Ala Thr Thr Ala Leu Met Ser Asn Gln Ile Ala Ser
275 280 285

Ile Gln Ile Leu Asp Pro Gly Asn Ala Gly Val Arg Ser Leu Ser Glu
290 295 300

Met Arg Ser Val Thr Lys Lys Ala Ala Val Val Ile Ala Gly Phe Gly
305 310 315 320

Asp Asp Pro Thr Gln Ile Ile Glu Glu Gly Ile Met Ala Lys Asp Ala
325 330 335

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

Sequence

Thr Ser Ser Gly Val Ser Lys Gly Glu Ile Glu Gly Leu Ile Ala Leu
355 360 365

Val Glu Thr Leu Val Asp Asn Asp Lys Lys Ala Ala Lys Leu Ile Lys
370 375 380

Met Ile Asp Gln Val Lys Ser His Ala Asp Tyr Ala Arg Val Lys Gln
385 390 395 400

Ala Ile Tyr Asn Ala
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<210> 81
<211> 1110
<212> DNA
<213> artificial sequence

<220>
<223> M gene of FJ619036

<400> 81
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agggttagatt caattggcga tgtgcagaat gccaaagagt cctcgatatt cgtgactcta 180
tatggtttca tccaagcaat taaggagaat tcagatcgat cgaaattctt ccatccaaaa 240
gatgacttca aacctgagac agtcactgca ggactggtag tagtgggtgc aatccgaatg 300
atggctgatg tcaataccat ctctaatagat gactagcgc tggagatcac tgtaagaaa 360
tctgcaactt ctcaagagaa aatgacgggtg atgttcaca atagcccccc ttcattgaga 420
actgcaataa ctatccgagc aggagggttc atctcgaatg cagacgaaaa tataaaatgt 480
gccagcaagt tgactgcagg agtgcagtac atattccgtc caatgtttgt ttcaatcact 540
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ctactgtata gtgtgatgtt ggaggtagga ttcaaagtgg acatcgggaa ggatcatccc 660
caggcaaaaa tgctgaagag ggtcacaatt ggcgatgcag acacatactg gggatttgca 720
tggttccacc tgtgcaattt caaaaagaca tcctctaagg gaaagccgag aacgctagac 780
gaactgagga caaaagtcaa aaatatgggg ttgaaattgg agttacatga cctatgggggt 840
ccgactattg tgggtccaaat cactggcaag agcagcaaata atgctcaagg atttttttct 900
tccaatggta cttgttgctt cccaatcagc agatctgcac cagagcttgg gaagcttctg 960
tggtcctgct cagcaactat tgggtgacgca acagttgtta tccaatcaag cgagaagggg 1020
gaactcctaa ggtctgatga tctcgagata cgagggtgctg tggcctccaa gaaaggtaga 1080
ctgagctcat ttcacccctt caaaaaatga 1110

<210> 82
<211> 369

Sequence

<212> PRT
<213> artificial sequence

<220>
<223> M protein of ACN88143

<400> 82

Met Ala Tyr Thr Thr Leu Lys Leu Trp Val Asp Glu Gly Asp Met Ser
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Ser Ser Leu Leu Ser Phe Pro Leu Val Leu Lys Glu Thr Asp Arg Gly
20 25 30

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

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

Gln Ala Ile Lys Glu Asn Ser Asp Arg Ser Lys Phe Phe His Pro Lys
65 70 75 80

Asp Asp Phe Lys Pro Glu Thr Val Thr Ala Gly Leu Val Val Val Gly
85 90 95

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

Ala Leu Glu Ile Thr Val Lys Lys Ser Ala Thr Ser Gln Glu Lys Met
115 120 125

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

Ile Arg Ala Gly Gly Phe Ile Ser Asn Ala Asp Glu Asn Ile Lys Cys
145 150 155 160

Ala Ser Lys Leu Thr Ala Gly Val Gln Tyr Ile Phe Arg Pro Met Phe
165 170 175

Val Ser Ile Thr Lys Leu His Asn Gly Lys Leu Tyr Arg Val Pro Lys
180 185 190

Ser Ile His Ser Ile Ser Ser Thr Leu Leu Tyr Ser Val Met Leu Glu
195 200 205

Val Gly Phe Lys Val Asp Ile Gly Lys Asp His Pro Gln Ala Lys Met
210 215 220

Leu Lys Arg Val Thr Ile Gly Asp Ala Asp Thr Tyr Trp Gly Phe Ala
225 230 235 240

Trp Phe His Leu Cys Asn Phe Lys Lys Thr Ser Ser Lys Gly Lys Pro
245 250 255

Ala Val Ala Ser Lys Lys Gly Arg Leu Ser Ser Phe His Pro Phe Lys
355 360 365

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Sequence

```

ggaattaaac agcaagacgt taattcgcta tatgaagccg gactaatcac aggacaagtc      780
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gaggtaactg gtgtgctgac gacagaatta gtcactgtta gtgtaacaac agacaagggg      900
gaaggggaaag caattgtacc ccaatttgta gctgaaagtc ggggtgactat tgaggagctt      960
gatgtagcat cttgtaaatt cagcagcaca accctatact gcaggcaggt caacacaagg     1020
gcacttcccc cgctagtggc tagctgtctc cgaggtaact atgatgattg tcaatatacc     1080
acagagattg gagcattatc atcccggtat ataacactag atggaggggt cttagtcaat     1140
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gctgcagtaa catatgttga tgctacaata tgcaaaacaa ttcaattgga tgacatacaa     1260
ctccagttgg aagggtcact atcatcagtt tatgcaagga acattctaat tgagatcagt     1320
caggtgacta cctccggttc tttggatata agcagtgaga tagggaacat caataatacg     1380
gtgaatcgtg tggaggatit aatccaccaa tcggaggaat ggctggcaaa agttaaccca     1440
cacattgtta ataatactac actaattgta ctctgtgtgt taagtgcgct tgctgtgatc     1500
tggctggcag tattaacggc tattataata tacttgagaa caaagttgaa gactatatcg     1560
gcattggctg taaccaatac aatacagtct aatccctatg ttaaccaaac gaaacgtgaa     1620
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<210> 84
 <211> 543
 <212> PRT
 <213> artificial sequence

<220>
 <223> F protein of ACN88144

<400> 84

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

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

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```

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

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```

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

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```

Thr Thr Cys Leu Arg Glu Thr Ile Thr Thr Tyr Asn Asn Thr Val Asn
65           70           75           80

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```

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

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Sequence

Glu Thr Tyr Pro Gln Thr Arg Leu Ile Gly Ala Val Ile Gly Ser Ile
100 105 110

Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu
115 120 125

Lys Gln Ala Gln Asp Asn Ala Arg Asn Ile Leu Ala Leu Lys Glu Ala
130 135 140

Leu Ser Lys Thr Asn Glu Ala Val Lys Glu Leu Ser Ser Gly Leu Gln
145 150 155 160

Gln Thr Ala Ile Ala Leu Gly Lys Ile Gln Ser Phe Val Asn Glu Glu
165 170 175

Ile Leu Pro Ser Ile Asn Gln Leu Ser Cys Glu Val Thr Ala Asn Lys
180 185 190

Leu Gly Val Tyr Leu Ser Leu Tyr Leu Thr Glu Leu Thr Thr Ile Phe
195 200 205

Gly Ala Gln Leu Thr Asn Pro Ala Leu Thr Ser Leu Ser Tyr Gln Ala
210 215 220

Leu Tyr Asn Leu Cys Gly Gly Asn Met Ala Met Leu Thr Gln Lys Ile
225 230 235 240

Gly Ile Lys Gln Gln Asp Val Asn Ser Leu Tyr Glu Ala Gly Leu Ile
245 250 255

Thr Gly Gln Val Ile Gly Tyr Asp Ser Gln Tyr Gln Leu Leu Val Ile
260 265 270

Gln Val Asn Tyr Pro Ser Ile Ser Glu Val Thr Gly Val Arg Ala Thr
275 280 285

Glu Leu Val Thr Val Ser Val Thr Thr Asp Lys Gly Glu Gly Lys Ala
290 295 300

Ile Val Pro Gln Phe Val Ala Glu Ser Arg Val Thr Ile Glu Glu Leu
305 310 315 320

Asp Val Ala Ser Cys Lys Phe Ser Ser Thr Thr Leu Tyr Cys Arg Gln
325 330 335

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

Asn Tyr Asp Asp Cys Gln Tyr Thr Thr Glu Ile Gly Ala Leu Ser Ser
355 360 365

Sequence

Arg Tyr Ile Thr Leu Asp Gly Gly Val Leu Val Asn Cys Lys Ser Ile
370 375 380

Val Cys Arg Cys Leu Asn Pro Ser Lys Ile Ile Ser Gln Asn Thr Asn
385 390 395 400

Ala Ala Val Thr Tyr Val Asp Ala Thr Ile Cys Lys Thr Ile Gln Leu
405 410 415

Asp Asp Ile Gln Leu Gln Leu Glu Gly Ser Leu Ser Ser Val Tyr Ala
420 425 430

Arg Asn Ile Ser Ile Glu Ile Ser Gln Val Thr Thr Ser Gly Ser Leu
435 440 445

Asp Ile Ser Ser Glu Ile Gly Asn Ile Asn Asn Thr Val Asn Arg Val
450 455 460

Glu Asp Leu Ile His Gln Ser Glu Glu Trp Leu Ala Lys Val Asn Pro
465 470 475 480

His Ile Val Asn Asn Thr Thr Leu Ile Val Leu Cys Val Leu Ser Ala
485 490 495

Leu Ala Val Ile Trp Leu Ala Val Leu Thr Ala Ile Ile Ile Tyr Leu
500 505 510

Arg Thr Lys Leu Lys Thr Ile Ser Ala Leu Ala Val Thr Asn Thr Ile
515 520 525

Gln Ser Asn Pro Tyr Val Asn Gln Thr Lys Arg Glu Ser Lys Phe
530 535 540

<210> 85
<211> 1734
<212> DNA
<213> artificial sequence

<220>
<223> HN gene of FJ619036

<400> 85
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attgttagca tagttcaa at tggaatttg aaaattcctt ctgtagggga tctggcggac 180
gaggttggtaa cacctttgaa aaccactctg tctgatacac tcaggaatcc aattaaccag 240
ataaatgaca tattcaggat tgttgccctt gatattccat tgcaagtaac tagtatccaa 300
aaagacctcg caagtcaatt tagcatgttg atagatagtt taaatgctat caaattgggc 360
aacgggacca accttatcat acctacatca gataaggagt atgcaggagg aatttgaaac 420
cctgtcttta ctgtcgatgc tggagggttct ataggattca agcaatttag cttaatagaa 480

Sequence

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gccagtgcac ctagtatgta tatctcaatg ggggttctcc atgtgtcttc atctggcact      660
cctatctttc ttactactgc aagtgaactg atagacgatg gagttaatcg taagtcatgc      720
agtattgtag caaccaatt cggtctgtgac attttgtgca gtattgtcat agagaaggag      780
ggagatgatt attggtctga tactccgact ccaatgcgcc acggccgttt ttcattcaat      840
gggagttttg tagaaaccga actaccctgtg tccagtatgt tctcgtcatt ctctgccaac      900
taccctgctg tgggatcagg cgaaattgta aaagatagaa tattattccc aatttacgga      960
ggtataaagc agacttcacc agagtgtacc gaattagtga aatatggact ctttgtgtca     1020
acacctacaa ctgtatgtca gagtagctgg acttatgacc aggtaaaagc agcgtatagg     1080
ccagattaca tatcaggccg gttctgggca caagtgatac tcagctgcgc tcttgatgca     1140
gtcgcattat caagttgtat tgtaaagatt atgaatagca gcacagtgat gatggcagca     1200
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Thr Thr Gly Cys Leu Ala Leu Ser Ile Val Ser Ile Val Gln Ile Gly
 35 40 45

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

Sequence

Pro Leu Lys Thr Thr Leu Ser Asp Thr Leu Arg Asn Pro Ile Asn Gln
65 70 75 80

Ile Asn Asp Ile Phe Arg Ile Val Ala Leu Asp Ile Pro Leu Gln Val
85 90 95

Thr Ser Ile Gln Lys Asp Leu Ala Ser Gln Phe Ser Met Leu Ile Asp
100 105 110

Ser Leu Asn Ala Ile Lys Leu Gly Asn Gly Thr Asn Leu Ile Ile Pro
115 120 125

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

His Pro Ser Phe Ile Ala Gly Pro Thr Thr Thr Arg Gly Cys Thr Arg
165 170 175

Ile Pro Thr Phe His Met Ser Glu Ser His Trp Cys Tyr Ser His Asn
180 185 190

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195 200 205

Ser Met Gly Val Leu His Val Ser Ser Ser Gly Thr Pro Ile Phe Leu
210 215 220

Thr Thr Ala Ser Glu Leu Ile Asp Asp Gly Val Asn Arg Lys Ser Cys
225 230 235 240

Ser Ile Val Ala Thr Gln Phe Gly Cys Asp Ile Leu Cys Ser Ile Val
245 250 255

Ile Glu Lys Glu Gly Asp Asp Tyr Trp Ser Asp Thr Pro Thr Pro Met
260 265 270

Arg His Gly Arg Phe Ser Phe Asn Gly Ser Phe Val Glu Thr Glu Leu
275 280 285

Pro Val Ser Ser Met Phe Ser Ser Phe Ser Ala Asn Tyr Pro Ala Val
290 295 300

Gly Ser Gly Glu Ile Val Lys Asp Arg Ile Leu Phe Pro Ile Tyr Gly
305 310 315 320

Gly Ile Lys Gln Thr Ser Pro Glu Phe Thr Glu Leu Val Lys Tyr Gly
325 330 335

Sequence

Leu Phe Val Ser Thr Pro Thr Thr Val Cys Gln Ser Ser Trp Thr Tyr
 340 345 350
 Asp Gln Val Lys Ala Ala Tyr Arg Pro Asp Tyr Ile Ser Gly Arg Phe
 355 360 365
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 370 375 380
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 385 390 395 400
 Glu Gly Arg Ile Ile Lys Ile Gly Ile Asp Tyr Phe Tyr Tyr Gln Arg
 405 410 415
 Ser Ser Ser Trp Trp Pro Leu Ala Phe Val Thr Lys Leu Asp Pro Gln
 420 425 430
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 435 440 445
 Pro Gln Ser Lys Phe Pro Arg Pro Ser Tyr Ser Glu Asn Tyr Cys Thr
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 Lys Pro Ala Val Cys Pro Ala Thr Cys Val Thr Gly Val Tyr Ser Asp
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 Gly Gln Tyr Leu Asp Ala Pro Val Gly Arg Thr Tyr Pro Arg Phe Gly
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Asn

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Sequence

<212> DNA
<213> artificial sequence

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Sequence

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Sequence

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Sequence

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<210> 88
<211> 2238
<212> PRT
<213> artificial sequence

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<220>
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Gly Leu Pro Met Pro Ala Asp Leu Arg Gln Lys Ser Val Val Met His
35     40     45
Ile Pro Asp His Ile Leu Glu Lys Ser Glu Tyr Arg Ile Lys His Arg
50     55     60
Leu Gly Lys Ile Lys Ser Asp Ile Ala His Tyr Cys Gln Tyr Phe Asn
65     70     75     80
Ile Asn Leu Ala Asn Leu Asp Pro Ile Thr His Pro Lys Ser Leu Tyr
85     90     95
Trp Leu Ser Arg Leu Thr Ile Ala Ser Ala Gly Thr Phe Arg His Met
100    105    110
Lys Asp Arg Ile Leu Cys Thr Val Gly Ser Glu Phe Gly His Lys Ile
115    120    125

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Sequence

Gln Asp Leu Phe Ser Leu Leu Ser His Lys Leu Val Gly Asn Gly Asp
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Leu Phe Asn Gln Ser Leu Ser Gly Thr Arg Leu Thr Ala Ser Pro Leu
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Ser Pro Leu Cys Asn Gln Phe Val Ser Asp Ile Lys Ser Ala Val Thr
165 170 175

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

Met Arg Tyr Leu Ile Lys Gln Ser Arg Thr Thr Asn Ser Ala His Leu
195 200 205

Thr Glu Ile Ile Lys Glu Glu Trp Gly Leu Val Gly Ile Thr Pro Asp
210 215 220

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

Phe Glu Met Val Leu Met Tyr Ser Asp Val Leu Glu Ser Arg Asp Asn
245 250 255

Ile Val Leu Val Gly Arg Leu Ser Thr Phe Leu Gln Pro Val Val Ser
260 265 270

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

Gly Asp Thr Ile Tyr Glu Ile Ile Ala Val Leu Glu Ser Leu Ser Tyr
290 295 300

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

Phe Ser Phe Asn Met Asn Glu Leu Asp Asn Thr Leu Ser Lys Arg Val
325 330 335

Asp Pro Lys His Lys Asn Thr Ile Met Ser Ile Ile Arg Gln Cys Phe
340 345 350

Ser Asn Leu Asp Val Asp Gln Ala Ala Glu Met Leu Cys Leu Met Arg
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Leu Phe Gly His Pro Met Leu Thr Ala Pro Asp Ala Ala Ala Lys Val
370 375 380

Arg Lys Ala Met Cys Ala Pro Lys Leu Val Glu His Asp Thr Ile Leu
385 390 395 400

Sequence

Gln Thr Leu Ser Phe Phe Lys Gly Ile Ile Ile Asn Gly Tyr Arg Arg
405 410 415

Ser His Ser Gly Leu Trp Pro Asn Val Glu Pro Ser Ser Ile Tyr Asp
420 425 430

Asp Asp Leu Arg Gln Leu Tyr Leu Glu Ser Ala Glu Ile Ser His His
435 440 445

Phe Met Leu Lys Asn Tyr Lys Ser Leu Ser Met Ile Glu Phe Lys Lys
450 455 460

Ser Ile Asp Tyr Asp Leu His Asp Asp Leu Ser Thr Phe Leu Lys Asp
465 470 475 480

Arg Ala Ile Cys Arg Pro Lys Ser Gln Trp Asp Val Ile Phe Arg Lys
485 490 495

Ser Leu Arg Arg Ser His Thr Arg Ser Gln Tyr Met Asp Glu Ile Lys
500 505 510

Ser Asn Arg Leu Leu Ile Asp Phe Leu Asp Ser Ala Asp Phe Asp Pro
515 520 525

Glu Lys Glu Phe Ala Tyr Val Thr Thr Met Asp Tyr Leu His Asp Asn
530 535 540

Glu Phe Cys Ala Ser Tyr Ser Leu Lys Glu Lys Glu Ile Lys Thr Thr
545 550 555 560

Gly Arg Ile Phe Ala Lys Met Thr Arg Asn Met Arg Ser Cys Gln Val
565 570 575

Ile Leu Glu Ser Leu Leu Ser Lys His Ile Cys Lys Phe Phe Lys Glu
580 585 590

Asn Gly Val Ser Met Glu Gln Leu Ser Leu Thr Lys Ser Leu Leu Ala
595 600 605

Met Ser Gln Leu Ser Pro Lys Val Ser Thr Leu Gln Asp Thr Ala Ser
610 615 620

Arg His Val Gly Asn Ser Lys Ser Gln Ile Ala Thr Ser Asn Pro Ser
625 630 635 640

Arg His His Ser Thr Thr Asn Gln Met Ser Leu Ser Asn Arg Lys Thr
645 650 655

Val Val Ala Thr Phe Leu Thr Thr Asp Leu Glu Lys Tyr Cys Leu Gln
660 665 670

Sequence

Trp Arg Tyr Ser Thr Ile Lys Leu Phe Ala Gln Ala Leu Asn Gln Leu
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 705 710 715 720
 Leu Glu Asp Ile Asp Lys Ala Pro Asn Asp Asp Ile Phe Ile Val Ser
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 Pro Arg Gly Gly Ile Glu Gly Leu Cys Gln Lys Met Trp Thr Met Ile
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 Ser Ile Ser Ala Ile His Cys Val Ala Glu Lys Ile Gly Ala Arg Val
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 Val Glu Asn Gly Phe Glu Lys Asp Thr Ala Phe Val Leu Asn Leu Val
 885 890 895
 Tyr Ile Met Thr Gln Ile Leu Phe Asp Glu His Tyr Ser Ile Val Cys
 900 905 910
 Asp His Asn Ser Val Lys Ser Leu Ile Gly Ser Lys Asn Tyr Arg Asn
 915 920 925
 Leu Leu Tyr Ser Ser Leu Ile Pro Gly Gln Leu Gly Gly Phe Asn Phe
 930 935 940

Sequence

Ile Asn Ile Ser Arg Leu Phe Thr Arg Asn Ile Gly Asp Pro Val Thr
945 950 955 960

Cys Ser Leu Ser Asp Leu Lys Cys Phe Ile Ala Ala Gly Leu Leu Pro
965 970 975

Pro Tyr Val Leu Lys Asn Val Val Leu Arg Glu Pro Gly Pro Gly Thr
980 985 990

Trp Leu Thr Leu Cys Ser Asp Pro Tyr Thr Leu Asn Ile Pro Tyr Thr
995 1000 1005

Gln Leu Pro Thr Thr Tyr Leu Lys Lys His Thr Gln Arg Ser Leu
1010 1015 1020

Ile Ser Arg Ala Val Asn Pro Leu Leu Ala Gly Val Gln Val Pro
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Asn Gln His Glu Glu Glu Glu Met Leu Ala Arg Phe Leu Leu Asp
1040 1045 1050

Arg Glu Tyr Val Met Pro Arg Val Ala His Val Thr Leu Glu Thr
1055 1060 1065

Ser Val Leu Gly Lys Arg Lys Gln Ile Gln Gly Leu Ile Asp Thr
1070 1075 1080

Thr Pro Thr Ile Ile Arg Thr Ser Leu Val Asn Leu Pro Val Ser
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Arg Lys Lys Cys Glu Lys Ile Ile Asn Tyr Ser Leu Asn Tyr Ile
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Ala Glu Cys His Asp Ser Leu Leu Ser Gln Ile Cys Phe Ser Asp
1115 1120 1125

Asn Lys Glu Tyr Leu Trp Ser Thr Ser Leu Ile Ser Val Glu Thr
1130 1135 1140

Cys Ser Val Thr Ile Ala Asp Tyr Leu Arg Ala Val Ser Trp Ser
1145 1150 1155

Asn Ile Leu Gly Gly Arg Ser Ile Ser Gly Val Thr Thr Pro Asp
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Sequence

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Lys	Met	Arg	Val	Pro	Tyr	Leu	Gly	Ser	Lys	Thr	Glu	Glu	Arg	Lys
1220						1225					1230			
Thr	Ala	Ser	Met	Ala	Ala	Ile	Lys	Gly	Met	Ser	His	His	Leu	Arg
1235						1240					1245			
Ala	Val	Leu	Arg	Gly	Thr	Ser	Val	Phe	Ile	Trp	Ala	Ser	Gly	Asp
1250						1255					1260			
Thr	Asp	Ile	Asn	Trp	Asp	Asn	Ala	Leu	Gln	Ile	Ala	Gln	Ser	Arg
1265						1270					1275			
Cys	Asn	Ile	Thr	Leu	Asp	Gln	Met	Arg	Leu	Leu	Thr	Pro	Ile	Pro
1280						1285					1290			
Ser	Ser	Ser	Asn	Ile	Gln	Arg	Arg	Leu	Asp	Asp	Gly	Ile	Ser	Thr
1295						1300					1305			
Gln	Lys	Phe	Thr	Pro	Ala	Ser	Leu	Ala	Arg	Ile	Thr	Ser	Ser	Val
1310						1315					1320			
His	Ile	Cys	Asn	Asp	Ser	Gln	Arg	Leu	Glu	Lys	Asp	Gly	Ser	Ser
1325						1330					1335			
Val	Asp	Ser	Asn	Leu	Ile	Tyr	Gln	Gln	Ile	Met	Leu	Leu	Gly	Leu
1340						1345					1350			
Ser	Ile	Phe	Glu	Thr	Met	Tyr	Ser	Met	Asp	Gln	Lys	Trp	Val	Phe
1355						1360					1365			
Asn	Asn	His	Thr	Leu	His	Leu	His	Thr	Gly	His	Ser	Cys	Cys	Pro
1370						1375					1380			
Arg	Glu	Leu	Asp	Ile	Ser	Leu	Val	Asn	Pro	Pro	Arg	His	Gln	Thr
1385						1390					1395			
Pro	Glu	Leu	Thr	Ser	Thr	Thr	Thr	Asn	Pro	Phe	Leu	Tyr	Asp	Gln
1400						1405					1410			
Leu	Pro	Leu	Asn	Gln	Asp	Asn	Leu	Thr	Thr	Leu	Glu	Ile	Lys	Thr
1415						1420					1425			
Phe	Lys	Phe	Asn	Glu	Leu	Asn	Ile	Asp	Gly	Leu	Asp	Phe	Gly	Glu
1430						1435					1440			
Gly	Ile	Gln	Leu	Leu	Ser	Arg	Cys	Thr	Ala	Arg	Leu	Met	Ala	Glu
1445						1450					1455			

Sequence

Cys	Ile	Leu	Glu	Glu	Gly	Ile	Gly	Ser	Ser	Val	Lys	Asn	Glu	Ala
1460						1465					1470			
Ile	Val	Asn	Phe	Asp	Asn	Ser	Val	Asn	Trp	Ile	Ser	Glu	Cys	Leu
1475						1480					1485			
Met	Cys	Asp	Ile	Arg	Ser	Leu	Cys	Val	Asn	Leu	Gly	Gln	Glu	Ile
1490						1495					1500			
Leu	Cys	Ser	Leu	Ala	Tyr	Gln	Met	Tyr	Tyr	Leu	Arg	Ile	Arg	Gly
1505						1510					1515			
Arg	Arg	Ala	Ile	Leu	Asn	Tyr	Leu	Asp	Thr	Thr	Leu	Gln	Arg	Ile
1520						1525					1530			
Pro	Val	Ile	Gln	Leu	Ala	Asn	Ile	Ala	Leu	Thr	Ile	Ser	His	Pro
1535						1540					1545			
Glu	Ile	Phe	Arg	Arg	Ile	Val	Asn	Thr	Gly	Ile	His	Asn	Gln	Ile
1550						1555					1560			
Lys	Gly	Pro	Tyr	Val	Ala	Thr	Thr	Asp	Phe	Ile	Ala	Ala	Ser	Arg
1565						1570					1575			
Asp	Ile	Ile	Leu	Ser	Gly	Ala	Arg	Glu	Tyr	Leu	Ser	Tyr	Leu	Ser
1580						1585					1590			
Ser	Gly	Gln	Glu	Asp	Cys	Tyr	Thr	Phe	Phe	Asn	Cys	Gln	Asp	Gly
1595						1600					1605			
Asp	Leu	Thr	Pro	Lys	Met	Glu	Gln	Tyr	Leu	Ala	Arg	Arg	Ala	Cys
1610						1615					1620			
Leu	Leu	Thr	Leu	Leu	Tyr	Asn	Thr	Gly	His	Gln	Ile	Pro	Ile	Ile
1625						1630					1635			
Arg	Ser	Leu	Thr	Pro	Ile	Glu	Lys	Cys	Lys	Val	Leu	Thr	Glu	Tyr
1640						1645					1650			
Asn	Gln	Gln	Ile	Glu	Tyr	Ala	Asp	Gln	Glu	Phe	Ser	Ser	Val	Leu
1655						1660					1665			
Lys	Val	Val	Asn	Ala	Leu	Leu	Gln	Asn	Pro	Asn	Ile	Asp	Ala	Leu
1670						1675					1680			
Val	Ser	Asn	Leu	Tyr	Phe	Thr	Thr	Arg	Arg	Val	Leu	Ser	Asn	Leu
1685						1690					1695			
Arg	Ser	Cys	Asp	Lys	Ala	Ile	Ser	Tyr	Ile	Glu	Tyr	Leu	Tyr	Thr
1700						1705					1710			

Sequence

Glu Asp Phe Gly Glu Lys Glu Asp Thr Val Gln Tyr Asp Ile Met
 1715 1720 1725
 Thr Thr Asn Asp Ile Ile Leu Thr His Gly Leu Phe Thr Gln Ile
 1730 1735 1740
 Glu Ile Ser Tyr Gln Gly Ser Ser Leu His Lys Phe Leu Thr Pro
 1745 1750 1755
 Asp Asn Ala Pro Gly Ser Leu Ile Pro Phe Ser Ile Ser Pro Asn
 1760 1765 1770
 Ser Leu Ala Cys Asp Pro Leu His His Leu Leu Lys Ser Val Gly
 1775 1780 1785
 Thr Ser Ser Thr Ser Trp Tyr Lys Tyr Ala Ile Ala Tyr Ala Val
 1790 1795 1800
 Ser Glu Lys Arg Ser Ala Arg Leu Gly Gly Ser Leu Tyr Ile Gly
 1805 1810 1815
 Glu Gly Ser Gly Ser Val Met Thr Leu Leu Glu Tyr Leu Glu Pro
 1820 1825 1830
 Ser Val Asp Ile Phe Tyr Asn Ser Leu Phe Ser Asn Gly Met Asn
 1835 1840 1845
 Pro Pro Gln Arg Asn Tyr Gly Leu Met Pro Leu Gln Phe Val Asn
 1850 1855 1860
 Ser Val Val Tyr Lys Asn Leu Thr Ala Lys Ser Glu Cys Lys Leu
 1865 1870 1875
 Gly Phe Val Gln Gln Phe Lys Pro Leu Trp Arg Asp Ile Asp Ile
 1880 1885 1890
 Glu Thr Asn Val Thr Asp Pro Ser Phe Val Asn Phe Ala Leu Asn
 1895 1900 1905
 Glu Ile Pro Met Gln Ser Leu Lys Arg Val Asn Cys Asp Val Glu
 1910 1915 1920
 Phe Asp Arg Gly Met Pro Ile Glu Arg Val Ile Gln Gly Tyr Thr
 1925 1930 1935
 His Ile Leu Leu Val Ala Thr Tyr Gly Leu Gln Gln Asp Ser Ile
 1940 1945 1950
 Leu Trp Val Lys Val Tyr Arg Thr Ser Glu Lys Val Phe Gln Phe
 1955 1960 1965

Sequence

Leu Leu Ser Ala Met Ile Met Ile Phe Gly Tyr Val Lys Ile His
 1970 1975 1980
 Arg Asn Gly Tyr Met Ser Ala Lys Asp Glu Glu Tyr Ile Leu Met
 1985 1990 1995
 Ser Asp Cys Lys Glu Pro Val Asn Tyr Thr Ala Val Pro Asn Ile
 2000 2005 2010
 Leu Thr Arg Val Ser Asp Leu Val Ser Lys Asn Leu Ser Leu Ile
 2015 2020 2025
 His Pro Glu Asp Leu Arg Lys Val Arg Cys Glu Thr Asp Ser Leu
 2030 2035 2040
 Asn Leu Lys Cys Asn His Ile Tyr Glu Lys Ile Ile Ala Arg Lys
 2045 2050 2055
 Ile Pro Leu Gln Val Ser Ser Thr Asp Ser Leu Leu Leu Gln Leu
 2060 2065 2070
 Gly Gly Val Ile Asn Ser Val Gly Ser Thr Asp Pro Arg Glu Val
 2075 2080 2085
 Ala Thr Leu Ser Ser Ile Glu Cys Met Asp Tyr Val Val Ser Ser
 2090 2095 2100
 Ile Asp Leu Ala Ile Leu Glu Ala Asn Ile Val Ile Ser Glu Ser
 2105 2110 2115
 Ala Asp Leu Asp Leu Ala Leu Met Leu Gly Pro Phe Asn Leu Asn
 2120 2125 2130
 Lys Leu Lys Lys Ile Asp Thr Ile Leu Lys Ser Ser Thr Tyr Gln
 2135 2140 2145
 Leu Ile Pro Tyr Trp Leu Arg Tyr Glu Tyr Ser Ile Asn Pro Arg
 2150 2155 2160
 Ser Leu Ser Phe Leu Ile Thr Lys Leu Gln Gln Cys Arg Ile Ser
 2165 2170 2175
 Trp Ser Asp Met Ile Thr Ile Ser Glu Phe Cys Lys Lys Ser Lys
 2180 2185 2190
 Arg Pro Ile Phe Ile Lys Arg Val Ile Gly Asn Gln Arg Leu Lys
 2195 2200 2205
 Ser Phe Phe Asn Glu Ser Ser Ser Ile Val Leu Thr Arg Ala Glu
 2210 2215 2220

Sequence

Val Lys Val Cys Ile Lys Phe Leu Gly Ala Ile Ile Lys Leu Lys
2225 2230 2235