

SEQUENCE LISTING

<110> SANOFI

<120> CHO EXPRESSION SYSTEM

<130> FR2012-007

<160> 14

<170> PatentIn version 3.3

<210> 1

<211> 373

<212> PRT

<213> Homo sapiens

<400> 1

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

Tyr Met Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
20 25 30

Ile Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
35 40 45

Ser Glu Pro Lys Cys Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly
50 55 60

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

Pro Ala Ala Met Phe Arg Asp Pro Phe Arg Lys Asp Pro Asn Lys Leu
85 90 95

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

Leu Arg His Thr Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
115 120 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
130 135 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
145 150 155 160

Tyr Tyr Cys Gly Val Gly Ala Asp Arg Ala Tyr Gly Arg Asp Ile Val
165 170 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Ala Gly
180 185 190

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
Page 1

SEQUENCE LISTING

195

200

205

Cys Glu Gly Ile Ser Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
210 215 220

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

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
245 250 255

Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Lys Tyr Ile Glu Glu
260 265 270

Ala Ile Glu Lys Leu Ser Lys Arg His Gln Tyr His Ile Arg Ala Tyr
275 280 285

Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
290 295 300

Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
305 310 315 320

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

Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Phe Ser Val Thr
340 345 350

Glu Ala Leu Ile Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
355 360 365

Phe Gln Tyr Lys Asn
370

<210> 2
<211> 373
<212> PRT
<213> Canis lupus

<400> 2

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

Tyr Met Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
20 25 30

Ile Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
35 40 45

Ser Glu Pro Lys Gly Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly
50 55 60

SEQUENCE LISTING

Ser 65 Ser Thr Phe Gln 70 Ser Glu Gly Ser Asn 75 Ser Asp Met Tyr Leu Val 80
 Pro Ala Ala Met Phe 85 Arg Asp Pro Phe Arg 90 Lys Asp Pro Asn Lys 95 Leu
 Val Phe Cys Glu 100 Val Phe Lys Tyr Asn 105 Arg Lys Pro Ala Glu Thr Asn 110
 Leu Arg His 115 Thr Cys Lys Arg Ile 120 Met Asp Met Val Ser 125 Asn Gln His
 Pro Trp 130 Phe Gly Met Glu Gln 135 Glu Tyr Thr Leu Met 140 Gly Thr Asp Gly
 His 145 Pro Phe Gly Trp Pro 150 Ser Asn Gly Phe Pro 155 Gly Pro Gln Gly Pro 160
 Tyr Tyr Cys Gly Val 165 Gly Ala Asp Lys Ala 170 Tyr Gly Arg Asp Ile Val 175
 Glu Ala His Tyr 180 Arg Ala Cys Leu Tyr 185 Ala Gly Ile Lys Ile 190 Ala Gly
 Thr Asn Ala 195 Glu Val Met Pro Ala 200 Gln Trp Glu Phe Gln 205 Ile Gly Pro
 Cys Glu 210 Gly Ile Asp Met Gly 215 Asp His Leu Trp Val 220 Ala Arg Phe Ile
 Leu 225 His Arg Val Cys Glu 230 Asp Phe Gly Val Ile 235 Ala Thr Phe Asp Pro 240
 Lys Pro Ile Pro Gly 245 Asn Trp Asn Gly Ala 250 Gly Cys His Thr Asn 255 Phe
 Ser Thr Lys Ala 260 Met Arg Glu Glu Asn 265 Gly Leu Lys Tyr Ile 270 Glu Glu
 Ser Ile Glu 275 Lys Leu Ser Lys Arg 280 His Gln Tyr His Ile 285 Arg Ala Tyr
 Asp Pro 290 Lys Gly Gly Leu Asp 295 Asn Ala Arg Arg Leu 300 Thr Gly Phe His
 Glu Thr Ser Asn Ile 310 Asn Asp Phe Ser Ala Gly 315 Val Ala Asn Arg Gly 320
 Ala Ser Ile Arg Ile 325 Pro Arg Thr Val Gly 330 Gln Glu Lys Lys Gly 335 Tyr

SEQUENCE LISTING

Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Phe Ser Val Thr
340 345 350

Glu Ala Leu Ile Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
355 360 365

Phe Gln Tyr Lys Asn
370

<210> 3
<211> 373
<212> PRT
<213> Cricetulus griseus

<400> 3

Met Ala Thr Ser Ala Ser Ser His Leu Asn Lys Asn Ile Lys Gln Met
1 5 10 15

Tyr Leu Cys Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp
20 25 30

Val Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
35 40 45

Cys Glu Pro Lys Cys Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly
50 55 60

Ser Ser Thr Phe Gln Ser Glu Gly Ser Asn Ser Asp Met Tyr Leu Ser
65 70 75 80

Pro Val Ala Met Phe Arg Asp Pro Phe Arg Arg Asp Pro Asn Lys Leu
85 90 95

Val Phe Cys Glu Val Phe Lys Tyr Asn Arg Lys Pro Ala Glu Thr Asn
100 105 110

Leu Arg His Ser Cys Lys Arg Ile Met Asp Met Val Ser Asn Gln His
115 120 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Met Gly Thr Asp Gly
130 135 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
145 150 155 160

Tyr Tyr Cys Gly Val Gly Ala Asp Lys Ala Tyr Gly Arg Asp Ile Val
165 170 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Thr Gly
180 185 190

SEQUENCE LISTING

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Pro
195 200 205

Cys Glu Gly Ile Arg Met Gly Asp His Leu Trp Val Ala Arg Phe Ile
210 215 220

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

Lys Pro Ile Pro Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
245 250 255

Ser Thr Lys Ala Met Arg Glu Glu Asn Gly Leu Lys His Ile Glu Glu
260 265 270

Ala Ile Glu Lys Leu Ser Lys Arg His Arg Tyr His Ile Arg Ala Tyr
275 280 285

Asp Pro Lys Gly Gly Leu Asp Asn Ala Arg Arg Leu Thr Gly Phe His
290 295 300

Glu Thr Ser Asn Ile Asn Asp Phe Ser Ala Gly Val Ala Asn Arg Ser
305 310 315 320

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

Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Phe Ala Val Thr
340 345 350

Glu Ala Ile Val Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
355 360 365

Phe Gln Tyr Lys Asn
370

<210> 4
<211> 370
<212> PRT
<213> Saccharomyces cerevisiae

<400> 4

Met Ala Glu Ala Ser Ile Glu Lys Thr Gln Ile Leu Gln Lys Tyr Leu
1 5 10 15

Glu Leu Asp Gln Arg Gly Arg Ile Ile Ala Glu Tyr Val Trp Ile Asp
20 25 30

Gly Thr Gly Asn Leu Arg Ser Lys Gly Arg Thr Leu Lys Lys Arg Ile
35 40 45

SEQUENCE LISTING

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

SEQUENCE LISTING

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

Ser Asn Ile Asp Pro Tyr Leu Val Thr Gly Ile Met Cys Glu Thr Val
340 345 350

Cys Gly Ala Ile Asp Asn Ala Asp Met Thr Lys Glu Phe Glu Arg Glu
355 360 365

Ser Ser
370

<210> 5
<211> 373
<212> PRT
<213> Xenopus laevis

<400> 5

Met Ala Thr Ser Ala Ser Ala Gln Leu Ser Lys Ala Ile Lys Gln Met
1 5 10 15

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

Ile Asp Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp
35 40 45

Ser Glu Pro Lys Thr Ile Glu Asp Leu Pro Glu Trp Asn Phe Asp Gly
50 55 60

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

Pro Val Ala Met Phe Arg Asp Pro Phe Arg Arg Asp Pro Asn Lys Leu
85 90 95

Val Leu Cys Glu Val Leu Lys Tyr Asn Arg Lys Thr Ala Glu Thr Asn
100 105 110

Leu Arg His Thr Cys Asn Gln Ile Met Asp Met Val Gly Asn Glu His
115 120 125

Pro Trp Phe Gly Met Glu Gln Glu Tyr Thr Leu Leu Gly Met Asp Gly
130 135 140

His Pro Phe Gly Trp Pro Ser Asn Gly Phe Pro Gly Pro Gln Gly Pro
145 150 155 160

Tyr Tyr Cys Gly Val Gly Ala Asn Lys Ala Tyr Gly Arg Asp Ile Val
165 170 175

Glu Ala His Tyr Arg Ala Cys Leu Tyr Ala Gly Val Lys Ile Ala Gly
Page 7

SEQUENCE LISTING

180

185

190

Thr Asn Ala Glu Val Met Pro Ala Gln Trp Glu Phe Gln Ile Gly Thr
195 200 205

Cys Glu Gly Ile Asp Met Gly Asp His Leu Trp Ile Ala Arg Phe Ile
210 215 220

Leu His Arg Val Cys Glu Asp Phe Gly Ile Ile Val Ser Phe Asp Pro
225 230 235 240

Lys Pro Ile Thr Gly Asn Trp Asn Gly Ala Gly Cys His Thr Asn Phe
245 250 255

Ser Thr Lys Ser Met Arg Glu Glu Gly Gly Leu Lys His Ile Glu Glu
260 265 270

Ser Ile Glu Arg Leu Ser Lys Arg His Glu Tyr His Ile Arg Met Tyr
275 280 285

Asp Pro Arg Gly Gly Lys Asp Asn Ala Arg Arg Leu Thr Gly Phe His
290 295 300

Glu Thr Ser Ser Ile His Glu Phe Ser Ala Gly Val Ala Asn Arg Gly
305 310 315 320

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

Phe Glu Asp Arg Arg Pro Ser Ala Asn Cys Asp Pro Tyr Ala Val Thr
340 345 350

Glu Ala Val Ile Arg Thr Cys Leu Leu Asn Glu Thr Gly Asp Glu Pro
355 360 365

Leu Glu Tyr Lys Asn
370

<210> 6
<211> 354
<212> PRT
<213> Arabidopsis thaliana

<400> 6

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

Gly Lys Ile Ile Ala Glu Tyr Ile Trp Ile Gly Gly Ser Gly Met Asp
20 25 30

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

SEQUENCE LISTING

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

SEQUENCE LISTING

Thr Glu Lys Glu Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ala Ser
325 330 335

Asn Met Asp Pro Tyr Val Val Thr Ser Met Ile Ala Glu Thr Thr Ile
340 345 350

Leu Gly

<210> 7

<211> 369

<212> PRT

<213> Drosophila melanogaster

<400> 7

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

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

Gln Ala Thr Tyr Val Trp Ile Asp Gly Thr Gly Glu Asp Leu Arg Cys
35 40 45

Lys Asp Arg Thr Leu Asp Phe Ile Pro Gln Ser Pro Lys Glu Leu Pro
50 55 60

Val Trp Asn Tyr Asp Gly Ser Ser Cys Tyr Gln Ala Glu Gly Ser Asn
65 70 75 80

Ser Asp Thr Tyr Leu Tyr Pro Val Ala Ile Tyr Lys Asp Pro Phe Arg
85 90 95

Arg Gly Asn Asn Ile Leu Val Met Cys Asp Thr Tyr Lys Phe Asp Gly
100 105 110

Thr Pro Thr Asp Thr Asn Lys Arg Lys Thr Cys Leu Glu Val Ala Asn
115 120 125

Lys Cys Ala Ala Glu Glu Pro Trp Phe Gly Ile Glu Gln Glu Tyr Thr
130 135 140

Phe Leu Asp Phe Asp Gly His Pro Leu Gly Trp Pro Lys Asn Gly Phe
145 150 155 160

Pro Gly Pro Gln Gly Pro Tyr Tyr Cys Gly Val Gly Ala Asn Lys Val
165 170 175

Tyr Ala Arg Asp Ile Val Asp Ala His Tyr Arg Ala Cys Leu Tyr Ala
180 185 190

SEQUENCE LISTING

Gly Ile Lys Val Ser Gly Thr Asn Ala Glu Val Met Pro Ala Gln Trp
195 200 205

Glu Phe Gln Val Gly Pro Cys Glu Gly Ile Ser Ile Gly Asp Asp Leu
210 215 220

Trp Met Ala Arg Phe Leu Leu His Arg Ile Ser Glu Glu Phe Gly Ile
225 230 235 240

Val Ser Thr Leu Asp Pro Lys Pro Met Pro Gly Asp Trp Asn Gly Ala
245 250 255

Gly Ala His Thr Asn Val Ser Thr Lys Ala Met Arg Glu Asp Gly Gly
260 265 270

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

Arg His Ile Arg Ala Tyr Asp Pro Lys Gln Gly Gln Asp Asn Ala Arg
290 295 300

Arg Leu Thr Gly Lys His Glu Thr Ser Ser Ile Asn Asp Phe Ser Ala
305 310 315 320

Gly Val Ala Asn Arg Gly Cys Ser Ile Arg Ile Pro Arg Gly Val Asn
325 330 335

Asp Asp Gly Lys Gly Tyr Phe Glu Asp Arg Arg Pro Ser Ser Asn Cys
340 345 350

Asp Pro Tyr Ser Val Val Glu Ala Ile Leu Arg Thr Ile Cys Leu Asp
355 360 365

Glu

<210> 8
<211> 1122
<212> DNA
<213> Homo sapiens

<400> 8
atgaccacct ccgcctccag ccacctgaac aagggcatca aacaggtgta catgagcctg 60
ccccagggcg agaaggtgca ggccatgtac atctggatcg acggcaccgg cgagggactg 120
cgggtgcaaga ccagaaccct ggactccgag cctaagtgcg tggaagaact gcccgagtgg 180
aacttcgacg gtcctccac cctgcagtcc gagggctcca actccgacat gtacctggtg 240
cctgccgcca tggtccggga ccctttccgg aaggacccca acaagctggt gctgtgcbag 300
gtgttcaagt acaacagacg gcctgccgag acaaacctgc ggcatacctg caagcggatc 360
atggacatgg tgtccaacca gcacccttgg tttggcatgg aacaggagta caccctgatg 420

SEQUENCE LISTING

```

ggcaccgacg gccacccctt cggctggcct tctaacggct tccctggccc ccagggcccc 480
tactattgtg gcgtgggcg cgaccgggccc tacggcagag atatcgtgga agcccactac 540
cgggcctgcc tgtacgccgg agtgaagatc gccggcacca acgccgaagt gatgcccgcc 600
cagtgggagt tccagatcgg cccttgcgag ggcattctcca tgggcgatca cctgtgggtg 660
gcccggttca tcctgcacag agtgtgagag gacttcggcg tgatcgccac cttcgacccc 720
aagcccatcc ccggcaactg gaacggcgct ggctgccaca ccaacttctc caccaaggcc 780
atgcgggaag agaacggcct gaagtacatc gaggaagcca tcgagaagct gtccaagcgg 840
caccagtacc acatcagagc ctacgaccct aagggcgggc tggacaacgc cagaaggctg 900
accggctttc acgagacatc caacatcaac gacttctctg ccggcgtggc caacagatcc 960
gcctccatcc ggatccctag aaccgtgggc caggaaaaga agggctactt cgaggacaga 1020
cggccctccg ccaactgcga ccccttttagc gtgaccgagg ccctgatccg gacctgcctg 1080
ctgaacgaga caggcgacga gcccttccag tacaagaact ga 1122

```

```

<210> 9
<211> 1122
<212> DNA
<213> Canis lupus

```

```

<400> 9
atggccacct ccgcctccag ccacctgaac aagggcatca aacagggtgta catgagcctg 60
ccccagggcg agaagggtga ggccatgtac atctggatcg acggcaccgg cgagggactg 120
cgggtgaaga ccagaaccct ggactccgag cccaagggcg tggaagaact gcccgagtgg 180
aacttcgacg gtcctccac cttccagtcc gagggctcca actccgacat gtacctggtg 240
cctgccgcca tgttccggga ccttttccgg aaggacccca acaagctggt gttctgcgag 300
gtgttcaagt acaaccggaa gcccgccgag acaaacctgc ggcatacctg caagcggatc 360
atggacatgg tgtccaacca gcacccttgg tttggcatgg aacaggagta caccctgatg 420
ggcaccgacg gccacccctt cggctggcct tctaacggct tccctggccc ccagggcccc 480
tactattgtg gcgtgggcg cgacaaggcc tacggcagag acatcgtgga agcccactac 540
cgggcctgcc tgtacgccgg catcaagatc gctggcacca acgccgaagt gatgcccgcc 600
cagtgggagt tccagatcgg cccttgcgag ggcattcgaca tgggcgatca cctgtgggtg 660
gcccggttca tcctgcacag agtgtgagag gacttcggcg tgatcgccac cttcgacccc 720
aagcccatcc ccggcaactg gaacggcgct ggctgccaca ccaacttctc caccaaggcc 780
atgcgggaag agaacggcct gaagtacatc gaggaatcca tcgagaagct gtccaagcgg 840
caccagtacc acatccgggc ctacgacccc aagggcgggc tggataacgc cagacggctg 900
accggcttcc acgagacatc caacatcaac gacttctctg ccggcgtggc caacagaggc 960
gcctccatcc ggatcccccg gaccgtgggc caggaaaaga agggctactt cgaggacaga 1020
cggccctccg ccaactgcga ccccttttagc gtgaccgagg ccctgatccg gacctgcctg 1080

```

SEQUENCE LISTING

ctgaacgaga caggcgacga gcccttccag tacaagaact ga 1122

<210> 10
<211> 1122
<212> DNA
<213> *Cricetulus griseus*

<400> 10
atggccacct cagcaagttc ccacttgaac aaaaacatca agcaaagtga cttgtgcctg 60
ccccaggggtg agaaagtcca agccatgtat atctgggttg atggtactgg agaaggactg 120
cgctgcaaaa cccgcaccct ggactgtgag cccaagtgtg tagaagagtt acctgagtgg 180
aattttgatg gctctagtag ctttcagtct gagggctcca acagtgacat gtatctcagc 240
cctgttgcca tgtttcggga ccccttccgc agagatccca acaagctggg gttctgtgaa 300
gttttcaagt acaaccggaa gcctgcagag accaatttaa ggcactcgtg taaacggata 360
atggacatgg tgagcaacca gcaccctgg tttggaatgg aacaggagta tactctgatg 420
ggaacagatg ggcacccttt tggttggcct tccaatggct ttcctggggc ccaaggtccg 480
tattactgtg gtgtgggctg agacaaagcc tatggcaggg atatcgtgga ggctcactac 540
cgcgctgtg tgtatgtg ggtcaagatt acaggaacaa atgctgaggt catgcctgcc 600
cagtgggaat tccaaatagg accctgtgaa ggaatccgca tgggagatca tctctgggtg 660
gcccgtttca tcttgcatcg agtatgtgaa gactttgggg taatagcaac ctttgacccc 720
aagcccattc ctgggaactg gaatggtgca ggctgccata ccaacttttag caccaaggcc 780
atgcgggagg agaatggtct gaagcacatc gaggaggcca tcgagaaact aagcaagcgg 840
caccggtacc acattcgagc ctacgatccc aagggggggc tggacaatgc ccgtcgtctg 900
actgggttcc acgaaacgtc caacatcaac gacttttctg ctggtgtcgc caatcgcagt 960
gccagcatcc gcattccccg gactgtcggc caggagaaga aaggttactt tgaagaccgc 1020
cgcccctctg ccaattgtga cccctttgca gtgacagaag ccatcgtccg cacatgcctt 1080
ctcaatgaga ctggcgacga gcccttccaa taaaaaact aa 1122

<210> 11
<211> 1113
<212> DNA
<213> *Saccharomyces cerevisiae*

<400> 11
atggccgagg cctccatcga aaagaccag atcctgcaga agtacctgga actggaccag 60
cggggcagaa tcattgccga gtacgtgtgg atcgacggca cgggcaacct gcggtctaag 120
ggccggaccc tgaagaagcg gatcacctcc atcgaccagc tgcccagagt gaacttcgac 180
ggctcctcca ccaaccaggc ccctggccac gactccgaca tctacctgaa gcccgaggcc 240
tactaccccg accccttcag acggggcgac aacatcgtgg tgctggccgc ctgtacaac 300
aacgacggca ccccaacaa gttcaaccac cggcacgagg ccgccaagct gttcgccgcc 360
cacaaggacg aggaaatttg gttcggcctg gaacaggagt acaccctgtt cgatatgtac 420

SEQUENCE LISTING

gacgacgtgt acggctggcc caagggcggc tatcctgccc ctcagggccc ctactactgt	480
ggcgtgggcg ctggcaaggt gtacgccaga gacatgatcg aggcccacta ccgggcctgc	540
ctgtacgccg gcctggaaat ctccggcatc aacgccgaag tgatgccctc ccagtgggag	600
ttccaggtgg gaccctgcac cggcatcgac atgggcgacc agctgtggat ggcccggtag	660
ttcctgcacc ggggtggccga ggaattcggc atcaagatca gcttccaccc caagcccctg	720
aagggcgact ggaacggcgc tggatgccac gccaacgtgt ccaccaaaga gatgcggcag	780
cctggcggca ccaagtacat cgagcaggcc atcgagaagc tgtccaagcg gcacgccgag	840
cacatcaagc tgtacggctc cgacaacgac atgcggctga ccggcagaca cgagacagcc	900
tccatgaccg ctttctccag cggcgtggcc aaccggggct cctccatccg gatccctaga	960
agcgtggcca aagagggcta cggctacttc gaggacagac ggctgcctc caacatcgac	1020
ccctacctgg tgacaggcat catgtgagag acagtgtgag gcgccatcga caacgccgac	1080
atgaccaaag agttcgagag agagtctctc tga	1113

<210> 12
 <211> 1122
 <212> DNA
 <213> *Xenopus laevis*

<400> 12	
atggccacct ccgcctccgc ccagctgtcc aaggccatca agcagatgta cctggaactg	60
cctcagggcg acaaggtgca ggccatgtac atctggatcg acggcaccgg cgagggactg	120
cgggtgcaaga ccagaacctt ggactccgag cccaagacca tcgaggacct gcccgagtgg	180
aacttcgacg gtcctccac ccaccagtcc gagggctcca actccgacat gtacctgac	240
cccgtggcca tgttccggga ccctttccgg cgggacccca acaagctggg gctgtgagag	300
gtgctgaagt acaacagaaa gaccgccgag acaaacctgc ggcacacctg taaccagatc	360
atggacatgg tgggaaacga gcacccttgg tttggcatgg aacaggagta caccctgctg	420
ggcatggacg gccaccctt cggctggcct tccaacggct ttcctggccc ccagggcccc	480
tactattgag gcgtgggag caacaaggcc tacggcagag acatcgtgga agcccactac	540
cgggcctgcc tgtacgccg cgtgaagatc gccggcacca acgccgaagt gatgcccgcc	600
cagtgggagt tccagatcgg cacatgcgag ggcacgaca tgggagacca cctgtggatc	660
ggccggttca tcctgcacag agtgtgagag gacttcggca tcacgtgtc cttcgacccc	720
aagcccatca ccggcaactg gaacggcgct ggctgccaca ccaacttctc caccaagtcc	780
atgcgggaag agggcggcct gaagcacatc gaggaatcca tcgagcggct gtccaagcgg	840
cacgagtacc acatcaggat gtacgacccc agaggcggca aggacaacgc cagacggctg	900
accggcttcc acgagacatc ctccatccac gagttctctg ctggcgtggc caacagaggc	960
gcctccatcc ggatcccaag actggtggga caggaaaaga agggctactt cgaggacaga	1020
cggccctccg ccaactgcga cccttacgct gtgaccgagg ccgtgatccg gacctgcctg	1080
ctgaacgaga caggcgacga gccctggag tacaagaact ga	1122

SEQUENCE LISTING

<210> 13
 <211> 1065
 <212> DNA
 <213> *Arabidopsis thaliana*

<400> 13
 atgtccctgc tgtccgacct ggtgaacctg aacctgaccg acgccaccgg caagatcatt 60
 gccgagtaca tctggatcgg cggctccggc atggacatcc ggtctaaggc ccggaccctg 120
 cctggccctg tgaccgacct ctccaagctg cccaagtgga actacgacgg ctctccacc 180
 ggccaggccg ctggcgagga ctccgaagtg atcctgtatc cacaggccat cttcaaggac 240
 cctttccgga agggcaacaa catcctggtg atgtgcgacg cctacacccc tgccggcgac 300
 cccatcccta ccaacaagcg gcacaacgcc gccaaagtct tctcccaccc cgacgtggcc 360
 aaagaggaac cttggtacgg catcgagcag gactacaccc tgatgcagaa agacgtgaac 420
 tggcccatcg gctggcccgt gggcggctat cctggccctc agggacctta ctactcggc 480
 gtgggcgccg acaaggccat cggcagagac atcgtggacg cccactacaa ggcctgcctg 540
 tacgccggca tcggcatctc tggcatcaac ggcgaagtga tgcccggcca gtgggagttc 600
 cagggtgggac ccgtggaagg catctcctcc ggcgatcagg tgtgggtggc cagatacctg 660
 ctggaacgga tcaccgagat ctccggcgtg atcgtgtcct tcgaccccaa gcccgtgccc 720
 ggcgattgga atggcgctgg cgccactgc aactactcca ccaagaccat gcggaacgac 780
 ggcggcctgg aagtgatcaa gaaggctatc ggcaagctgc agctgaagca caaagagcat 840
 atcgccgcct acggcgaggg caacgagcgg agactgaccg gcaagcacga gacagccgac 900
 atcaacacct tcagctgggg cgtggccaac aggggcgctt ctgtgcgcggt gggccgggat 960
 accgagaaaag agggcaaggg ctacttcgag gacagacggc ctgcctccaa catggacccc 1020
 tacgtggtga catccatgat cgccgagaca accatcctgg gctga 1065

<210> 14
 <211> 1110
 <212> DNA
 <213> *Drosophila melanogaster*

<400> 14
 atgtccgccc ggatcctgga agattccccc aacgcccgga tcaacaagac catcctggac 60
 agatacctga gcctgccact gcaggaaaac atcgtccagg ccacctacgt gtggatcgac 120
 ggcacaggcg aggacctgcg gtgcaaggac cggaccctgg acttcatccc ccagtccccc 180
 aaagaactgc ccgtgtggaa ctacgacggc tccagctgct accaggccga gggctccaac 240
 tccgacacct acctgtacct cgtggccatc tacaaggacc ctttcagacg gggcaacaac 300
 atcctggtga tgtgcgacac ctacaagttc gatggcacc caccgacac caacaagaga 360
 aagacctgcc tggaagtggc caacaagtgt gccgccgagg aaccttggtt tggcatcgag 420
 caggagtaca ctttcctgga cttcgacggc cccccctgg gctggcccaa gaatggcttt 480
 cctggacccc agggccccta ctattgcggc gtgggcgcca acaaggtgta cgccagagac 540

SEQUENCE LISTING

atcgtggacg	cccactaccg	ggcctgcctg	tacgccggaa	tcaaggtgtc	cggcaccaac	600
gccgaagtga	tgcccgccca	gtgggagttc	caggtgggac	cttgcgaggg	catctccatc	660
ggcgacgacc	tgtggatggc	ccggttcctg	ctgcaccgga	tctccgagga	attcggcatac	720
gtgtccaccc	tggaccccaa	gcccataccc	ggcgattgga	atggcgctgg	cgcccacacc	780
aacgtgtcca	ccaaggccat	gagagaggac	ggcggcatcc	gggacatcga	gaaggccgtg	840
gccaagctgt	ccaagtgccca	cgagcggcac	atccgggcct	acgaccctaa	gcagggccag	900
gacaacgcca	gacggctgac	cggcaagcac	gagacatcct	ccatcaacga	cttctctgcc	960
ggcgtggcca	accgggggctg	ctccatcaga	atccctcggg	gcgtgaacga	cgacggcaag	1020
ggctacttcg	aggacagacg	gccctcctcc	aactgcgacc	cttactccgt	ggtggaagcc	1080
atcctgcgga	ccatctgcct	ggacgagtga				1110