SEQUENCE LISTING

<110> SELEXIS S.A.

<120> PRODUCTS AND METHODS FOR ENHANCED TRANSGENE EXPRESSION AND PROCESSING

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atatatatat atatatatat atatatatat atatgacaca tgatctcact ctgttgccta 600

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aacaaaacta agaagaccaa agcagcagca gcagcagcag cagcagcacc tgccgcagca 360

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35 40 45

Phe Glu Pro Ala Asp Asn Lys Cys Leu Leu Arg Ala Thr Asp Gly Lys
50 55 60

Lys Lys Ile Ser Thr Val Val Ser Ser Lys Glu Val Asn Lys Phe Gln
65 70 75 80

Met Ala Tyr Ser Asn Leu Leu Arg Ala Asn Met Asp Gly Leu Lys Lys
85 90 95

Arg Asp Lys Lys Asn Lys Thr Lys Lys Thr Lys Ala Ala Ala Ala Ala
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35 40 45

Pro Leu Phe Gly Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp
50 55 60

Met Arg Val Ile Leu Ala Ser Asn Arg Gly Thr Leu Met Glu Leu Gly
65 70 75 80

Ile Ser Pro Ile Val Thr Ser Gly Leu Ile Met Gln Leu Leu Ala Gly
85 90 95

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

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

Ile Val Tyr Val Met Thr Gly Met Tyr Gly Asp Pro Ser Glu Met Gly
130 135 140

Ala Gly Ile Cys Leu Leu Ile Thr Ile Gln Leu Phe Val Ala Gly Leu
145 150 155 160

Ile Val Leu Leu Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly Leu Gly
165 170 175

Ser Gly Ile Ser Leu Phe Ile Ala Thr Asn Ile Cys Glu Thr Ile Val
180 185 190

Trp Lys Ala Phe Ser Pro Thr Thr Val Asn Thr Gly Arg Gly Met Glu
195 200 205

Phe Glu Gly Ala Ile Ile Ala Leu Phe His Leu Leu Ala Thr Arg Thr
210 215 220

Asp Lys Val Arg Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn Leu Pro
225 230 235 240

Asn Leu Met Asn Leu Ile Ala Thr Ile Phe Val Phe Ala Val Val Ile

245 250 255

Tyr Phe Gln Gly Phe Arg Val Asp Leu Pro Ile Lys Ser Ala Arg Tyr
260 265 270

Arg Gly Gln Tyr Asn Thr Tyr Pro Ile Lys Leu Phe Tyr Thr Ser Asn
275 280 285

Ile Pro Ile Ile Leu Gln Ser Ala Leu Val Ser Asn Leu Tyr Val Ile
290 295 300

Ser Gln Met Leu Ser Ala Arg Phe Ser Gly Asn Leu Leu Val Ser Leu
305 310 315 320

Leu Gly Thr Trp Ser Asp Thr Ser Ser Gly Gly Pro Ala Arg Ala Tyr
325 330 335

Pro Val Gly Gly Leu Cys Tyr Tyr Leu Ser Pro Pro Glu Ser Phe Gly
340 345 350

Ser Val Leu Glu Asp Pro Val His Ala Val Val Tyr Ile Val Phe Met
355 360 365

Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr Trp Ile Glu Val Ser Gly
370 375 380

Ser Ser Ala Lys Asp Val Ala Lys Gln Leu Lys Glu Gln Gln Met Val
385 390 395 400

Met Arg Gly His Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr
405 410 415

Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser
420 425 430

Val Leu Ala Asp Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu
435 440 445

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gaagattcac ctgggctcaa agttggccct gttccagtat tggttatgag tcttctgttc 240

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20 25 30

Gln Arg Lys Asn Ala Ser Cys Gly Thr Arg Ser Ala Gly Arg Thr Thr
35 40 45

Ser Ala Gly Thr Gly Gly Met Trp Arg Phe Tyr Thr Glu Asp Ser Pro
50 55 60

Gly Leu Lys Val Gly Pro Val Pro Val Leu Val Met Ser Leu Leu Phe
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<400> 19

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Phe Gln Lys Ile Ala Met Ala Thr Ala Ile Gly Phe Ala Ile Met Gly
35 40 45

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caaatggcca aaatgatgga tcctagggtt cttcatcaca tgggtggtat ggcaggactt 1440

cagtcaatga tgaggcagtt tcaacagggt gctgctggca acatgaaagg catgatggga 1500

ttcaataata tgtaa 1515

<210> 21
<211> 504
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hSRP54

<400> 21

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

Leu Ser Asn Ala Thr Ile Ile Asn Glu Glu Val Leu Asn Ala Met Leu
20 25 30

Lys Glu Val Cys Thr Ala Leu Leu Glu Ala Asp Val Asn Ile Lys Leu
35 40 45

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

Met Ala Ser Gly Leu Asn Lys Arg Lys Met Ile Gln His Ala Val Phe
65 70 75 80

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

Thr Lys Gly Lys Gln Asn Val Ile Met Phe Val Gly Leu Gln Gly Ser
100 105 110

Gly Lys Thr Thr Thr Cys Ser Lys Leu Ala Tyr Tyr Tyr Gln Arg Lys
115 120 125

Gly Trp Lys Thr Cys Leu Ile Cys Ala Asp Thr Phe Arg Ala Gly Ala
130 135 140

Phe Asp Gln Leu Lys Gln Asn Ala Thr Lys Ala Arg Ile Pro Phe Tyr
145 150 155 160

Gly Ser Tyr Thr Glu Met Asp Pro Val Ile Ile Ala Ser Glu Gly Val
165 170 175

Glu Lys Phe Lys Asn Glu Asn Phe Glu Ile Ile Ile Val Asp Thr Ser
180 185 190

Gly Arg His Lys Gln Glu Asp Ser Leu Phe Glu Glu Met Leu Gln Val
195 200 205

Ala Asn Ala Ile Gln Pro Asp Asn Ile Val Tyr Val Met Asp Ala Ser
210 215 220

Ile Gly Gln Ala Cys Glu Ala Gln Ala Lys Ala Phe Lys Asp Lys Val
225 230 235 240

Asp Val Ala Ser Val Ile Val Thr Lys Leu Asp Gly His Ala Lys Gly
245 250 255

Gly Gly Ala Leu Ser Ala Val Ala Ala Thr Lys Ser Pro Ile Ile Phe
260 265 270

Ile Gly Thr Gly Glu His Ile Asp Asp Phe Glu Pro Phe Lys Thr Gln
275 280 285

Pro Phe Ile Ser Lys Leu Leu Gly Met Gly Asp Ile Glu Gly Leu Ile
290 295 300

Asp Lys Val Asn Glu Leu Lys Leu Asp Asp Asn Glu Ala Leu Ile Glu
305 310 315 320

Lys Leu Lys His Gly Gln Phe Thr Leu Arg Asp Met Tyr Glu Gln Phe
325 330 335

Gln Asn Ile Met Lys Met Gly Pro Phe Ser Gln Ile Leu Gly Met Ile
340 345 350

Pro Gly Phe Gly Thr Asp Phe Met Ser Lys Gly Asn Glu Gln Glu Ser
355 360 365

Met Ala Arg Leu Lys Lys Leu Met Thr Ile Met Asp Ser Met Asn Asp
370 375 380

Gln Glu Leu Asp Ser Thr Asp Gly Ala Lys Val Phe Ser Lys Gln Pro
385 390 395 400

Gly Arg Ile Gln Arg Val Ala Arg Gly Ser Gly Val Ser Thr Arg Asp
405 410 415

Val Gln Glu Leu Leu Thr Gln Tyr Thr Lys Phe Ala Gln Met Val Lys
420 425 430

Lys Met Gly Gly Ile Lys Gly Leu Phe Lys Gly Gly Asp Met Ser Lys
435 440 445

Asn Val Ser Gln Ser Gln Met Ala Lys Leu Asn Gln Gln Met Ala Lys
450 455 460

Met Met Asp Pro Arg Val Leu His His Met Gly Gly Met Ala Gly Leu
465 470 475 480

Gln Ser Met Met Arg Gln Phe Gln Gln Gly Ala Ala Gly Asn Met Lys
485 490 495

Gly Met Met Gly Phe Asn Asn Met
500

<210> 22
<211> 249
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hSRP9

<400> 22
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gaccctatga aggcacgtgt ggttctcaaa tataggcatt ctgatgggaa cttgtgtgtt 120

aaagtaacag atgatttagt tagacagtgt cttgctctat tgctcaggct gcagtgcagt 180

ggcatgatca tagctcactg catcctcgac ctcctgggct caagcggtcc tcttgcttca 240

gcctcctga 249

<210> 23
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hSRP9

<400> 23

Met Pro Gln Tyr Gln Thr Trp Glu Glu Phe Ser Arg Ala Ala Glu Lys

1 5 10 15

Leu Tyr Leu Ala Asp Pro Met Lys Ala Arg Val Val Leu Lys Tyr Arg
20 25 30

His Ser Asp Gly Asn Leu Cys Val Lys Val Thr Asp Asp Leu Val Arg
35 40 45

Gln Cys Leu Ala Leu Leu Leu Arg Leu Gln Cys Ser Gly Met Ile Ile
50 55 60

Ala His Cys Ile Leu Asp Leu Leu Gly Ser Ser Gly Pro Leu Ala Ser
65 70 75 80

Ala Ser

<210> 24
<211> 1917
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hSRPRalpha

<400> 24
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gttagcgact catgcaccgg acccgttaac gcgttgattc gttccgtgct gctgcaggaa 120

cggggaggta acaactcctt cacccatgag gcactcacac tcaagtataa actggacaac 180

cagtttgagc tggtgtttgt ggttggtttt cagaagatcc tgacactgac atatgtagac 240

aaattgatag atgacgtgca tcggctgttt cgggacaagt accgcacaga gatccaacag 300

caaagtgctt taagtttatt aaatggcact tttgatttcc aaaatgactt cctgcggctc 360

cttcgtgaag cagaggagag cagtaagatc cgtgctccca ctaccatgaa gaaatttgaa 420

gattctgaaa aggccaagaa acctgtgagg tccatgattg agacacgggg ggaaaagccc 480

aaggaaaaag caaagaatag caaaaaaaag ggggccaaga aggaaggttc tgatggtcct 540

ttggctacca gcaaaccagt ccctgcagaa aagtcaggtc ttccagtggg tcctgagaac 600

ggagtagaac tttccaaaga ggagctgatc cgcaggaagc gcgaggagtt cattcagaag 660

catgggaggg gtatggagaa gtccaacaag tccacgaagt cagatgctcc aaaggagaag 720

ggcaaaaaag caccccgggt gtgggaactg ggtggctgtg ctaacaaaga agtgttggat 780

tacagtactc ccaccaccaa tggaacccct gaggctgcct tgtctgagga catcaacctg 840

attcgaggga ctgggtctgg ggggcagctt caggatctgg actgcagcag ctctgatgac 900

gaaggggctg ctcaaaactc taccaaacct agtgcgacca agggaacact gggtggcatg 960

tttggtatgc tgaagggcct tgtgggttca aagagcttga gtcgtgaaga catggaatct 1020

gtgctggaca agatgcgtga tcatctcatt gctaagaacg tggctgcaga cattgccgtc 1080

cagctctgtg aatctgttgc caacaagttg gaagggaagg tgatggggac gttcagcacg 1140

gtgacttcca cagtaaagca agccctacag gagtccctgg tgcagattct gcagccacag 1200

cgtcgtgtag acatgctccg ggacatcatg gatgcccagc gtcgccagcg cccttatgtc 1260

gtcaccttct gcggcgttaa tggagtgggg aaatctacta atcttgccaa gatttccttc 1320

tggttgttag agaatggctt cagtgtcctc attgctgcct gtgatacatt tcgtgctggg 1380

gccgtggagc agctgcgtac acacacccgg cgtttgagtg ccctacaccc tccagagaag 1440

catggtggcc gcaccatggt gcagttgttt gaaaagggct atggcaagga tgctgctggc 1500

attgccatgg aagccattgc ttttgcacgt aaccaaggct ttgacgtggt gctggtggac 1560

acggcaggcc gcatgcaaga caatgcccct ctgatgactg ccctggccaa actcattact 1620

gtcaatacac ctgatttggt gctgtttgta ggagaagcct tagtaggcaa tgaagccgtg 1680

gaccagctgg tcaagttcaa cagagccttg gctgaccatt ctatggctca gacacctcgg 1740

ctcattgatg gcattgttct taccaaattt gataccattg atgacaaggt gggagctgct 1800

atttctatga cgtacatcac aagcaaaccc atcgtctttg tgggcaccgg ccagacctac 1860

tgtgacctac gcagcctcaa tgccaaggct gtggtggctg ccctcatgaa ggcttaa 1917

<210> 25
<211> 638
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hSRPRalpha

<400> 25

Met Leu Asp Phe Phe Thr Ile Phe Ser Lys Gly Gly Leu Val Leu Trp
1 5 10 15

Cys Phe Gln Gly Val Ser Asp Ser Cys Thr Gly Pro Val Asn Ala Leu
20 25 30

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

His Glu Ala Leu Thr Leu Lys Tyr Lys Leu Asp Asn Gln Phe Glu Leu
50 55 60

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

Lys Leu Ile Asp Asp Val His Arg Leu Phe Arg Asp Lys Tyr Arg Thr
85 90 95

Glu Ile Gln Gln Gln Ser Ala Leu Ser Leu Leu Asn Gly Thr Phe Asp

100 105 110

Phe Gln Asn Asp Phe Leu Arg Leu Leu Arg Glu Ala Glu Glu Ser Ser
115 120 125

Lys Ile Arg Ala Pro Thr Thr Met Lys Lys Phe Glu Asp Ser Glu Lys
130 135 140

Ala Lys Lys Pro Val Arg Ser Met Ile Glu Thr Arg Gly Glu Lys Pro
145 150 155 160

Lys Glu Lys Ala Lys Asn Ser Lys Lys Lys Gly Ala Lys Lys Glu Gly
165 170 175

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

Gly Leu Pro Val Gly Pro Glu Asn Gly Val Glu Leu Ser Lys Glu Glu
195 200 205

Leu Ile Arg Arg Lys Arg Glu Glu Phe Ile Gln Lys His Gly Arg Gly
210 215 220

Met Glu Lys Ser Asn Lys Ser Thr Lys Ser Asp Ala Pro Lys Glu Lys
225 230 235 240

Gly Lys Lys Ala Pro Arg Val Trp Glu Leu Gly Gly Cys Ala Asn Lys
245 250 255

Glu Val Leu Asp Tyr Ser Thr Pro Thr Thr Asn Gly Thr Pro Glu Ala
260 265 270

Ala Leu Ser Glu Asp Ile Asn Leu Ile Arg Gly Thr Gly Ser Gly Gly
275 280 285

Gln Leu Gln Asp Leu Asp Cys Ser Ser Ser Asp Asp Glu Gly Ala Ala
290 295 300

Gln Asn Ser Thr Lys Pro Ser Ala Thr Lys Gly Thr Leu Gly Gly Met
305 310 315 320

Phe Gly Met Leu Lys Gly Leu Val Gly Ser Lys Ser Leu Ser Arg Glu
325 330 335

Asp Met Glu Ser Val Leu Asp Lys Met Arg Asp His Leu Ile Ala Lys
340 345 350

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

Lys Leu Glu Gly Lys Val Met Gly Thr Phe Ser Thr Val Thr Ser Thr

370 375 380

Val Lys Gln Ala Leu Gln Glu Ser Leu Val Gln Ile Leu Gln Pro Gln
385 390 395 400

Arg Arg Val Asp Met Leu Arg Asp Ile Met Asp Ala Gln Arg Arg Gln
405 410 415

Arg Pro Tyr Val Val Thr Phe Cys Gly Val Asn Gly Val Gly Lys Ser
420 425 430

Thr Asn Leu Ala Lys Ile Ser Phe Trp Leu Leu Glu Asn Gly Phe Ser
435 440 445

Val Leu Ile Ala Ala Cys Asp Thr Phe Arg Ala Gly Ala Val Glu Gln
450 455 460

Leu Arg Thr His Thr Arg Arg Leu Ser Ala Leu His Pro Pro Glu Lys
465 470 475 480

His Gly Gly Arg Thr Met Val Gln Leu Phe Glu Lys Gly Tyr Gly Lys
485 490 495

Asp Ala Ala Gly Ile Ala Met Glu Ala Ile Ala Phe Ala Arg Asn Gln
500 505 510

Gly Phe Asp Val Val Leu Val Asp Thr Ala Gly Arg Met Gln Asp Asn
515 520 525

Ala Pro Leu Met Thr Ala Leu Ala Lys Leu Ile Thr Val Asn Thr Pro
530 535 540

Asp Leu Val Leu Phe Val Gly Glu Ala Leu Val Gly Asn Glu Ala Val
545 550 555 560

Asp Gln Leu Val Lys Phe Asn Arg Ala Leu Ala Asp His Ser Met Ala
565 570 575

Gln Thr Pro Arg Leu Ile Asp Gly Ile Val Leu Thr Lys Phe Asp Thr
580 585 590

Ile Asp Asp Lys Val Gly Ala Ala Ile Ser Met Thr Tyr Ile Thr Ser
595 600 605

Lys Pro Ile Val Phe Val Gly Thr Gly Gln Thr Tyr Cys Asp Leu Arg
610 615 620

Ser Leu Asn Ala Lys Ala Val Val Ala Ala Leu Met Lys Ala
625 630 635

<210> 26

<211> 816
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hSRPRbeta

<400> 26
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gtggtggcgg ttcttgcggt gctgctgacg ctagtcttct ggaagttaat ccggagcaga 180
aggagcagtc agagagctgt tcttcttgtt ggcctttgtg attccgggaa aacgttgctc 240
tttgtcaggt tgttaacagg cctttataga gacactcaga cgtccattac tgacagctgt 300
gctgtataca gagtcaacaa taacaggggc aatagtctga ccttgattga ccttcccggc 360
catgagagtt tgaggcttca gttcttagag cggtttaagt cttcagccag ggctattgtg 420
tttgttgtgg atagtgcagc attccagcga gaggtgaaag atgtggctga gtttctgtat 480
caagtcctca ttgacagtat gggtctgaag aatacaccat cattcttaat agcctgcaat 540
aagcaagata ttgcaatggc aaaatcagca aagttaattc aacagcagct ggagaaagaa 600
ctcaacacct tacgagttac ccgttctgct gcccccagca cactggacag ttccagcact 660
gcccctgctc agctggggaa gaaaggcaaa gagtttgaat tctcacagtt gcccctcaaa 720
gtggagttcc tggagtgcag tgccaagggt ggaagagggg acgtgggctc tgctgacatc 780
caggacttgg agaaatggct ggctaaaatt gcctga 816

<210> 27
<211> 271
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hSRPRbeta

<400> 27

Met Ala Ser Ala Asp Ser Arg Arg Val Ala Asp Gly Gly Gly Ala Gly
1 5 10 15

Gly Thr Phe Gln Pro Tyr Leu Asp Thr Leu Arg Gln Glu Leu Gln Gln
20 25 30

Thr Asp Pro Thr Leu Leu Ser Val Val Val Ala Val Leu Ala Val Leu
35 40 45

Leu Thr Leu Val Phe Trp Lys Leu Ile Arg Ser Arg Arg Ser Ser Gln
50 55 60

Arg Ala Val Leu Leu Val Gly Leu Cys Asp Ser Gly Lys Thr Leu Leu

65 70 75 80

Phe Val Arg Leu Leu Thr Gly Leu Tyr Arg Asp Thr Gln Thr Ser Ile
85 90 95

Thr Asp Ser Cys Ala Val Tyr Arg Val Asn Asn Asn Arg Gly Asn Ser
100 105 110

Leu Thr Leu Ile Asp Leu Pro Gly His Glu Ser Leu Arg Leu Gln Phe
115 120 125

Leu Glu Arg Phe Lys Ser Ser Ala Arg Ala Ile Val Phe Val Val Asp
130 135 140

Ser Ala Ala Phe Gln Arg Glu Val Lys Asp Val Ala Glu Phe Leu Tyr
145 150 155 160

Gln Val Leu Ile Asp Ser Met Gly Leu Lys Asn Thr Pro Ser Phe Leu
165 170 175

Ile Ala Cys Asn Lys Gln Asp Ile Ala Met Ala Lys Ser Ala Lys Leu
180 185 190

Ile Gln Gln Gln Leu Glu Lys Glu Leu Asn Thr Leu Arg Val Thr Arg
195 200 205

Ser Ala Ala Pro Ser Thr Leu Asp Ser Ser Ser Thr Ala Pro Ala Gln
210 215 220

Leu Gly Lys Lys Gly Lys Glu Phe Glu Phe Ser Gln Leu Pro Leu Lys
225 230 235 240

Val Glu Phe Leu Glu Cys Ser Ala Lys Gly Gly Arg Gly Asp Val Gly
245 250 255

Ser Ala Asp Ile Gln Asp Leu Glu Lys Trp Leu Ala Lys Ile Ala
260 265 270

<210> 28
<211> 1779
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hCANX

<400> 28
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catgatggac atgatgatga tgtgattgat attgaggatg accttgacga tgtcattgaa 120

gaggtagaag actcaaaacc agataccact gctcctcctt catctcccaa ggttacttac 180

aaagctccag ttccaacagg ggaagtatat tttgctgatt cttttgacag aggaactctg 240

tcagggtgga ttttatccaa agccaagaaa gacgataccg atgatgaaat tgccaaatat 300

gatggaaagt gggaggtaga ggaaatgaag gagtcaaagc ttccaggtga taaaggactt 360

gtgttgatgt ctcgggccaa gcatcatgcc atctctgcta aactgaacaa gcccttcctg 420

tttgacacca agcctctcat tgttcagtat gaggttaatt tccaaaatgg aatagaatgt 480

ggtggtgcct atgtgaaact gctttctaaa acaccagaac tcaacctgga tcagttccat 540

gacaagaccc cttatacgat tatgtttggt ccagataaat gtggagagga ctataaactg 600

cacttcatct tccgacacaa aaaccccaaa acgggtatct atgaagaaaa acatgctaag 660

aggccagatg cagatctgaa gacctatttt actgataaga aaacacatct ttacacacta 720

atcttgaatc cagataatag ttttgaaata ctggttgacc aatctgtggt gaatagtgga 780

aatctgctca atgacatgac tcctcctgta aatccttcac gtgaaattga ggacccagaa 840

gaccggaagc ccgaggattg ggatgaaaga ccaaaaatcc cagatccaga agctgtcaag 900

ccagatgact gggatgaaga tgcccctgct aagattccag atgaagaggc cacaaaaccc 960

gaaggctggt tagatgatga gcctgagtac gtacctgatc cagacgcaga gaaacctgag 1020

gattgggatg aagacatgga tggagaatgg gaggctcctc agattgccaa ccctagatgt 1080

gagtcagctc ctggatgtgg tgtctggcag cgacctgtga ttgacaaccc caattataaa 1140

ggcaaatgga agcctcctat gattgacaat cccagttacc agggaatctg gaaacccagg 1200

aaaataccaa atccagattt ctttgaagat ctggaacctt tcagaatgac tccttttagt 1260

gctattggtt tggagctgtg gtccatgacc tctgacattt tttttgacaa ctttatcatt 1320

tgtgctgatc gaagaatagt tgatgattgg gccaatgatg gatggggcct gaagaaagct 1380

gctgatgggg ctgctgagcc aggcgttgtg gggcagatga tcgaggcagc tgaagagcgc 1440

ccgtggctgt gggtagtcta tattctaact gtagcccttc ctgtgttcct ggttatcctc 1500

ttctgctgtt ctggaaagaa acagaccagt ggtatggagt ataagaaaac tgatgcacct 1560

caaccggatg tgaaggaaga ggaagaagag aaggaagagg aaaaggacaa gggagatgag 1620

gaggaggaag gagaagagaa acttgaagag aaacagaaaa gtgatgctga agaagatggt 1680

ggcactgtca gtcaagagga ggaagacaga aaacctaaag cagaggagga tgaaattttg 1740

aacagatcac caagaaacag aaagccacga agagagtga 1779

<210> 29
<211> 592
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hCANX

<400> 29

Met Glu Gly Lys Trp Leu Leu Cys Met Leu Leu Val Leu Gly Thr Ala

1 5 10 15

Ile Val Glu Ala His Asp Gly His Asp Asp Asp Val Ile Asp Ile Glu
20 25 30

Asp Asp Leu Asp Asp Val Ile Glu Glu Val Glu Asp Ser Lys Pro Asp
35 40 45

Thr Thr Ala Pro Pro Ser Ser Pro Lys Val Thr Tyr Lys Ala Pro Val
50 55 60

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

Ser Gly Trp Ile Leu Ser Lys Ala Lys Lys Asp Asp Thr Asp Asp Glu
85 90 95

Ile Ala Lys Tyr Asp Gly Lys Trp Glu Val Glu Glu Met Lys Glu Ser
100 105 110

Lys Leu Pro Gly Asp Lys Gly Leu Val Leu Met Ser Arg Ala Lys His
115 120 125

His Ala Ile Ser Ala Lys Leu Asn Lys Pro Phe Leu Phe Asp Thr Lys
130 135 140

Pro Leu Ile Val Gln Tyr Glu Val Asn Phe Gln Asn Gly Ile Glu Cys
145 150 155 160

Gly Gly Ala Tyr Val Lys Leu Leu Ser Lys Thr Pro Glu Leu Asn Leu
165 170 175

Asp Gln Phe His Asp Lys Thr Pro Tyr Thr Ile Met Phe Gly Pro Asp
180 185 190

Lys Cys Gly Glu Asp Tyr Lys Leu His Phe Ile Phe Arg His Lys Asn
195 200 205

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

Asp Leu Lys Thr Tyr Phe Thr Asp Lys Lys Thr His Leu Tyr Thr Leu
225 230 235 240

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

Val Asn Ser Gly Asn Leu Leu Asn Asp Met Thr Pro Pro Val Asn Pro
260 265 270

Ser Arg Glu Ile Glu Asp Pro Glu Asp Arg Lys Pro Glu Asp Trp Asp

275 280 285

Glu Arg Pro Lys Ile Pro Asp Pro Glu Ala Val Lys Pro Asp Asp Trp
290 295 300

Asp Glu Asp Ala Pro Ala Lys Ile Pro Asp Glu Glu Ala Thr Lys Pro
305 310 315 320

Glu Gly Trp Leu Asp Asp Glu Pro Glu Tyr Val Pro Asp Pro Asp Ala
325 330 335

Glu Lys Pro Glu Asp Trp Asp Glu Asp Met Asp Gly Glu Trp Glu Ala
340 345 350

Pro Gln Ile Ala Asn Pro Arg Cys Glu Ser Ala Pro Gly Cys Gly Val
355 360 365

Trp Gln Arg Pro Val Ile Asp Asn Pro Asn Tyr Lys Gly Lys Trp Lys
370 375 380

Pro Pro Met Ile Asp Asn Pro Ser Tyr Gln Gly Ile Trp Lys Pro Arg
385 390 395 400

Lys Ile Pro Asn Pro Asp Phe Phe Glu Asp Leu Glu Pro Phe Arg Met
405 410 415

Thr Pro Phe Ser Ala Ile Gly Leu Glu Leu Trp Ser Met Thr Ser Asp
420 425 430

Ile Phe Phe Asp Asn Phe Ile Ile Cys Ala Asp Arg Arg Ile Val Asp
435 440 445

Asp Trp Ala Asn Asp Gly Trp Gly Leu Lys Lys Ala Ala Asp Gly Ala
450 455 460

Ala Glu Pro Gly Val Val Gly Gln Met Ile Glu Ala Ala Glu Glu Arg
465 470 475 480

Pro Trp Leu Trp Val Val Tyr Ile Leu Thr Val Ala Leu Pro Val Phe
485 490 495

Leu Val Ile Leu Phe Cys Cys Ser Gly Lys Lys Gln Thr Ser Gly Met
500 505 510

Glu Tyr Lys Lys Thr Asp Ala Pro Gln Pro Asp Val Lys Glu Glu Glu
515 520 525

Glu Glu Lys Glu Glu Glu Lys Asp Lys Gly Asp Glu Glu Glu Glu Gly
530 535 540

Glu Glu Lys Leu Glu Glu Lys Gln Lys Ser Asp Ala Glu Glu Asp Gly

545 550 555 560

Gly Thr Val Ser Gln Glu Glu Glu Asp Arg Lys Pro Lys Ala Glu Glu
565 570 575

Asp Glu Ile Leu Asn Arg Ser Pro Arg Asn Arg Lys Pro Arg Arg Glu
580 585 590

<210> 30
<211> 972
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hUCP4

<400> 30
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agcaaattcc tactgtccgg ctgcgcggct accgtggccg agctagcaac ctttcccctg 120

gatctcacaa aaactcgact ccaaatgcaa ggagaagcag ctcttgctcg gttgggagac 180

ggtgcaagag aatctgcccc ctatagggga atggtgcgca cagccctagg gatcattgaa 240

gaggaaggct ttctaaagct ttggcaagga gtgacacccg ccatttacag acacgtagtg 300

tattctggag gtcgaatggt cacatatgaa catctccgag aggttgtgtt tggcaaaagt 360

gaagatgagc attatcccct ttggaaatca gtcattggag ggatgatggc tggtgttatt 420

ggccagtttt tagccaatcc aactgaccta gtgaaggttc agatgcaaat ggaaggaaaa 480

aggaaactgg aaggaaaacc attgcgattt cgtggtgtac atcatgcatt tgcaaaaatc 540

ttagctgaag gaggaatacg agggctttgg gcaggctggg tacccaatat acaaagagca 600

gcactggtga atatgggaga tttaaccact tatgatacag tgaaacacta cttggtattg 660

aatacaccac ttgaggacaa tatcatgact cacggtttat caagtttatg ttctggactg 720

gtagcttcta ttctgggaac accagccgat gtcatcaaaa gcagaataat gaatcaacca 780

cgagataaac aaggaagggg acttttgtat aaatcatcga ctgactgctt gattcaggct 840

gttcaaggtg aaggattcat gagtctatat aaaggctttt taccatcttg gctgagaatg 900

acccccttggt caatggtgtt ctggcttact tatgaaaaaa tcagagagat gagtggagtc 960

agtccatttt aa 972

<210> 31
<211> 323
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hUCP4

<400> 31

Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln Arg
1 5 10 15

Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala Thr Val
20 25 30

Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr Arg Leu Gln
35 40 45

Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp Gly Ala Arg Glu
50 55 60

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

Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly Val Thr Pro Ala Ile Tyr
85 90 95

Arg His Val Val Tyr Ser Gly Gly Arg Met Val Thr Tyr Glu His Leu
100 105 110

Arg Glu Val Val Phe Gly Lys Ser Glu Asp Glu His Tyr Pro Leu Trp
115 120 125

Lys Ser Val Ile Gly Gly Met Met Ala Gly Val Ile Gly Gln Phe Leu
130 135 140

Ala Asn Pro Thr Asp Leu Val Lys Val Gln Met Gln Met Glu Gly Lys
145 150 155 160

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

Phe Ala Lys Ile Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly
180 185 190

Trp Val Pro Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu
195 200 205

Thr Thr Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu
210 215 220

Glu Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
225 230 235 240

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

Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr Lys Ser
260 265 270

Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly Phe Met Ser
275 280 285

Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met Thr Pro Trp Ser
290 295 300

Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg Glu Met Ser Gly Val
305 310 315 320

Ser Pro Phe

<210> 32
<211> 1014
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hCMPSAT

<400> 32
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accctgatgg ctgcagtcta taccatagct ttaagataca caaggacatc agacaaagaa 120

ctctactttt caaccacagc cgtgtgtatc acagaagtta taaagttatt gctaagtgtg 180

ggaattttag ctaaagaaac tggtagtctg ggtagattca aagcatcttt aagagaaaat 240

gtcttgggga gccccaagga actgttgaag ttaagtgtgc catcgttagt gtatgctgtt 300

cagaacaaca tggctttcct agctcttagc aatctggatg cagcagtgta ccaggtgacc 360

taccagttga agattccgtg tactgcttta tgcactgttt taatgttaaa ccggacactc 420

agcaaattac agtgggtttc agtttttatg ctgtgtgctg gagttacgct tgtacagtgg 480

aaaccagccc aagctacaaa agtggtggtg gaacaaaatc cattattagg gtttggcgct 540

atagctattg ctgtattgtg ctcaggattt gcaggagtat attttgaaaa agttttaaag 600

agttcagata cttctctttg ggtgagaaac attcaaatgt atctatcagg gattattgtg 660

acattagctg gcgtctactt gtcagatgga gctgaaatta aagaaaaagg atttttctat 720

ggttacacat attatgtctg gtttgtcatc tttcttgcaa gtgttggtgg cctctacact 780

tctgttgtgg ttaagtacac agacaacatc atgaaaggct tttctgcagc agcggccatt 840

gtcctttcca ccattgcttc agtaatgctg tttggattac agataacact caccttgcc 900

ctgggtactc ttcttgtatg tgtttccata tatctctatg gattacccag acaagacact 960

acatccatcc aacaaggaga aacagcttca aaggagagag ttattggtgt gtga 1014

<210> 33
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hCMPSAT

<400> 33

Met Ala Ala Pro Arg Asp Asn Val Thr Leu Leu Phe Lys Leu Tyr Cys
1 5 10 15

Leu Ala Val Met Thr Leu Met Ala Ala Val Tyr Thr Ile Ala Leu Arg
20 25 30

Tyr Thr Arg Thr Ser Asp Lys Glu Leu Tyr Phe Ser Thr Thr Ala Val
35 40 45

Cys Ile Thr Glu Val Ile Lys Leu Leu Leu Ser Val Gly Ile Leu Ala
50 55 60

Lys Glu Thr Gly Ser Leu Gly Arg Phe Lys Ala Ser Leu Arg Glu Asn
65 70 75 80

Val Leu Gly Ser Pro Lys Glu Leu Leu Lys Leu Ser Val Pro Ser Leu
85 90 95

Val Tyr Ala Val Gln Asn Asn Met Ala Phe Leu Ala Leu Ser Asn Leu
100 105 110

Asp Ala Ala Val Tyr Gln Val Thr Tyr Gln Leu Lys Ile Pro Cys Thr
115 120 125

Ala Leu Cys Thr Val Leu Met Leu Asn Arg Thr Leu Ser Lys Leu Gln
130 135 140

Trp Val Ser Val Phe Met Leu Cys Ala Gly Val Thr Leu Val Gln Trp
145 150 155 160

Lys Pro Ala Gln Ala Thr Lys Val Val Val Glu Gln Asn Pro Leu Leu
165 170 175

Gly Phe Gly Ala Ile Ala Ile Ala Val Leu Cys Ser Gly Phe Ala Gly
180 185 190

Val Tyr Phe Glu Lys Val Leu Lys Ser Ser Asp Thr Ser Leu Trp Val
195 200 205

Arg Asn Ile Gln Met Tyr Leu Ser Gly Ile Ile Val Thr Leu Ala Gly
210 215 220

Val Tyr Leu Ser Asp Gly Ala Glu Ile Lys Glu Lys Gly Phe Phe Tyr
225 230 235 240

Gly Tyr Thr Tyr Tyr Val Trp Phe Val Ile Phe Leu Ala Ser Val Gly

245 250 255

Gly Leu Tyr Thr Ser Val Val Val Lys Tyr Thr Asp Asn Ile Met Lys
260 265 270

Gly Phe Ser Ala Ala Ala Ala Ile Val Leu Ser Thr Ile Ala Ser Val
275 280 285

Met Leu Phe Gly Leu Gln Ile Thr Leu Thr Phe Ala Leu Gly Thr Leu
290 295 300

Leu Val Cys Val Ser Ile Tyr Leu Tyr Gly Leu Pro Arg Gln Asp Thr
305 310 315 320

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

Val

<210> 34
<211> 1212
<212> DNA
<213> Artificial Sequence

<220>
<223> Optimized Sequence

<220>
<221> misc_feature
<223> rST6Gal1

<400> 34
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gccgtgatct gcgtgtggaa gaagggctcc gactacgagg ctctgaccct gcaggccaaa 120

gaattccaga tgcccaagtc ccaagaaaag gtggcaatgg gctccgccag ccaggtggtg 180

ttctccaact ccaagcagga ccctaaagag gacatcccta tcctgtccta ccacagagtg 240

accgccaaag tgaagcctca gcctagcttc caggtctggg acaaggactc cacctacagc 300

aagctgaacc ctcggctgct gaagatctgg cggaactacc tgaacatgaa caagtacaag 360

gtgtcctaca agggccctgg ccctggcgtg aagttctccg tggaggccct gaggtgccac 420

ctgagggacc acgtgaacgt gtccatgatc gaggccaccg acttcccatt caacaccacc 480

gagtgggagg gctacctgcc taaagagaac ttccggacca aagtgggccc ttggcagaga 540

tgcgccgtgg tgtcctccgc cggctccctg aagaactctc agctgggccg ggagatcgac 600

aaccacgacg ccgtgctgag gttcaacggc gctcctaccg acaacttcca gcaggacgtg 660

ggctccaaga ccaccatcag actgatgaac agccagctgg tgaccaccga gaagcggttt 720

ctgaaggact ccctgtacac cgagggcatc ctgatcgtgt gggacccttc cgtgtaccac 780

gccgacatcc ctaagtggta tcagaagccc gactacaact tcttcgagac atacaagtcc 840

taccggcggc tgaacccttc ccagcctttc tacatcctga agccccagat gccttgggag 900

ctgtgggaca tcatccagga aatctccgcc gacctgatcc agcctaaccc tccttcctcc 960

ggcatgctgg gcatcatcat catgatgacc ctgtgcgacc aggtggacat ctacgagttt 1020

ctgccttcca agagaaagac cgacgtgtgc tactaccacc agaagttctt cgactccgcc 1080

tgcacaatgg gcgcctacca ccccctgctg ttcgagaaga acatggtgaa gcacctgaac 1140

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atccggtgct ga 1212

<210> 35
<211> 403
<212> PRT
<213> Rattus norvegicus

<220>
<221> MISC_FEATURE
<223> rST6Gal1

<400> 35

Met Ile His Thr Asn Leu Lys Lys Lys Phe Ser Leu Phe Ile Leu Val
1 5 10 15

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

Glu Ala Leu Thr Leu Gln Ala Lys Glu Phe Gln Met Pro Lys Ser Gln
35 40 45

Glu Lys Val Ala Met Gly Ser Ala Ser Gln Val Val Phe Ser Asn Ser
50 55 60

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

Thr Ala Lys Val Lys Pro Gln Pro Ser Phe Gln Val Trp Asp Lys Asp
85 90 95

Ser Thr Tyr Ser Lys Leu Asn Pro Arg Leu Leu Lys Ile Trp Arg Asn
100 105 110

Tyr Leu Asn Met Asn Lys Tyr Lys Val Ser Tyr Lys Gly Pro Gly Pro
115 120 125

Gly Val Lys Phe Ser Val Glu Ala Leu Arg Cys His Leu Arg Asp His
130 135 140

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

Glu Trp Glu Gly Tyr Leu Pro Lys Glu Asn Phe Arg Thr Lys Val Gly
165 170 175

Pro Trp Gln Arg Cys Ala Val Val Ser Ser Ala Gly Ser Leu Lys Asn
180 185 190

Ser Gln Leu Gly Arg Glu Ile Asp Asn His Asp Ala Val Leu Arg Phe
195 200 205

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

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

Leu Lys Asp Ser Leu Tyr Thr Glu Gly Ile Leu Ile Val Trp Asp Pro
245 250 255

Ser Val Tyr His Ala Asp Ile Pro Lys Trp Tyr Gln Lys Pro Asp Tyr
260 265 270

Asn Phe Phe Glu Thr Tyr Lys Ser Tyr Arg Arg Leu Asn Pro Ser Gln
275 280 285

Pro Phe Tyr Ile Leu Lys Pro Gln Met Pro Trp Glu Leu Trp Asp Ile
290 295 300

Ile Gln Glu Ile Ser Ala Asp Leu Ile Gln Pro Asn Pro Pro Ser Ser
305 310 315 320

Gly Met Leu Gly Ile Ile Ile Met Met Thr Leu Cys Asp Gln Val Asp
325 330 335

Ile Tyr Glu Phe Leu Pro Ser Lys Arg Lys Thr Asp Val Cys Tyr Tyr
340 345 350

His Gln Lys Phe Phe Asp Ser Ala Cys Thr Met Gly Ala Tyr His Pro
355 360 365

Leu Leu Phe Glu Lys Asn Met Val Lys His Leu Asn Glu Gly Thr Asp
370 375 380

Glu Asp Ile Tyr Leu Phe Gly Lys Ala Thr Leu Ser Gly Phe Arg Asn
385 390 395 400

Ile Arg Cys

<210> 36
<211> 957
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hCOMSC

<400> 36
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ttgatcacta tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 120

catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga ggatgagcgc 180

atggagctca gtaagagctt tcgagtatac tgtattatcc ttgtaaaacc caaagatgtg 240

agtctttggg ctgcagtaaa ggagacttgg accaaacact gtgacaaagc agagttcttc 300

agttctgaaa atgttaaagt gtttgagtca attaatatgg acacaaatga catgtggtta 360

atgatgagaa aagcttacaa atacgccttt gataagtata gagaccaata caactggttc 420

ttccttgcac gccccactac gtttgctatc attgaaaacc taaagtattt tttgttaaaa 480

aaggatccat cacagccttt ctatctaggc cacactataa aatctggaga ccttgaatat 540

gtgggtatgg aaggaggaat tgtcttaagt gtagaatcaa tgaaaagact taacagcctt 600

ctcaatatcc cagaaaagtg tcctgaacag ggagggatga tttggaagat atctgaagat 660

aaacagctag cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 720

gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga ggcaatgact 780

tatcacccca accaggtagt agaaggctgt tgttcagata tggctgttac ttttaatgga 840

ctgactccaa atcagatgca tgtgatgatg tatggggtat accgccttag ggcatttggg 900

catattttca atgatgcatt ggttttctta cctccaaatg gttctgacaa tgactga 957

<210> 37
<211> 318
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hCOMSC

<400> 37

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser
1 5 10 15

Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly His
20 25 30

Gly Asn Arg Met His His His Glu His His His Leu Gln Ala Pro Asn
35 40 45

Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg Met Glu Leu Ser
50 55 60

Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val Lys Pro Lys Asp Val
65 70 75 80

Ser Leu Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys
85 90 95

Ala Glu Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn
100 105 110

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

Ala Phe Asp Lys Tyr Arg Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg
130 135 140

Pro Thr Thr Phe Ala Ile Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys
145 150 155 160

Lys Asp Pro Ser Gln Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly
165 170 175

Asp Leu Glu Tyr Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu
180 185 190

Ser Met Lys Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro
195 200 205

Glu Gln Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala
210 215 220

Val Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
225 230 235 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile Lys
245 250 255

Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys Cys Ser
260 265 270

Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val
275 280 285

Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Ile Phe Asn
290 295 300

Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser Asp Asn Asp
305 310 315

<210> 38
<211> 1092
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hT-Synthase

<400> 38
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cttttatgtt ctcagctatt tagtattttg ttgggagaaa aggttgacac ccagcctaat 120

gttcttcata atgatcctca tgcaaggcat tcagatgata atggacagaa tcatctagaa 180

ggacaaatga acttcaatgc agattctagc caacataaag atgagaacac agacattgct 240

gaaaacctct atcagaaagt tagaattctt tgctgggtta tgaccggccc tcaaaaccta 300

gagaaaaagg ccaaacacgt caaagctact tgggcccagc gttgtaacaa agtgttgttt 360

atgagttcag aagaaaataa agacttccct gctgtgggac tgaaaaccaa agaaggcaga 420

gatcaactat actggaaaac aattaaagct tttcagtatg ttcatgaaca ttatttagaa 480

gatgctgatt ggtttttgaa agcagatgat gacacgtatg tcatactaga caatttgagg 540

tggcttcttt caaaatacga ccctgaagaa cccatttact ttgggagaag atttaagcct 600

tatgtaaagc agggctacat gagtggagga gcaggatatg tactaagcaa agaagccttg 660

aaaagatttg ttgatgcatt taaaacagac aagtgtacac atagttcctc cattgaagac 720

ttagcactgg ggagatgcat ggaaattatg aatgtagaag caggagattc cagagatacc 780

attggaaaag aaacttttca tccctttgtg ccagaacacc atttaattaa aggttatcta 840

cctagaacgt tttggtactg gaattacaac tattatcctc ctgtagaggg tcctggttgc 900

tgctctgatc ttgcagtttc ttttcactat gttgattcta caaccatgta tgagttagaa 960

tacctcgttt atcatcttcg tccatatggt tatttataca gatatcaacc taccttacct 1020

gaacgtatac taaaggaaat tagtcaagca aacaaaaatg aagatacaaa agtgaagtta 1080

ggaaatcctt ga 1092

<210> 39
<211> 363
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hT-Synthase

<400> 39

Met Ala Ser Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Cys Gly Ser
1 5 10 15

Ala Ile Gly Phe Leu Leu Cys Ser Gln Leu Phe Ser Ile Leu Leu Gly
20 25 30

Glu Lys Val Asp Thr Gln Pro Asn Val Leu His Asn Asp Pro His Ala
35 40 45

Arg His Ser Asp Asp Asn Gly Gln Asn His Leu Glu Gly Gln Met Asn
50 55 60

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

Glu Asn Leu Tyr Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly
85 90 95

Pro Gln Asn Leu Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala
100 105 110

Gln Arg Cys Asn Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp
115 120 125

Phe Pro Ala Val Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr
130 135 140

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

Asp Ala Asp Trp Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu
165 170 175

Asp Asn Leu Arg Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile
180 185 190

Tyr Phe Gly Arg Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser
195 200 205

Gly Gly Ala Gly Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val
210 215 220

Asp Ala Phe Lys Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp
225 230 235 240

Leu Ala Leu Gly Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp
245 250 255

Ser Arg Asp Thr Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu
260 265 270

His His Leu Ile Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn
275 280 285

Tyr Asn Tyr Tyr Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu
290 295 300

Ala Val Ser Phe His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu
305 310 315 320

Tyr Leu Val Tyr His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln
325 330 335

Pro Thr Leu Pro Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys
340 345 350

Asn Glu Asp Thr Lys Val Lys Leu Gly Asn Pro
355 360

<210> 40
<211> 1605
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hP4HA1

<400> 40
atgatctggt atatattaat tataggaatt ctgcttcccc agtctttggc tcatccaggc 60

ttttttactt caattggtca gatgactgat ttgatccata ctgagaaaga tctggtgact 120

tctctgaaag attatattaa ggcagaagag gacaagttag aacaaataaa aaaatgggca 180

gagaagttag atcggctaac tagtacagcg acaaaagatc cagaaggatt tgttgggcat 240

ccagtaaatg cattcaaatt aatgaaacgt ctgaatactg agtggagtga gttggagaat 300

ctggtcctta aggatatgtc agatggcttt atctctaacc taaccattca gagacagtac 360

tttcctaatg atgaagatca ggttggggca gccaaagctc tgttacgtct ccaggatacc 420

tacaatttgg atacagatac catctcaaag ggtaatcttc caggagtgaa acacaaatct 480

tttctaacgg ctgaggactg ctttgagttg ggcaaagtgg cctatacaga agcagattat 540

taccatacgg aactgtggat ggaacaagcc ctaaggcaac tggatgaagg cgagatttct 600

accatagata aagtctctgt tctagattat ttgagctatg cggtatatca gcagggagac 660

ctggataagg cacttttgct cacaaagaag cttcttgaac tagatcctga acatcagaga 720

gctaatggta acttaaaata ttttgagtat ataatggcta aagaaaaaga tgtcaataag 780

tctgcttcag atgaccaatc tgatcagaaa actacaccaa agaaaaaagg ggttgctgtg 840

gattacctgc cagagagaca gaagtacgaa atgctgtgcc gtggggaggg tatcaaaatg 900

acccctcgga gacagaaaaa actcttttgc cgctaccatg atggaaaccg taatcctaaa 960

tttattctgg ctccagctaa acaggaggat gaatgggaca agcctcgtat tattcgcttc 1020

catgatatta tttctgatgc agaaattgaa atcgtcaaag acctagcaaa accaaggctg 1080

agccgagcta cagtacatga ccctgagact ggaaaattga ccacagcaca gtacagagta 1140

tctaagagtg cctggctctc tggctatgaa aatcctgtgg tgtctcgaat taatatgaga 1200

atacaagatc taacaggact agatgtttcc acagcagagg aattacaggt agcaaattat 1260

ggagttggag gacagtatga accccatttt gactttgcac ggaaagatga gccagatgct 1320

ttcaaagagc tggggacagg aaatagaatt gctacatggc tgttttatat gagtgatgtg 1380

tctgcaggag gagccactgt ttttcctgaa gttggagcta gtgtttggcc caaaaaagga 1440

actgctgttt tctggtataa tctgtttgcc agtggagaag gagattatag tacacggcat 1500

gcagcctgtc cagtgctagt tggcaacaaa tgggtatcca ataaatggct ccatgaacgt 1560

ggacaagaat ttcgaagacc ttgtacgttg tcagaattgg aatga 1605

<210> 41
<211> 534
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hP4HA1

<400> 41

Met Ile Trp Tyr Ile Leu Ile Ile Gly Ile Leu Leu Pro Gln Ser Leu
1 5 10 15

Ala His Pro Gly Phe Phe Thr Ser Ile Gly Gln Met Thr Asp Leu Ile
20 25 30

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

Glu Glu Asp Lys Leu Glu Gln Ile Lys Lys Trp Ala Glu Lys Leu Asp
50 55 60

Arg Leu Thr Ser Thr Ala Thr Lys Asp Pro Glu Gly Phe Val Gly His
65 70 75 80

Pro Val Asn Ala Phe Lys Leu Met Lys Arg Leu Asn Thr Glu Trp Ser
85 90 95

Glu Leu Glu Asn Leu Val Leu Lys Asp Met Ser Asp Gly Phe Ile Ser
100 105 110

Asn Leu Thr Ile Gln Arg Gln Tyr Phe Pro Asn Asp Glu Asp Gln Val
115 120 125

Gly Ala Ala Lys Ala Leu Leu Arg Leu Gln Asp Thr Tyr Asn Leu Asp
130 135 140

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

Phe Leu Thr Ala Glu Asp Cys Phe Glu Leu Gly Lys Val Ala Tyr Thr
165 170 175

Glu Ala Asp Tyr Tyr His Thr Glu Leu Trp Met Glu Gln Ala Leu Arg
180 185 190

Gln Leu Asp Glu Gly Glu Ile Ser Thr Ile Asp Lys Val Ser Val Leu
195 200 205

Asp Tyr Leu Ser Tyr Ala Val Tyr Gln Gln Gly Asp Leu Asp Lys Ala
210 215 220

Leu Leu Leu Thr Lys Lys Leu Leu Glu Leu Asp Pro Glu His Gln Arg
225 230 235 240

Ala Asn Gly Asn Leu Lys Tyr Phe Glu Tyr Ile Met Ala Lys Glu Lys
245 250 255

Asp Val Asn Lys Ser Ala Ser Asp Asp Gln Ser Asp Gln Lys Thr Thr
260 265 270

Pro Lys Lys Lys Gly Val Ala Val Asp Tyr Leu Pro Glu Arg Gln Lys
275 280 285

Tyr Glu Met Leu Cys Arg Gly Glu Gly Ile Lys Met Thr Pro Arg Arg
290 295 300

Gln Lys Lys Leu Phe Cys Arg Tyr His Asp Gly Asn Arg Asn Pro Lys
305 310 315 320

Phe Ile Leu Ala Pro Ala Lys Gln Glu Asp Glu Trp Asp Lys Pro Arg
325 330 335

Ile Ile Arg Phe His Asp Ile Ile Ser Asp Ala Glu Ile Glu Ile Val
340 345 350

Lys Asp Leu Ala Lys Pro Arg Leu Ser Arg Ala Thr Val His Asp Pro
355 360 365

Glu Thr Gly Lys Leu Thr Thr Ala Gln Tyr Arg Val Ser Lys Ser Ala
370 375 380

Trp Leu Ser Gly Tyr Glu Asn Pro Val Val Ser Arg Ile Asn Met Arg
385 390 395 400

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

Val Ala Asn Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe
420 425 430

Ala Arg Lys Asp Glu Pro Asp Ala Phe Lys Glu Leu Gly Thr Gly Asn
435 440 445

Arg Ile Ala Thr Trp Leu Phe Tyr Met Ser Asp Val Ser Ala Gly Gly
450 455 460

Ala Thr Val Phe Pro Glu Val Gly Ala Ser Val Trp Pro Lys Lys Gly
465 470 475 480

Thr Ala Val Phe Trp Tyr Asn Leu Phe Ala Ser Gly Glu Gly Asp Tyr
485 490 495

Ser Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Asn Lys Trp Val
500 505 510

Ser Asn Lys Trp Leu His Glu Arg Gly Gln Glu Phe Arg Arg Pro Cys
515 520 525

Thr Leu Ser Glu Leu Glu
530

<210> 42
<211> 1527
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hP4HB

<400> 42
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gaggaggagg accacgtcct ggtgctgcgg aaaagcaact tcgcggaggc gctggcggcc 120

cacaagtacc tgctggtgga gttctatgcc ccttggtgtg gccactgcaa ggctctggcc 180

cctgagtatg ccaaagccgc tgggaagctg aaggcagaag gttccgagat caggttggcc 240

aaggtggacg ccacggagga gtctgacctg gcccagcagt acggcgtgcg cggctatccc 300

accatcaagt tcttcaggaa tggagacacg gcttccccca aggaatatac agctggcaga 360

gaggctgatg acatcgtgaa ctggctgaag aagcgcacgg gcccggctgc caccaccctg 420

cctgacggcg cagctgcaga gtccttggtg gagtccagcg aggtggctgt catcggcttc 480

ttcaaggacg tggagtcgga ctctgccaag cagtttttgc aggcagcaga ggccatcgat 540

gacataccat ttgggatcac ttccaacagt gacgtgttct ccaaatacca gctcgacaaa 600

gatggggttg tcctctttaa gaagtttgat gaaggccgga acaactttga aggggaggtc 660

accaaggaga acctgctgga ctttatcaaa cacaaccagc tgcccccttgt catcgagttc 720

accgagcaga cagccccgaa gatttttgga ggtgaaatca agactcacat cctgctgttc 780

ttgcccaaga gtgtgtctga ctatgacggc aaactgagca acttcaaaac agcagccgag 840

agcttcaagg gcaagatcct gttcatcttc atcgacagcg accacaccga caaccagcgc 900

atcctcgagt tctttggcct gaagaaggaa gagtgcccgg ccgtgcgcct catcaccctg 960

gaggaggaga tgaccaagta caagcccgaa tcggaggagc tgacggcaga gaggatcaca 1020

gagttctgcc accgcttcct ggagggcaaa atcaagcccc acctgatgag ccaggagctg 1080

ccggaggact gggacaagca gcctgtcaag gtgcttgttg ggaagaactt tgaagacgtg 1140

gcttttgatg agaaaaaaaa cgtctttgtg gagttctatg ccccatggtg tggtcactgc 1200

aaacagttgg ctcccatttg ggataaactg ggagagacgt acaaggacca tgagaacatc 1260

gtcatcgcca agatggactc gactgccaac gaggtggagg ccgtcaaagt gcacagcttc 1320

cccacactca agttctttcc tgccagtgcc gacaggacgg tcattgatta caacggggaa 1380

cgcacgctgg atggttttaa gaaattcctg gagagcggtg gccaggatgg ggcaggggat 1440

gatgacgatc tcgaggacct ggaagaagca gaggagccag acatggagga agacgatgat 1500

cagaaagctg tgaaagatga actgtaa 1527

<210> 43
<211> 508
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hP4HB

<400> 43

Met Leu Arg Arg Ala Leu Leu Cys Leu Ala Val Ala Ala Leu Val Arg
1 5 10 15

Ala Asp Ala Pro Glu Glu Glu Asp His Val Leu Val Leu Arg Lys Ser
20 25 30

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

Tyr Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro Glu Tyr Ala
50 55 60

Lys Ala Ala Gly Lys Leu Lys Ala Glu Gly Ser Glu Ile Arg Leu Ala
65 70 75 80

Lys Val Asp Ala Thr Glu Glu Ser Asp Leu Ala Gln Gln Tyr Gly Val
85 90 95

Arg Gly Tyr Pro Thr Ile Lys Phe Phe Arg Asn Gly Asp Thr Ala Ser
100 105 110

Pro Lys Glu Tyr Thr Ala Gly Arg Glu Ala Asp Asp Ile Val Asn Trp
115 120 125

Leu Lys Lys Arg Thr Gly Pro Ala Ala Thr Thr Leu Pro Asp Gly Ala
130 135 140

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

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

Glu Ala Ile Asp Asp Ile Pro Phe Gly Ile Thr Ser Asn Ser Asp Val
180 185 190

Phe Ser Lys Tyr Gln Leu Asp Lys Asp Gly Val Val Leu Phe Lys Lys
195 200 205

Phe Asp Glu Gly Arg Asn Asn Phe Glu Gly Glu Val Thr Lys Glu Asn
210 215 220

Leu Leu Asp Phe Ile Lys His Asn Gln Leu Pro Leu Val Ile Glu Phe
225 230 235 240

Thr Glu Gln Thr Ala Pro Lys Ile Phe Gly Gly Glu Ile Lys Thr His
245 250 255

Ile Leu Leu Phe Leu Pro Lys Ser Val Ser Asp Tyr Asp Gly Lys Leu
260 265 270

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

Ile Phe Ile Asp Ser Asp His Thr Asp Asn Gln Arg Ile Leu Glu Phe
290 295 300

Phe Gly Leu Lys Lys Glu Glu Cys Pro Ala Val Arg Leu Ile Thr Leu
305 310 315 320

Glu Glu Glu Met Thr Lys Tyr Lys Pro Glu Ser Glu Glu Leu Thr Ala
325 330 335

Glu Arg Ile Thr Glu Phe Cys His Arg Phe Leu Glu Gly Lys Ile Lys
340 345 350

Pro His Leu Met Ser Gln Glu Leu Pro Glu Asp Trp Asp Lys Gln Pro
355 360 365

Val Lys Val Leu Val Gly Lys Asn Phe Glu Asp Val Ala Phe Asp Glu
370 375 380

Lys Lys Asn Val Phe Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys
385 390 395 400

Lys Gln Leu Ala Pro Ile Trp Asp Lys Leu Gly Glu Thr Tyr Lys Asp
405 410 415

His Glu Asn Ile Val Ile Ala Lys Met Asp Ser Thr Ala Asn Glu Val
420 425 430

Glu Ala Val Lys Val His Ser Phe Pro Thr Leu Lys Phe Phe Pro Ala
435 440 445

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

Gly Phe Lys Lys Phe Leu Glu Ser Gly Gly Gln Asp Gly Ala Gly Asp
465 470 475 480

Asp Asp Asp Leu Glu Asp Leu Glu Glu Ala Glu Glu Pro Asp Met Glu
485 490 495

Glu Asp Asp Asp Gln Lys Ala Val Lys Asp Glu Leu
500 505

<210> 44
<211> 603
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hGILZ

<400> 44
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ctggacctgg cccatcggag tgggctccag cgaggcagca gcggggagaa caacaacccg 120

ggcagcccta cagtgagcaa ctttcggcag ctgcaggaaa agctggtctt tgagaacctc 180

aataccgaca agctcaacag cataatgcgg caggattcgc tagagccggt gctgcgggac 240

ccctgctacc tgatcaacga gggcatctgc aaccgcaaca tcgaccagac catgctctcc 300

atcctgctct tcttccacag tgcctccgga gccagcgtgg tggccataga caacaagatc 360

gaacaggcca tggatctggt gaagaatcat ctgatgtatg ctgtgagaga ggaggtggag 420

atcctgaagg agcagatccg agagctggtg gagaagaact cccagctaga gcgtgagaac 480

accctgttga agaccctggc aagcccagag cagctggaga agttccagtc ctgtctgagc 540

cctgaagagc cagctcccga atccccacaa gtgcccgagg cccctggtgg ttctgcggtg 600

taa 603

<210> 45
<211> 200
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hGILZ

<400> 45

Met Ala Gln Ser Lys Leu Asp Cys Arg Ser Pro Val Gly Leu Asp Cys
1 5 10 15

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

Ser Ser Gly Glu Asn Asn Asn Pro Gly Ser Pro Thr Val Ser Asn Phe
35 40 45

Arg Gln Leu Gln Glu Lys Leu Val Phe Glu Asn Leu Asn Thr Asp Lys
50 55 60

Leu Asn Ser Ile Met Arg Gln Asp Ser Leu Glu Pro Val Leu Arg Asp
65 70 75 80

Pro Cys Tyr Leu Ile Asn Glu Gly Ile Cys Asn Arg Asn Ile Asp Gln
85 90 95

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

Val Val Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys
115 120 125

Asn His Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu
130 135 140

Gln Ile Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn
145 150 155 160

Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln
165 170 175

Ser Cys Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro
180 185 190

Glu Ala Pro Gly Gly Ser Ala Val
195 200

<210> 46
<211> 651
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hCyPB

<400> 46
atgctgcgcc tctccgaacg caacatgaag gtgctccttg ccgccgccct catcgcgggg 60

tccgtcttct tcctgctgct gccgggacct tctgcggccg atgagaagaa gaaggggccc 120

aaagtcaccg tcaaggtgta ttttgaccta cgaattggag atgaagatgt aggccgggtg 180

atctttggtc tcttcggaaa gactgttcca aaaacagtgg ataattttgt ggccttagct 240

acaggagaga aaggatttgg ctacaaaaac agcaaattcc atcgtgtaat caaggacttc 300

atgatccagg gcggagactt caccagggga gatggcacag gaggaaagag catctacggt 360

gagcgcttcc ccgatgagaa cttcaaactg aagcactacg ggcctggctg ggtgagcatg 420

gccaacgcag gcaaagacac caacggctcc cagttcttca tcacgacagt caagacagcc 480

tggctagatg gcaagcatgt ggtgtttggc aaagttctag agggcatgga ggtggtgcgg 540

aaggtggaga gcaccaagac agacagccgg gataaacccc tgaaggatgt gatcatcgca 600

gactgcggca agatcgaggt ggagaagccc tttgccatcg ccaaggagta g 651

<210> 47
<211> 216
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hCyPB

<400> 47

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

Leu Ile Ala Gly Ser Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala
20 25 30

Ala Asp Glu Lys Lys Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe
35 40 45

Asp Leu Arg Ile Gly Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu
50 55 60

Phe Gly Lys Thr Val Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala
65 70 75 80

Thr Gly Glu Lys Gly Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val
85 90 95

Ile Lys Asp Phe Met Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly
100 105 110

Thr Gly Gly Lys Ser Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe
115 120 125

Lys Leu Lys His Tyr Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly
130 135 140

Lys Asp Thr Asn Gly Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala
145 150 155 160

Trp Leu Asp Gly Lys His Val Val Phe Gly Lys Val Leu Glu Gly Met
165 170 175

Glu Val Val Arg Lys Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys
180 185 190

Pro Leu Lys Asp Val Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu
195 200 205

Lys Pro Phe Ala Ile Ala Lys Glu
210 215

<210> 48
<211> 1818
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hNRF2

<400> 48
atgatggact tggagctgcc gccgccggga ctcccgtccc agcaggacat ggatttgatt 60
gacatacttt ggaggcaaga tatagatctt ggagtaagtc gagaagtatt tgacttcagt 120
cagcgacgga aagagtatga gctggaaaaa cagaaaaaac ttgaaaagga aagacaagaa 180
caactccaaa aggagcaaga gaaagccttt ttcgctcagt tacaactaga tgaagagaca 240
ggtgaatttc tcccaattca gccagcccag cacatccagt cagaaaccag tggatctgcc 300
aactactccc aggttgccca cattcccaaa tcagatgctt tgtactttga tgactgcatg 360
cagcttttgg cgcagacatt cccgtttgta gatgacaatg aggtttcttc ggctacgttt 420
cagtcacttg ttcctgatat tcccggtcac atcgagagcc cagtcttcat tgctactaat 480
caggctcagt cacctgaaac ttctgttgct caggtagccc ctgttgattt agacggtatg 540
caacaggaca ttgagcaagt ttgggaggag ctattatcca ttcctgagtt acagtgtctt 600
aatattgaaa atgacaagct ggttgagact accatggttc caagtccaga agccaaactg 660
acagaagttg acaattatca tttttactca tctatacccct caatggaaaa agaagtaggt 720
aactgtagtc cacattttct taatgctttt gaggattcct tcagcagcat cctctccaca 780
gaagacccca accagttgac agtgaactca ttaaattcag atgccacagt caacacagat 840
tttggtgatg aattttattc tgctttcata gctgagccca gtatcagcaa cagcatgccc 900
tcacctgcta ctttaagcca ttcactctct gaacttctaa atgggcccat tgatgtttct 960
gatctatcac tttgcaaagc tttcaaccaa aaccaccctg aaagcacagc agaattcaat 1020
gattctgact ccggcatttc actaaacaca agtcccagtg tggcatcacc agaacactca 1080
gtggaatctt ccagctatgg agacacacta cttggcctca gtgattctga agtggaagag 1140

ctagatagtg cccctggaag tgtcaaacag aatggtccta aaacaccagt acattcttct 1200

ggggatatgg tacaaccctt gtcaccatct caggggcaga gcactcacgt gcatgatgcc 1260

caatgtgaga acacaccaga gaaagaattg cctgtaagtc ctggtcatcg gaaaacccca 1320

ttcacaaaag acaaacattc aagccgcttg gaggctcatc tcacaagaga tgaacttagg 1380

gcaaaagctc tccatatccc attccctgta gaaaaaatca ttaacctccc tgttgttgac 1440

ttcaacgaaa tgatgtccaa agagcagttc aatgaagctc aacttgcatt aattcgggat 1500

atacgtagga ggggtaagaa taaagtggct gctcagaatt gcagaaaaag aaaactggaa 1560

aatatagtag aactagagca agatttagat catttgaaag atgaaaaaga aaaattgctc 1620

aaagaaaaag gagaaaatga caaaagcctt cacctactga aaaaacaact cagcacctta 1680

tatctcgaag ttttcagcat gctacgtgat gaagatggaa aaccttattc tcctagtgaa 1740

tactccctgc agcaaacaag agatggcaat gttttccttg ttcccaaaag taagaagcca 1800

gatgttaaga aaaactag 1818

<210> 49
<211> 605
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hNRF2

<400> 49

Met Met Asp Leu Glu Leu Pro Pro Pro Gly Leu Pro Ser Gln Gln Asp
1 5 10 15

Met Asp Leu Ile Asp Ile Leu Trp Arg Gln Asp Ile Asp Leu Gly Val
20 25 30

Ser Arg Glu Val Phe Asp Phe Ser Gln Arg Arg Lys Glu Tyr Glu Leu
35 40 45

Glu Lys Gln Lys Lys Leu Glu Lys Glu Arg Gln Glu Gln Leu Gln Lys
50 55 60

Glu Gln Glu Lys Ala Phe Phe Ala Gln Leu Gln Leu Asp Glu Glu Thr
65 70 75 80

Gly Glu Phe Leu Pro Ile Gln Pro Ala Gln His Ile Gln Ser Glu Thr
85 90 95

Ser Gly Ser Ala Asn Tyr Ser Gln Val Ala His Ile Pro Lys Ser Asp
100 105 110

Ala Leu Tyr Phe Asp Asp Cys Met Gln Leu Leu Ala Gln Thr Phe Pro
115 120 125

Phe Val Asp Asp Asn Glu Val Ser Ser Ala Thr Phe Gln Ser Leu Val
130 135 140

Pro Asp Ile Pro Gly His Ile Glu Ser Pro Val Phe Ile Ala Thr Asn
145 150 155 160

Gln Ala Gln Ser Pro Glu Thr Ser Val Ala Gln Val Ala Pro Val Asp
165 170 175

Leu Asp Gly Met Gln Gln Asp Ile Glu Gln Val Trp Glu Glu Leu Leu
180 185 190

Ser Ile Pro Glu Leu Gln Cys Leu Asn Ile Glu Asn Asp Lys Leu Val
195 200 205

Glu Thr Thr Met Val Pro Ser Pro Glu Ala Lys Leu Thr Glu Val Asp
210 215 220

Asn Tyr His Phe Tyr Ser Ser Ile Pro Ser Met Glu Lys Glu Val Gly
225 230 235 240

Asn Cys Ser Pro His Phe Leu Asn Ala Phe Glu Asp Ser Phe Ser Ser
245 250 255

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

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

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

Leu Ser His Ser Leu Ser Glu Leu Leu Asn Gly Pro Ile Asp Val Ser
305 310 315 320

Asp Leu Ser Leu Cys Lys Ala Phe Asn Gln Asn His Pro Glu Ser Thr
325 330 335

Ala Glu Phe Asn Asp Ser Asp Ser Gly Ile Ser Leu Asn Thr Ser Pro
340 345 350

Ser Val Ala Ser Pro Glu His Ser Val Glu Ser Ser Ser Tyr Gly Asp
355 360 365

Thr Leu Leu Gly Leu Ser Asp Ser Glu Val Glu Glu Leu Asp Ser Ala
370 375 380

Pro Gly Ser Val Lys Gln Asn Gly Pro Lys Thr Pro Val His Ser Ser
385 390 395 400

Gly Asp Met Val Gln Pro Leu Ser Pro Ser Gln Gly Gln Ser Thr His
405 410 415

Val His Asp Ala Gln Cys Glu Asn Thr Pro Glu Lys Glu Leu Pro Val
420 425 430

Ser Pro Gly His Arg Lys Thr Pro Phe Thr Lys Asp Lys His Ser Ser
435 440 445

Arg Leu Glu Ala His Leu Thr Arg Asp Glu Leu Arg Ala Lys Ala Leu
450 455 460

His Ile Pro Phe Pro Val Glu Lys Ile Ile Asn Leu Pro Val Val Asp
465 470 475 480

Phe Asn Glu Met Met Ser Lys Glu Gln Phe Asn Glu Ala Gln Leu Ala
485 490 495

Leu Ile Arg Asp Ile Arg Arg Arg Gly Lys Asn Lys Val Ala Ala Gln
500 505 510

Asn Cys Arg Lys Arg Lys Leu Glu Asn Ile Val Glu Leu Glu Gln Asp
515 520 525

Leu Asp His Leu Lys Asp Glu Lys Glu Lys Leu Leu Lys Glu Lys Gly
530 535 540

Glu Asn Asp Lys Ser Leu His Leu Leu Lys Lys Gln Leu Ser Thr Leu
545 550 555 560

Tyr Leu Glu Val Phe Ser Met Leu Arg Asp Glu Asp Gly Lys Pro Tyr
565 570 575

Ser Pro Ser Glu Tyr Ser Leu Gln Gln Thr Arg Asp Gly Asn Val Phe
580 585 590

Leu Val Pro Lys Ser Lys Lys Pro Asp Val Lys Lys Asn
595 600 605

<210> 50
<211> 2754
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hHK1

<400> 50
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aagattgaca agtatctcta tgccatgcgg ctctccgatg aaactctcat agatatcatg 120

actcgcttca ggaaggagat gaagaatggc ctctcccggg attttaatcc aacagccaca 180
gtcaagatgt tgccaacatt cgtaaggtcc attcctgatg gctctgaaaa gggagatttc 240
attgccctgg atcttggtgg gtcttccttt cgaattctgc gggtgcaagt gaatcatgag 300
aaaaaccaga atgttcacat ggagtccgag gtttatgaca ccccagagaa catcgtgcac 360
ggcagtggaa gccagctttt tgatcatgtt gctgagtgcc tgggagattt catggagaaa 420
aggaagatca aggacaagaa gttacctgtg ggattcacgt tttcttttcc ttgccaacaa 480
tccaaaatag atgaggccat cctgatcacc tggacaaagc gatttaaagc gagcggagtg 540
gaaggagcag atgtggtcaa actgcttaac aaagccatca aaaagcgagg ggactatgat 600
gccaacatcg tagctgtggt gaatgacaca gtgggcacca tgatgacctg tggctatgac 660
gaccagcact gtgaagtcgg cctgatcatc ggcactggca ccaatgcttg ctacatggag 720
gaactgaggc acattgatct ggtggaagga gacgagggga ggatgtgtat caatacagaa 780
tggggagcct ttggagacga tggatcatta gaagacatcc ggacagagtt tgacagggag 840
atagaccggg gatccctcaa ccctggaaaa cagctgtttg agaagatggt cagtggcatg 900
tacttgggag agctggttcg actgatccta gtcaagatgg ccaaggaggg cctcttattt 960
gaagggcgga tcaccccgga gctgctcacc cgagggaagt ttaacaccag tgatgtgtca 1020
gccatcgaaa agaataagga aggcctccac aatgccaaag aaatcctgac ccgcctggga 1080
gtggagccgt ccgatgatga ctgtgtctca gtccagcacg tttgcaccat tgtctcattt 1140
cgctcagcca acttggtggc tgccacactg ggcgccatct tgaaccgcct gcgtgataac 1200
aagggcacac ccaggctgcg gaccacggtt ggtgtcgacg gatctcttta caagacgcac 1260
ccacagtatt cccggcgttt ccacaagact ctaaggcgct tggtgccaga ctccgatgtg 1320
cgcttcctcc tctcggagag tggcagcggc aaggggggctg ccatggtgac ggcggtggcc 1380
taccgcttgg ccgagcagca ccggcagata gaggagaccc tggctcattt ccacctcacc 1440
aaggacatgc tgctggaggt gaagaagagg atgcgggccg agatggagct ggggctgagg 1500
aagcagacgc acaacaatgc cgtggttaag atgctgccct ccttcgtccg gagaactccc 1560
gacgggaccg agaatggtga cttcttggcc ctggatcttg gaggaaccaa tttccgtgtg 1620
ctgctggtga aaatccgtag tgggaaaaag agaacggtgg aaatgcacaa caagatctac 1680
gccattccta ttgaaatcat gcagggcact ggggaagagc tgtttgatca cattgtctcc 1740
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acgttctcat ttccctgcca gcagacgagt ctggacgcgg gaatcttgat cacgtggaca 1860
aagggtttta aggcaacaga ctgcgtgggc cacgatgtag tcaccttact aagggatgcg 1920
ataaaaagga gagaggaatt tgacctggac gtggtggctg tggtcaacga cacagtgggc 1980
accatgatga cctgtgctta tgaggagccc acctgtgagg ttggactcat tgttgggacc 2040
ggcagcaatg cctgctacat ggaggagatg aagaacgtgg agatggtgga gggggaccag 2100
gggcagatgt gcatcaacat ggagtggggg gcctttgggg acaacgggtg tctggatgat 2160

atcaggacac actacgacag actggtggac gaatattccc taaatgctgg gaaacaaagg 2220

tatgagaaga tgatcagtgg tatgtacctg ggtgaaatcg tccgcaacat cttaatcgac 2280

ttcaccaaga agggattcct cttccgaggg cagatctctg agacgctgaa gacccggggc 2340

atctttgaga ccaagtttct ctctcagatc gagagtgacc gattagcact gctccaggtc 2400

cgggctatcc tccagcagct aggtctgaat agcacctgcg atgacagtat cctcgtcaag 2460

acagtgtgcg gggtggtgtc caggagggcc gcacagctgt gtggcgcagg catggctgcg 2520

gttgtggata agatccgcga gaacagagga ctggaccgtc tgaatgtgac tgtgggagtg 2580

gacgggacac tctacaagct tcatccacac ttctccagaa tcatgcacca gacggtgaag 2640

gaactgtcac caaaatgtaa cgtgtccttc ctcctgtctg aggatggcag cggcaagggg 2700

gccgccctca tcacggccgt gggcgtgcgg ttacgcacag aggcaagcag ctaa 2754

<210> 51
<211> 917
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hHK1

<400> 51

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

Asp Gln Val Lys Lys Ile Asp Lys Tyr Leu Tyr Ala Met Arg Leu Ser
20 25 30

Asp Glu Thr Leu Ile Asp Ile Met Thr Arg Phe Arg Lys Glu Met Lys
35 40 45

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

Pro Thr Phe Val Arg Ser Ile Pro Asp Gly Ser Glu Lys Gly Asp Phe
65 70 75 80

Ile Ala Leu Asp Leu Gly Gly Ser Ser Phe Arg Ile Leu Arg Val Gln
85 90 95

Val Asn His Glu Lys Asn Gln Asn Val His Met Glu Ser Glu Val Tyr
100 105 110

Asp Thr Pro Glu Asn Ile Val His Gly Ser Gly Ser Gln Leu Phe Asp
115 120 125

His Val Ala Glu Cys Leu Gly Asp Phe Met Glu Lys Arg Lys Ile Lys
130 135 140

Asp Lys Lys Leu Pro Val Gly Phe Thr Phe Ser Phe Pro Cys Gln Gln
145 150 155 160

Ser Lys Ile Asp Glu Ala Ile Leu Ile Thr Trp Thr Lys Arg Phe Lys
165 170 175

Ala Ser Gly Val Glu Gly Ala Asp Val Val Lys Leu Leu Asn Lys Ala
180 185 190

Ile Lys Lys Arg Gly Asp Tyr Asp Ala Asn Ile Val Ala Val Val Asn
195 200 205

Asp Thr Val Gly Thr Met Met Thr Cys Gly Tyr Asp Asp Gln His Cys
210 215 220

Glu Val Gly Leu Ile Ile Gly Thr Gly Thr Asn Ala Cys Tyr Met Glu
225 230 235 240

Glu Leu Arg His Ile Asp Leu Val Glu Gly Asp Glu Gly Arg Met Cys
245 250 255

Ile Asn Thr Glu Trp Gly Ala Phe Gly Asp Asp Gly Ser Leu Glu Asp
260 265 270

Ile Arg Thr Glu Phe Asp Arg Glu Ile Asp Arg Gly Ser Leu Asn Pro
275 280 285

Gly Lys Gln Leu Phe Glu Lys Met Val Ser Gly Met Tyr Leu Gly Glu
290 295 300

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

Glu Gly Arg Ile Thr Pro Glu Leu Leu Thr Arg Gly Lys Phe Asn Thr
325 330 335

Ser Asp Val Ser Ala Ile Glu Lys Asn Lys Glu Gly Leu His Asn Ala
340 345 350

Lys Glu Ile Leu Thr Arg Leu Gly Val Glu Pro Ser Asp Asp Asp Cys
355 360 365

Val Ser Val Gln His Val Cys Thr Ile Val Ser Phe Arg Ser Ala Asn
370 375 380

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

Lys Gly Thr Pro Arg Leu Arg Thr Thr Val Gly Val Asp Gly Ser Leu
405 410 415

Tyr Lys Thr His Pro Gln Tyr Ser Arg Arg Phe His Lys Thr Leu Arg
420 425 430

Arg Leu Val Pro Asp Ser Asp Val Arg Phe Leu Leu Ser Glu Ser Gly
435 440 445

Ser Gly Lys Gly Ala Ala Met Val Thr Ala Val Ala Tyr Arg Leu Ala
450 455 460

Glu Gln His Arg Gln Ile Glu Glu Thr Leu Ala His Phe His Leu Thr
465 470 475 480

Lys Asp Met Leu Leu Glu Val Lys Lys Arg Met Arg Ala Glu Met Glu
485 490 495

Leu Gly Leu Arg Lys Gln Thr His Asn Asn Ala Val Val Lys Met Leu
500 505 510

Pro Ser Phe Val Arg Arg Thr Pro Asp Gly Thr Glu Asn Gly Asp Phe
515 520 525

Leu Ala Leu Asp Leu Gly Gly Thr Asn Phe Arg Val Leu Leu Val Lys
530 535 540

Ile Arg Ser Gly Lys Lys Arg Thr Val Glu Met His Asn Lys Ile Tyr
545 550 555 560

Ala Ile Pro Ile Glu Ile Met Gln Gly Thr Gly Glu Glu Leu Phe Asp
565 570 575

His Ile Val Ser Cys Ile Ser Asp Phe Leu Asp Tyr Met Gly Ile Lys
580 585 590

Gly Pro Arg Met Pro Leu Gly Phe Thr Phe Ser Phe Pro Cys Gln Gln
595 600 605

Thr Ser Leu Asp Ala Gly Ile Leu Ile Thr Trp Thr Lys Gly Phe Lys
610 615 620

Ala Thr Asp Cys Val Gly His Asp Val Val Thr Leu Leu Arg Asp Ala
625 630 635 640

Ile Lys Arg Arg Glu Glu Phe Asp Leu Asp Val Val Ala Val Val Asn
645 650 655

Asp Thr Val Gly Thr Met Met Thr Cys Ala Tyr Glu Glu Pro Thr Cys
660 665 670

Glu Val Gly Leu Ile Val Gly Thr Gly Ser Asn Ala Cys Tyr Met Glu
675 680 685

Glu Met Lys Asn Val Glu Met Val Glu Gly Asp Gln Gly Gln Met Cys
690 695 700

Ile Asn Met Glu Trp Gly Ala Phe Gly Asp Asn Gly Cys Leu Asp Asp
705 710 715 720

Ile Arg Thr His Tyr Asp Arg Leu Val Asp Glu Tyr Ser Leu Asn Ala
725 730 735

Gly Lys Gln Arg Tyr Glu Lys Met Ile Ser Gly Met Tyr Leu Gly Glu
740 745 750

Ile Val Arg Asn Ile Leu Ile Asp Phe Thr Lys Lys Gly Phe Leu Phe
755 760 765

Arg Gly Gln Ile Ser Glu Thr Leu Lys Thr Arg Gly Ile Phe Glu Thr
770 775 780

Lys Phe Leu Ser Gln Ile Glu Ser Asp Arg Leu Ala Leu Leu Gln Val
785 790 795 800

Arg Ala Ile Leu Gln Gln Leu Gly Leu Asn Ser Thr Cys Asp Asp Ser
805 810 815

Ile Leu Val Lys Thr Val Cys Gly Val Val Ser Arg Arg Ala Ala Gln
820 825 830

Leu Cys Gly Ala Gly Met Ala Ala Val Val Asp Lys Ile Arg Glu Asn
835 840 845

Arg Gly Leu Asp Arg Leu Asn Val Thr Val Gly Val Asp Gly Thr Leu
850 855 860

Tyr Lys Leu His Pro His Phe Ser Arg Ile Met His Gln Thr Val Lys
865 870 875 880

Glu Leu Ser Pro Lys Cys Asn Val Ser Phe Leu Leu Ser Glu Asp Gly
885 890 895

Ser Gly Lys Gly Ala Ala Leu Ile Thr Ala Val Gly Val Arg Leu Arg
900 905 910

Thr Glu Ala Ser Ser
915

<210> 52
<211> 1578
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hPDI

<400> 52
atgagccgcc agcttctgcc tgtactgctg ctgctgctgc tcagggcttc gtgcccatgg 60
ggtcaggaac agggagcgag gagcccctcg gaggagcctc cagaggagga aatccccaag 120
gaggatggga tcttggtgct gagccgccac accctgggcc tggccctgcg ggagcaccct 180
gccctgctgg tggaattcta tgccccgtgg tgtgggcact gccaggccct ggcccccgag 240
tacagcaagg cagctgccgt gctcgcggcc gagtcaatgg tggtcacgct ggccaaggtg 300
gatgggcccg cgcagcgcga gctggctgag gagtttggtg tgacggagta ccctacgctc 360
aagttcttcc gcaatgggaa ccgcacgcac ccggaggagt acacaggacc acgggacgct 420
gagggcattg ccgagtggct gcgacggcgg gtggggccca gtgccatgcg gctggaggac 480
gaggcggccg cccaggcgct gatcggtggc cgggacctag tggtcattgg cttcttccag 540
gacctgcagg acgaggacgt ggccaccttc ttggccttgg cccaggacgc cctggacatg 600
acctttggcc tcacagaccg gccgcggctc tttcagcagt ttggcctcac caaggacact 660
gtggttctct tcaagaagtt tgatgagggg cgggcagact tccccgtgga cgaggagctt 720
ggcctggacc tgggggatct gtcgcgcttc ctggtcacac acagcatgcg cctggtcacg 780
gagttcaaca gccagacgtc tgccaagatc ttcgcggcca ggatcctcaa ccacctgctg 840
ctgtttgtca accagacgct ggctgcgcac cgggagctcc tagcgggctt tggggaggca 900
gctccccgct tccgggggca ggtgctgttc gtggtggtgg acgtggcggc cgacaatgag 960
cacgtgctgc agtactttgg actcaaggct gaggcagccc ccactctgcg cttggtcaac 1020
cttgaaacca ctaagaagta tgcgcctgtg gatgggggcc ctgtcaccgc agcgtccatc 1080
actgctttct gccatgcagt cctcaacggc caagtcaagc cctatctcct gagccaggag 1140
atacccccctg attgggatca gcggccagtt aagaccctcg tgggcaagaa ttttgagcag 1200
gtggcttttg acgaaaccaa gaatgtgttt gtcaagttct atgccccgtg gtgcacccac 1260
tgcaaggaga tggcccctgc ctgggaggca ttggctgaga agtaccaaga ccacgaggac 1320
atcatcattg ctgagctgga tgccacggcc aacgagctgg atgccttcgc tgtgcacggc 1380
ttccctactc tcaagtactt cccagcaggg ccaggtcgga aggtgattga atacaaaagc 1440
accagggacc tggagacttt ctccaagttc ctggacaacg ggggcgtgct gcccacggag 1500
gagccccgg aggagccagc agccccgttc ccggagccac cggccaactc cactatgggg 1560
tccaaggagg aactgtag 1578

<210> 53
<211> 525
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE

<223> hPDI

<400> 53

Met Ser Arg Gln Leu Leu Pro Val Leu Leu Leu Leu Leu Leu Arg Ala
1 5 10 15

Ser Cys Pro Trp Gly Gln Glu Gln Gly Ala Arg Ser Pro Ser Glu Glu
20 25 30

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

Arg His Thr Leu Gly Leu Ala Leu Arg Glu His Pro Ala Leu Leu Val
50 55 60

Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Ala Leu Ala Pro Glu
65 70 75 80

Tyr Ser Lys Ala Ala Ala Val Leu Ala Ala Glu Ser Met Val Val Thr
85 90 95

Leu Ala Lys Val Asp Gly Pro Ala Gln Arg Glu Leu Ala Glu Glu Phe
100 105 110

Gly Val Thr Glu Tyr Pro Thr Leu Lys Phe Phe Arg Asn Gly Asn Arg
115 120 125

Thr His Pro Glu Glu Tyr Thr Gly Pro Arg Asp Ala Glu Gly Ile Ala
130 135 140

Glu Trp Leu Arg Arg Arg Val Gly Pro Ser Ala Met Arg Leu Glu Asp
145 150 155 160

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

Gly Phe Phe Gln Asp Leu Gln Asp Glu Asp Val Ala Thr Phe Leu Ala
180 185 190

Leu Ala Gln Asp Ala Leu Asp Met Thr Phe Gly Leu Thr Asp Arg Pro
195 200 205

Arg Leu Phe Gln Gln Phe Gly Leu Thr Lys Asp Thr Val Val Leu Phe
210 215 220

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

Gly Leu Asp Leu Gly Asp Leu Ser Arg Phe Leu Val Thr His Ser Met
245 250 255

Arg Leu Val Thr Glu Phe Asn Ser Gln Thr Ser Ala Lys Ile Phe Ala
260 265 270

Ala Arg Ile Leu Asn His Leu Leu Leu Phe Val Asn Gln Thr Leu Ala
275 280 285

Ala His Arg Glu Leu Leu Ala Gly Phe Gly Glu Ala Ala Pro Arg Phe
290 295 300

Arg Gly Gln Val Leu Phe Val Val Val Asp Val Ala Ala Asp Asn Glu
305 310 315 320

His Val Leu Gln Tyr Phe Gly Leu Lys Ala Glu Ala Ala Pro Thr Leu
325 330 335

Arg Leu Val Asn Leu Glu Thr Thr Lys Lys Tyr Ala Pro Val Asp Gly
340 345 350

Gly Pro Val Thr Ala Ala Ser Ile Thr Ala Phe Cys His Ala Val Leu
355 360 365

Asn Gly Gln Val Lys Pro Tyr Leu Leu Ser Gln Glu Ile Pro Pro Asp
370 375 380

Trp Asp Gln Arg Pro Val Lys Thr Leu Val Gly Lys Asn Phe Glu Gln
385 390 395 400

Val Ala Phe Asp Glu Thr Lys Asn Val Phe Val Lys Phe Tyr Ala Pro
405 410 415

Trp Cys Thr His Cys Lys Glu Met Ala Pro Ala Trp Glu Ala Leu Ala
420 425 430

Glu Lys Tyr Gln Asp His Glu Asp Ile Ile Ile Ala Glu Leu Asp Ala
435 440 445

Thr Ala Asn Glu Leu Asp Ala Phe Ala Val His Gly Phe Pro Thr Leu
450 455 460

Lys Tyr Phe Pro Ala Gly Pro Gly Arg Lys Val Ile Glu Tyr Lys Ser
465 470 475 480

Thr Arg Asp Leu Glu Thr Phe Ser Lys Phe Leu Asp Asn Gly Gly Val
485 490 495

Leu Pro Thr Glu Glu Pro Pro Glu Glu Pro Ala Ala Pro Phe Pro Glu
500 505 510

Pro Pro Ala Asn Ser Thr Met Gly Ser Lys Glu Glu Leu
515 520 525

<210> 54
<211> 492
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hPIN1

<400> 54
atggcggacg aggagaagct gccgcccggc tgggagaagc gcatgagccg cagctcaggc 60

cgagtgtact acttcaacca catcactaac gccagccagt gggagcggcc cagcggcaac 120

agcagcagtg gtggcaaaaa cgggcagggg gagcctgcca gggtccgctg ctcgcacctg 180

ctggtgaagc acagccagtc acggcggccc tcgtcctggc ggcaggagaa gatcacccgg 240

accaaggagg aggccctgga gctgatcaac ggctacatcc agaagatcaa gtcgggagag 300

gaggactttg agtctctggc ctcacagttc agcgactgca gctcagccaa ggccagggga 360

gacctgggtg ccttcagcag aggtcagatg cagaagccat ttgaagacgc ctcgtttgcg 420

ctgcggacgg gggagatgag cgggcccgtg ttcacggatt ccggcatcca catcatcctc 480

cgcactgagt ga 492

<210> 55
<211> 163
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hPIN1

<400> 55

Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
1 5 10 15

Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser
20 25 30

Gln Trp Glu Arg Pro Ser Gly Asn Ser Ser Ser Gly Gly Lys Asn Gly
35 40 45

Gln Gly Glu Pro Ala Arg Val Arg Cys Ser His Leu Leu Val Lys His
50 55 60

Ser Gln Ser Arg Arg Pro Ser Ser Trp Arg Gln Glu Lys Ile Thr Arg
65 70 75 80

Thr Lys Glu Glu Ala Leu Glu Leu Ile Asn Gly Tyr Ile Gln Lys Ile
85 90 95

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

Cys Ser Ser Ala Lys Ala Arg Gly Asp Leu Gly Ala Phe Ser Arg Gly
115 120 125

Gln Met Gln Lys Pro Phe Glu Asp Ala Ser Phe Ala Leu Arg Thr Gly
130 135 140

Glu Met Ser Gly Pro Val Phe Thr Asp Ser Gly Ile His Ile Ile Leu
145 150 155 160

Arg Thr Glu

<210> 56
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hSEPW1

<400> 56
atggctctcg ccgtccgagt cgtttattgt ggcgcttgag gctacaagtc caagtatctt 60

cagctcaaga agaagttaga agatgagttc cccggccgcc tggacatctg cggcgaggga 120

actccccagg ccaccgggtt ctttgaagtg atggtagccg ggaagttgat tcactctaag 180

aagaaaggcg atggctacgt ggacacagaa agcaagtttc tgaagttggt ggccgccatc 240

aaagccgcct tggctcaggg ctaa 264

<210> 57
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hSEPW1

<220>
<221> MISC_FEATURE
<222> (13)..(13)
<223> Special amino acid selenocysteine (U)

<400> 57

Met Ala Leu Ala Val Arg Val Val Tyr Cys Gly Ala Xaa Gly Tyr Lys
1 5 10 15

Ser Lys Tyr Leu Gln Leu Lys Lys Lys Leu Glu Asp Glu Phe Pro Gly
20 25 30

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

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

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

Lys Ala Ala Leu Ala Gln Gly
85

<210> 58
<211> 1254
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hCALR

<400> 58
atgctgctat ccgtgccgct gctgctcggc ctcctcggcc tggccgtcgc cgagcctgcc 60

gtctacttca aggagcagtt tctggacgga gacgggtgga cttcccgctg gatcgaatcc 120

aaacacaagt cagattttgg caaattcgtt ctcagttccg gcaagttcta cggtgacgag 180

gagaaagata aaggtttgca gacaagccag gatgcacgct tttatgctct gtcggccagt 240

ttcgagcctt tcagcaacaa aggccagacg ctggtggtgc agttcacggt gaaacatgag 300

cagaacatcg actgtggggg cggctatgtg aagctgtttc ctaatagttt ggaccagaca 360

gacatgcacg gagactcaga atacaacatc atgtttggtc ccgacatctg tggccctggc 420

accaagaagg ttcatgtcat cttcaactac aagggcaaga acgtgctgat caacaaggac 480

atccgttgca aggatgatga gtttacacac ctgtacacac tgattgtgcg gccagacaac 540

acctatgagg tgaagattga caacagccag gtggagtccg gctccttgga agacgattgg 600

gacttcctgc cacccaagaa gataaaggat cctgatgctt caaaaccgga agactgggat 660

gagcgggcca agatcgatga tcccacagac tccaagcctg aggactggga caagcccgag 720

catatccctg accctgatgc taagaagccc gaggactggg atgaagagat ggacggagag 780

tgggaacccc cagtgattca gaaccctgag tacaagggtg agtggaagcc ccggcagatc 840

gacaacccag attacaaggg cacttggatc cacccagaaa ttgacaaccc cgagtattct 900

cccgatccca gtatctatgc ctatgataac tttggcgtgc tgggcctgga cctctggcag 960

gtcaagtctg gcaccatctt tgacaacttc ctcatcacca acgatgaggc atacgctgag 1020

gagtttggca acgagacgtg gggcgtaaca aaggcagcag agaaacaaat gaaggacaaa 1080

caggacgagg agcagaggct taaggaggag gaagaagaca agaaacgcaa agaggaggag 1140

gaggcagagg acaaggagga tgatgaggac aaagatgagg atgaggagga tgaggaggac 1200

aaggaggaag atgaggagga agatgtcccc ggccaggcca aggacgagct gtag 1254

<210> 59

<211> 417
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hCALR

<400> 59

Met Leu Leu Ser Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Val
1 5 10 15

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

Trp Thr Ser Arg Trp Ile Glu Ser Lys His Lys Ser Asp Phe Gly Lys
35 40 45

Phe Val Leu Ser Ser Gly Lys Phe Tyr Gly Asp Glu Glu Lys Asp Lys
50 55 60

Gly Leu Gln Thr Ser Gln Asp Ala Arg Phe Tyr Ala Leu Ser Ala Ser
65 70 75 80

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

Val Lys His Glu Gln Asn Ile Asp Cys Gly Gly Gly Tyr Val Lys Leu
100 105 110

Phe Pro Asn Ser Leu Asp Gln Thr Asp Met His Gly Asp Ser Glu Tyr
115 120 125

Asn Ile Met Phe Gly Pro Asp Ile Cys Gly Pro Gly Thr Lys Lys Val
130 135 140

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

Ile Arg Cys Lys Asp Asp Glu Phe Thr His Leu Tyr Thr Leu Ile Val
165 170 175

Arg Pro Asp Asn Thr Tyr Glu Val Lys Ile Asp Asn Ser Gln Val Glu
180 185 190

Ser Gly Ser Leu Glu Asp Asp Trp Asp Phe Leu Pro Pro Lys Lys Ile
195 200 205

Lys Asp Pro Asp Ala Ser Lys Pro Glu Asp Trp Asp Glu Arg Ala Lys
210 215 220

Ile Asp Asp Pro Thr Asp Ser Lys Pro Glu Asp Trp Asp Lys Pro Glu

225 230 235 240

His Ile Pro Asp Pro Asp Ala Lys Lys Pro Glu Asp Trp Asp Glu Glu
245 250 255

Met Asp Gly Glu Trp Glu Pro Pro Val Ile Gln Asn Pro Glu Tyr Lys
260 265 270

Gly Glu Trp Lys Pro Arg Gln Ile Asp Asn Pro Asp Tyr Lys Gly Thr
275 280 285

Trp Ile His Pro Glu Ile Asp Asn Pro Glu Tyr Ser Pro Asp Pro Ser
290 295 300

Ile Tyr Ala Tyr Asp Asn Phe Gly Val Leu Gly Leu Asp Leu Trp Gln
305 310 315 320

Val Lys Ser Gly Thr Ile Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu
325 330 335

Ala Tyr Ala Glu Glu Phe Gly Asn Glu Thr Trp Gly Val Thr Lys Ala
340 345 350

Ala Glu Lys Gln Met Lys Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys
355 360 365

Glu Glu Glu Glu Asp Lys Lys Arg Lys Glu Glu Glu Glu Ala Glu Asp
370 375 380

Lys Glu Asp Asp Glu Asp Lys Asp Glu Asp Glu Glu Asp Glu Glu Asp
385 390 395 400

Lys Glu Glu Asp Glu Glu Glu Asp Val Pro Gly Gln Ala Lys Asp Glu
405 410 415

Leu

<210> 60
<211> 656
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> DroBiP

<400> 60

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

Arg Ala Glu Glu Lys Lys Glu Lys Asp Lys Glu Leu Gly Thr Val Ile

Gly Ile Asp Leu Gly Thr Thr Tyr Ser Cys Val Gly Val Tyr Lys Asn
35 40 45

Gly Arg Val Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro
50 55 60

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

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

Lys Arg Leu Ile Gly Arg Glu Trp Ser Asp Thr Asn Val Gln His Asp
100 105 110

Ile Lys Phe Phe Pro Phe Lys Val Val Glu Lys Asn Ser Lys Pro His
115 120 125

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

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

Leu Gly Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe
165 170 175

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

Leu Gln Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala
195 200 205

Tyr Gly Leu Asp Lys Lys Glu Gly Glu Lys Asn Val Leu Val Phe Asp
210 215 220

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

Val Phe Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu
245 250 255

Asp Phe Asp Gln Arg Val Met Asp His Phe Ile Lys Leu Tyr Lys Lys
260 265 270

Lys Lys Gly Lys Asp Ile Arg Lys Asp Asn Arg Ala Val Gln Lys Leu
275 280 285

Arg Arg Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Gly Ser His Gln

290 295 300

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

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

Ser Thr Leu Lys Pro Val Gln Lys Val Leu Glu Asp Ala Asp Met Asn
340 345 350

Lys Lys Asp Val His Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile
355 360 365

Pro Lys Val Gln Gln Leu Val Lys Asp Phe Phe Gly Gly Lys Glu Pro
370 375 380

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

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

Leu Asp Val Asn Pro Leu Thr Met Gly Ile Glu Thr Val Gly Gly Val
420 425 430

Met Thr Lys Leu Ile Pro Arg Asn Thr Val Ile Pro Thr Lys Lys Ser
435 440 445

Gln Val Phe Ser Thr Ala Ser Asp Asn Gln His Thr Val Thr Ile Gln
450 455 460

Val Tyr Glu Gly Glu Arg Pro Met Thr Lys Asp Asn His Leu Leu Gly
465 470 475 480

Lys Phe Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Ile Pro Gln
485 490 495

Ile Glu Val Ser Phe Glu Ile Asp Ala Asn Gly Ile Leu Gln Val Ser
500 505 510

Ala Glu Asp Lys Gly Thr Gly Asn Lys Glu Lys Ile Val Ile Thr Asn
515 520 525

Asp Gln Asn Arg Leu Thr Pro Glu Asp Ile Asp Arg Met Ile Arg Asp
530 535 540

Ala Glu Lys Phe Ala Asp Glu Asp Lys Lys Leu Lys Glu Arg Val Glu
545 550 555 560

Ser Arg Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile

565 570 575

Gly Asp Lys Asp Lys Leu Gly Ala Lys Leu Ser Asp Asp Glu Lys Asn
580 585 590

Lys Leu Glu Ser Ala Ile Asp Glu Ser Ile Lys Trp Leu Glu Gln Asn
595 600 605

Pro Asp Ala Asp Pro Glu Glu Tyr Lys Lys Gln Lys Lys Asp Leu Glu
610 615 620

Ala Ile Val Gln Pro Val Ile Ala Lys Leu Tyr Gln Gly Ala Gly Gly
625 630 635 640

Ala Pro Pro Pro Glu Gly Gly Asp Asp Ala Asp Leu Lys Asp Glu Leu
645 650 655

<210> 61
<211> 1371
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hDDOST

<400> 61
atggggtact tccggtgtgc aggtgctggg tccttcggca ggaggaggaa gatggagccc 60
agcaccgcgg cccgggcttg ggccctcttt tggttgctgc tgcccttgct tggcgcggtt 120
tgcgccagcg gaccccgcac cttagtgctg ctggacaacc tcaacgtgcg ggagactcat 180
tcgcttttct tccggagcct gaaggaccgg ggctttgagc tcacattcaa gaccgctgat 240
gaccccagcc tgtctctcat aaagtatggg gaattcctct atgacaatct catcatttc 300
tccccttcgg tagaagattt tggaggcaac atcaacgtgg agaccatcag tgcctttatt 360
gacggcggag gcagtgtgct ggtagctgcc agctccgaca ttggtgaccc tcttcgagag 420
ctgggcagtg agtgcgggat tgagtttgac gaggagaaaa cggctgtcat tgaccatcac 480
aactatgaca tctcagacct tggccagcat acgctcatcg tggctgacac tgagaacctg 540
ctgaaggccc caaccatcgt tgggaaatca tctctaaatc ccatcctctt tcgaggtgtt 600
gggatggtgg ccgatcctga taacccttg gtgctggaca tcctgacggg ctcttccacc 660
tcttactcct tcttcccgga caagcctatc acccagtatc cacatgcggt ggggaagaac 720
accctcctca ttgctgggct ccaggccagg aacaatgccc gcgtcatctt cagcggctcc 780
ctcgacttct tcagcgactc cttcttcaac tcagcagtgc agaaggcggc gcccggctcc 840
cagaggtatt cccagacagg caactatgaa ctagctgtgg ccctctcccg ctgggtgttc 900
aaggaggagg gtgtcctccg tgtggggcct gtgtcccatc atcgggtggg cgagacagcc 960
ccacccaatg cctacactgt cactgaccta gtggagtata gcatcgtgat ccagcagctc 1020

tcaaatggca aatgggtccc ctttgatggc gatgacattc agctggagtt tgtccgcatt 1080

gatccttttg tgaggacctt cctgaagaag aaaggtggca aatacagtgt tcagttcaag 1140

ttgcccgacg tgtatggtgt attccagttt aaagtggatt acaaccggct aggctacaca 1200

cacctgtact cttccactca ggtatccgtg cggccactcc agcacacgca gtatgagcgc 1260

ttcatcccct cggcctaccc ctactacgcc agcgccttct ccatgatgct ggggctcttc 1320

atcttcagca tcgtcttctt gcacatgaag gagaaggaga agtccgactg a 1371

<210> 62
<211> 456
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hDDOST

<400> 62

Met Gly Tyr Phe Arg Cys Ala Gly Ala Gly Ser Phe Gly Arg Arg Arg
1 5 10 15

Lys Met Glu Pro Ser Thr Ala Ala Arg Ala Trp Ala Leu Phe Trp Leu
20 25 30

Leu Leu Pro Leu Leu Gly Ala Val Cys Ala Ser Gly Pro Arg Thr Leu
35 40 45

Val Leu Leu Asp Asn Leu Asn Val Arg Glu Thr His Ser Leu Phe Phe
50 55 60

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

Asp Pro Ser Leu Ser Leu Ile Lys Tyr Gly Glu Phe Leu Tyr Asp Asn
85 90 95

Leu Ile Ile Phe Ser Pro Ser Val Glu Asp Phe Gly Gly Asn Ile Asn
100 105 110

Val Glu Thr Ile Ser Ala Phe Ile Asp Gly Gly Gly Ser Val Leu Val
115 120 125

Ala Ala Ser Ser Asp Ile Gly Asp Pro Leu Arg Glu Leu Gly Ser Glu
130 135 140

Cys Gly Ile Glu Phe Asp Glu Glu Lys Thr Ala Val Ile Asp His His
145 150 155 160

Asn Tyr Asp Ile Ser Asp Leu Gly Gln His Thr Leu Ile Val Ala Asp
165 170 175

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

Asn Pro Ile Leu Phe Arg Gly Val Gly Met Val Ala Asp Pro Asp Asn
195 200 205

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

Phe Pro Asp Lys Pro Ile Thr Gln Tyr Pro His Ala Val Gly Lys Asn
225 230 235 240

Thr Leu Leu Ile Ala Gly Leu Gln Ala Arg Asn Asn Ala Arg Val Ile
245 250 255

Phe Ser Gly Ser Leu Asp Phe Phe Ser Asp Ser Phe Phe Asn Ser Ala
260 265 270

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

Tyr Glu Leu Ala Val Ala Leu Ser Arg Trp Val Phe Lys Glu Glu Gly
290 295 300

Val Leu Arg Val Gly Pro Val Ser His His Arg Val Gly Glu Thr Ala
305 310 315 320

Pro Pro Asn Ala Tyr Thr Val Thr Asp Leu Val Glu Tyr Ser Ile Val
325 330 335

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

Ile Gln Leu Glu Phe Val Arg Ile Asp Pro Phe Val Arg Thr Phe Leu
355 360 365

Lys Lys Lys Gly Gly Lys Tyr Ser Val Gln Phe Lys Leu Pro Asp Val
370 375 380

Tyr Gly Val Phe Gln Phe Lys Val Asp Tyr Asn Arg Leu Gly Tyr Thr
385 390 395 400

His Leu Tyr Ser Ser Thr Gln Val Ser Val Arg Pro Leu Gln His Thr
405 410 415

Gln Tyr Glu Arg Phe Ile Pro Ser Ala Tyr Pro Tyr Tyr Ala Ser Ala
420 425 430

Phe Ser Met Met Leu Gly Leu Phe Ile Phe Ser Ile Val Phe Leu His
435 440 445

Met Lys Glu Lys Glu Lys Ser Asp
450 455

<210> 63
<211> 1023
<212> DNA
<213> Homo sapiens

<220>
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<223> hHSP40

<400> 63
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gccgaggaga agttcaagga gatcgctgag gcctacgacg tgctcagcga cccgcgcaag 180

cgcgagatct tcgaccgcta cggggaggaa ggcctaaagg ggagtggccc cagtggcggt 240

agcggcggtg gtgccaatgg tacctctttc agctacacat tccatggaga ccctcatgcc 300

atgtttgctg agttcttcgg tggcagaaat ccctttgaca ccttttttgg gcagcggaac 360

ggggaggaag gcatggacat tgatgaccca ttctctggct tccctatggg catgggtggc 420

ttcaccaacg tgaactttgg ccgctcccgc tctgcccaag agcccgcccg aaagaagcaa 480

gatcccccag tcacccacga ccttcgagtc tcccttgaag agatctacag cggctgtacc 540

aagaagatga aaatctccca caagcggcta aaccccgacg gaaagagcat tcgaaacgaa 600

gacaaaatat tgaccatcga agtgaagaag gggtggaaag aaggaaccaa aatcactttc 660

cccaaggaag gagaccagac ctccaacaac attccagctg atatcgtctt tgttttaaag 720

gacaagcccc acaatatctt taagagagat ggctctgatg tcatttatcc tgccaggatc 780

agcctccggg aggctctgtg tggctgcaca gtgaacgtcc ccactctgga cggcaggacg 840

atacccgtcg tattcaaaga tgttatcagg cctggcatgc ggcgaaaagt tcctggagaa 900

ggcctccccc tccccaaaac acccgagaaa cgtggggacc tcattattga gtttgaagtg 960

atcttccccg aaaggattcc ccagacatca agaaccgtac ttgagcaggt tcttccaata 1020

tag 1023

<210> 64
<211> 340
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hHSP40

<400> 64

Met Gly Lys Asp Tyr Tyr Gln Thr Leu Gly Leu Ala Arg Gly Ala Ser
1 5 10 15

Asp Glu Glu Ile Lys Arg Ala Tyr Arg Arg Gln Ala Leu Arg Tyr His
20 25 30

Pro Asp Lys Asn Lys Glu Pro Gly Ala Glu Glu Lys Phe Lys Glu Ile
35 40 45

Ala Glu Ala Tyr Asp Val Leu Ser Asp Pro Arg Lys Arg Glu Ile Phe
50 55 60

Asp Arg Tyr Gly Glu Glu Gly Leu Lys Gly Ser Gly Pro Ser Gly Gly
65 70 75 80

Ser Gly Gly Gly Ala Asn Gly Thr Ser Phe Ser Tyr Thr Phe His Gly
85 90 95

Asp Pro His Ala Met Phe Ala Glu Phe Phe Gly Gly Arg Asn Pro Phe
100 105 110

Asp Thr Phe Phe Gly Gln Arg Asn Gly Glu Glu Gly Met Asp Ile Asp
115 120 125

Asp Pro Phe Ser Gly Phe Pro Met Gly Met Gly Gly Phe Thr Asn Val
130 135 140

Asn Phe Gly Arg Ser Arg Ser Ala Gln Glu Pro Ala Arg Lys Lys Gln
145 150 155 160

Asp Pro Pro Val Thr His Asp Leu Arg Val Ser Leu Glu Glu Ile Tyr
165 170 175

Ser Gly Cys Thr Lys Lys Met Lys Ile Ser His Lys Arg Leu Asn Pro
180 185 190

Asp Gly Lys Ser Ile Arg Asn Glu Asp Lys Ile Leu Thr Ile Glu Val
195 200 205

Lys Lys Gly Trp Lys Glu Gly Thr Lys Ile Thr Phe Pro Lys Glu Gly
210 215 220

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

Asp Lys Pro His Asn Ile Phe Lys Arg Asp Gly Ser Asp Val Ile Tyr
245 250 255

Pro Ala Arg Ile Ser Leu Arg Glu Ala Leu Cys Gly Cys Thr Val Asn
260 265 270

Val Pro Thr Leu Asp Gly Arg Thr Ile Pro Val Val Phe Lys Asp Val
275 280 285

Ile Arg Pro Gly Met Arg Arg Lys Val Pro Gly Glu Gly Leu Pro Leu
290 295 300

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

Ile Phe Pro Glu Arg Ile Pro Gln Thr Ser Arg Thr Val Leu Glu Gln
325 330 335

Val Leu Pro Ile
340

<210> 65
<211> 1662
<212> DNA
<213> Homo sapiens

<220>
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<223> hATP5A1

<400> 65
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gtctccagaa atgctttggg ttcatctttc attgctgcaa ggaacttcca tgcctctaac 120
actcatcttc aaaagactgg gactgctgag atgtcctcta ttcttgaaga gcgtattctt 180
ggagctgata cctctgttga tcttgaagaa actgggcgtg tcttaagtat tggtgatggt 240
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aatgataaac taattaagga aggagatata gtgaagagga caggagccat tgtggacgtt 420
ccagttggtg aggagctgtt gggtcgtgta gttgatgccc ttggtaatgc tattgatgga 480
aagggtccaa ttggttccaa gacgcgtagg cgagttggtc tgaaagcccc cggtatcatt 540
cctcgaattt cagtgcggga accaatgcag actggcatta aggctgtgga tagcttggtg 600
ccaattggtc gtggtcagcg tgaactgatt attggtgacc gacagactgg gaaaacctca 660
attgctattg acacaatcat taaccagaaa cgtttcaatg atggatctga tgaaaagaag 720
aagctgtact gtatttatgt tgctattggt caaaagagat ccactgttgc ccagttggtg 780
aagagactta cagatgcaga tgccatgaag tacaccattg tggtgtcggc tacggcctcg 840
gatgctgccc cacttcagta cctggctcct tactctggct gttccatggg agagtatttt 900
agagacaatg gcaaacatgc tttgatcatc tatgacgact tatccaaaca ggctgttgct 960
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tacaaaggta tccgccctgc aattaacgtt ggtctgtctg tatctcgtgt cggatccgct 1260

gcccaaacca gggctatgaa gcaggtagca ggtaccatga agctggaatt ggctcagtat 1320

cgtgaggttg ctgcttttgc ccagttcggt tctgacctcg atgctgccac tcaacaactt 1380

ttgagtcgtg gcgtgcgtct aactgagttg ctgaagcaag gacagtattc tcccatggct 1440

attgaagaac aagtggctgt tatctatgcg ggtgtaaggg gatatcttga taaactggag 1500

cccagcaaga ttacaaagtt tgagaatgct ttcttgtctc atgtcgtcag ccagcaccaa 1560

gccttgttgg gcactatcag ggctgatgga aagatctcag aacaatcaga tgcaaagctg 1620

aaagagattg taacaaattt cttggctgga tttgaagctt aa 1662

<210> 66
<211> 553
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hATP5A1

<400> 66

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Arg Ala Gly Leu Val Ser Arg Asn Ala Leu Gly Ser Ser Phe Ile Ala
20 25 30

Ala Arg Asn Phe His Ala Ser Asn Thr His Leu Gln Lys Thr Gly Thr
35 40 45

Ala Glu Met Ser Ser Ile Leu Glu Glu Arg Ile Leu Gly Ala Asp Thr
50 55 60

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

Ile Ala Arg Val His Gly Leu Arg Asn Val Gln Ala Glu Glu Met Val
85 90 95

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

Asn Val Gly Val Val Val Phe Gly Asn Asp Lys Leu Ile Lys Glu Gly
115 120 125

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

Glu Leu Leu Gly Arg Val Val Asp Ala Leu Gly Asn Ala Ile Asp Gly
145 150 155 160

Lys Gly Pro Ile Gly Ser Lys Thr Arg Arg Arg Val Gly Leu Lys Ala
165 170 175

Pro Gly Ile Ile Pro Arg Ile Ser Val Arg Glu Pro Met Gln Thr Gly
180 185 190

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

Leu Ile Ile Gly Asp Arg Gln Thr Gly Lys Thr Ser Ile Ala Ile Asp
210 215 220

Thr Ile Ile Asn Gln Lys Arg Phe Asn Asp Gly Ser Asp Glu Lys Lys
225 230 235 240

Lys Leu Tyr Cys Ile Tyr Val Ala Ile Gly Gln Lys Arg Ser Thr Val
245 250 255

Ala Gln Leu Val Lys Arg Leu Thr Asp Ala Asp Ala Met Lys Tyr Thr
260 265 270

Ile Val Val Ser Ala Thr Ala Ser Asp Ala Ala Pro Leu Gln Tyr Leu
275 280 285

Ala Pro Tyr Ser Gly Cys Ser Met Gly Glu Tyr Phe Arg Asp Asn Gly
290 295 300

Lys His Ala Leu Ile Ile Tyr Asp Asp Leu Ser Lys Gln Ala Val Ala
305 310 315 320

Tyr Arg Gln Met Ser Leu Leu Leu Arg Arg Pro Pro Gly Arg Glu Ala
325 330 335

Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu Glu Arg Ala
340 345 350

Ala Lys Met Asn Asp Ala Phe Gly Gly Gly Ser Leu Thr Ala Leu Pro
355 360 365

Val Ile Glu Thr Gln Ala Gly Asp Val Ser Ala Tyr Ile Pro Thr Asn
370 375 380

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

Tyr Lys Gly Ile Arg Pro Ala Ile Asn Val Gly Leu Ser Val Ser Arg
405 410 415

Val Gly Ser Ala Ala Gln Thr Arg Ala Met Lys Gln Val Ala Gly Thr
420 425 430

Met Lys Leu Glu Leu Ala Gln Tyr Arg Glu Val Ala Ala Phe Ala Gln
435 440 445

Phe Gly Ser Asp Leu Asp Ala Ala Thr Gln Gln Leu Leu Ser Arg Gly
450 455 460

Val Arg Leu Thr Glu Leu Leu Lys Gln Gly Gln Tyr Ser Pro Met Ala
465 470 475 480

Ile Glu Glu Gln Val Ala Val Ile Tyr Ala Gly Val Arg Gly Tyr Leu
485 490 495

Asp Lys Leu Glu Pro Ser Lys Ile Thr Lys Phe Glu Asn Ala Phe Leu
500 505 510

Ser His Val Val Ser Gln His Gln Ala Leu Leu Gly Thr Ile Arg Ala
515 520 525

Asp Gly Lys Ile Ser Glu Gln Ser Asp Ala Lys Leu Lys Glu Ile Val
530 535 540

Thr Asn Phe Leu Ala Gly Phe Glu Ala
545 550

<210> 67
<211> 3129
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hSERCA2

<400> 67
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ttaccggctg aagaaggaaa aaccttgctg gaacttgtga ttgagcagtt tgaagacttg 180
ctagttagga ttttattact ggcagcatgt atatcttttg ttttggcttg gtttgaagaa 240
ggtgaagaaa caattacagc ctttgtagaa ccttttgtaa ttttactcat attagtagcc 300
aatgcaattg tgggtgtatg gcaggaaaga aatgctgaaa atgccatcga agcccttaag 360
gaatatgagc ctgaaatggg caaagtgtat cgacaggaca gaaagagtgt gcagcggatt 420
aaagctaaag acatagttcc tggtgatatt gtagaaattg ctgttggtga caaagttcct 480
gctgatataa ggttaacttc catcaaatct accacactaa gagttgacca gtcaattctc 540
acaggtgaat ctgtctctgt catcaagcac actgatcccg tccctgaccc acgagctgtc 600
aaccaagata aaaagaacat gctgttttct ggtacaaaca ttgctgctgg gaaagctatg 660
ggagtggtgg tagcaactgg agttaacacc gaaattggca agatccggga tgaaatggtg 720

gcaacagaac aggagagaac acccccttcag caaaaactag atgaatttgg ggaacagctt 780

tccaaagtca tctcccttat ttgcattgca gtctggatca taaatattgg gcacttcaat 840

gacccggttc atggagggtc ctggatcaga ggtgctattt actactttaa aattgcagtg 900

gccctggctg tagcagccat tcctgaaggt ctgcctgcag tcatcaccac ctgcctggct 960

cttggaactc gcagaatggc aaagaaaaat gccattgttc gaagcctccc gtctgtggaa 1020

acccttggtt gtacttctgt tatctgctca gacaagactg gtacacttac aacaaaccag 1080

atgtcagtct gcaggatgtt cattctggac agagtggaag gtgatacttg ttcccttaat 1140

gagtttacca taactggatc aacttatgca cctattggag aagtgcataa agatgataaa 1200

ccagtgaatt gtcaccagta tgatggtctg gtagaattag caacaatttg tgctctttgt 1260

aatgactctg ctttggatta caatgaggca aagggtgtgt atgaaaaagt tggagaagct 1320

acagagactg ctctcacttg cctagtagag aagatgaatg tatttgatac cgaattgaag 1380

ggtctttcta aaatagaacg tgcaaatgcc tgcaactcag tcattaaaca gctgatgaaa 1440

aaggaattca ctctagagtt ttcacgtgac agaaagtcaa tgtcggttta ctgtacacca 1500

aataaaccaa gcaggacatc aatgagcaag atgtttgtga agggtgctcc tgaaggtgtc 1560

attgacaggt gcacccacat tcgagttgga agtactaagg ttcctatgac ctctggagtc 1620

aaacagaaga tcatgtctgt cattcgagag tggggtagtg gcagcgacac actgcgatgc 1680

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gccaacttta ttaaatatga gaccaatctg accttcgttg gctgcgtggg catgctggat 1800

cctccgagaa tcgaggtggc ctcctccgtg aagctgtgcc ggcaagcagg catccgggtc 1860

atcatgatca ctggggacaa caagggcact gctgtggcca tctgtcgccg catcggcatc 1920

ttcgggcagg atgaggacgt gacgtcaaaa gctttcacag gccgggagtt tgatgaactc 1980

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tcccacaagt ctaaaatcgt agaatttctt cagtcttttg atgagattac agctatgact 2100

ggcgatggcg tgaacgatgc tcctgctctg aagaaagccg agattggcat tgctatgggc 2160

tctggcactg cggtggctaa aaccgcctct gagatggtcc tggcggatga caacttctcc 2220

accattgtgg ctgccgttga ggaggggcgg gcaatctaca acaacatgaa acagttcatc 2280

cgctacctca tctcgtccaa cgtcggggaa gttgtctgta ttttcctgac agcagccctt 2340

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tctgttctag taactataga aatgtgtaac gccctcaaca gcttgtccga aaaccagtcc 2760

ttgctgagga tgccccctg ggagaacatc tggctcgtgg gctccatctg cctgtccatg 2820

tcactccact tcctgatcct ctatgtcgaa cccttgccac tcatcttcca gatcacaccg 2880

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gccaccaaat cctgctcgtt ctcggcatgc accgatggga tttcctggcc gtttgtgctg 3060

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<210> 68
<211> 1042
<212> PRT
<213> Homo sapiens

<220>
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<223> hSERCA2

<400> 68

Met Glu Asn Ala His Thr Lys Thr Val Glu Glu Val Leu Gly His Phe
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Gly Val Asn Glu Ser Thr Gly Leu Ser Leu Glu Gln Val Lys Lys Leu
20 25 30

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

Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile
50 55 60

Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu
65 70 75 80

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

Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala
100 105 110

Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys
115 120 125

Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp
130 135 140

Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro
145 150 155 160

Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp

165 170 175

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

Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu
195 200 205

Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val Val
210 215 220

Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val
225 230 235 240

Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu Phe
245 250 255

Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp
260 265 270

Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp
275 280 285

Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val
290 295 300

Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala
305 310 315 320

Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu
325 330 335

Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys
340 345 350

Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile
355 360 365

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

Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp Lys
385 390 395 400

Pro Val Asn Cys His Gln Tyr Asp Gly Leu Val Glu Leu Ala Thr Ile
405 410 415

Cys Ala Leu Cys Asn Asp Ser Ala Leu Asp Tyr Asn Glu Ala Lys Gly
420 425 430

Val Tyr Glu Lys Val Gly Glu Ala Thr Glu Thr Ala Leu Thr Cys Leu

435 440 445

Val Glu Lys Met Asn Val Phe Asp Thr Glu Leu Lys Gly Leu Ser Lys
450 455 460

Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met Lys
465 470 475 480

Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser Val
485 490 495

Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met Phe
500 505 510

Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile Arg
515 520 525

Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys Ile
530 535 540

Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg Cys
545 550 555 560

Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met His
565 570 575

Leu Glu Asp Ser Ala Asn Phe Ile Lys Tyr Glu Thr Asn Leu Thr Phe
580 585 590

Val Gly Cys Val Gly Met Leu Asp Pro Pro Arg Ile Glu Val Ala Ser
595 600 605

Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile Thr
610 615 620

Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly Ile
625 630 635 640

Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg Glu
645 650 655

Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn Ala
660 665 670

Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu
675 680 685

Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val
690 695 700

Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly

705 710 715 720

Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp
725 730 735

Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile
740 745 750

Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val
755 760 765

Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu
770 775 780

Ala Leu Ile Pro Val Gln Leu Leu Trp Val Asn Leu Val Thr Asp Gly
785 790 795 800

Leu Pro Ala Thr Ala Leu Gly Phe Asn Pro Pro Asp Leu Asp Ile Met
805 810 815

Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu
820 825 830

Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val
835 840 845

Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val
850 855 860

Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro
865 870 875 880

Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro Met
885 890 895

Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu
900 905 910

Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp Glu
915 920 925

Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe
930 935 940

Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro
945 950 955 960

Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro Val
965 970 975

Ile Leu Met Asp Glu Thr Leu Lys Phe Val Ala Arg Asn Tyr Leu Glu

980 985 990

Pro Gly Lys Glu Cys Val Gln Pro Ala Thr Lys Ser Cys Ser Phe Ser
995 1000 1005

Ala Cys Thr Asp Gly Ile Ser Trp Pro Phe Val Leu Leu Ile Met
1010 1015 1020

Pro Leu Val Ile Trp Val Tyr Ser Thr Asp Thr Asn Phe Ser Asp
1025 1030 1035

Met Phe Trp Ser
1040

<210> 69
<211> 1938
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hPDIA4

<400> 69
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gaagaggagg aggaggagga agatgatgat gaggaagaag acgacttgga agttaaggaa 180
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gatgcaacct cagcgtctgt gctggccagc aggtttgatg tgagtggcta ccccaccatc 420
aagatcctta agaaggggca ggctgtagac tacgagggct ccagaaccca ggaagaaatt 480
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aaggagctca gcaagcgttc tcctccaatt cccctggcaa aggtcgacgc caccgcagaa 720
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aaggatggag acgatgtcat catcatcggg gtctttaagg gggagagtga cccagcctac 960
cagcaatacc aggatgccgc taacaacctg agagaagatt acaaatttca ccacactttc 1020
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aaggtgtcaa acgatgctaa gcgctacacc aggcgccccc tggtggtcgt ctactacagt 1260

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gagagtggga agaagttcgc catggagcca gaggagtttg actctgacac cctccgcgag 1500

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aagaacaaca agggacccgt caaggtcgtg gtgggaaaga cctttgactc cattgtgatg 1620

gaccccaaga aggacgtcct catcgagttc tacgcgccat ggtgcgggca ctgcaagcag 1680

ctagagcccg tgtacaacag cctggccaag aagtacaagg gccaaaaggg cctggtcatc 1740

gccaagatgg acgccactgc caacgacgtc cccagcgacc gctataaggt ggagggcttc 1800

cccaccatct acttcgcccc cagtggggac aaaaagaacc cagttaaatt tgagggtgga 1860

gacagagatc tggagcattt gagcaagttt atagaagaac atgccacaaa actgagcagg 1920

accaaggaag agctttga 1938

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<212> PRT
<213> Homo sapiens

<220>
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<223> hPDIA4

<400> 70

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Gln Leu Leu Ala Val Ala Gly Ala Glu Gly Pro Asp Glu Asp Ser Ser
20 25 30

Asn Arg Glu Asn Ala Ile Glu Asp Glu Glu Glu Glu Glu Glu Glu Asp
35 40 45

Asp Asp Glu Glu Glu Asp Asp Leu Glu Val Lys Glu Glu Asn Gly Val
50 55 60

Leu Val Leu Asn Asp Ala Asn Phe Asp Asn Phe Val Ala Asp Lys Asp
65 70 75 80

Thr Val Leu Leu Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Gln
85 90 95

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

Pro Pro Ile Pro Val Ala Lys Ile Asp Ala Thr Ser Ala Ser Val Leu
115 120 125

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

Lys Gly Gln Ala Val Asp Tyr Glu Gly Ser Arg Thr Gln Glu Glu Ile
145 150 155 160

Val Ala Lys Val Arg Glu Val Ser Gln Pro Asp Trp Thr Pro Pro Pro
165 170 175

Glu Val Thr Leu Val Leu Thr Lys Glu Asn Phe Asp Glu Val Val Asn
180 185 190

Asp Ala Asp Ile Ile Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His
195 200 205

Cys Lys Lys Leu Ala Pro Glu Tyr Glu Lys Ala Ala Lys Glu Leu Ser
210 215 220

Lys Arg Ser Pro Pro Ile Pro Leu Ala Lys Val Asp Ala Thr Ala Glu
225 230 235 240

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

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

Tyr Gly Ile Val Asp Tyr Met Ile Glu Gln Ser Gly Pro Pro Ser Lys
275 280 285

Glu Ile Leu Thr Leu Lys Gln Val Gln Glu Phe Leu Lys Asp Gly Asp
290 295 300

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

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

His His Thr Phe Ser Thr Glu Ile Ala Lys Phe Leu Lys Val Ser Gln
340 345 350

Gly Gln Leu Val Val Met Gln Pro Glu Lys Phe Gln Ser Lys Tyr Glu
355 360 365

Pro Arg Ser His Met Met Asp Val Gln Gly Ser Thr Gln Asp Ser Ala
370 375 380

Ile Lys Asp Phe Val Leu Lys Tyr Ala Leu Pro Leu Val Gly His Arg
385 390 395 400

Lys Val Ser Asn Asp Ala Lys Arg Tyr Thr Arg Arg Pro Leu Val Val
405 410 415

Val Tyr Tyr Ser Val Asp Phe Ser Phe Asp Tyr Arg Ala Ala Thr Gln
420 425 430

Phe Trp Arg Ser Lys Val Leu Glu Val Ala Lys Asp Phe Pro Glu Tyr
435 440 445

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

Leu Gly Leu Ser Glu Ser Gly Glu Asp Val Asn Ala Ala Ile Leu Asp
465 470 475 480

Glu Ser Gly Lys Lys Phe Ala Met Glu Pro Glu Glu Phe Asp Ser Asp
485 490 495

Thr Leu Arg Glu Phe Val Thr Ala Phe Lys Lys Gly Lys Leu Lys Pro
500 505 510

Val Ile Lys Ser Gln Pro Val Pro Lys Asn Asn Lys Gly Pro Val Lys
515 520 525

Val Val Val Gly Lys Thr Phe Asp Ser Ile Val Met Asp Pro Lys Lys
530 535 540

Asp Val Leu Ile Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Lys Gln
545 550 555 560

Leu Glu Pro Val Tyr Asn Ser Leu Ala Lys Lys Tyr Lys Gly Gln Lys
565 570 575

Gly Leu Val Ile Ala Lys Met Asp Ala Thr Ala Asn Asp Val Pro Ser
580 585 590

Asp Arg Tyr Lys Val Glu Gly Phe Pro Thr Ile Tyr Phe Ala Pro Ser
595 600 605

Gly Asp Lys Lys Asn Pro Val Lys Phe Glu Gly Gly Asp Arg Asp Leu
610 615 620

Glu His Leu Ser Lys Phe Ile Glu Glu His Ala Thr Lys Leu Ser Arg
625 630 635 640

Thr Lys Glu Glu Leu
645

<210> 71
<211> 1941
<212> DNA
<213> Homo sapiens

<220>
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<223> hHSC70 /HSPA8

<400> 71
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tatgtcgcct ttacggacac tgaacggttg atcggtgatg ccgcaaagaa tcaagttgca 180
atgaacccca ccaacacagt ttttgatgcc aaacgtctga ttggacgcag atttgatgat 240
gctgttgtcc agtctgatat gaaacattgg ccctttatgg tggtgaatga tgctggcagg 300
cccaaggtcc aagtagaata caagggagag accaaaagct tctatccaga ggaggtgtct 360
tctatggttc tgacaaagat gaaggaaatt gcagaagcct accttgggaa gactgttacc 420
aatgctgtgg tcacagtgcc agcttacttt aatgactctc agcgtcaggc taccaaagat 480
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ggaggtggca cttttgatgt gtcaatcctc actattgagg atggaatctt tgaggtcaag 660
tctacagctg gagacaccca cttgggtgga gaagattttg acaaccgaat ggtcaaccat 720
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aagattaacg atgaggacaa acagaagatt ctggacaagt gtaatgaaat tatcaactgg 1740

cttgataaga atcagactgc tgagaaggaa gaatttgaac atcaacagaa agagctggag 1800

aaagtttgca accccatcat caccaagctg taccagagtg caggaggcat gccaggagga 1860

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accattgaag aggttgatta a 1941

<210> 72
<211> 646
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hHSC70 /HSPA8

<400> 72

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Cys Val Gly Val Phe Gln His Gly Lys Val Glu Ile Ile Ala Asn Asp
20 25 30

Gln Gly Asn Arg Thr Thr Pro Ser Tyr Val Ala Phe Thr Asp Thr Glu
35 40 45

Arg Leu Ile Gly Asp Ala Ala Lys Asn Gln Val Ala Met Asn Pro Thr
50 55 60

Asn Thr Val Phe Asp Ala Lys Arg Leu Ile Gly Arg Arg Phe Asp Asp
65 70 75 80

Ala Val Val Gln Ser Asp Met Lys His Trp Pro Phe Met Val Val Asn
85 90 95

Asp Ala Gly Arg Pro Lys Val Gln Val Glu Tyr Lys Gly Glu Thr Lys
100 105 110

Ser Phe Tyr Pro Glu Glu Val Ser Ser Met Val Leu Thr Lys Met Lys
115 120 125

Glu Ile Ala Glu Ala Tyr Leu Gly Lys Thr Val Thr Asn Ala Val Val
130 135 140

Thr Val Pro Ala Tyr Phe Asn Asp Ser Gln Arg Gln Ala Thr Lys Asp
145 150 155 160

Ala Gly Thr Ile Ala Gly Leu Asn Val Leu Arg Ile Ile Asn Glu Pro
165 170 175

Thr Ala Ala Ala Ile Ala Tyr Gly Leu Asp Lys Lys Val Gly Ala Glu

180 185 190

Arg Asn Val Leu Ile Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser
195 200 205

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

Asp Thr His Leu Gly Gly Glu Asp Phe Asp Asn Arg Met Val Asn His
225 230 235 240

Phe Ile Ala Glu Phe Lys Arg Lys His Lys Lys Asp Ile Ser Glu Asn
245 250 255

Lys Arg Ala Val Arg Arg Leu Arg Thr Ala Cys Glu Arg Ala Lys Arg
260 265 270

Thr Leu Ser Ser Ser Thr Gln Ala Ser Ile Glu Ile Asp Ser Leu Tyr
275 280 285

Glu Gly Ile Asp Phe Tyr Thr Ser Ile Thr Arg Ala Arg Phe Glu Glu
290 295 300

Leu Asn Ala Asp Leu Phe Arg Gly Thr Leu Asp Pro Val Glu Lys Ala
305 310 315 320

Leu Arg Asp Ala Lys Leu Asp Lys Ser Gln Ile His Asp Ile Val Leu
325 330 335

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

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

Val Ala Tyr Gly Ala Ala Val Gln Ala Ala Ile Leu Ser Gly Asp Lys
370 375 380

Ser Glu Asn Val Gln Asp Leu Leu Leu Leu Asp Val Thr Pro Leu Ser
385 390 395 400

Leu Gly Ile Glu Thr Ala Gly Gly Val Met Thr Val Leu Ile Lys Arg
405 410 415

Asn Thr Thr Ile Pro Thr Lys Gln Thr Gln Thr Phe Thr Thr Tyr Ser
420 425 430

Asp Asn Gln Pro Gly Val Leu Ile Gln Val Tyr Glu Gly Glu Arg Ala
435 440 445

Met Thr Lys Asp Asn Asn Leu Leu Gly Lys Phe Glu Leu Thr Gly Ile

450 455 460

Pro Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile
465 470 475 480

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

Lys Glu Asn Lys Ile Thr Ile Thr Asn Asp Lys Gly Arg Leu Ser Lys
500 505 510

Glu Asp Ile Glu Arg Met Val Gln Glu Ala Glu Lys Tyr Lys Ala Glu
515 520 525

Asp Glu Lys Gln Arg Asp Lys Val Ser Ser Lys Asn Ser Leu Glu Ser
530 535 540

Tyr Ala Phe Asn Met Lys Ala Thr Val Glu Asp Glu Lys Leu Gln Gly
545 550 555 560

Lys Ile Asn Asp Glu Asp Lys Gln Lys Ile Leu Asp Lys Cys Asn Glu
565 570 575

Ile Ile Asn Trp Leu Asp Lys Asn Gln Thr Ala Glu Lys Glu Glu Phe
580 585 590

Glu His Gln Gln Lys Glu Leu Glu Lys Val Cys Asn Pro Ile Ile Thr
595 600 605

Lys Leu Tyr Gln Ser Ala Gly Gly Met Pro Gly Gly Met Pro Gly Gly
610 615 620

Phe Pro Gly Gly Gly Ala Pro Pro Ser Gly Gly Ala Ser Ser Gly Pro
625 630 635 640

Thr Ile Glu Glu Val Asp
645

<210> 73
<211> 3000
<212> DNA
<213> Homo sapiens

<220>
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<223> hHYOU1

<400> 73
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ggcagtgagt ccatgaaggt ggccattgtc aaacctggag tgcccatgga aattgtcttg 180

aataaggaat ctcggaggaa aacaccggtg atcgtgaccc tgaaagaaaa tgaaagattc 240

tttggagaca gtgcagcaag catggcgatt aagaatccaa aggctacgct acgttacttc 300

cagcacctcc tggggaagca ggcagataac ccccatgtag ctctttacca ggcccgcttc 360

ccggagcacg agctgacttt cgacccacag aggcagactg tgcactttca gatcagctcg 420

cagctgcagt tctcacctga ggaagtgttg ggcatggttc tcaattattc tcgttctcta 480

gctgaagatt ttgcagagca gcccatcaag gatgcagtga tcaccgtgcc agtcttcttc 540

aaccaggccg agcgccgagc tgtgctgcag gctgctcgta tggctggcct caaagtgctg 600

cagctcatca atgacaacac cgccactgcc ctcagctatg gtgtcttccg ccggaaagat 660

attaacacca ctgcccagaa tatcatgttc tatgacatgg gctcaggcag caccgtatgc 720

accattgtga cctaccagat ggtgaagact aaggaagctg ggatgcagcc acagctgcag 780

atccggggag taggatttga ccgtaccctg gggggcctgg agatggagct ccggcttcga 840

gaacgcctgg ctgggctttt caatgagcag cgcaagggtc agagagcaaa ggatgtgcgg 900

gagaacccgc gtgccatggc caagctgctg cgtgaggcta atcggctcaa aaccgtcctc 960

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gcaaaagtga ctcgtgtgga atttgaggag ttgtgtgcag acttgtttga gcgggtgcct 1080

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gtccaggagg aagaggagag ccctgcagag gggagcaagg acgagcctgg ggagcaggtg 1860

gagctcaagg aggaagctga ggccccagtg gaggatggct ctcagccccc acccccctgaa 1920

cctaagggag atgcaacccc tgagggagaa aaggccacag aaaaagaaaa tggggacaag 1980

tctgaggccc agaaaccaag tgagaaggca gaggcagggc ctgagggcgt cgctccagcc 2040

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gaagtgtcca cagaggagca gcgtgaggag atctctggga agctcagcgc cgcatccacc 2340

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gaggtgcagt atctgctcaa taaggccaag tttaccaagc cccggccccg gcctaaggac 2760

aagaatggga cccgggcaga gccacccctc aatgccagtg ccagtgacca gggggagaag 2820

gtcatccctc cagcaggcca gactgaagat gcagagccca tttcagaacc tgagaaagta 2880

gagactggat ccgagccagg agacactgag cctttggagt taggaggtcc tggagcagaa 2940

cctgaacaga aagaacaatc gacaggacag aagcggcctt tgaagaacga cgaactataa 3000

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<211> 999
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hHYOU1

<400> 74

Met Ala Asp Lys Val Arg Arg Gln Arg Pro Arg Arg Arg Val Cys Trp
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20 25 30

Leu Ala Val Met Ser Val Asp Leu Gly Ser Glu Ser Met Lys Val Ala
35 40 45

Ile Val Lys Pro Gly Val Pro Met Glu Ile Val Leu Asn Lys Glu Ser
50 55 60

Arg Arg Lys Thr Pro Val Ile Val Thr Leu Lys Glu Asn Glu Arg Phe
65 70 75 80

Phe Gly Asp Ser Ala Ala Ser Met Ala Ile Lys Asn Pro Lys Ala Thr
85 90 95

Leu Arg Tyr Phe Gln His Leu Leu Gly Lys Gln Ala Asp Asn Pro His
100 105 110

Val Ala Leu Tyr Gln Ala Arg Phe Pro Glu His Glu Leu Thr Phe Asp

115 120 125

Pro Gln Arg Gln Thr Val His Phe Gln Ile Ser Ser Gln Leu Gln Phe
130 135 140

Ser Pro Glu Glu Val Leu Gly Met Val Leu Asn Tyr Ser Arg Ser Leu
145 150 155 160

Ala Glu Asp Phe Ala Glu Gln Pro Ile Lys Asp Ala Val Ile Thr Val
165 170 175

Pro Val Phe Phe Asn Gln Ala Glu Arg Arg Ala Val Leu Gln Ala Ala
180 185 190

Arg Met Ala Gly Leu Lys Val Leu Gln Leu Ile Asn Asp Asn Thr Ala
195 200 205

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

Ala Gln Asn Ile Met Phe Tyr Asp Met Gly Ser Gly Ser Thr Val Cys
225 230 235 240

Thr Ile Val Thr Tyr Gln Met Val Lys Thr Lys Glu Ala Gly Met Gln
245 250 255

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

Leu Glu Met Glu Leu Arg Leu Arg Glu Arg Leu Ala Gly Leu Phe Asn
275 280 285

Glu Gln Arg Lys Gly Gln Arg Ala Lys Asp Val Arg Glu Asn Pro Arg
290 295 300

Ala Met Ala Lys Leu Leu Arg Glu Ala Asn Arg Leu Lys Thr Val Leu
305 310 315 320

Ser Ala Asn Ala Asp His Met Ala Gln Ile Glu Gly Leu Met Asp Asp
325 330 335

Val Asp Phe Lys Ala Lys Val Thr Arg Val Glu Phe Glu Glu Leu Cys
340 345 350

Ala Asp Leu Phe Glu Arg Val Pro Gly Pro Val Gln Gln Ala Leu Gln
355 360 365

Ser Ala Glu Met Ser Leu Asp Glu Ile Glu Gln Val Ile Leu Val Gly
370 375 380

Gly Ala Thr Arg Val Pro Arg Val Gln Glu Val Leu Leu Lys Ala Val

385 390 395 400

Gly Lys Glu Glu Leu Gly Lys Asn Ile Asn Ala Asp Glu Ala Ala Ala
405 410 415

Met Gly Ala Val Tyr Gln Ala Ala Ala Leu Ser Lys Ala Phe Lys Val
420 425 430

Lys Pro Phe Val Val Arg Asp Ala Val Val Tyr Pro Ile Leu Val Glu
435 440 445

Phe Thr Arg Glu Val Glu Glu Glu Pro Gly Ile His Ser Leu Lys His
450 455 460

Asn Lys Arg Val Leu Phe Ser Arg Met Gly Pro Tyr Pro Gln Arg Lys
465 470 475 480

Val Ile Thr Phe Asn Arg Tyr Ser His Asp Phe Asn Phe His Ile Asn
485 490 495

Tyr Gly Asp Leu Gly Phe Leu Gly Pro Glu Asp Leu Arg Val Phe Gly
500 505 510

Ser Gln Asn Leu Thr Thr Val Lys Leu Lys Gly Val Gly Asp Ser Phe
515 520 525

Lys Lys Tyr Pro Asp Tyr Glu Ser Lys Gly Ile Lys Ala His Phe Asn
530 535 540

Leu Asp Glu Ser Gly Val Leu Ser Leu Asp Arg Val Glu Ser Val Phe
545 550 555 560

Glu Thr Leu Val Glu Asp Ser Ala Glu Glu Glu Ser Thr Leu Thr Lys
565 570 575

Leu Gly Asn Thr Ile Ser Ser Leu Phe Gly Gly Gly Thr Thr Pro Asp
580 585 590

Ala Lys Glu Asn Gly Thr Asp Thr Val Gln Glu Glu Glu Glu Ser Pro
595 600 605

Ala Glu Gly Ser Lys Asp Glu Pro Gly Glu Gln Val Glu Leu Lys Glu
610 615 620

Glu Ala Glu Ala Pro Val Glu Asp Gly Ser Gln Pro Pro Pro Pro Glu
625 630 635 640

Pro Lys Gly Asp Ala Thr Pro Glu Gly Glu Lys Ala Thr Glu Lys Glu
645 650 655

Asn Gly Asp Lys Ser Glu Ala Gln Lys Pro Ser Glu Lys Ala Glu Ala

660 665 670

Gly Pro Glu Gly Val Ala Pro Ala Pro Glu Gly Glu Lys Lys Gln Lys
675 680 685

Pro Ala Arg Lys Arg Arg Met Val Glu Glu Ile Gly Val Glu Leu Val
690 695 700

Val Leu Asp Leu Pro Asp Leu Pro Glu Asp Lys Leu Ala Gln Ser Val
705 710 715 720

Gln Lys Leu Gln Asp Leu Thr Leu Arg Asp Leu Glu Lys Gln Glu Arg
725 730 735

Glu Lys Ala Ala Asn Ser Leu Glu Ala Phe Ile Phe Glu Thr Gln Asp
740 745 750

Lys Leu Tyr Gln Pro Glu Tyr Gln Glu Val Ser Thr Glu Glu Gln Arg
755 760 765

Glu Glu Ile Ser Gly Lys Leu Ser Ala Ala Ser Thr Trp Leu Glu Asp
770 775 780

Glu Gly Val Gly Ala Thr Thr Val Met Leu Lys Glu Lys Leu Ala Glu
785 790 795 800

Leu Arg Lys Leu Cys Gln Gly Leu Phe Phe Arg Val Glu Glu Arg Lys
805 810 815

Lys Trp Pro Glu Arg Leu Ser Ala Leu Asp Asn Leu Leu Asn His Ser
820 825 830

Ser Met Phe Leu Lys Gly Ala Arg Leu Ile Pro Glu Met Asp Gln Ile
835 840 845

Phe Thr Glu Val Glu Met Thr Thr Leu Glu Lys Val Ile Asn Glu Thr
850 855 860

Trp Ala Trp Lys Asn Ala Thr Leu Ala Glu Gln Ala Lys Leu Pro Ala
865 870 875 880

Thr Glu Lys Pro Val Leu Leu Ser Lys Asp Ile Glu Ala Lys Met Met
885 890 895

Ala Leu Asp Arg Glu Val Gln Tyr Leu Leu Asn Lys Ala Lys Phe Thr
900 905 910

Lys Pro Arg Pro Arg Pro Lys Asp Lys Asn Gly Thr Arg Ala Glu Pro
915 920 925

Pro Leu Asn Ala Ser Ala Ser Asp Gln Gly Glu Lys Val Ile Pro Pro

930 935 940

Ala Gly Gln Thr Glu Asp Ala Glu Pro Ile Ser Glu Pro Glu Lys Val
945 950 955 960

Glu Thr Gly Ser Glu Pro Gly Asp Thr Glu Pro Leu Glu Leu Gly Gly
965 970 975

Pro Gly Ala Glu Pro Glu Gln Lys Glu Gln Ser Thr Gly Gln Lys Arg
980 985 990

Pro Leu Lys Asn Asp Glu Leu
995

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<211> 1305
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hCMP-SAS

<400> 75
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aagaacatta agcacctggc gggggtcccg ctcattggct gggtcctgcg tgcggccctg 240

gattcagggg ccttccagag tgtatgggtt tcgacagacc atgatgaaat tgagaatgtg 300

gccaaacaat ttggtgcaca agttcatcga agaagttctg aagtttcaaa agacagctct 360

acctcactag atgccatcat agaatttctt aattatcata atgaggttga cattgtagga 420

aatattcaag ctacttctcc atgtttacat cctactgatc ttcaaaaagt tgcagaaatg 480

attcgagaag aaggatatga ttctgttttc tctgttgtga gacgccatca gtttcgatgg 540

agtgaaattc agaaaggagt tcgtgaagtg accgaacctc tgaatttaaa tccagctaaa 600

cggcctcgtc gacaagactg ggatggagaa ttatatgaaa atggctcatt ttattttgct 660

aaaagacatt tgatagagat gggttacttg cagggtggaa aaatggcata ctacgaaatg 720

cgagctgaac atagtgtgga tatagatgtg gatattgatt ggcctattgc agagcaaaga 780

gtattaagat atggctattt tggcaaagag aagcttaagg aaataaaact tttggtttgc 840

aatattgatg gatgtctcac caatggccac atttatgtat caggagacca aaaagaaata 900

atatcttatg atgtaaaaga tgctattggg ataagtttat taaagaaaag tggtattgag 960

gtgaggctaa tctcagaaag ggcctgttca aagcagacgc tgtcttcttt aaaactggat 1020

tgcaaaatgg aagtcagtgt atcagacaag ctagcagttg tagatgaatg gagaaaagaa 1080

atgggcctgt gctggaaaga agtggcatat cttggaaatg aagtgtctga tgaagagtgc 1140

ttgaagagag tgggcctaag tggcgctcct gctgatgcct gttctactgc ccagaaggct 1200

gttggataca tttgcaaatg taatggtggc cgtggtgcca tccgagaatt tgcagagcac 1260

atttgcctac taatggaaaa ggttaataat tcatgccaaa aatag 1305

<210> 76
<211> 434
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hCMP-SAS

<400> 76

Met Asp Ser Val Glu Lys Gly Ala Ala Thr Ser Val Ser Asn Pro Arg
1 5 10 15

Gly Arg Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg
20 25 30

Gly Gly Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu
35 40 45

Ile Leu Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys
50 55 60

His Leu Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu
65 70 75 80

Asp Ser Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu
85 90 95

Ile Glu Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser
100 105 110

Ser Glu Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu
115 120 125

Phe Leu Asn Tyr His Asn Glu Val Asp Ile Val Gly Asn Ile Gln Ala
130 135 140

Thr Ser Pro Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met
145 150 155 160

Ile Arg Glu Glu Gly Tyr Asp Ser Val Phe Ser Val Val Arg Arg His
165 170 175

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

Pro Leu Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp

195 200 205

Gly Glu Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu
210 215 220

Ile Glu Met Gly Tyr Leu Gln Gly Gly Lys Met Ala Tyr Tyr Glu Met
225 230 235 240

Arg Ala Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile
245 250 255

Ala Glu Gln Arg Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu
260 265 270

Lys Glu Ile Lys Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn
275 280 285

Gly His Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp
290 295 300

Val Lys Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu
305 310 315 320

Val Arg Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser
325 330 335

Leu Lys Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala
340 345 350

Val Val Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val
355 360 365

Ala Tyr Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val
370 375 380

Gly Leu Ser Gly Ala Pro Ala Asp Ala Cys Ser Thr Ala Gln Lys Ala
385 390 395 400

Val Gly Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu
405 410 415

Phe Ala Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys
420 425 430

Gln Lys

<210> 77
<211> 1353
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hBeclin-1

<400> 77
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tgcagccagc ccctgaaact ggacacgagt ttcaagatcc tggaccgtgt caccatccag 120

gaactcacag ctccattact taccacagcc caggcgaaac caggagagac ccaggaggaa 180

gagactaact caggagagga gccatttatt gaaactcctc gccaggatgg tgtctctcgc 240

agattcatcc ccccagccag gatgatgtcc acagaaagtg ccaacagctt cactctgatt 300

ggggaggcat ctgatggcgg caccatggag aacctcagcc gaagactgaa ggtcactggg 360

gacctttttg acatcatgtc gggccagaca gatgtggatc acccactctg tgaggaatgc 420

acagatactc ttttagacca gctggacact cagctcaacg tcactgaaaa tgagtgtcag 480

aactacaaac gctgtttgga gatcttagag caaatgaatg aggatgacag tgaacagtta 540

cagatggagc taaaggagct ggcactagag gaggagaggc tgatccagga gctggaagac 600

gtggaaaaga accgcaagat agtggcagaa aatctcgaga aggtccaggc tgaggctgag 660

agactggatc aggaggaagc tcagtatcag agagaataca gtgaatttaa acgacagcag 720

ctggagctgg atgatgagct gaagagtgtt gaaaaccaga tgcgttatgc ccagacgcag 780

ctggataagc tgaagaaaac caacgtcttt aatgcaacct tccacatctg gcacagtgga 840

cagtttggca caatcaataa cttcaggctg ggtcgcctgc ccagtgttcc cgtggaatgg 900

aatgagatta atgctgcttg gggccagact gtgttgctgc tccatgctct ggccaataag 960

atgggtctga aatttcagag ataccgactt gttccttacg gaaaccattc atatctggag 1020

tctctgacag acaaatctaa ggagctgccg ttatactgtt ctgggggttt gcggtttttc 1080

tgggacaaca agtttgacca tgcaatggtg gctttcctgg actgtgtgca gcagttcaaa 1140

gaagaggttg agaaaggcga gacacgtttt tgtcttccct acaggatgga tgtggagaaa 1200

ggcaagattg aagacacagg aggcagtggc ggctcctatt ccatcaaaac ccagtttaac 1260

tctgaggagc agtggacaaa agctctcaag ttcatgctga cgaatcttaa gtggggtctt 1320

gcttgggtgt cctcacaatt ttataacaaa tga 1353

<210> 78
<211> 450
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hBeclin-1

<400> 78

Met Glu Gly Ser Lys Thr Ser Asn Asn Ser Thr Met Gln Val Ser Phe
1 5 10 15

Val Cys Gln Arg Cys Ser Gln Pro Leu Lys Leu Asp Thr Ser Phe Lys
20 25 30

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

Thr Ala Gln Ala Lys Pro Gly Glu Thr Gln Glu Glu Glu Thr Asn Ser
50 55 60

Gly Glu Glu Pro Phe Ile Glu Thr Pro Arg Gln Asp Gly Val Ser Arg
65 70 75 80

Arg Phe Ile Pro Pro Ala Arg Met Met Ser Thr Glu Ser Ala Asn Ser
85 90 95

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

Ser Arg Arg Leu Lys Val Thr Gly Asp Leu Phe Asp Ile Met Ser Gly
115 120 125

Gln Thr Asp Val Asp His Pro Leu Cys Glu Glu Cys Thr Asp Thr Leu
130 135 140

Leu Asp Gln Leu Asp Thr Gln Leu Asn Val Thr Glu Asn Glu Cys Gln
145 150 155 160

Asn Tyr Lys Arg Cys Leu Glu Ile Leu Glu Gln Met Asn Glu Asp Asp
165 170 175

Ser Glu Gln Leu Gln Met Glu Leu Lys Glu Leu Ala Leu Glu Glu Glu
180 185 190

Arg Leu Ile Gln Glu Leu Glu Asp Val Glu Lys Asn Arg Lys Ile Val
195 200 205

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

Glu Glu Ala Gln Tyr Gln Arg Glu Tyr Ser Glu Phe Lys Arg Gln Gln
225 230 235 240

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

Ala Gln Thr Gln Leu Asp Lys Leu Lys Lys Thr Asn Val Phe Asn Ala
260 265 270

Thr Phe His Ile Trp His Ser Gly Gln Phe Gly Thr Ile Asn Asn Phe
275 280 285

Arg Leu Gly Arg Leu Pro Ser Val Pro Val Glu Trp Asn Glu Ile Asn
290 295 300

Ala Ala Trp Gly Gln Thr Val Leu Leu Leu His Ala Leu Ala Asn Lys
305 310 315 320

Met Gly Leu Lys Phe Gln Arg Tyr Arg Leu Val Pro Tyr Gly Asn His
325 330 335

Ser Tyr Leu Glu Ser Leu Thr Asp Lys Ser Lys Glu Leu Pro Leu Tyr
340 345 350

Cys Ser Gly Gly Leu Arg Phe Phe Trp Asp Asn Lys Phe Asp His Ala
355 360 365

Met Val Ala Phe Leu Asp Cys Val Gln Gln Phe Lys Glu Glu Val Glu
370 375 380

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

Gly Lys Ile Glu Asp Thr Gly Gly Ser Gly Gly Ser Tyr Ser Ile Lys
405 410 415

Thr Gln Phe Asn Ser Glu Glu Gln Trp Thr Lys Ala Leu Lys Phe Met
420 425 430

Leu Thr Asn Leu Lys Trp Gly Leu Ala Trp Val Ser Ser Gln Phe Tyr
435 440 445

Asn Lys
450

<210> 79
<211> 1077
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hERdj3

<400> 79
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attaaaaagg cctataggaa actagccctg cagcttcatc ccgaccggaa ccctgatgat 180
ccacaagccc aggagaaatt ccaggatctg ggtgctgctt atgaggttct gtcagatagt 240
gagaaacgga aacagtacga tacttatggt gaagaaggat taaaagatgg tcatcagagc 300
tcccatggag acatttttc acacttcttt ggggattttg gtttcatgtt tggaggaacc 360

cctcgtcagc aagacagaaa tattccaaga ggaagtgata ttattgtaga tctagaagtc 420

actttggaag aagtatatgc aggaaatttt gtggaagtag ttagaaacaa acctgtggca 480

aggcaggctc ctggcaaacg gaagtgcaat tgtcggcaag agatgcggac cacccagctg 540

ggccctgggc gcttccaaat gacccaggag gtggtctgcg acgaatgccc taatgtcaaa 600

ctagtgaatg aagaacgaac gctggaagta gaaatagagc ctggggtgag agacggcatg 660

gagtacccct ttattggaga aggtgagcct cacgtggatg gggagcctgg agatttacgg 720

ttccgaatca aagttgtcaa gcacccaata tttgaaagga gaggagatga tttgtacaca 780

aatgtgacaa tctcattagt tgagtcactg gttggctttg agatggatat tactcacttg 840

gatggtcaca aggtacatat ttcccgggat aagatcacca ggccaggagc gaagctatgg 900

aagaaagggg aagggctccc caactttgac aacaacaata tcaagggctc tttgataatc 960

acttttgatg tggattttcc aaaagaacag ttaacagagg aagcgagaga aggtatcaaa 1020

cagctactga aacaagggtc agtgcagaag gtatacaatg gactgcaagg atattga 1077

<210> 80
<211> 358
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hERdj3

<400> 80

Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu
1 5 10 15

Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val
20 25 30

Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu
35 40 45

Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln
50 55 60

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

Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp
85 90 95

Gly His Gln Ser Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp
100 105 110

Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile
115 120 125

Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu
130 135 140

Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala
145 150 155 160

Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg
165 170 175

Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val
180 185 190

Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu
195 200 205

Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe
210 215 220

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

Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp
245 250 255

Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu Val Gly
260 265 270

Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val His Ile Ser
275 280 285

Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu
290 295 300

Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile
305 310 315 320

Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg
325 330 335

Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr
340 345 350

Asn Gly Leu Gln Gly Tyr
355

<210> 81
<211> 1764
<212> DNA
<213> Cricetulus griseus

<220>

<221> misc_feature
<223> CHO_AGE

<400> 81
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aaaggcggca tgcttctgag ctcaggacag gcctgttgtg aggagaaggg cctggatgct 180
gaggacggtg gtggggacag caatgacctc agcagcgtca gcgagaccac agacagcaca 240
gatgtcaaag acagctcaga gacctctctg actctgcctc ctagagcctc accctgccct 300
gcaggctttt ggattcttga aactggagct agccaaagac agtttcaggc ctggtttact 360
gcggaggagg gtccgctgcc accttcgcct ccttttggcc ctgaactgac ttgcagatgg 420
agcagtctag aacagctaaa ggacatcttg gcgctcggag cacagcctca ctgggtccac 480
aagctccaag gcttctggtt tgttgaggtt atcttgtcag caaaaagatt acaggacatg 540
gagaaggagc gggcttcact gcaggcctgg aaggatcgtg tggcaaagga acttgacagc 600
gtggtcgctt tctggctgca gcactcccat gatcaggaac acgggggttt cttcacatgc 660
cttgcccgca atgggcaggt ctatgatgac cttaaatata tctggctgca ggggagacag 720
gtatggatgt attgtcgctt gtaccgcaat tttgagcgct tccgccgcgc tgagcttcta 780
gatgctgcaa aagcaggtgg tgagtttttg ctgcgttttg cacgggtggc accgcctgcc 840
aagaagtgtg cctttgtgtt gactcgggac ggccgtccag tgaaggtgca gcggaccatt 900
ttcagcgagt gtttctacac cattgctatg aatgagcttt ggagagtaac aaaggaatca 960
cgttaccaga atgaagctgt ggagatgatg gaccagattg tccactgggt acgggaagac 1020
ccagctgggc taggccggcc tcagctctca gggaccccgg atgcagagtc catggcagtg 1080
cccatgatgc tgatgaatct ggtggaccag ctttccgagg aagatgaggc actgacaaag 1140
aaatatgcag agctatggga ctggtgtgcc cagaggattc ttcagcatgt gcagagggat 1200
ggaaaagcta tactagagaa tgtatctcat gatggcaagg aactcactgg ttgccttgga 1260
agacatcaga acccaggcca cgcaatagag gctggctggt tcctgctcca gtatgcccgc 1320
aagaaaggtg acgccaaact tcgtgcacac atcatcgaca agtttctctt gttgcctttc 1380
cgctctggat gggacgctga gcatgggggc ctcttctact tccaggatgt tgatggtttc 1440
tgccccaccc agctggagtg ggacatgaag ctgtggtggc cacacaatga agccatgatt 1500
tccttcctaa tgggttacag ggacagtggt gacccagcct tgctacaaat cttcaatcag 1560
gtggctgagt acaccttcaa gcattttcat gatcccgaga acggcgaatg gttcggctat 1620
ctgaaccgag agggcaaggt ggccctcaac tttaagggag gcccatttaa aggctgcttc 1680
cacgtgccgc ggtgcctggc catgtgcgag aagatgttgg gagacctgct ccaccgtggg 1740
agcgcccctg ctggctcgaa ataa 1764

<210> 82
<211> 587
<212> PRT

<213> Cricetulus griseus

<220>
<221> MISC_FEATURE
<223> CHO_AGE

<400> 82

Met Lys Gly Ile Leu Trp Gly Ala Phe Cys Gly Lys Ala Asn Glu Leu
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Arg Gln Arg Leu Glu Leu Lys Glu Lys Gly Arg His Val Val Leu Glu
20 25 30

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

Gly Gln Ala Cys Cys Glu Glu Lys Gly Leu Asp Ala Glu Asp Gly Gly
50 55 60

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

Asp Val Lys Asp Ser Ser Glu Thr Ser Leu Thr Leu Pro Pro Arg Ala
85 90 95

Ser Pro Cys Pro Ala Gly Phe Trp Ile Leu Glu Thr Gly Ala Ser Gln
100 105 110

Arg Gln Phe Gln Ala Trp Phe Thr Ala Glu Glu Gly Pro Leu Pro Pro
115 120 125

Ser Pro Pro Phe Gly Pro Glu Leu Thr Cys Arg Trp Ser Ser Leu Glu
130 135 140

Gln Leu Lys Asp Ile Leu Ala Leu Gly Ala Gln Pro His Trp Val His
145 150 155 160

Lys Leu Gln Gly Phe Trp Phe Val Glu Val Ile Leu Ser Ala Lys Arg
165 170 175

Leu Gln Asp Met Glu Lys Glu Arg Ala Ser Leu Gln Ala Trp Lys Asp
180 185 190

Arg Val Ala Lys Glu Leu Asp Ser Val Val Ala Phe Trp Leu Gln His
195 200 205

Ser His Asp Gln Glu His Gly Gly Phe Phe Thr Cys Leu Ala Arg Asn
210 215 220

Gly Gln Val Tyr Asp Asp Leu Lys Tyr Ile Trp Leu Gln Gly Arg Gln
225 230 235 240

Val Trp Met Tyr Cys Arg Leu Tyr Arg Asn Phe Glu Arg Phe Arg Arg
245 250 255

Ala Glu Leu Leu Asp Ala Ala Lys Ala Gly Gly Glu Phe Leu Leu Arg
260 265 270

Phe Ala Arg Val Ala Pro Pro Ala Lys Lys Cys Ala Phe Val Leu Thr
275 280 285

Arg Asp Gly Arg Pro Val Lys Val Gln Arg Thr Ile Phe Ser Glu Cys
290 295 300

Phe Tyr Thr Ile Ala Met Asn Glu Leu Trp Arg Val Thr Lys Glu Ser
305 310 315 320

Arg Tyr Gln Asn Glu Ala Val Glu Met Met Asp Gln Ile Val His Trp
325 330 335

Val Arg Glu Asp Pro Ala Gly Leu Gly Arg Pro Gln Leu Ser Gly Thr
340 345 350

Pro Asp Ala Glu Ser Met Ala Val Pro Met Met Leu Met Asn Leu Val
355 360 365

Asp Gln Leu Ser Glu Glu Asp Glu Ala Leu Thr Lys Lys Tyr Ala Glu
370 375 380

Leu Trp Asp Trp Cys Ala Gln Arg Ile Leu Gln His Val Gln Arg Asp
385 390 395 400

Gly Lys Ala Ile Leu Glu Asn Val Ser His Asp Gly Lys Glu Leu Thr
405 410 415

Gly Cys Leu Gly Arg His Gln Asn Pro Gly His Ala Ile Glu Ala Gly
420 425 430

Trp Phe Leu Leu Gln Tyr Ala Arg Lys Lys Gly Asp Ala Lys Leu Arg
435 440 445

Ala His Ile Ile Asp Lys Phe Leu Leu Leu Pro Phe Arg Ser Gly Trp
450 455 460

Asp Ala Glu His Gly Gly Leu Phe Tyr Phe Gln Asp Val Asp Gly Phe
465 470 475 480

Cys Pro Thr Gln Leu Glu Trp Asp Met Lys Leu Trp Trp Pro His Asn
485 490 495

Glu Ala Met Ile Ser Phe Leu Met Gly Tyr Arg Asp Ser Gly Asp Pro
500 505 510

Ala Leu Leu Gln Ile Phe Asn Gln Val Ala Glu Tyr Thr Phe Lys His
515 520 525

Phe His Asp Pro Glu Asn Gly Glu Trp Phe Gly Tyr Leu Asn Arg Glu
530 535 540

Gly Lys Val Ala Leu Asn Phe Lys Gly Gly Pro Phe Lys Gly Cys Phe
545 550 555 560

His Val Pro Arg Cys Leu Ala Met Cys Glu Lys Met Leu Gly Asp Leu
565 570 575

Leu His Arg Gly Ser Ala Pro Ala Gly Ser Lys
580 585

<210> 83
<211> 1818
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> hWip1

<400> 83
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atggaggacg ttactcaaat cgttgtggag cccgaaccga cggctgaaga aaagccctcg 120

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ggcgaagtct cggggaaagg cccagcggtg gcagcccgag aggctcgcga ccctctcccg 240

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ttcgccgtgt gcgacgggca cggcgggcgg gaggcggcac agtttgcccg ggagcacttg 360

tggggtttca tcaagaagca gaagggtttc acctcgtccg agccggctaa ggtttgcgct 420

gccatccgca aaggctttct cgcttgtcac cttgccatgt ggaagaaact ggcggaatgg 480

ccaaagacta tgacgggtct tcctagcaca tcagggacaa ctgccagtgt ggtcatcatt 540

cggggcatga agatgtatgt agctcacgta ggtgactcag gggtggttct tggaattcag 600

gatgacccga aggatgactt tgtcagagct gtggaggtga cacaggacca taagccagaa 660

cttcccaagg aaagagaacg aatcgaagga cttggtggga gtgtaatgaa caagtctggg 720

gtgaatcgtg tagtttggaa acgacctcga ctcactcaca atggacctgt tagaaggagc 780

acagttattg accagattcc ttttctggca gtagcaagag cacttggtga tttgtggagc 840

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ccaccacaag atgccatctc aatgtgccag gaccaagagg agaaaaaata cctgatgggt 1020

gagcatggac aatcttgtgc caaaatgctt gtgaatcgag cattgggccg ctggaggcag 1080

cgtatgctcc gagcagataa cactagtgcc atagtaatct gcatctctcc agaagtggac 1140

aatcagggaa actttaccaa tgaagatgag ttatacctga acctgactga cagcccttcc 1200

tataatagtc aagaaacctg tgtgatgact ccttccccat gttctacacc accagtcaag 1260

tcactggagg aggatccatg gccaagggtg aattctaagg accatatacc tgccctggtt 1320

cgtagcaatg ccttctcaga gaatttttta gaggtttcag ctgagatagc tcgagagaat 1380

gtccaaggtg tagtcatacc ctcaaaagat ccagaaccac ttgaagaaaa ttgcgctaaa 1440

gccctgactt taaggataca tgattctttg aataatagcc ttccaattgg ccttgtgcct 1500

actaattcaa caaacactgt catggaccaa aaaaatttga agatgtcaac tcctggccaa 1560

atgaaagccc aagaaattga aagaacccct ccaacaaact ttaaaaggac attagaagag 1620

tccaattctg gccccctgat gaagaagcat agacgaaatg gcttaagtcg aagtagtggt 1680

gctcagcctg caagtctccc cacaacctca cagcgaaaga actctgttaa actcaccatg 1740

cgacgcagac ttaggggcca gaagaaaatt ggaaatcctt tacttcatca acacaggaaa 1800

actgtttgtg tttgctga 1818

<210> 84
<211> 605
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hWip1

<400> 84

Met Ala Gly Leu Tyr Ser Leu Gly Val Ser Val Phe Ser Asp Gln Gly
1 5 10 15

Gly Arg Lys Tyr Met Glu Asp Val Thr Gln Ile Val Val Glu Pro Glu
20 25 30

Pro Thr Ala Glu Glu Lys Pro Ser Pro Arg Arg Ser Leu Ser Gln Pro
35 40 45

Leu Pro Pro Arg Pro Ser Pro Ala Ala Leu Pro Gly Gly Glu Val Ser
50 55 60

Gly Lys Gly Pro Ala Val Ala Ala Arg Glu Ala Arg Asp Pro Leu Pro
65 70 75 80

Asp Ala Gly Ala Ser Pro Ala Pro Ser Arg Cys Cys Arg Arg Arg Ser
85 90 95

Ser Val Ala Phe Phe Ala Val Cys Asp Gly His Gly Gly Arg Glu Ala
100 105 110

Ala Gln Phe Ala Arg Glu His Leu Trp Gly Phe Ile Lys Lys Gln Lys

120 125

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

Gly Phe Leu Ala Cys His Leu Ala Met Trp Lys Lys Leu Ala Glu Trp
145 150 155 160

Pro Lys Thr Met Thr Gly Leu Pro Ser Thr Ser Gly Thr Thr Ala Ser
165 170 175

Val Val Ile Ile Arg Gly Met Lys Met Tyr Val Ala His Val Gly Asp
180 185 190

Ser Gly Val Val Leu Gly Ile Gln Asp Asp Pro Lys Asp Asp Phe Val
195 200 205

Arg Ala Val Glu Val Thr Gln Asp His Lys Pro Glu Leu Pro Lys Glu
210 215 220

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

Val Asn Arg Val Val Trp Lys Arg Pro Arg Leu Thr His Asn Gly Pro
245 250 255

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

Arg Ala Leu Gly Asp Leu Trp Ser Tyr Asp Phe Phe Ser Gly Glu Phe
275 280 285

Val Val Ser Pro Glu Pro Asp Thr Ser Val His Thr Leu Asp Pro Gln
290 295 300

Lys His Lys Tyr Ile Ile Leu Gly Ser Asp Gly Leu Trp Asn Met Ile
305 310 315 320

Pro Pro Gln Asp Ala Ile Ser Met Cys Gln Asp Gln Glu Glu Lys Lys
325 330 335

Tyr Leu Met Gly Glu His Gly Gln Ser Cys Ala Lys Met Leu Val Asn
340 345 350

Arg Ala Leu Gly Arg Trp Arg Gln Arg Met Leu Arg Ala Asp Asn Thr
355 360 365

Ser Ala Ile Val Ile Cys Ile Ser Pro Glu Val Asp Asn Gln Gly Asn
370 375 380

Phe Thr Asn Glu Asp Glu Leu Tyr Leu Asn Leu Thr Asp Ser Pro Ser

385 390 395 400

Tyr Asn Ser Gln Glu Thr Cys Val Met Thr Pro Ser Pro Cys Ser Thr
405 410 415

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

Lys Asp His Ile Pro Ala Leu Val Arg Ser Asn Ala Phe Ser Glu Asn
435 440 445

Phe Leu Glu Val Ser Ala Glu Ile Ala Arg Glu Asn Val Gln Gly Val
450 455 460

Val Ile Pro Ser Lys Asp Pro Glu Pro Leu Glu Glu Asn Cys Ala Lys
465 470 475 480

Ala Leu Thr Leu Arg Ile His Asp Ser Leu Asn Asn Ser Leu Pro Ile
485 490 495

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

Leu Lys Met Ser Thr Pro Gly Gln Met Lys Ala Gln Glu Ile Glu Arg
515 520 525

Thr Pro Pro Thr Asn Phe Lys Arg Thr Leu Glu Glu Ser Asn Ser Gly
530 535 540

Pro Leu Met Lys Lys His Arg Arg Asn Gly Leu Ser Arg Ser Ser Gly
545 550 555 560

Ala Gln Pro Ala Ser Leu Pro Thr Thr Ser Gln Arg Lys Asn Ser Val
565 570 575

Lys Leu Thr Met Arg Arg Arg Leu Arg Gly Gln Lys Lys Ile Gly Asn
580 585 590

Pro Leu Leu His Gln His Arg Lys Thr Val Cys Val Cys
595 600 605

<210> 85
<211> 741
<212> DNA
<213> Homo sapiens

<220>
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<223> hRTP4

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gggtggaagc aataccaaca gagagcattt ggctggttcc ggtgttcctc ctgccagcga 180

agttgggctt ccgcccaagt gcagattctg tgccacacgt actgggagca ctggacatcc 240

cagggtcagg tgcgtatgag gctctttggc caaaggtgcc agaagtgctc ctggtcccaa 300

tatgagatgc ctgagttctc ctcggatagc accatgagga ttctgagcaa cctggtgcag 360

catatactga agaaatacta tggaaatggc acgaggaagt ctccagaaat gccagtaatc 420

ctggaagtgt ccctggaagg atcccatgac acagccaatt gtgaggcatg cactttgggc 480

atctgtggac agggcttaaa aagctgcatg acaaagccgt ccaaatccct actcccccac 540

ctaaagactg ggaattcctc acctggaatt ggtgctgtgt acctcgcaaa ccaagccaag 600

aaccagtcag ctgaggcaaa agaggctaag gggagtgggt atgagaaatt agggcccagt 660

cgagacccag atccactgaa catctgtgtc tttattttgc tgcttgtatt tattgtagtc 720

aaatgcttta catcagaatg a 741

<210> 86
<211> 246
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hRTP4

<400> 86

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

Leu Gln Leu Asp Cys Leu Ala Gln Gly Trp Lys Gln Tyr Gln Gln Arg
35 40 45

Ala Phe Gly Trp Phe Arg Cys Ser Ser Cys Gln Arg Ser Trp Ala Ser
50 55 60

Ala Gln Val Gln Ile Leu Cys His Thr Tyr Trp Glu His Trp Thr Ser
65 70 75 80

Gln Gly Gln Val Arg Met Arg Leu Phe Gly Gln Arg Cys Gln Lys Cys
85 90 95

Ser Trp Ser Gln Tyr Glu Met Pro Glu Phe Ser Ser Asp Ser Thr Met
100 105 110

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

Asn Gly Thr Arg Lys Ser Pro Glu Met Pro Val Ile Leu Glu Val Ser
130 135 140

Leu Glu Gly Ser His Asp Thr Ala Asn Cys Glu Ala Cys Thr Leu Gly
145 150 155 160

Ile Cys Gly Gln Gly Leu Lys Ser Cys Met Thr Lys Pro Ser Lys Ser
165 170 175

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

Val Tyr Leu Ala Asn Gln Ala Lys Asn Gln Ser Ala Glu Ala Lys Glu
195 200 205

Ala Lys Gly Ser Gly Tyr Glu Lys Leu Gly Pro Ser Arg Asp Pro Asp
210 215 220

Pro Leu Asn Ile Cys Val Phe Ile Leu Leu Leu Val Phe Ile Val Val
225 230 235 240

Lys Cys Phe Thr Ser Glu
245

<210> 87
<211> 765
<212> DNA
<213> Homo sapiens

<220>
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<223> hREEP2

<400> 87
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tactggatcg tctttgcctt cttcaccacg gccgagacgc tcacggatat agtgctctcc 180

tggttcccct tctactttga actgaagatc gccttcgtga tatggctgct gtccccttac 240

accaagggct ccagcgtgct ctaccgcaag ttcgtgcacc caacgctgtc caacaaggag 300

aaggagatcg acgagtacat cacgcaggcc cgagacaaga gctatgagac catgatgagg 360

gtgggcaaga ggggcctgaa ccttgccgcc aatgctgcag tcacagctgc cgccaagggc 420

caggggtgc tgtcagagaa gctccgcagc ttcagcatgc aggacctgac cctgatccgg 480

gacgaggacg cactgcccct gcagaggcct gacggccgcc tccgacccag ccctggcagc 540

ctcctggaca ccatcgagga cttaggagat gaccctgccc tgagtctaag gtccagcaca 600

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<210> 88
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> hREEP2

<400> 88

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

Lys Glu Tyr Val Lys Trp Met Met Tyr Trp Ile Val Phe Ala Phe Phe
35 40 45

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

Tyr Phe Glu Leu Lys Ile Ala Phe Val Ile Trp Leu Leu Ser Pro Tyr
65 70 75 80

Thr Lys Gly Ser Ser Val Leu Tyr Arg Lys Phe Val His Pro Thr Leu
85 90 95

Ser Asn Lys Glu Lys Glu Ile Asp Glu Tyr Ile Thr Gln Ala Arg Asp
100 105 110

Lys Ser Tyr Glu Thr Met Met Arg Val Gly Lys Arg Gly Leu Asn Leu
115 120 125

Ala Ala Asn Ala Ala Val Thr Ala Ala Ala Lys Gly Gln Gly Val Leu
130 135 140

Ser Glu Lys Leu Arg Ser Phe Ser Met Gln Asp Leu Thr Leu Ile Arg
145 150 155 160

Asp Glu Asp Ala Leu Pro Leu Gln Arg Pro Asp Gly Arg Leu Arg Pro
165 170 175

Ser Pro Gly Ser Leu Leu Asp Thr Ile Glu Asp Leu Gly Asp Asp Pro
180 185 190

Ala Leu Ser Leu Arg Ser Ser Thr Asn Pro Ala Asp Ser Arg Thr Glu
195 200 205

Ala Ser Glu Asp Asp Met Gly Asp Lys Ala Pro Lys Arg Ala Lys Pro

210 215 220

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

Thr Arg Pro Lys Lys Lys Thr Ser Gly Gly Gly Asp Ser Ala
245 250

<210> 89
<211> 783
<212> DNA
<213> Homo sapiens

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<223> hDPM1

<400> 89
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ccgctcatcg tgtggctgct ggtgaaaagc ttctccgaga gtggaatcaa ctatgaaatt 180

ataatcatag atgatggaag cccagatgga acaagggatg ttgctgaaca gttggagaag 240

atctatgggt cagacagaat tcttctaaga ccacgagaga aaaagttggg actaggaact 300

gcatatattc atggaatgaa acatgccaca ggaaactaca tcattattat ggatgctgat 360

ctctcacacc atccaaaatt tattcctgaa tttattagga agcaaaagga gggtaatttt 420

gatattgtct ctggaactcg ctacaaagga aatggaggtg tatatggctg ggatttgaaa 480

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tctgatttaa caggaagttt cagattatac cgaaaagaag ttctagagaa attaatagaa 600

aaatgtgttt ctaaaggcta cgtcttccag atggagatga ttgttcgggc aagacagttg 660

aattatacta ttggcgaggt tccaatatca tttgtggatc gtgtttatgg tgaatccaag 720

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<210> 90
<211> 260
<212> PRT
<213> Homo sapiens

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<223> hDPM1

<400> 90

Met Ala Ser Leu Glu Val Ser Arg Ser Pro Arg Arg Ser Arg Arg Glu
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Leu Glu Val Arg Ser Pro Arg Gln Asn Lys Tyr Ser Val Leu Leu Pro

Thr Tyr Asn Glu Arg Glu Asn Leu Pro Leu Ile Val Trp Leu Leu Val
35 40 45

Lys Ser Phe Ser Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp
50 55 60

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

Ile Tyr Gly Ser Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu
85 90 95

Gly Leu Gly Thr Ala Tyr Ile His Gly Met Lys His Ala Thr Gly Asn
100 105 110

Tyr Ile Ile Ile Met Asp Ala Asp Leu Ser His His Pro Lys Phe Ile
115 120 125

Pro Glu Phe Ile Arg Lys Gln Lys Glu Gly Asn Phe Asp Ile Val Ser
130 135 140

Gly Thr Arg Tyr Lys Gly Asn Gly Gly Val Tyr Gly Trp Asp Leu Lys
145 150 155 160

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

Arg Pro Gly Ala Ser Asp Leu Thr Gly Ser Phe Arg Leu Tyr Arg Lys
180 185 190

Glu Val Leu Glu Lys Leu Ile Glu Lys Cys Val Ser Lys Gly Tyr Val
195 200 205

Phe Gln Met Glu Met Ile Val Arg Ala Arg Gln Leu Asn Tyr Thr Ile
210 215 220

Gly Glu Val Pro Ile Ser Phe Val Asp Arg Val Tyr Gly Glu Ser Lys
225 230 235 240

Leu Gly Gly Asn Glu Ile Val Ser Phe Leu Lys Gly Leu Leu Thr Leu
245 250 255

Phe Ala Thr Thr
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<210> 91
<211> 2109
<212> DNA
<213> Homo sapiens

<220>
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<223> hDRiP78

<400> 91
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gactcagcag ggactgctcc taatggtacc cgctgcctca cagagcactc tggtcctaag 180
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gctgatcttc aggatttctt gagtcggatc tttcaagtac ccccagggca gatgcccaat 1980

gggaacttct ttgcagctcc tcagcctgcc cctggagccg ctgcagcctc taagcccaac 2040

agcacagtac ccaagggaga agccaaacct aagcggcgga agaaagtgag gaggcccttc 2100

caacgttga 2109

<210> 92
<211> 702
<212> PRT
<213> Homo sapiens

<220>
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<223> hDRiP78

<400> 92

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

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

Gly Thr Arg Cys Leu Thr Glu His Ser Gly Pro Lys His Thr Gln His
50 55 60

Pro Asn Pro Ala His Trp Leu Asp Pro Ser His Gly Pro Pro Gly Gly
65 70 75 80

Pro Gly Pro Pro Arg Asp Ala Glu Asp Pro Asp Gln Ser Glu Thr Ser
85 90 95

Ser Glu Glu Glu Ser Gly Val Asp Gln Glu Leu Ser Lys Glu Asn Glu
100 105 110

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

Cys Asn Cys Gln Gly Thr Pro Gly Ile Pro Glu Gly Pro Tyr Ser Glu
130 135 140

Gly Gly Asn Gly Ser Ser Ser Asn Phe Cys His His Cys Thr Ser Pro
145 150 155 160

Ala Leu Gly Glu Asp Glu Leu Glu Glu Glu Tyr Asp Asp Glu Glu Ser
165 170 175

Leu Lys Phe Pro Ser Asp Phe Ser Arg Val Ser Ser Gly Lys Lys Pro

180 185 190

Pro Ser Arg Arg Gln Arg His Arg Phe Pro Thr Lys Glu Asp Thr Arg
195 200 205

Glu Gly Gly Arg Arg Asp Pro Arg Ser Pro Gly Arg His Arg Leu Gly
210 215 220

Arg Lys Arg Ser Gln Ala Asp Lys Arg Lys Gly Leu Gly Leu Trp Gly
225 230 235 240

Ala Glu Glu Leu Cys Gln Leu Gly Gln Ala Gly Phe Trp Trp Leu Ile
245 250 255

Glu Leu Leu Val Leu Val Gly Glu Tyr Val Glu Thr Cys Gly His Leu
260 265 270

Ile Tyr Ala Cys Arg Gln Leu Lys Ser Ser Asp Leu Asp Leu Phe Arg
275 280 285

Val Trp Met Gly Val Trp Thr Gly Arg Leu Gly Gly Trp Ala Gln Val
290 295 300

Met Phe Gln Phe Leu Ser Gln Gly Phe Tyr Cys Gly Val Gly Leu Phe
305 310 315 320

Thr Arg Phe Leu Lys Leu Leu Gly Ala Leu Leu Leu Leu Ala Leu Ala
325 330 335

Leu Phe Leu Gly Phe Leu Gln Leu Gly Trp Arg Phe Leu Val Gly Leu
340 345 350

Gly Asp Arg Leu Gly Trp Arg Asp Lys Ala Thr Trp Leu Phe Ser Trp
355 360 365

Leu Asp Ser Pro Ala Leu Gln Arg Cys Leu Thr Leu Leu Arg Asp Ser
370 375 380

Arg Pro Trp Gln Arg Leu Val Arg Ile Val Gln Trp Gly Trp Leu Glu
385 390 395 400

Leu Pro Trp Val Lys Gln Asn Ile Asn Arg Gln Gly Asn Ala Pro Val
405 410 415

Ala Ser Gly Arg Tyr Cys Gln Pro Glu Glu Glu Val Ala Arg Leu Leu
420 425 430

Thr Met Ala Gly Val Pro Glu Asp Glu Leu Asn Pro Phe His Val Leu
435 440 445

Gly Val Glu Ala Thr Ala Ser Asp Val Glu Leu Lys Lys Ala Tyr Arg

450 455 460

Gln Leu Ala Val Met Val His Pro Asp Lys Asn His His Pro Arg Ala
465 470 475 480

Glu Glu Ala Phe Lys Val Leu Arg Ala Ala Trp Asp Ile Val Ser Asn
485 490 495

Ala Glu Lys Arg Lys Glu Tyr Glu Met Lys Arg Met Ala Glu Asn Glu
500 505 510

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

Lys Glu Ala Met Asn Thr Met Met Cys Ser Arg Cys Gln Gly Lys His
530 535 540

Arg Arg Phe Glu Met Asp Arg Glu Pro Lys Ser Ala Arg Tyr Cys Ala
545 550 555 560

Glu Cys Asn Arg Leu His Pro Ala Glu Glu Gly Asp Phe Trp Ala Glu
565 570 575

Ser Ser Met Leu Gly Leu Lys Ile Thr Tyr Phe Ala Leu Met Asp Gly
580 585 590

Lys Val Tyr Asp Ile Thr Glu Trp Ala Gly Cys Gln Arg Val Gly Ile
595 600 605

Ser Pro Asp Thr His Arg Val Pro Tyr His Ile Ser Phe Gly Ser Arg
610 615 620

Ile Pro Gly Thr Arg Gly Arg Gln Arg Ala Thr Pro Asp Ala Pro Pro
625 630 635 640

Ala Asp Leu Gln Asp Phe Leu Ser Arg Ile Phe Gln Val Pro Pro Gly
645 650 655

Gln Met Pro Asn Gly Asn Phe Phe Ala Ala Pro Gln Pro Ala Pro Gly
660 665 670

Ala Ala Ala Ala Ser Lys Pro Asn Ser Thr Val Pro Lys Gly Glu Ala
675 680 685

Lys Pro Lys Arg Arg Lys Lys Val Arg Arg Pro Phe Gln Arg
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<210> 93
<211> 1020
<212> DNA
<213> Cricetulus griseus

<220>
<221> misc_feature
<223> Rad51

<400> 93
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<210> 94
<211> 1053
<212> DNA
<213> Cricetulus griseus

<220>
<221> misc_feature
<223> Rad51b

<400> 94
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ccactctatt ttaacacaga agaaaaactg cttttgatga gcagtaaagt tcatcttcac 540

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<211> 1101
<212> DNA
<213> Cricetulus griseus

<220>
<221> misc_feature
<223> Rad51c

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gttgggatat ctaaagagga agctttagaa actctacaaa ttgtaagaag agagagtctc 180

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acaataagac ttatttttca ctgggagcaa aagcaaaggt ttgcaacatt gtacaagtca 960

ccaagccaga aggagtccac aataccattt cagatcacac cacagggatt tagagatgct 1020

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gaaccagagg aaggatgctg a 1101

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gatgtgctgg gcaaagacat tctcctgtgt gaccctatac ccctggacac tgaagtgaca 4680

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ccaaaatata aacatgatta tgtttctcac taa 5973

<210> 110

<211> 384
<212> DNA
<213> Human cytomegalovirus

<220>
<221> misc_feature
<223> CMV IE enhancer

<400> 110
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ccaacgaccc ccgcccattg acgtcaataa tgacgtatgt tcccatagta acgccaatag 180

ggactttcca ttgacgtcaa tgggtggagt atttacggta aactgcccac ttggcagtac 240

atcaagtgta tcatatgcca agtacgcccc ctattgacgt caatgacggt aaatggcccg 300

cctggcatta tgcccagtac atgaccttat gggactttcc tacttggcag tacatctacg 360

tattagtcat cgctattacc atgg 384

<210> 111
<211> 799
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Human GAPDH promoter

<400> 111
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caaagtcctc ctgtttcatc caagcgtgta agggtccccg tccttgactc cctagtgtcc 180

tgctgcccac agtccagtcc tgggaaccag caccgatcac ctcccatcgg gccaatctca 240

gtcccttccc ccctacgtcg gggcccacac gctcggtgcg tgcccagttg aaccaggcgg 300

ctgcggaaaa aaaaaagcgg ggagaaagta gggcccggct actagcggtt ttacgggcgc 360

acgtagctca ggcctcaaga ccttgggctg ggactggctg agcctggcgg gaggcggggt 420

ccgagtcacc gcctgccgcc gcgcccccgg tttctataaa ttgagcccgc agcctcccgc 480

ttcgctctct gctcctcctg ttcgacagtc agccgcatct tcttttgcgt cgccaggtga 540

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aggccggatg tgttcgcgcc gctgcggggt gggcccgggc ggcctccgca ttgcaggggc 660

gggcggagga cgtgatgcgg cgcgggctgg gcatggaggc ctggtggggg aggggagggg 720

aggcgtgtgt gtcggccggg gccactaggc gctcactgtt ctctccctcc gcgcagccga 780

gccacatcgc tcagacacc 799

<210> 112
<211> 1188
<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<223> Human Ef1 alpha promoter

<400> 112
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tgggaaagtg atgtcgtgta ctggctccgc ctttttcccg agggtggggg agaaccgtat 180

ataagtgcag tagtcgccgt gaacgttctt tttcgcaacg ggtttgccgc cagaacacag 240

gtaagtgccg tgtgtggttc ccgcgggcct ggcctcttta cgggttatgg cccttgcgtg 300

ccttgaatta cttccacctg gctgcagtac gtgattcttg atcccgagct tcgggttgga 360

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gcctttccgt cctcagccgt cgcttcatgt gactccacgg agtaccgggc gccgtccagg 960

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tatgcgatgg agtttcccca cactgagtgg gtggagactg aagttaggcc agcttggcac 1080

ttgatgtaat tctccttgga atttgccctt tttgagtttg gatcttggtt cattctcaag 1140

cctcagacag tggttcaaag ttttttttctt ccatttcagg tgtcgtga 1188

<210> 113
<211> 985
<212> DNA
<213> Simian cytomegalovirus

<220>
<221> misc_feature
<223> CMV promoter

<400> 113
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gacctgtgcc aattcaatat ggcgtatatg gactcgtgcc aattcaatat ggtggatctg 120

gaccccagcc aattcaatat ggcggacttg gcaccatgcc aattcaatat ggcggacttg 180

gcactgtgcc aactggggag gggtctactt ggcacggtgc caagtttgag gaggggtctt 240

ggccctgtgc caagtccgcc atattgaatt ggcatggtgc caataatggc ggccatattg 300

gctatatgcc aggatcaata tataggcaat atccaatatg gccctatgcc aatatggcta 360

ttggccaggt tcaatactat gtattggccc tatgccatat agtattccat atatgggttt 420

tcctattgac gtagatagcc cctcccaatg ggcggtccca tataccatat atggggcttc 480

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<210> 114
<211> 197
<212> DNA
<213> Simian virus 40

<220>
<221> misc_feature
<223> SV40 promoter

<400> 114
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ctccgcccag ttccgcccat tctccgcccc atcgctgact aatttttttt atttatgcag 120

aggccgaggc cgcctcggcc tctgagctat tccagaagta gtgaggaggc ttttttggag 180

gcctaggctt ttgcaaa 197

<210> 115
<211> 999
<212> DNA
<213> Cricetulus griseus

<220>
<221> misc_feature
<223> CHO Actb promoter

<400> 115
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ccatcctctt cctcaatctc gctttctctc tctctctctt ttttttttt ttttttttt 120

ttttttttt tttgcaaaag gaggggagag ggggtaaaaa aatgctgcac tgtgcggcta 180

ggccggtgag tgagcggcgc ggagccaatc agcgctcgcc gttccgaaag ttgcctttta 240

tggctcgagt ggccgctgtg gcgtcctata aaacccggcg gcgcaacgcg cagccactgt 300

cgagtccgcg tccacccgcg agcacaggcc tttcgcagct ctttcttcgc cgctccacac 360

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<210> 116
<211> 683
<212> DNA
<213> Cricetulus griseus

<220>
<221> misc_feature
<223> CHO Hspa5 promoter

<400> 116
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gggaaggacc caagtcccac cgcccagagg gaactgacac gcagaccccg cagcagtccc 120

cgggggccgg gtgacgggag gacctggacg gttaccggcg gaaacggtct cgggttgaga 180

ggtcacctga gggacaggca gctgctgaac caataggacc ggcgcacagg gcggatgctg 240

cctctcattg gcggccgttg agagtaacca gtagccaatg agtcagcccg gggggcgtag 300

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gaccaatcag cgtcctccaa cgagaagcgc cttcaccaat cggaggcctc cacgacgggg 420

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gatcggaacg ccgccgcgct ccgggactac agcctgttgc tggacttcga gactgcagac 660

ggaccgaccg ctgagcactg gcc 683