

SEQUENCE LISTING

<110> Firmenich SA
Pfister, Patrick
Rogers, Matthew E
Kao, Huey-Ling
Abibi, Claude Ayome

<120> Method of identifying malodor modulating compounds

<130> 10020/WO

<160> 55

<170> PatentIn version 3.5

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<211> 957

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Leu Ile Met Leu Thr Val Cys Ser Gly Asn Leu Phe Lys Phe Pro Met
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Tyr Phe Phe Leu Asn Phe Leu Ser Phe Val Asp Ile Cys Tyr Ser Ser
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Val Thr Ala Pro Lys Met Ile Ile Asp Leu Leu Val Lys Lys Lys Thr
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Ile Ser Tyr Val Gly Cys Met Leu Gln Leu Phe Val Val His Phe Phe
 100 105 110

Gly Cys Thr Glu Ile Phe Ile Leu Thr Val Met Ala Tyr Asp Arg Tyr
 115 120 125

Val Ala Ile Cys Lys Pro Leu His Tyr Met Thr Met Met Asp Arg Glu
 130 135 140

Arg Cys Asn Lys Met Leu Leu Gly Thr Trp Ile Gly Gly Phe Leu His
 145 150 155 160

Ser Ile Ile Gln Val Ala Leu Val Val Gln Leu Pro Phe Cys Gly Pro
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Asn Glu Ile Asp His Tyr Phe Cys Asp Val His Pro Val Leu Lys Leu
 180 185 190

Ala Cys Thr Asp Thr Tyr Ile Val Gly Ile Phe Val Thr Ala Asn Ser
 195 200 205

Gly Thr Ile Ala Leu Gly Ser Phe Val Ile Leu Leu Ile Ser Tyr Thr
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Val Ile Leu Met Ser Leu Arg Lys Gln Ser Ser Glu Gly Arg Arg Lys
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Ala Leu Ser Thr Cys Gly Ser His Ile Ala Val Val Ile Ile Phe Phe
 245 250 255

Gly Pro Cys Thr Phe Met Tyr Met Arg Pro Asp Thr Thr Phe Ser Glu
 260 265 270

Asp Lys Met Val Ala Ile Phe Tyr Thr Ile Ile Thr Pro Met Leu Asn
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Thr Val Ala Met Ser Pro Arg Val Tyr Leu Pro Leu Ile Ile Ala Ser
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Tyr Ala Gly Gly Val Val His Gly Ala Ile His Thr Val Ala Thr Phe
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Ser Leu Ser Phe Cys Gly Ser Asn Glu Ile Lys His Val Phe Cys Asp
180 185 190

Ile Pro Ala Leu Leu Ala Leu Ser Cys Ser Asp Thr His Thr Asn Glu
195 200 205

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

His Ser Ala Glu Gly Arg Arg Lys Val Phe Ser Thr Cys Gly Ser His
245 250 255

Leu Thr Gly Val Ser Ile Tyr His Gly Thr Ile Leu Phe Thr Tyr Met
260 265 270

Arg Pro Ser Ser Ser Tyr Ala Ser Asn His Asp Met Val Val Ser Ile
275 280 285

Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu
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Asp Ser

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 35 40 45

Ile His Leu Asp Val Gln Leu His Thr Pro Met Tyr Phe Phe Leu Thr
50 55 60

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

Thr Leu Gln Asn Thr Leu Thr Ser Ile Lys Asn Ile Ser Phe Met Gly
85 90 95

Cys Phe Thr Gln Leu Tyr Phe Phe Val Leu Leu Ala Ala Ser Glu Cys
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Phe Ile Leu Ser Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn
115 120 125

Pro Leu His Tyr Pro Val Ile Met Ser Pro Arg Arg Ser Tyr Thr Leu
130 135 140

Ile Thr Val Ser Tyr Met Ile Gly Val Leu Asp Ser Ser Val Thr Val
145 150 155 160

Phe Cys Leu Ser Thr Leu Asp Phe Cys Asn Ser Lys Val Ile His His
165 170 175

Phe Phe Cys Asp Thr Phe Pro Ile Leu Ala Leu Ser Cys Ser Asp Thr
180 185 190

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

Leu Ser Leu Ile Thr Ile Ser Ser Ser Tyr Val Ser Ile Leu Ser Thr
210 215 220

Ile Leu Lys Ile Asn Ser Ser Ser Gly Lys His Lys Ala Phe Ser Thr
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Cys Ala Ser His Leu Ile Gly Val Thr Val Phe Tyr Gly Thr Met Ile
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Phe Thr Tyr Leu Lys Pro Ser Thr Ser Tyr Ser Leu Gly Lys Asp Gln

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270

Val Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu
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Val Phe Ser Leu Ala Leu Cys Gly Asn Ser Gly Met Ile His Leu Ile
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Arg Val Asp Pro Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
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Leu Ser Leu Met Asp Leu Met Tyr Ile Ser Thr Thr Val Pro Lys Met
65 70 75 80

Ala Phe Asn Phe Leu Ser Gly Gln Lys Ser Ile Ser Phe Leu Gly Cys
85 90 95

Gly Val Gln Ser Phe Phe Phe Leu Thr Met Ala Cys Ser Glu Gly Leu
100 105 110

Leu Leu Ala Ser Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro
115 120 125

Leu His Tyr Pro Ile Arg Met Ser Lys Ile Met Cys Leu Lys Met Ile
130 135 140

Ile Gly Ser Trp Ile Leu Gly Ser Ile Asn Ser Leu Ala His Thr Val
145 150 155 160

Tyr Ala Leu His Ile Pro Tyr Cys His Ser Arg Ser Ile Asn His Phe
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Phe Cys Asp Val Pro Ala Met Leu Pro Leu Ala Cys Met Asp Thr Trp
180 185 190

Val Tyr Glu Tyr Met Val Phe Val Ser Thr Ser Leu Phe Leu Leu Leu

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Pro Phe Leu Gly Ile Thr Ala Ser Tyr Gly Arg Val Leu Phe Ala Val
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Phe His Met Arg Ser Lys Glu Gly Lys Lys Lys Ala Phe Thr Thr Cys
 225 230 235 240

Ser Thr His Leu Thr Val Val Thr Phe Tyr Tyr Ala Pro Phe Val Tyr
 245 250 255

Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp Lys Ile
 260 265 270

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

Met Ile Ala Asp Phe Leu Ser Gly Ser Arg Thr Ile Ser Phe Ala Gly
 85 90 95

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

130

135

140

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

Thr His Tyr Glu Arg Gly Val Tyr Val Ser Gly Ile Ile Phe Leu Leu
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Ile Pro Phe Ser Met Ile Ser Ile Ser Tyr Val Gln Ile Leu Leu Thr
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Val Phe Gln Met Gln Ser Ser Gly Ala Arg Gln Lys Ser Phe Ser Thr
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Cys Ser Phe His Met Val Val Val Ile Met Tyr Tyr Gly Pro Phe Ile
 245 250 255

Phe Thr Tyr Met Arg Pro Arg Ser Tyr His Thr Pro Gly Gln Asp Lys
 260 265 270

Phe Leu Ala Ile Phe Tyr Thr Ile Leu Thr Pro Thr Leu Asn Pro Ile
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Val	Leu	Phe	Phe	Ile	Ile	Tyr	Ile	Leu	Thr	Leu	Met	Gly	Asn	Ala	Ser
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Ile	Ile	Cys	Ala	Val	Cys	Tyr	Asp	Lys	Lys	Leu	His	Ser	Pro	Met	Tyr
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Leu	Leu	Leu	Ala	Asn	Phe	Ser	Phe	Leu	Glu	Ile	Trp	Tyr	Val	Thr	Ser
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 tgcttcctgc agttctatctt cttcttctcc tttggttcta cagaatgctt tttcctggca 360
 gtcattggcat ttgatcgata ccttgccatc tgtagggcac tacattatcc ttctctcatg 420
 actgggcacc tctgcaacat ccttgtgatc agttgctggg tgcttggttt cctctggttc 480
 cctgtacca tcatcatcat ctcccagatg tccttctgtg ggtccagaat tatagaccac 540
 ttctgtgtg acccaggccc tcttttggcc cttgcctgtt ccagagcccc attgatggag 600
 gttttctgga caattataat gtctatgctc ctggttattc ctttctctt catcatggga 660
 acttacatat tggtcctaag agctgtgttt agacttcctt caagagatgg acaaaaaaag 720
 gccttctcca cttgcgggtc tcatctcaca gtagtttcac tcttttattg ctcagtgatg 780
 aaaatgtatt tgagcccaac atctgagcat gaagctggaa tgcagaagct tgtaactcta 840
 ttttattctg tgggtactcc actacttaat cctgtgatat acagtctgag gaacaaagat 900
 atgaaaaatg ccctgcagaa gattttaaga acataa 936

<210> 14
 <211> 311
 <212> PRT
 <213> Mus musculus

<400> 14

Met Lys Thr Leu Ser Ser Pro Ser Asn Ser Ser Thr Ile Thr Gly Phe

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

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

Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr
 245 250 255

Cys Ser Val Met Lys Met Tyr Leu Ser Pro Thr Ser Glu His Glu Ala
 260 265 270

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

Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Asp Met Lys Asn Ala
 290 295 300

Leu Gln Lys Ile Leu Arg Thr
 305 310

<210> 15
 <211> 918
 <212> DNA
 <213> Mus musculus

<400> 15
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 aaccttggct taatctttgt catctggaag gaccctcatc ttcacacacc catgtacctt 180
 ttccttggaa atttggcctt tgctgatgcc tgtaattcat cctctgtgac accaaagatg 240
 cttatgaaat ttttaaataa gaatgacatg atatccatgg gtgagtgttt tgctcaattt 300
 tatttctttt gttcaagtgt aactgcagaa gccttcattc tggtagctat ggcctatgac 360
 cgctatgtag ccatatgcaa acctctgctc tatgtagtgg tgatgtccaa cagactctgt 420
 attcagttca taggtgtatc ctatctaatt ggacttctac atggcttact tcatgtagga 480
 ttgttattta ggtaaagtt ttgtagttcc aatgtaatag attatttcta ctgtgacatc 540
 ctgccacttt ataggatttc ttgcactgac ccatcgatca atgtactggg agctttcatt 600
 atgggtattt tattacaagt gagtaccttt atgagtatta tagtctccta tgtccgtgtc 660
 ctctttgcca tcctgagaac aaagtctgag aggggcagaa acaaagcctt ctctacttgc 720
 agttcccacc tgtcatctgt gtctttgttc tatggcactc tcttcatcat atatgtcctc 780

tctggctctg acacagataa ttatcagggt aaaatgtatt cactgttcta taccattatc	840
attcctctgc taaacccctt catttacagc ctaagaaata aagaagtcac cggtgccttg	900
agaaaagtca gaaaatga	918

<210> 16
 <211> 305
 <212> PRT
 <213> Mus musculus

<400> 16

Met	Glu	Leu	Asn	Arg	Thr	Gln	Leu	Thr	Glu	Phe	Val	Leu	Arg	Gly	Ile
1				5					10					15	

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

Ile	Tyr	Val	Ile	Thr	Met	Val	Gly	Asn	Leu	Gly	Leu	Ile	Phe	Val	Ile
		35					40					45			

Trp	Lys	Asp	Pro	His	Leu	His	Thr	Pro	Met	Tyr	Leu	Phe	Leu	Gly	Asn
	50					55					60				

Leu	Ala	Phe	Ala	Asp	Ala	Cys	Asn	Ser	Ser	Ser	Val	Thr	Pro	Lys	Met
65					70					75					80

Leu	Met	Lys	Phe	Leu	Asn	Lys	Asn	Asp	Met	Ile	Ser	Met	Gly	Glu	Cys
				85					90					95	

Phe	Ala	Gln	Phe	Tyr	Phe	Phe	Cys	Ser	Ser	Val	Thr	Ala	Glu	Ala	Phe
			100					105					110		

Ile	Leu	Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys	Pro
		115					120					125			

Leu	Leu	Tyr	Val	Val	Val	Met	Ser	Asn	Arg	Leu	Cys	Ile	Gln	Phe	Ile
	130					135					140				

Gly	Val	Ser	Tyr	Leu	Ile	Gly	Leu	Leu	His	Gly	Leu	Leu	His	Val	Gly
145					150					155					160

Leu Leu Phe Arg Leu Thr Phe Cys Ser Ser Asn Val Ile Asp Tyr Phe
165 170 175

Tyr Cys Asp Ile Leu Pro Leu Tyr Arg Ile Ser Cys Thr Asp Pro Ser
180 185 190

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

Thr Phe Met Ser Ile Ile Val Ser Tyr Val Arg Val Leu Phe Ala Ile
210 215 220

Leu Arg Thr Lys Ser Glu Arg Gly Arg Asn Lys Ala Phe Ser Thr Cys
225 230 235 240

Ser Ser His Leu Ser Ser Val Ser Leu Phe Tyr Gly Thr Leu Phe Ile
245 250 255

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

Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn Pro Phe Ile
275 280 285

Tyr Ser Leu Arg Asn Lys Glu Val Ile Gly Ala Leu Arg Lys Val Arg
290 295 300

Lys
305

<210> 17
<211> 951
<212> DNA
<213> Mus musculus

<400> 17
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gtcacaggta actgtggact tatctacctc atcagtcattg aggaggctct gcaccggccc 180
atgtactact ttctagccat gttgtctgct acagatatct ctgggtgtaa tacaattgtc 240
cccagtatgt tatgcatctt ttggttcagt gtcaaggaga ttgatttcaa tgcctgcctt 300

gtacagatgt ttttcatcca catgttaaca ggcattggagt ctggtgtgct catgcttatg 360
gctctcgacc gctatgtggc tatatgctat ccattacgct atactaccat actcaccaac 420
actatgatta ccaagattgg attggcagca cttgttagaa gtgtgttact catggtccct 480
tttgctttcc tgatcaagcg tcttcatac tgtagaggaa acctcatcca acatacctat 540
tgtgatcaca tggctgtggc taaactatcc tgtggcaata ttaagattaa tgctatctat 600
ggctcttataa ttgctatatt tattgggggt tttgatatat tctgtatctc catgtcttat 660
gccatgatta tccatgctgt ggtgaagcta tcttcggcag atgctcgcca taaagccttc 720
agtacctgta catcacacat atgtgctatt gttattacct atgtcccagc attcttcaac 780
ttctttactc atcgctttgg gagaaccact ataccccatc atatccacat tattatagcc 840
aacctgtatc tattgctacc tcccaccttg aatccaattg tatatggagt aaagaccaag 900
cagattcgtg aagggtgat caaactgttt gctagacaaa aagttgtttg a 951

<210> 18
<211> 316
<212> PRT
<213> Mus musculus

<400> 18

Met Pro Gly Val Asn Thr Ser Ser Leu Thr Pro Arg Tyr Phe Ile Leu
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Asn Gly Ile Pro Gly Leu Glu Ala Ala His Ile Trp Ile Ser Leu Pro
20 25 30

Phe Phe Ile Met Tyr Leu Ile Ala Val Thr Gly Asn Cys Gly Leu Ile
35 40 45

Tyr Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe
50 55 60

Leu Ala Met Leu Ser Ala Thr Asp Ile Ser Gly Cys Asn Thr Ile Val
65 70 75 80

Pro Ser Met Leu Cys Ile Phe Trp Phe Ser Val Lys Glu Ile Asp Phe
85 90 95

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

<210> 19
 <211> 954
 <212> DNA
 <213> Mus musculus

<400> 19
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 ctagtaggca accttggcct tgtatatctc atttactatg aggaatcctt acatcgccca 180
 atgtatttct ttctggccat gctttctctc atagacctgt ttacttgacac aaccactgtc 240
 cccaatgccc tcttcatttt ctgggtcaaa ctcaaggaaa ttaacttcac tgcttgcccta 300
 gttcagatgt tctttgtgca cggattcaca ggtgtggagt ctgggggtact catgctcatg 360
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 cctgtcattg ccaaagctgg gcttgccacc ttcttgagag gtgtgttact gatgattcct 480
 tttccattct tgggttaaagc tttgcccttc tgccgaagca atgtcatctc ccatacatat 540
 tgtgaccaca tgtctgtggt aaagttatcc tgtgccagca tcaaaatcaa tgtcatctat 600
 ggtctcatgg ttgcatttct gattggagtg ttgacatat gttgtatatc tgtgtcctac 660
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 agcacctgca cagcccacat atctgccatc atcattactt atgttccagc cttcttcacc 780
 ttctttactc atcgtttttg aggtcacacc atccctcctt ctcttcatat cattgtggct 840
 aatctttatc ttcttctccc tccaactcta aatcccattg tttatgggat gaagacccaa 900
 cagatcagag atagtatcat taaattcttt cacggtgaaa aaggttcaag gtga 954

<210> 20
 <211> 317
 <212> PRT
 <213> Mus musculus

<400> 20

Met Leu Ile Ser Asn Asn Ser Tyr Glu Ala Pro Gln Ser Phe Ile Leu
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Asn Gly Ile Pro Gly Leu Glu Ala Val His Ile Trp Ile Ser Leu Pro
 20 25 30

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

Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His Arg Pro Met Tyr Phe Phe
 50 55 60

Leu Ala Met Leu Ser Leu Ile Asp Leu Phe Thr Cys Thr Thr Thr Val
 65 70 75 80

Pro Asn Ala Leu Phe Ile Phe Trp Phe Lys Leu Lys Glu Ile Asn Phe
 85 90 95

Thr Ala Cys Leu Val Gln Met Phe Phe Val His Gly Phe Thr Gly Val
 100 105 110

Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125

Cys Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala
 130 135 140

Lys Ala Gly Leu Ala Thr Phe Leu Arg Gly Val Leu Leu Met Ile Pro
 145 150 155 160

Phe Pro Phe Leu Val Lys Arg Leu Pro Phe Cys Arg Ser Asn Val Ile
 165 170 175

Ser His Thr Tyr Cys Asp His Met Ser Val Val Lys Leu Ser Cys Ala
 180 185 190

Ser Ile Lys Ile Asn Val Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
 195 200 205

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

Arg Ala Val Val Ser Leu Ser Ser Ala Asp Ala Arg Gln Lys Ala Phe
 225 230 235 240

Ser Thr Cys Thr Ala His Ile Ser Ala Ile Ile Ile Thr Tyr Val Pro
 245 250 255

Ala Phe Phe Thr Phe Phe Thr His Arg Phe Gly Gly His Thr Ile Pro
260 265 270

Pro Ser Leu His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro
275 280 285

Thr Leu Asn Pro Ile Val Tyr Gly Met Lys Thr Lys Gln Ile Arg Asp
290 295 300

Ser Ile Ile Lys Phe Phe His Gly Glu Lys Gly Ser Arg
305 310 315

<210> 21
<211> 936
<212> DNA
<213> Mus musculus

<400> 21
atgcaaaacc agagttttgt aacagaattc atattccttg gactttcaca gaaccctaaa 60
gtccagaaaa tagtttttat tgtattttta tttgtctaca ttgcaactgt tgggggcaac 120
atgataattg tgggtgacat tgtctgtagc ccagcattga tagactgccc catgtacttc 180
tttttggcat tcttgtccct attggatgca tgcttctctt ctgtcatcac accaaagatg 240
gttgtggact ccctgtatga gaagaaaact atctcctttg aaggatgtat gatgcagtta 300
tttgctgagc acttccttgc agcagtagaa gtgattgtct tgacagccat ggcctatgac 360
cgctatgtag caatttgcaa gcccttgcac tactcttcca tcatgaactg gaggtcttgt 420
ggcacactta tggggatagc atggacaggg ggcttcttgc attctatcat acaaattatc 480
ttcacgttgc aattgccctt ctgtggacca aatgtcatcg atcatttcat gtgtgacttg 540
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aacagtgggt ctatctgcat cataatcttc tctattttgc tgggtctccta tgggtgcatc 660
ctgttctctc tgaaagctca cagttctgaa gggcgatgga aagctctctc cacatgtgga 720
tcccacattg cagttgtgggt tttgttcttt gtcccgtgta tatttattha tgcacgtcct 780
ccatctgctt tctcctttga taaaatgggt gcgatatttt atactatcct aactcccttg 840
ctcaatcctg tgatttatac ttttcggaat aaggacatga aaaatgctat gaagaaagtg 900
tggaagaggt tggcagtggt ttctgatgga aagtga 936

<210> 22
 <211> 311
 <212> PRT
 <213> Mus musculus

<400> 22

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

Tyr Ile Ala Thr Val Gly Gly Asn Met Ile Ile Val Val Thr Ile Val
 35 40 45

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

Leu Ser Leu Leu Asp Ala Cys Phe Ser Ser Val Ile Thr Pro Lys Met
 65 70 75 80

Val Val Asp Ser Leu Tyr Glu Lys Lys Thr Ile Ser Phe Glu Gly Cys
 85 90 95

Met Met Gln Leu Phe Ala Glu His Phe Leu Ala Ala Val Glu Val Ile
 100 105 110

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

Leu His Tyr Ser Ser Ile Met Asn Trp Arg Leu Cys Gly Thr Leu Met
 130 135 140

Gly Ile Ala Trp Thr Gly Gly Phe Leu His Ser Ile Ile Gln Ile Ile
 145 150 155 160

Phe Thr Leu Gln Leu Pro Phe Cys Gly Pro Asn Val Ile Asp His Phe
 165 170 175

Met Cys Asp Leu Phe Pro Leu Leu Glu Leu Ala Cys Thr Asp Thr His
 180 185 190

Ile Phe Gly Leu Leu Val Val Ala Asn Ser Gly Ser Ile Cys Ile Ile
 195 200 205

Ile Phe Ser Ile Leu Leu Val Ser Tyr Gly Val Ile Leu Phe Ser Leu
 210 215 220

Lys Ala His Ser Ser Glu Gly Arg Trp Lys Ala Leu Ser Thr Cys Gly
 225 230 235 240

Ser His Ile Ala Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Ile
 245 250 255

Tyr Ala Arg Pro Pro Ser Ala Phe Ser Phe Asp Lys Met Val Ala Ile
 260 265 270

Phe Tyr Thr Ile Leu Thr Pro Leu Leu Asn Pro Val Ile Tyr Thr Phe
 275 280 285

Arg Asn Lys Asp Met Lys Asn Ala Met Lys Lys Val Trp Lys Arg Leu
 290 295 300

Ala Val Val Ser Asp Gly Lys
 305 310

<210> 23
 <211> 975
 <212> DNA
 <213> Homo sapiens

<400> 23
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 acaatgtaca tcatcttcct tgtggggaat cttggtcttg tgtacctcat ttattatgag 180
 gagtccttac atcatccgat gtatTTTTTT tttggccatg ctctctccct cattgacctc 240
 cttacctgca ccaccactct acccaatgca ctctgcatct tctggttcag tctcaaagaa 300
 attaacttca atgcttgctt ggcccagatg ttctttgttc atgggttcac aggtgtggag 360
 tctggggtgc tcatgctcat ggctctagac cgctatgtag ccatttgcta ccctttgcgt 420
 tatgctacca cactcaccaa ccctatcatt gccaaaggctg agcttgccac cttcctgagg 480

ggtgtattgc tgatgattcc tttcccatc ttggttaagc gtttgccttt ctgccaaagc 540
 aatattatct cccatacgta ctgcgaccac atgtctgtag taaagctatc ttgtgccagc 600
 atcaaggcca atgtaatcta tgggtctaagc gttgctctcc tgattggagt gtttgacatt 660
 tgttgtatat ctttgtctta cactttgatc ctcaaggcag cgatcagcct ctcttcatca 720
 gatgctcggc agaaggcttt cagcacctgc actgcccata tatctgccat catcatcacc 780
 tatgttccag cattcttcac tttctttgcc caccgttttg ggggacacac aattccccct 840
 tctcttcaca tcattgtggc taatctttat cttcttcttc cccaactct aaaccctatt 900
 gtttatggag taaagacaaa acagatacgc aagagtgtca taaagttctt ccagggtgat 960
 aagggtgcag gttga 975

<210> 24
 <211> 324
 <212> PRT
 <213> Homo sapiens

<400> 24

Met Pro Leu Phe Asn Ser Leu Cys Trp Phe Pro Thr Ile His Val Thr
1 5 10 15

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

Val Trp Ile Ser Leu Pro Leu Cys Thr Met Tyr Ile Ile Phe Leu Val
35 40 45

Gly Asn Leu Gly Leu Val Tyr Leu Ile Tyr Tyr Glu Glu Ser Leu His
50 55 60

His Pro Met Tyr Phe Phe Phe Gly His Ala Leu Ser Leu Ile Asp Leu
65 70 75 80

Leu Thr Cys Thr Thr Thr Leu Pro Asn Ala Leu Cys Ile Phe Trp Phe
85 90 95

Ser Leu Lys Glu Ile Asn Phe Asn Ala Cys Leu Ala Gln Met Phe Phe
100 105 110

Val His Gly Phe Thr Gly Val Glu Ser Gly Val Leu Met Leu Met Ala

115

120

125

Leu Asp Arg Tyr Val Ala Ile Cys Tyr Pro Leu Arg Tyr Ala Thr Thr
 130 135 140

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

Gly Val Leu Leu Met Ile Pro Phe Pro Phe Leu Val Lys Arg Leu Pro
 165 170 175

Phe Cys Gln Ser Asn Ile Ile Ser His Thr Tyr Cys Asp His Met Ser
 180 185 190

Val Val Lys Leu Ser Cys Ala Ser Ile Lys Val Asn Val Ile Tyr Gly
 195 200 205

Leu Met Val Ala Leu Leu Ile Gly Val Phe Asp Ile Cys Cys Ile Ser
 210 215 220

Leu Ser Tyr Thr Leu Ile Leu Lys Ala Ala Ile Ser Leu Ser Ser Ser
 225 230 235 240

Asp Ala Arg Gln Lys Ala Phe Ser Thr Cys Thr Ala His Ile Ser Ala
 245 250 255

Ile Ile Ile Thr Tyr Val Pro Ala Phe Phe Thr Phe Phe Ala His Arg
 260 265 270

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

Leu Tyr Leu Leu Leu Pro Pro Thr Leu Asn Pro Ile Val Tyr Gly Val
 290 295 300

Lys Thr Lys Gln Ile Arg Lys Ser Val Ile Lys Phe Phe Gln Gly Asp
 305 310 315 320

Lys Gly Ala Gly

<210> 25
 <211> 939
 <212> DNA
 <213> Homo sapiens

<400> 25
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 caaactggaa tattttctctt gtgccttatc atcctcatat tctttctggc ctcggtgggt 120
 aactcggcca tgattcacct catccacgtg gatcctcgtc tccacacacc gatgtacttt 180
 cttctcagcc agctctccct tatggacctg atgtacatct ccaccaccgt cccaagatg 240
 gcgtacaact tcctgtccgg ccagaaaggc atctccttcc tgggatgtgg tgtgcaaagc 300
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 cgttatttgg ccatctgcca ctctctctat tatcctatcc gcatgagtaa aatgatgtgt 420
 gtgaagatga ttggaggctc ttggacactg ggggtccatca actccttggc acacacagtc 480
 ttgccccttc atattcccta ctgcaggctc agggctattg accatttctt ctgcgatgtc 540
 ccagccatgt tgcttcttgc ctgtacagat acttgggtct atgaatatat ggtttttgta 600
 agtacaagcc tctttctcct tttccctttc attggcatca cttcttcctg tggccgagtc 660
 ctatttgctg tctatcatat gcactcaaag gaggggagaa aaaaggcctt caccaccatt 720
 tcaacacatt taactgtagt gatcttttac tatgcacctt ttgtctacac ctatcttcgg 780
 cccaggaatc tccgctcacc agctgaagac aagatcctgg cagtcttcta caccatcctt 840
 acccccatgc tcaatcccat tatctacagc ctgaggaata aggaagtcct gggggctatg 900
 aggagagtgt ttgggatatt ctctttcctg aaagaataa 939

<210> 26
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 26

Met Glu Lys Trp Asn His Thr Ser Asn Asp Phe Ile Leu Leu Gly Leu
 1 5 10 15

Leu Pro Pro Asn Gln Thr Gly Ile Phe Leu Leu Cys Leu Ile Ile Leu
 20 25 30

Ile Phe Phe Leu Ala Ser Val Gly Asn Ser Ala Met Ile His Leu Ile

35

40

45

His Val Asp Pro Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln
 50 55 60

Leu Ser Leu Met Asp Leu Met Tyr Ile Ser Thr Thr Val Pro Lys Met
 65 70 75 80

Ala Tyr Asn Phe Leu Ser Gly Gln Lys Gly Ile Ser Phe Leu Gly Cys
 85 90 95

Gly Val Gln Ser Phe Phe Phe Leu Thr Met Ala Cys Ser Glu Gly Leu
 100 105 110

Leu Leu Thr Ser Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys His Ser
 115 120 125

Leu Tyr Tyr Pro Ile Arg Met Ser Lys Met Met Cys Val Lys Met Ile
 130 135 140

Gly Gly Ser Trp Thr Leu Gly Ser Ile Asn Ser Leu Ala His Thr Val
 145 150 155 160

Phe Ala Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asp His Phe
 165 170 175

Phe Cys Asp Val Pro Ala Met Leu Leu Leu Ala Cys Thr Asp Thr Trp
 180 185 190

Val Tyr Glu Tyr Met Val Phe Val Ser Thr Ser Leu Phe Leu Leu Phe
 195 200 205

Pro Phe Ile Gly Ile Thr Ser Ser Cys Gly Arg Val Leu Phe Ala Val
 210 215 220

Tyr His Met His Ser Lys Glu Gly Arg Lys Lys Ala Phe Thr Thr Ile
 225 230 235 240

Ser Thr His Leu Thr Val Val Ile Phe Tyr Tyr Ala Pro Phe Val Tyr
 245 250 255

Thr Tyr Leu Arg Pro Arg Asn Leu Arg Ser Pro Ala Glu Asp Lys Ile
 260 265 270

Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Ile Ile
 275 280 285

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

Gly Ile Phe Ser Phe Leu Lys Glu
 305 310

<210> 27
 <211> 879
 <212> DNA
 <213> Homo sapiens

<400> 27
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 actccaatgt attttctgct cagccatctc tccttaatgg atatcttgca tgtttccaac 120
 atcgttccca aaatggtcac taactttctg tcaggcagca gaactatttc atttgcaggt 180
 tgtgggttcc aggtatttct gtccctcacc ctcctgggtg gtgagtgctt tctcctggct 240
 gcaatgtcct gtgatcgcta tgtggctatc tgtcaccgc tgcgctatcc gattcttatg 300
 aaggagtatg ccagcgctct catggctgga ggctcctggc tcattggggg tttcaactcc 360
 acagtccaca cagcttatgc actgcagttt cccttctgtg gctctagggc aattgatcac 420
 ttcttctgtg aagtccctgc catgttgaag ttgtcctgtg cagacacaac acgctatgaa 480
 cgagggggtt gtgtaagtgc tgtgatcttc ctgctgatcc ctttctcctt gatctctgct 540
 tcttatggcc aaattattct tactgtcctc cagatgaaat catcagaggc aaggaaaaag 600
 tcattttcca cttgttcctt ccacatgatt gtgggtcacga tgtactatgg gccatttatt 660
 ttacatata tgagacctaa atcataccac actccagggc aggataagtt cctggcaata 720
 ttctatacga tcctcacacc cacactcaac cttttcatct acagcttttag gaataaagat 780
 gttctggcgg tgatgaaaaa tatgctcaaa agtaactttc tgcacaaaaa aatgaatagg 840
 aaaattcctg aatgtgtgtt ctgtctatct ctatgttaa 879

<210> 28
 <211> 292

<212> PRT
<213> Homo sapiens

<400> 28

Met Ser Val Thr Glu Asn Thr Leu Met Ile Leu Leu Ile Arg Ser Asp
1 5 10 15

Ser Arg Leu His Thr Pro Met Tyr Phe Leu Leu Ser His Leu Ser Leu
20 25 30

Met Asp Ile Leu His Val Ser Asn Ile Val Pro Lys Met Val Thr Asn
35 40 45

Phe Leu Ser Gly Ser Arg Thr Ile Ser Phe Ala Gly Cys Gly Phe Gln
50 55 60

Val Phe Leu Ser Leu Thr Leu Leu Gly Gly Glu Cys Leu Leu Leu Ala
65 70 75 80

Ala Met Ser Cys Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg Tyr
85 90 95

Pro Ile Leu Met Lys Glu Tyr Ala Ser Ala Leu Met Ala Gly Gly Ser
100 105 110

Trp Leu Ile Gly Val Phe Asn Ser Thr Val His Thr Ala Tyr Ala Leu
115 120 125

Gln Phe Pro Phe Cys Gly Ser Arg Ala Ile Asp His Phe Phe Cys Glu
130 135 140

Val Pro Ala Met Leu Lys Leu Ser Cys Ala Asp Thr Thr Arg Tyr Glu
145 150 155 160

Arg Gly Val Cys Val Ser Ala Val Ile Phe Leu Leu Ile Pro Phe Ser
165 170 175

Leu Ile Ser Ala Ser Tyr Gly Gln Ile Ile Leu Thr Val Leu Gln Met
180 185 190

Lys Ser Ser Glu Ala Arg Lys Lys Ser Phe Ser Thr Cys Ser Phe His
195 200 205

Met Ile Val Val Thr Met Tyr Tyr Gly Pro Phe Ile Phe Thr Tyr Met
 210 215 220

Arg Pro Lys Ser Tyr His Thr Pro Gly Gln Asp Lys Phe Leu Ala Ile
 225 230 235 240

Phe Tyr Thr Ile Leu Thr Pro Thr Leu Asn Pro Phe Ile Tyr Ser Phe
 245 250 255

Arg Asn Lys Asp Val Leu Ala Val Met Lys Asn Met Leu Lys Ser Asn
 260 265 270

Phe Leu His Lys Lys Met Asn Arg Lys Ile Pro Glu Cys Val Phe Cys
 275 280 285

Leu Phe Leu Cys
 290

<210> 29
 <211> 1113
 <212> DNA
 <213> Homo sapiens

<400> 29
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 atgactatga taccacaaat tgatctgaag caaatTTTcc tttgtcctaa ttgcagacta 120
 tacatgatcc ctgttggagc tttcatcttt tccttgggaa acatgcaaaa ccaaagcttt 180
 gtaactgagt ttgtcctcct gggactttca cagaatccaa atgttcagga aatagtattt 240
 gttgtatttt tgTTTgtcta cattgcaact gttgggggca acatgctaatt ttagtagtaacc 300
 attctcagca gccctgctct tctgggtgtct cctatgtact tcttcttggg cttcctgtcc 360
 ttcctggatg cgtgcttctc atctgtcatc accccaaaga tgattgtaga ctccctctat 420
 gtgacaaaaa ccatctcttt tgaaggctgc atgatgcagc tctttgctga acatttcttt 480
 gctgggggtgg aggtgattgt cctcacagcc atggcctatg atcgttatgt ggccatttgc 540
 aagcccttgc attactcttc tatcatgaac aggaggctct gtggcattct gatgggggta 600
 gcctggacag ggggcctctt gcattccatg atacaaattc tttttacttt ccagcttccc 660
 ttttgtggcc ccaatgtcat caatcacttt atgtgtgact tgtaccggtt actggagctt 720

gcctgcactg atactcacat ctttggcctc atggtgggtca tcaacagtgg gtttatctgc 780
atcataaact tctccttggt gcttgtctcc tatgctgtca tcttgctctc tctgagaaca 840
cacagttctg aagggcgctg gaaagctctc tccacctgtg gatctcacat tgctgtttgtg 900
atTTTgttct ttgtcccatg catatttgta tatacacgac ctccatctgc tttttccctt 960
gacaaaatgg cggcaatatt ttatatcatc ttaaattcct tgctcaatcc tttgatttac 1020
actttcagga ataaggaagt aaaacaggcc atgaggagaa tatggaacag actgatgggtg 1080
gtttctgatg agaaagaaaa tattaaactt taa 1113

<210> 30
<211> 370
<212> PRT
<213> Homo sapiens

<400> 30

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

Thr Asn Leu Leu Met Thr Met Ile Pro Gln Ile Asp Leu Lys Gln Ile
20 25 30

Phe Leu Cys Pro Asn Cys Arg Leu Tyr Met Ile Pro Val Gly Ala Phe
35 40 45

Ile Phe Ser Leu Gly Asn Met Gln Asn Gln Ser Phe Val Thr Glu Phe
50 55 60

Val Leu Leu Gly Leu Ser Gln Asn Pro Asn Val Gln Glu Ile Val Phe
65 70 75 80

Val Val Phe Leu Phe Val Tyr Ile Ala Thr Val Gly Gly Asn Met Leu
85 90 95

Ile Val Val Thr Ile Leu Ser Ser Pro Ala Leu Leu Val Ser Pro Met
100 105 110

Tyr Phe Phe Leu Gly Phe Leu Ser Phe Leu Asp Ala Cys Phe Ser Ser
115 120 125

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

Arg Ile Trp Asn Arg Leu Met Val Val Ser Asp Glu Lys Glu Asn Ile
 355 360 365

Lys Leu
 370

<210> 31
 <211> 930
 <212> DNA
 <213> Homo sapiens

<400> 31
 atggatatat cagagggaaa taagactctt gtgacagagt ttgtttctcac aggacttaca 60
 gatcgaccat ggctgcacgt cctcttcttt gttgtgtttt tgggtgtcta tctcatcacc 120
 atggtgggca accttggact gatagttcta atttggaacg acccccatct tcatatgccc 180
 atgtacttat tccttgggtgg ttttagccttt tcagatgctt gtacttcaac ctctataacc 240
 cctaggatgc tgggtcaattt cttagacaag actgcaatga tatccctagc tgagtgcac 300
 acccagtttt acttttttgc ttccagtgc actacagaat gcttcctcct ggtgatgatg 360
 gcctatgacc gctatgtagc catatgtaat cccttgcttt atccagtgat gatgtccaac 420
 aaactcagcg ctgagttgct aagtatttca tatgtaattg gtttcctgca tcctctgggt 480
 catgtgagtt tactattgcg actaactttc tgcaggttta acataatata ttatttctac 540
 tgtgaaattt tacaactggt caaaatttca tgcaatggtc catctattaa cgcactaatg 600
 atatttattt ttgggtgcttt tatacaaata ccacttttaa tgactatcat aatctcttat 660
 actcgtgtgc tctttgatat tctgaaaaaa aagtctgaaa agggcagaag caaagccttc 720
 tccacatgcg gcgcccactct gctttctgtc tcattgtact acggaactct gatcttcatg 780
 tatgtgcgtc ctgcatctgg cttagctgaa gaccaagaca aagtgtattc tctgttttac 840
 acgattataa ttcccctgct aaaccattt atttacagct tgagaaataa aaaagtcatg 900
 catgcattga gaagagttat aaggaagtaa 930

<210> 32
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 32

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

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

Ser Thr Cys Gly Ala His Leu Leu Ser Val Ser Leu Tyr Tyr Gly Thr
 245 250 255

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

Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro Leu Leu Asn
 275 280 285

Pro Phe Ile Tyr Ser Leu Arg Asn Lys Lys Val Met His Ala Leu Arg
 290 295 300

Arg Val Ile Arg Lys
 305

<210> 33
 <211> 939
 <212> DNA
 <213> Homo sapiens

<400> 33
 atgatgggta gaaggaatga cacaaatgtg gctgacttca tccttacggg actgtcagac 60
 tctgaagagg tccagatggc tctgtttatg ctatttctcc tcatatacct aattactatg 120
 ctgggggaatg tgggggatgct attgataatc cgcctggacc tccagcttca cactcccatg 180
 tattttttcc ttactcacct gtcatttatt gacctcagtt actcaactgt cgtcacacct 240
 aaaaccttag cgaacttact gacttccaac tatatttcct tcacgggctg ctttgcccag 300
 atgttctgtt ttgtcttctt ggggtactgct gaatgttatc ttctctcctc aatggcctat 360
 gatcgctatg cagcgatctg cagtcctcta cactacacag ttattatgcc caaaaggctc 420
 tgcctcgctc tcatcactgg gccttatgtg attggcttta tggactcctt tgtcaatgtg 480
 gtttccatga gcagattgca tttctgtgac tcaaacataa ttcatcactt tttctgtgac 540
 acttccccaa ttttagctct gtcctgcact gacacagaca aactgaaat gctgatattc 600
 attatcgctg gttccaccct gatgggtgtcc cttatcacia tatctgcatc ctatgtgtcc 660
 attctctcta ccatcctgaa aattaattcc acttcaggaa agcagaaagc tttctctact 720

tgcgtctctc atctcttggg agtcaccatc ttctatggaa ctatgatttt tacttactta 780
 aagccaagaa agtcttattc cttgggaaga gatcaagtgg ctctgtgttt ttatactatt 840
 gtgattccca tgctgaatcc actcatttat agtcttagaa acagagaagt gaaaaatgct 900
 ctcattagag tcatgcagag aagacaggac tccaggtag 939

<210> 34
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 34

Met Met Gly Arg Arg Asn Asp Thr Asn Val Ala Asp Phe Ile Leu Thr
 1 5 10 15

Gly Leu Ser Asp Ser Glu Glu Val Gln Met Ala Leu Phe Met Leu Phe
 20 25 30

Leu Leu Ile Tyr Leu Ile Thr Met Leu Gly Asn Val Gly Met Leu Leu
 35 40 45

Ile Ile Arg Leu Asp Leu Gln Leu His Thr Pro Met Tyr Phe Phe Leu
 50 55 60

Thr His Leu Ser Phe Ile Asp Leu Ser Tyr Ser Thr Val Val Thr Pro
 65 70 75 80

Lys Thr Leu Ala Asn Leu Leu Thr Ser Asn Tyr Ile Ser Phe Thr Gly
 85 90 95

Cys Phe Ala Gln Met Phe Cys Phe Val Phe Leu Gly Thr Ala Glu Cys
 100 105 110

Tyr Leu Leu Ser Ser Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys Ser
 115 120 125

Pro Leu His Tyr Thr Val Ile Met Pro Lys Arg Leu Cys Leu Ala Leu
 130 135 140

Ile Thr Gly Pro Tyr Val Ile Gly Phe Met Asp Ser Phe Val Asn Val
 145 150 155 160

Val Ser Met Ser Arg Leu His Phe Cys Asp Ser Asn Ile Ile His His
165 170 175

Phe Phe Cys Asp Thr Ser Pro Ile Leu Ala Leu Ser Cys Thr Asp Thr
180 185 190

Asp Asn Thr Glu Met Leu Ile Phe Ile Ile Ala Gly Ser Thr Leu Met
195 200 205

Val Ser Leu Ile Thr Ile Ser Ala Ser Tyr Val Ser Ile Leu Ser Thr
210 215 220

Ile Leu Lys Ile Asn Ser Thr Ser Gly Lys Gln Lys Ala Phe Ser Thr
225 230 235 240

Cys Val Ser His Leu Leu Gly Val Thr Ile Phe Tyr Gly Thr Met Ile
245 250 255

Phe Thr Tyr Leu Lys Pro Arg Lys Ser Tyr Ser Leu Gly Arg Asp Gln
260 265 270

Val Ala Pro Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu
275 280 285

Ile Tyr Ser Leu Arg Asn Arg Glu Val Lys Asn Ala Leu Ile Arg Val
290 295 300

Met Gln Arg Arg Gln Asp Ser Arg
305 310

<210> 35
<211> 936
<212> DNA
<213> Homo sapiens

<400> 35
atgaaaatct tcaacagccc cagcaactcc agcaccttca ctggcttcat cctcctgggc 60
ttcccttgcc ccagggaggg gcagatcctc ctctttgtgc tcttcactgt tgtttacctc 120
ctgaccctca tgggcaatgg ttccatcatc tgtgctgtgc actgggatca gagactccac 180
gccccatgt acatcctgct cgccaacttc tccttcttgg agatatgtta tgtcacctcc 240

acagtcccca gcatgctggc caacttcctc tctgacacca agatcatctc gttctctggc 300
tgcttcctcc agttctactt tttcttctcc ttgggctcta cagaatgctt tttcctggca 360
gttatggcat ttgatcgata ccttgccatc tgtcggcctc tacgctatcc aaccattatg 420
accagacgtc tctgtaccaa tcttgtggtc aattgctggg tacttggttt catctggttc 480
ttgattccta tcgtcaacat ctcccaaatg tccttctgtg gatctaggat tattgaccac 540
ttcctatgtg acccagctcc tcttctaact ctacttgca aaaaaggccc tgtgatagag 600
cttgtctttt ctgtcttaag tcctctgcct gtctttatgc tctttctctt cattgtgggg 660
tcctatgctc tggtcgtgag agctgtgttg agggtcctt cagcagctgg gagaagaaag 720
gctttctcca cctgtgggtc tcacctggct gtggtttcac tgttctacgg ctcagtactg 780
gtcatgtatg ggagcccacc atctaagaat gaagctggaa agcagaagac tgtgactctg 840
ttttattctg ttgttacccc actgcttaac cctgtgatat atagtcttag gaacaaagat 900
atgagaaaag ctctgaagaa attttgggga acataa 936

<210> 36
<211> 311
<212> PRT
<213> Homo sapiens

<400> 36

Met Lys Ile Phe Asn Ser Pro Ser Asn Ser Ser Thr Phe Thr Gly Phe
1 5 10 15

Ile Leu Leu Gly Phe Pro Cys Pro Arg Glu Gly Gln Ile Leu Leu Phe
20 25 30

Val Leu Phe Thr Val Val Tyr Leu Leu Thr Leu Met Gly Asn Gly Ser
35 40 45

Ile Ile Cys Ala Val His Trp Asp Gln Arg Leu His Ala Pro Met Tyr
50 55 60

Ile Leu Leu Ala Asn Phe Ser Phe Leu Glu Ile Cys Tyr Val Thr Ser
65 70 75 80

Thr Val Pro Ser Met Leu Ala Asn Phe Leu Ser Asp Thr Lys Ile Ile
85 90 95

Ser Phe Ser Gly Cys Phe Leu Gln Phe Tyr Phe Phe Phe Ser Leu Gly
100 105 110

Ser Thr Glu Cys Phe Phe Leu Ala Val Met Ala Phe Asp Arg Tyr Leu
115 120 125

Ala Ile Cys Arg Pro Leu Arg Tyr Pro Thr Ile Met Thr Arg Arg Leu
130 135 140

Cys Thr Asn Leu Val Val Asn Cys Trp Val Leu Gly Phe Ile Trp Phe
145 150 155 160

Leu Ile Pro Ile Val Asn Ile Ser Gln Met Ser Phe Cys Gly Ser Arg
165 170 175

Ile Ile Asp His Phe Leu Cys Asp Pro Ala Pro Leu Leu Thr Leu Thr
180 185 190

Cys Lys Lys Gly Pro Val Ile Glu Leu Val Phe Ser Val Leu Ser Pro
195 200 205

Leu Pro Val Phe Met Leu Phe Leu Phe Ile Val Gly Ser Tyr Ala Leu
210 215 220

Val Val Arg Ala Val Leu Arg Val Pro Ser Ala Ala Gly Arg Arg Lys
225 230 235 240

Ala Phe Ser Thr Cys Gly Ser His Leu Ala Val Val Ser Leu Phe Tyr
245 250 255

Gly Ser Val Leu Val Met Tyr Gly Ser Pro Pro Ser Lys Asn Glu Ala
260 265 270

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

Leu Asn Pro Val Ile Tyr Ser Leu Arg Asn Lys Asp Met Arg Lys Ala
290 295 300

Leu Lys Lys Phe Trp Gly Thr
305 310

<210> 37
 <211> 966
 <212> DNA
 <213> Homo sapiens

<400> 37
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 gtcgtgggga actgtgggct catctgcctc atcagccatg aggaggccct gcaccggccc 180
 atgtactact tcctggccct gctctccttc actgatgtca ccttgtgcac caccatggta 240
 cctaatatgc tgtgcatatt ctggttcaac ctcaaggaga ttgactttaa cgcctgcctg 300
 gccagatgt tttttgtcca tatgctgaca gggatggagt ctggggtgct catgctcatg 360
 gccctggacc gctatgtggc catctgctac cccttacgct atgccaccat ccttaccaac 420
 cctgtcatcg ccaaggctgg tcttgccacc ttcttgagga atgtgatgct catcatccca 480
 ttactctcc tcaccaagcg cctgccctat tgccggggga acttcatccc ccacacctac 540
 tgtgaccata tgtctgtggc caaggtatcc tgtggcaatt tcaaggtcaa tgctatttat 600
 ggtctgatgg ttgctctcct gattggtgtg tttgatatct gctgtatctc tgtatcttac 660
 actatgattt tgcaggctgt tatgagcctg tcatcagcag atgctcgtca caaagccttc 720
 agcacctgca catctcacat gtgttcatt gtgatcacct atgttgctgc ttttttact 780
 tttttcactc atcgttttgt aggacacaat atcccaaacc acatacacat catcgtggcc 840
 aacctttatc tgctactgcc tcctaccatg aaccaattg tttatggagt caagaccaag 900
 cagattcagg aagggtgaat taaattttta cttggagaca aggttagttt tacctatgac 960
 aaatga 966

<210> 38
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 38

Met Ser Gly Asp Asn Ser Ser Ser Leu Thr Pro Gly Phe Phe Ile Leu
 1 5 10 15

Asn Gly Val Pro Gly Leu Glu Ala Thr His Ile Trp Ile Ser Leu Pro

20

25

30

Phe Cys Phe Met Tyr Ile Ile Ala Val Val Gly Asn Cys Gly Leu Ile
 35 40 45

Cys Leu Ile Ser His Glu Glu Ala Leu His Arg Pro Met Tyr Tyr Phe
 50 55 60

Leu Ala Leu Leu Ser Phe Thr Asp Val Thr Leu Cys Thr Thr Met Val
 65 70 75 80

Pro Asn Met Leu Cys Ile Phe Trp Phe Asn Leu Lys Glu Ile Asp Phe
 85 90 95

Asn Ala Cys Leu Ala Gln Met Phe Phe Val His Met Leu Thr Gly Met
 100 105 110

Glu Ser Gly Val Leu Met Leu Met Ala Leu Asp Arg Tyr Val Ala Ile
 115 120 125

Cys Tyr Pro Leu Arg Tyr Ala Thr Ile Leu Thr Asn Pro Val Ile Ala
 130 135 140

Lys Ala Gly Leu Ala Thr Phe Leu Arg Asn Val Met Leu Ile Ile Pro
 145 150 155 160

Phe Thr Leu Leu Thr Lys Arg Leu Pro Tyr Cys Arg Gly Asn Phe Ile
 165 170 175

Pro His Thr Tyr Cys Asp His Met Ser Val Ala Lys Val Ser Cys Gly
 180 185 190

Asn Phe Lys Val Asn Ala Ile Tyr Gly Leu Met Val Ala Leu Leu Ile
 195 200 205

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

Gln Ala Val Met Ser Leu Ser Ser Ala Asp Ala Arg His Lys Ala Phe
 225 230 235 240

Ser Thr Cys Thr Ser His Met Cys Ser Ile Val Ile Thr Tyr Val Ala
245 250 255

Ala Phe Phe Thr Phe Phe Thr His Arg Phe Val Gly His Asn Ile Pro
260 265 270

Asn His Ile His Ile Ile Val Ala Asn Leu Tyr Leu Leu Leu Pro Pro
275 280 285

Thr Met Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Gln Ile Gln Glu
290 295 300

Gly Val Ile Lys Phe Leu Leu Gly Asp Lys Val Ser Phe Thr Tyr Asp
305 310 315 320

Lys

<210> 39
<211> 915
<212> DNA
<213> Homo sapiens

<400> 39
atgtttatat taataagctt cacagaagaa tttgatgtgc aagtcttcct atttttatta 60
tttttagcaa tctatctatt cactctaata ggcaatttag ggctggttgt accgatcatt 120
ggggatttct ggcttcacag cccaatgtac tattttcttg gtgttttatc attcttggat 180
gtctgctatt ctacagttgt cactcaaaa atgttggtca atttcctggc aaaaaataaa 240
tctatttcat ttcttggatg tgcaacacag atgtttcttg cttgtacttt tggaaccaca 300
gaatgctttc tcttggctgc aatggcttat gatcgctatg tagccatcta caaccctctc 360
ctgtattcag tgagcatgtc acccagagtc tatgtgccac tcatcactgc ttcctatggt 420
gctagcattt tacatgctac tatacataca gtggctacat ttagcctgtc cttctgtgga 480
tccaatgaaa ttaggcatgt cttttgtaat atgcctcctc tccttgctat ttcttgttct 540
gacactcacg taatccagct tctattcttc tactttgtgg gctctattga gatagtcact 600
atcctgattg tcctgatctc ctatggtttt attctgttgg ccattctgaa gatgcagtct 660
gctgaaggga ggagaaaagt cttctctaca tgtggagctc acctaactgg agtgacaatt 720
tatcatggga caatcctctt catgtatgtg agaccaagtt ccagctacac ttcggacaat 780

gacatgatag tgtcaatatt ttataaccatt gtgattccca tgctgaatcc catcatctac 840
 agtttgcgga acaaagatgt aaaggaggca atcaaaagat tgcttgtgag aaattggttc 900
 ataaataagt tatag 915

<210> 40
 <211> 304
 <212> PRT
 <213> Homo sapiens

<400> 40

Met Phe Ile Leu Ile Ser Phe Thr Glu Glu Phe Asp Val Gln Val Phe
 1 5 10 15

Leu Phe Leu Leu Phe Leu Ala Ile Tyr Leu Phe Thr Leu Ile Gly Asn
 20 25 30

Leu Gly Leu Val Val Pro Ile Ile Gly Asp Phe Trp Leu His Ser Pro
 35 40 45

Met Tyr Tyr Phe Leu Gly Val Leu Ser Phe Leu Asp Val Cys Tyr Ser
 50 55 60

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

Ser Ile Ser Phe Leu Gly Cys Ala Thr Gln Met Phe Leu Ala Cys Thr
 85 90 95

Phe Gly Thr Thr Glu Cys Phe Leu Leu Ala Ala Met Ala Tyr Asp Arg
 100 105 110

Tyr Val Ala Ile Tyr Asn Pro Leu Leu Tyr Ser Val Ser Met Ser Pro
 115 120 125

Arg Val Tyr Val Pro Leu Ile Thr Ala Ser Tyr Val Ala Ser Ile Leu
 130 135 140

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

Ser Asn Glu Ile Arg His Val Phe Cys Asn Met Pro Pro Leu Leu Ala
165 170 175

Ile Ser Cys Ser Asp Thr His Val Ile Gln Leu Leu Phe Phe Tyr Phe
180 185 190

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

Gly Phe Ile Leu Leu Ala Ile Leu Lys Met Gln Ser Ala Glu Gly Arg
210 215 220

Arg Lys Val Phe Ser Thr Cys Gly Ala His Leu Thr Gly Val Thr Ile
225 230 235 240

Tyr His Gly Thr Ile Leu Phe Met Tyr Val Arg Pro Ser Ser Ser Tyr
245 250 255

Thr Ser Asp Asn Asp Met Ile Val Ser Ile Phe Tyr Thr Ile Val Ile
260 265 270

Pro Met Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys
275 280 285

Glu Ala Ile Lys Arg Leu Leu Val Arg Asn Trp Phe Ile Asn Lys Leu
290 295 300

<210> 41

<211> 936

<212> DNA

<213> Homo sapiens

<400> 41

atggaaaaaa taaacaacgt aactgaattc attttctggg gtctttctca gagcccagag 60

attgagaaag tttgttttgt ggtgttttct ttcttctaca taatcattct tctgggaaat 120

ctcctcatca tgctgacagt ttgcctgagc aacctgttta agtcacccat gtatttcttt 180

ctcagcttct tgtcttttgt ggacatttgt tactcttcag tcacagctcc caagatgatt 240

gttgacctgt tagcaaagga caaaaccatc tcctatgtgg ggtgcatgtt gcaactgttt 300

ggagtacatt tctttggttg cactgagatc ttcatcctta ctgtaatggc ctatgatcgt 360

tatgtggcta tctgtaaacc cctacattat atgaccatca tgaaccggga gacatgcaat 420

aaaatgttat tagggacgtg ggtaggtggg ttcttacact ccattatcca agtggctctg	480
gtagtccaac tacccttttg tggaccaat gagatagatc actacttttg tgatgttcac	540
cctgtgttga aacttgcctg cacagaaaca tacattgttg gtgttgttgt gacagccaac	600
agtggtagca ttgctctggg gagttttgtt atcttgctaa tctcctacag catcatccta	660
gtttccctga gaaagcagtc agcagaaggc aggcgcaaag ccctctccac ctgtggctcc	720
cacattgcca tggtcgttat ctttttcggc ccctgtactt ttatgtacat gcgccctgat	780
acgacctttt cagaggataa gatgggtggc gtatttttaca ccattatcac tcccatgtta	840
aatcctctga tttatacact gagaaatgca gaagtaaaga atgcaatgaa gaaactgtgg	900
ggcagaaatg ttttcttgga ggctaaaggg aaatag	936

<210> 42
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 42

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

Gln	Ser	Pro	Glu	Ile	Glu	Lys	Val	Cys	Phe	Val	Val	Phe	Ser	Phe	Phe
			20					25					30		

Tyr	Ile	Ile	Ile	Leu	Leu	Gly	Asn	Leu	Leu	Ile	Met	Leu	Thr	Val	Cys
		35					40				45				

Leu	Ser	Asn	Leu	Phe	Lys	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Phe	Leu
		50				55					60				

Ser	Phe	Val	Asp	Ile	Cys	Tyr	Ser	Ser	Val	Thr	Ala	Pro	Lys	Met	Ile
65					70					75				80	

Val	Asp	Leu	Leu	Ala	Lys	Asp	Lys	Thr	Ile	Ser	Tyr	Val	Gly	Cys	Met
				85					90					95	

Leu	Gln	Leu	Phe	Gly	Val	His	Phe	Phe	Gly	Cys	Thr	Glu	Ile	Phe	Ile
			100					105					110		

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

His Tyr Met Thr Ile Met Asn Arg Glu Thr Cys Asn Lys Met Leu Leu
130 135 140

Gly Thr Trp Val Gly Gly Phe Leu His Ser Ile Ile Gln Val Ala Leu
145 150 155 160

Val Val Gln Leu Pro Phe Cys Gly Pro Asn Glu Ile Asp His Tyr Phe
165 170 175

Cys Asp Val His Pro Val Leu Lys Leu Ala Cys Thr Glu Thr Tyr Ile
180 185 190

Val Gly Val Val Val Thr Ala Asn Ser Gly Thr Ile Ala Leu Gly Ser
195 200 205

Phe Val Ile Leu Leu Ile Ser Tyr Ser Ile Ile Leu Val Ser Leu Arg
210 215 220

Lys Gln Ser Ala Glu Gly Arg Arg Lys Ala Leu Ser Thr Cys Gly Ser
225 230 235 240

His Ile Ala Met Val Val Ile Phe Phe Gly Pro Cys Thr Phe Met Tyr
245 250 255

Met Arg Pro Asp Thr Thr Phe Ser Glu Asp Lys Met Val Ala Val Phe
260 265 270

Tyr Thr Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg
275 280 285

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

Phe Leu Glu Ala Lys Gly Lys
305 310

<210> 43
<211> 24
<212> DNA

<213> Artificial Sequence

<220>

<223> FLAG tag

<400> 43

gattacaagg acgacgacga taag

24

<210> 44

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> FLAG tag

<400> 44

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 45

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Rho tag

<400> 45

atgaacggga ccgagggccc aaacttctac gtgcctttct ccaacaagac gggcgtggtg

60

<210> 46

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Rho tag

<400> 46

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

Thr Gly Val Val
20

<210> 47

<211> 51

<212> DNA
<213> Artificial Sequence

<220>
<223> Lucy tag

<400> 47
atgagacccc agatcctgct gtcctggcc ctgctgaccc taggcctggc t 51

<210> 48
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Lucy tag

<400> 48

Met Arg Pro Gln Ile Leu Leu Leu Leu Ala Leu Leu Thr Leu Gly Leu
1 5 10 15

Ala

<210> 49
<211> 1376
<212> DNA
<213> Homo sapiens

<400> 49
atgggtctgt gctacagtct gcggccgctg cttttcgggg gccagggga cgacccctgc 60
gcggcctcgg agccgccggt ggaggacgcg cagcccgccc cggccccggc cctggcccca 120
gtccgggcgg ccgcaaggga cacggcccgg accctgctcc ctccggggcg cgaaggagagc 180
ccggcatgcg ctccggccaa agcagacaag ccgaaggaga agcggcagcg caccgagcag 240
cttagtgccg aggagcgca ggccggccaag gagcgcgagg cggtaagga ggcgaggaaa 300
gtgagccggg gcatcgaccg catgctgcgc gaccagaagc gcgacctgca gcagacgcac 360
cggctcctgc tgctcggggc tggtagtctt gggaaaagca ctatcgtaa acagatgagg 420
atcctgcacg tcaatgggtt taatcccag gaaaagaaac agaaaattct ggacatccgg 480
aaaaatgtta aagatgctat cgtgacaatt gtttcagcaa tgagtactat aatacctcca 540
gttccgctgg ccaaccctga aaaccaattt cgatcagact acatcaagag catagcccct 600
atcactgact ttgaatatc ccaggaattc ttgacctg tgaaaaaact ttgggacgat 660

gaaggcgtga aggcattgctt tgagagatcc aacgaatacc agctgattga ctgtgcacaa 720
 tacttcctgg aaagaatcga cagcgtcagc ttggttgact acacaccac agaccaggac 780
 ctctcagat gcagagtctt gacatctggg atttttgaga acgattccaa gtggacaaag 840
 taaacttcca catgtttgat gttggtggcc agagggatga gaggagaaaa tggatccagt 900
 gctttaacga tgtcacagct atcatttacg tcgcagcctg cagtagctac aacatggtga 960
 ttcgagaaga taacaacacc aacaggctga gagagtccct ggatcttttt gaaagcatct 1020
 ggaacaacag gtggttacgg accatttcta tcatcttggt cttgaacaaa caagatatgc 1080
 tggcagaaaa agtcttggca gggaaatcaa aaattgaaga ctatttccca gaatatgcaa 1140
 attatactgt tcctgaagac gcaacaccag atgcaggaga agatcccaaa gttacaagag 1200
 ccaagttctt tatccgggac ctgtttttga ggatcagcac ggccaccggt gacggcaaac 1260
 attactgcta cccgcacttc acctgcgccg tggacacaga gaacatccgc aggggtgttca 1320
 acgactgccg cgacatcatc cagcggatgc acctcaagca gtatgagctc ttgtga 1376

<210> 50
 <211> 458
 <212> PRT
 <213> Homo sapiens

<400> 50

Met Gly Leu Cys Tyr Ser Leu Arg Pro Leu Leu Phe Gly Gly Pro Gly
 1 5 10 15

Asp Asp Pro Cys Ala Ala Ser Glu Pro Pro Val Glu Asp Ala Gln Pro
 20 25 30

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

Ala Arg Thr Leu Leu Pro Arg Gly Gly Glu Gly Ser Pro Ala Cys Ala
 50 55 60

Arg Pro Lys Ala Asp Lys Pro Lys Glu Lys Arg Gln Arg Thr Glu Gln
 65 70 75 80

Leu Ser Ala Glu Glu Arg Glu Ala Ala Lys Glu Arg Glu Ala Val Lys
 85 90 95

Glu Ala Arg Lys Val Ser Arg Gly Ile Asp Arg Met Leu Arg Asp Gln
100 105 110

Lys Arg Asp Leu Gln Gln Thr His Arg Leu Leu Leu Leu Gly Ala Gly
115 120 125

Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His Val
130 135 140

Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln Lys Ile Leu Asp Ile Arg
145 150 155 160

Lys Asn Val Lys Asp Ala Ile Val Thr Ile Val Ser Ala Met Ser Thr
165 170 175

Ile Ile Pro Pro Val Pro Leu Ala Asn Pro Glu Asn Gln Phe Arg Ser
180 185 190

Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr Asp Phe Glu Tyr Ser Gln
195 200 205

Glu Phe Phe Asp His Val Lys Lys Leu Trp Asp Asp Glu Gly Val Lys
210 215 220

Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln
225 230 235 240

Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser Leu Val Asp Tyr Thr Pro
245 250 255

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

Glu Thr Arg Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val
275 280 285

Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp
290 295 300

Val Thr Ala Ile Ile Tyr Val Ala Ala Cys Ser Ser Tyr Asn Met Val

305		310		315		320
Ile Arg Glu Asp	Asn Asn Thr Asn Arg	Leu Arg Glu Ser	Leu Asp Leu			
	325	330	335			
Phe Glu Ser Ile	Trp Asn Asn Arg	Trp Leu Arg Thr	Ile Ser Ile Ile			
	340	345	350			
Leu Phe Leu Asn	Lys Gln Asp Met	Leu Ala Glu Lys	Val Leu Ala Gly			
	355	360	365			
Lys Ser Lys Ile	Glu Asp Tyr Phe	Pro Glu Tyr Ala	Asn Tyr Thr Val			
	370	375	380			
Pro Glu Asp Ala	Thr Pro Asp Ala	Gly Glu Asp Pro	Lys Val Thr Arg			
385	390	395	400			
Ala Lys Phe Phe	Ile Arg Asp Leu	Phe Leu Arg Ile	Ser Thr Ala Thr			
	405	410	415			
Gly Asp Gly Lys	His Tyr Cys Tyr	Pro His Phe Thr	Cys Ala Val Asp			
	420	425	430			
Thr Glu Asn Ile	Arg Arg Val Phe	Asn Asp Cys Arg	Asp Ile Ile Gln			
	435	440	445			
Arg Met His Leu	Lys Gln Tyr Glu	Leu Leu				
450	455					

<210> 51
 <211> 1125
 <212> DNA
 <213> Homo sapiens

<400> 51	
atggcccgggt cgctgacctg gcgctgctgc ccctggtgcc tgacggagga tgagaaggcc	60
gccgcccggg tggaccagga gatcaacagg atcctcttgg agcagaagaa gcaggaccgc	120
ggggagctga agctgctgct tttgggcca ggcgagagcg ggaagagcac cttcatcaag	180
cagatgcgga tcatccacgg cgccggctac tcggaggagg agcgcaaggg cttccggccc	240
ctggtctacc agaacatctt cgtgtccatg cgggccatga tcgaggccat ggagcggctg	300

cagattccat tcagcaggcc cgagagcaag caccacgcc gcctgggtcat gagccaggac 360
 ccctataaag tgaccacgtt tgagaagcgc tacgtgcgg ccatgcagt gctgtggagg 420
 gatgccggca tccgggcctg ctatgagcgt cggcgggaat tccacctgct cgattcagcc 480
 gtgtactacc tgtcccacct ggagcgcac accgaggagg gctacgtccc cacagctcag 540
 gacgtgctcc gcagccgcat gcccaccact ggcatcaacg agtactgctt ctccgtgcag 600
 aaaaccaacc tgcggatcgt ggacgtcggg ggccagaagt cagagcgtaa gaaatggatc 660
 cattgtttcg agaacgtgat cgccctcatc tacctggcct cactgagtga atacgaccag 720
 tgcctggagg agaacaacca ggagaaccgc atgaaggaga gcctcgcat gtttgggact 780
 atcctggaac taccctgggt caaaagcaca tccgtcatcc tctttctcaa caaaaccgac 840
 atcctggagg agaaaatccc cacctcccac ctggctacct atttcccag tttccagggc 900
 cctaagcagg atgctgaggc agccaagagg ttcacatcctgg acatgtacac gaggatgtac 960
 accgggtgcg tggacggccc cgagggcagc aagaaggcg cacgatcccg acgcctcttc 1020
 agccactaca catgtgccac agacacacag aacatccgca aggtcttcaa ggacgtgcgg 1080
 gactcgggtgc tcgcccgtc cctggacgag atcaacctgc tgtga 1125

<210> 52
 <211> 374
 <212> PRT
 <213> Homo sapiens

<400> 52

Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
 1 5 10 15

Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
 20 25 30

Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu
 35 40 45

Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
 50 55 60

Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
 65 70 75 80

Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
85 90 95

Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
100 105 110

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

Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
130 135 140

Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
145 150 155 160

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

Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
180 185 190

Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
195 200 205

Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
210 215 220

Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
225 230 235 240

Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
245 250 255

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

Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
275 280 285

Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
290 295 300

Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
305 310 315 320

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

Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
340 345 350

Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
355 360 365

Asp Glu Ile Asn Leu Leu
370

<210> 53
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein motif

<400> 53

Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys
1 5 10

<210> 54
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Protein motif

<400> 54

Phe Ser Thr Cys Ser Ser His
1 5

<210> 55
<211> 8
<212> PRT
<213> Artificial Sequence

<220>

<223> Protein motif

<400> 55

Pro	Met	Leu	Asn	Pro	Phe	Ile	Tyr
1				5			