

JPOXMLDOC01-seq1.app
SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> kokumi imparting agent

<130> Y1R-0607

<160> 4

<170> PatentIn version 3.1

<210> 1

<211> 4924

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (373)..(3609)

<223>

<400> 1

```

caacaggcac ctggctgcag ccaggaagga ccgcacgccc tttcgcgcag gagagtggaa      60
ggagggagct gtttgccagc accgaggtct tgcggcacag gcaacgcttg acctgagtct      120
tgcagaatga aaggcatcac aggaggcctc tgcattgatgt ggcttccaaa gactcaagga      180
ccaccacat tacaagtctg gattgaggaa ggcagaaatg gagattcaaa caccacgtct      240
tctattatatt tattaatcaa tctgtagaca tgtgtcccca ctgcagggag tgaactgctc      300
caagggagaa acttctggga gcctccaaac tcctagctgt ctcattccctt gccctggaga      360
gacggcagaa cc atg gca ttt tat agc tgc tgc tgg gtc ctc ttg gca ctc      411
                Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu
                1          5          10

acc tgg cac acc tct gcc tac ggg cca gac cag cga gcc caa aag aag      459
Thr Trp His Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys
                15          20          25

ggg gac att atc ctt ggg ggg ctc ttt cct att cat ttt gga gta gca      507
Gly Asp Ile Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala
                30          35          40          45

gct aaa gat caa gat ctc aaa tca agg ccg gag tct gtg gaa tgt atc      555
Ala Lys Asp Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile
                50          55          60

agg tat aat ttc cgt ggg ttt cgc tgg tta cag gct atg ata ttt gcc      603
Arg Tyr Asn Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala
                65          70          75

ata gag gag ata aac agc agc cca gcc ctt ctt ccc aac ttg acg ctg      651
Ile Glu Glu Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu
                80          85          90

gga tac agg ata ttt gac act tgc aac acc gtt tct aag gcc ttg gaa      699
Gly Tyr Arg Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu
                95          100          105

gcc acc ctg agt ttt gtt gct caa aac aaa att gat tct ttg aac ctt      747
Ala Thr Leu Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu
                110          115          120          125

gat gag ttc tgc aac tgc tca gag cac att ccc tct acg att gct gtg      795

```

JPOXMLDOC01-seq1.app

Asp	Glu	Phe	Cys	Asn	Cys	Ser	Glu	His	Ile	Pro	Ser	Thr	Ile	Ala	Val	
				130					135					140		
gtg	gga	gca	act	ggc	tca	ggc	gtc	tcc	acg	gca	gtg	gca	aat	ctg	ctg	843
Val	Gly	Ala	Thr	Gly	Ser	Gly	Val	Ser	Thr	Ala	Val	Ala	Asn	Leu	Leu	
			145					150					155			
ggg	ctc	ttc	tac	att	ccc	cag	gtc	agt	tat	gcc	tcc	tcc	agc	aga	ctc	891
Gly	Leu	Phe	Tyr	Ile	Pro	Gln	Val	Ser	Tyr	Ala	Ser	Ser	Ser	Arg	Leu	
		160					165					170				
ctc	agc	aac	aag	aat	caa	ttc	aag	tct	ttc	ctc	cga	acc	atc	ccc	aat	939
Leu	Ser	Asn	Lys	Asn	Gln	Phe	Lys	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	
	175					180					185					
gat	gag	cac	cag	gcc	act	gcc	atg	gca	gac	atc	atc	gag	tat	ttc	cgc	987
Asp	Glu	His	Gln	Ala	Thr	Ala	Met	Ala	Asp	Ile	Ile	Glu	Tyr	Phe	Arg	
190					195					200					205	
tgg	aac	tgg	gtg	ggc	aca	att	gca	gct	gat	gac	gac	tat	ggg	cgg	ccg	1035
Trp	Asn	Trp	Val	Gly	Thr	Ile	Ala	Ala	Asp	Asp	Asp	Tyr	Gly	Arg	Pro	
				210					215					220		
ggg	att	gag	aaa	ttc	cga	gag	gaa	gct	gag	gaa	agg	gat	atc	tgc	atc	1083
Gly	Ile	Glu	Lys	Phe	Arg	Glu	Glu	Ala	Glu	Glu	Arg	Asp	Ile	Cys	Ile	
			225					230					235			
gac	ttc	agt	gaa	ctc	atc	tcc	cag	tac	tct	gat	gag	gaa	gag	atc	cag	1131
Asp	Phe	Ser	Glu	Leu	Ile	Ser	Gln	Tyr	Ser	Asp	Glu	Glu	Glu	Ile	Gln	
		240					245					250				
cat	gtg	gta	gag	gtg	att	caa	aat	tcc	acg	gcc	aaa	gtc	atc	gtg	gtt	1179
His	Val	Val	Glu	Val	Ile	Gln	Asn	Ser	Thr	Ala	Lys	Val	Ile	Val	Val	
	255					260					265					
ttc	tcc	agt	ggc	cca	gat	ctt	gag	ccc	ctc	atc	aag	gag	att	gtc	cgg	1227
Phe	Ser	Ser	Gly	Pro	Asp	Leu	Glu	Pro	Leu	Ile	Lys	Glu	Ile	Val	Arg	
270					275					280					285	
cgc	aat	atc	acg	ggc	aag	atc	tgg	ctg	gcc	agc	gag	gcc	tgg	gcc	agc	1275
Arg	Asn	Ile	Thr	Gly	Lys	Ile	Trp	Leu	Ala	Ser	Glu	Ala	Trp	Ala	Ser	
				290					295				300			
tcc	tcc	ctg	atc	gcc	atg	cct	cag	tac	ttc	cac	gtg	gtt	ggc	ggc	acc	1323
Ser	Ser	Leu	Ile	Ala	Met	Pro	Gln	Tyr	Phe	His	Val	Val	Gly	Gly	Thr	
			305					310					315			
att	gga	ttc	gct	ctg	aag	gct	ggg	cag	atc	cca	ggc	ttc	cgg	gaa	ttc	1371
Ile	Gly	Phe	Ala	Leu	Lys	Ala	Gly	Gln	Ile	Pro	Gly	Phe	Arg	Glu	Phe	
		320					325					330				
ctg	aag	aag	gtc	cat	ccc	agg	aag	tct	gtc	cac	aat	ggg	ttt	gcc	aag	1419
Leu	Lys	Lys	Val	His	Pro	Arg	Lys	Ser	Val	His	Asn	Gly	Phe	Ala	Lys	
	335					340					345					
gag	ttt	tgg	gaa	gaa	aca	ttt	aac	tgc	cac	ctc	caa	gaa	ggg	gca	aaa	1467
Glu	Phe	Trp	Glu	Glu	Thr	Phe	Asn	Cys	His	Leu	Gln	Glu	Gly	Ala	Lys	
350					355					360					365	
gga	cct	tta	cct	gtg	gac	acc	ttt	ctg	aga	ggg	cac	gaa	gaa	agt	ggc	1515
Gly	Pro	Leu	Pro	Val	Asp	Thr	Phe	Leu	Arg	Gly	His	Glu	Glu	Ser	Gly	
				370					375					380		
gac	agg	ttt	agc	aac	agc	tcg	aca	gcc	ttc	cga	ccc	ctc	tgt	aca	ggg	1563
Asp	Arg	Phe	Ser	Asn	Ser	Ser	Thr	Ala	Phe	Arg	Pro	Leu	Cys	Thr	Gly	
			385					390					395			
gat	gag	aac	atc	agc	agt	gtc	gag	acc	cct	tac	ata	gat	tac	acg	cat	1611

Asp	Glu	Asn	Ile	Ser	Ser	Val	Glu	Thr	Pro	Tyr	Ile	Asp	Tyr	Thr	His	
		400					405					410				
tta	cgg	ata	tcc	tac	aat	gtg	tac	tta	gca	gtc	tac	tcc	att	gcc	cac	1659
Leu	Arg	Ile	Ser	Tyr	Asn	Val	Tyr	Leu	Ala	Val	Tyr	Ser	Ile	Ala	His	
	415					420					425					
gcc	ttg	caa	gat	ata	tat	acc	tgc	tta	cct	ggg	aga	ggg	ctc	ttc	acc	1707
Ala	Leu	Gln	Asp	Ile	Tyr	Thr	Cys	Leu	Pro	Gly	Arg	Gly	Leu	Phe	Thr	
430					435					440					445	
aat	ggc	tcc	tgt	gca	gac	atc	aag	aaa	gtt	gag	gcg	tgg	cag	gtc	ctg	1755
Asn	Gly	Ser	Cys	Ala	Asp	Ile	Lys	Lys	Val	Glu	Ala	Trp	Gln	Val	Leu	
				450					455					460		
aag	cac	cta	cgg	cat	cta	aac	ttt	aca	aac	aat	atg	ggg	gag	cag	gtg	1803
Lys	His	Leu	Arg	His	Leu	Asn	Phe	Thr	Asn	Asn	Met	Gly	Glu	Gln	Val	
			465					470					475			
acc	ttt	gat	gag	tgt	ggg	gac	ctg	gtg	ggg	aac	tat	tcc	atc	atc	aac	1851
Thr	Phe	Asp	Glu	Cys	Gly	Asp	Leu	Val	Gly	Asn	Tyr	Ser	Ile	Ile	Asn	
		480					485					490				
tgg	cac	ctc	tcc	cca	gag	gat	ggc	tcc	atc	gtg	ttt	aag	gaa	gtc	ggg	1899
Trp	His	Leu	Ser	Pro	Glu	Asp	Gly	Ser	Ile	Val	Phe	Lys	Glu	Val	Gly	
	495					500					505					
tat	tac	aac	gtc	tat	gcc	aag	aag	gga	gaa	aga	ctc	ttc	atc	aac	gag	1947
Tyr	Tyr	Asn	Val	Tyr	Ala	Lys	Lys	Gly	Glu	Arg	Leu	Phe	Ile	Asn	Glu	
510					515					520					525	
gag	aaa	atc	ctg	tgg	agt	ggg	ttc	tcc	agg	gag	gtg	ccc	ttc	tcc	aac	1995
Glu	Lys	Ile	Leu	Trp	Ser	Gly	Phe	Ser	Arg	Glu	Val	Pro	Phe	Ser	Asn	
				530					535					540		
tgc	agc	cga	gac	tgc	ctg	gca	ggg	acc	agg	aaa	ggg	atc	att	gag	ggg	2043
Cys	Ser	Arg	Asp	Cys	Leu	Ala	Gly	Thr	Arg	Lys	Gly	Ile	Ile	Glu	Gly	
			545					550					555			
gag	ccc	acc	tgc	tgc	ttt	gag	tgt	gtg	gag	tgt	cct	gat	ggg	gag	tat	2091
Glu	Pro	Thr	Cys	Cys	Phe	Glu	Cys	Val	Glu	Cys	Pro	Asp	Gly	Glu	Tyr	
		560					565					570				
agt	gat	gag	aca	gat	gcc	agt	gcc	tgt	aac	aag	tgc	cca	gat	gac	ttc	2139
Ser	Asp	Glu	Thr	Asp	Ala	Ser	Ala	Cys	Asn	Lys	Cys	Pro	Asp	Asp	Phe	
	575					580					585					
tgg	tcc	aat	gag	aac	cac	acc	tcc	tgc	att	gcc	aag	gag	atc	gag	ttt	2187
Trp	Ser	Asn	Glu	Asn	His	Thr	Ser	Cys	Ile	Ala	Lys	Glu	Ile	Glu	Phe	
590					595					600					605	
ctg	tcg	tgg	acg	gag	ccc	ttt	ggg	atc	gca	ctc	acc	ctc	ttt	gcc	gtg	2235
Leu	Ser	Trp	Thr	Glu	Pro	Phe	Gly	Ile	Ala	Leu	Thr	Leu	Phe	Ala	Val	
				610					615					620		
ctg	ggc	att	ttc	ctg	aca	gcc	ttt	gtg	ctg	ggg	gtg	ttt	atc	aag	ttc	2283
Leu	Gly	Ile	Phe	Leu	Thr	Ala	Phe	Val	Leu	Gly	Val	Phe	Ile	Lys	Phe	
			625					630					635			
cgc	aac	aca	ccc	att	gtc	aag	gcc	acc	aac	cga	gag	ctc	tcc	tac	ctc	2331
Arg	Asn	Thr	Pro	Ile	Val	Lys	Ala	Thr	Asn	Arg	Glu	Leu	Ser	Tyr	Leu	
		640					645					650				
ctc	ctc	ttc	tcc	ctg	ctc	tgc	tgc	ttc	tcc	agc	tcc	ctg	ttc	ttc	atc	2379
Leu	Leu	Phe	Ser	Leu	Leu	Cys	Cys	Phe	Ser	Ser	Ser	Leu	Phe	Phe	Ile	
	655					660					665					
ggg	gag	ccc	cag	gac	tgg	acg	tgc	cgc	ctg	cgc	cag	ccg	gcc	ttt	ggc	2427

Gly 670	Glu	Pro	Gln	Asp	Trp 675	Thr	Cys	Arg	Leu	Arg 680	Gln	Pro	Ala	Phe	Gly 685	
atc Ile	agc Ser	ttc Phe	gtg Val	ctc Leu 690	tgc Cys	atc Ile	tca Ser	tgc Cys	atc Ile 695	ctg Leu	gtg Val	aaa Lys	acc Thr	aac Asn 700	cgt Arg	2475
gtc Val	ctc Leu	ctg Leu	gtg Val 705	ttt Phe	gag Glu	gcc Ala	aag Lys	atc Ile 710	ccc Pro	acc Thr	agc Ser	ttc Phe	cac His 715	cgc Arg	aag Lys	2523
tgg Trp	tgg Trp	ggg Gly 720	ctc Leu	aac Asn	ctg Leu	cag Gln	ttc Phe 725	ctg Leu	ctg Leu	gtt Val	ttc Phe	ctc Leu 730	tgc Cys	acc Thr	ttc Phe	2571
atg Met	cag Gln 735	att Ile	gtc Val	atc Ile	tgt Cys	gtg Val 740	atc Ile	tgg Trp	ctc Leu	tac Tyr	acc Thr 745	gcg Ala	ccc Pro	ccc Pro	tca Ser	2619
agc Ser 750	tac Tyr	cgc Arg	aac Asn	cag Gln	gag Glu 755	ctg Leu	gag Glu	gat Asp	gag Glu	atc Ile 760	atc Ile	ttc Phe	atc Ile	acg Thr	tgc Cys 765	2667
cac His	gag Glu	ggc Gly	tcc Ser	ctc Leu 770	atg Met	gcc Ala	ctg Leu	ggc Gly	ttc Phe 775	ctg Leu	atc Ile	ggc Gly	tac Tyr	acc Thr 780	tgc Cys	2715
ctg Leu	ctg Leu	gct Ala	gcc Ala 785	atc Ile	tgc Cys	ttc Phe	ttc Phe	ttt Phe 790	gcc Ala	ttc Phe	aag Lys	tcc Ser	cgg Arg 795	aag Lys	ctg Leu	2763
ccg Pro	gag Glu	aac Asn 800	ttc Phe	aat Asn	gaa Glu	gcc Ala	aag Lys 805	ttc Phe	atc Ile	acc Thr	ttc Phe	agc Ser 810	atg Met	ctc Leu	atc Ile	2811
ttc Phe 815	ttc Phe	atc Ile	gtc Val	tgg Trp	atc Ile	tcc Ser 820	ttc Phe	att Ile	cca Pro	gcc Ala	tat Tyr 825	gcc Ala	agc Ser	acc Thr	tat Tyr	2859
ggc Gly 830	aag Lys	ttt Phe	gtc Val	tct Ser	gcc Ala 835	gta Val	gag Glu	gtg Val	att Ile	gcc Ala 840	atc Ile	ctg Leu	gca Ala	gcc Ala	agc Ser 845	2907
ttt Phe	ggc Gly	ttg Leu	ctg Leu	gcg Ala 850	tgc Cys	atc Ile	ttc Phe	ttc Phe	aac Asn 855	aag Lys	atc Ile	tac Tyr	atc Ile	att Ile 860	ctc Leu	2955
ttc Phe	aag Lys	cca Pro	tcc Ser 865	cgc Arg	aac Asn	acc Thr	atc Ile	gag Glu 870	gag Glu	gtg Val	cgt Arg	tgc Cys	agc Ser 875	acc Thr	gca Ala	3003
gct Ala	cac His	gct Ala 880	ttc Phe	aag Lys	gtg Val	gct Ala	gcc Ala 885	cgg Arg	gcc Ala	acg Thr	ctg Leu	cgc Arg 890	cgc Arg	agc Ser	aac Asn	3051
gtc Val	tcc Ser 895	cgc Arg	aag Lys	cgg Arg	tcc Ser	agc Ser 900	agc Ser	ctt Leu	gga Gly	ggc Gly	tcc Ser 905	acg Thr	gga Gly	tcc Ser	acc Thr	3099
ccc Pro 910	tcc Ser	tcc Ser	tcc Ser	atc Ile	agc Ser 915	agc Ser	aag Lys	agc Ser	aac Asn	agc Ser 920	gaa Glu	gac Asp	cca Pro	ttc Phe	cca Pro 925	3147
cag Gln	ccc Pro	gag Glu	agg Arg	cag Gln 930	aag Lys	cag Gln	cag Gln	cag Gln	ccg Pro 935	ctg Leu	gcc Ala	cta Leu	acc Thr	cag Gln 940	caa Gln	3195
gag	cag	cag	cag	cag	ccc	ctg	acc	ctc	cca	cag	cag	caa	cga	tct	cag	3243

JPOXMLDOC01-seq1.app

Glu Gln Gln Gln Gln Pro Leu Thr	Leu Pro Gln Gln Gln Arg Ser Gln	
945	950	955
cag cag ccc aga tgc aag cag aag gtc atc ttt ggc agc ggc acg gtc		3291
Gln Gln Pro Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val		
960	965	970
acc ttc tca ctg agc ttt gat gag cct cag aag aac gcc atg gcc cac		3339
Thr Phe Ser Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His		
975	980	985
agg aat tct acg cac cag aac tcc ctg gag gcc cag aaa agc agc gat		3387
Arg Asn Ser Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp		
990	995	1000
acg ctg acc cga cac cag cca tta ctc ccg ctg cag tgc ggg gaa		3432
Thr Leu Thr Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu		
1010	1015	1020
acg gac tta gat ctg acc gtc cag gaa aca ggt ctg caa gga cct		3477
Thr Asp Leu Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro		
1025	1030	1035
gtg ggt gga gac cag cgg cca gag gtg gag gac cct gaa gag ttg		3522
Val Gly Gly Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu		
1040	1045	1050
tcc cca gca ctt gta gtg tcc agt tca cag agc ttt gtc atc agt		3567
Ser Pro Ala Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser		
1055	1060	1065
ggt gga ggc agc act gtt aca gaa aac gta gtg aat tca taa		3609
Gly Gly Gly Ser Thr Val Thr Glu Asn Val Val Asn Ser		
1070	1075	
aatggaagga gaagactggg ctagggagaa tgcagagagg tttcttgggg tcccagggaa		3669
gaggaatcgc cccagactcc tttcctctga ggaagaaggg ataatagaca catcaaatgc		3729
cccgaattta gtcacaccat cttaaatagac agtgaattga cccatgttcc ctttaaaatt		3789
aaaaaaaaaga agagccttgt gtttctgtgg ttgcatttgt caaagcattg agatctccac		3849
ggtcagattt gctgttcacc cacatctaata gtctcttcct ctgttctatc ccaccaaca		3909
gctcagagat gaaactatgg ctttaaaacta ccctccagag tgtgcagact gatgggacat		3969
caaatttgcc accactagag ctgagagtct gaaagacaga atgtcaccag tcctgcccac		4029
tgccttgaca acagactgaa ttttaaatgt tcacaacata aggagaatgt atctctcct		4089
atztatgaaa accatatgat attttgtctc ctacctgctg ctgctattat gtaacatcca		4149
gaaggtttgc acccctccta taccatatgt ctgcttctgt ccaggacatg atactgatgc		4209
catgtttaga ttccaggatc acaagaatca cctcaaatgt ttaggaaggg actgcataaa		4269
ccaatgagct gtatctgtaa ttaatatctc tatatgtagc tttatcctta ggaaaatgct		4329
tctgttgtaa tagtccatgg acaatataaa ctgaaaaatg tcagtctggg ttatataagg		4389
cagtattatt gagctctatt tccccacccc actatcctca ctcccataag ctaagcctta		4449
tgtgagcccc ttcagggact caagggtcca gaagtccctc ccatctctac cccaaagaat		4509
tcctgaagcc agatccaccc tatccctgta cagagtaagt tctcaattat tggcctgcta		4569
atagctgcta gggtaggaaa gcgtgggttcc aagaaagatc caccctcaaa tgtcagagct		4629

JPOXMLDOC01-seq1.app

atgttccctc cagcagtggg attaatactg ccggtcaccc aggctctgga gccagagaga 4689
cagaccgggg ttcaagccat ggcttcgtca tttgcaagct gaggtagctgt aggcagggaa 4749
ccttaacctc tctaagccac agcttcttca tctttaaaat aaggataata atcattcttt 4809
ccccctcagag ctcttatgtg gattaaacga gataatgtat ataaagtact ttagcctggg 4869
acctagcaca caataagcat tcaataaata ttagttaata ttattaaaaa aaaaa 4924

<210> 2
<211> 1078
<212> PRT
<213> Homo sapiens

<400> 2

Met Ala Phe Tyr Ser Cys Cys Trp Val Leu Leu Ala Leu Thr Trp His
1 5 10 15

Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
20 25 30

Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
35 40 45

Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
50 55 60

Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
65 70 75 80

Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
85 90 95

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

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

Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
130 135 140

Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
145 150 155 160

Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
165 170 175

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

Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
Page 6

195

200

205

Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
 210 215 220
 Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
 225 230 235 240
 Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
 245 250 255
 Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
 260 265 270
 Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
 275 280 285
 Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
 290 295 300
 Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
 305 310 315 320
 Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
 325 330 335
 Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
 340 345 350
 Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
 355 360 365
 Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
 370 375 380
 Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
 385 390 395 400
 Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
 405 410 415
 Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
 420 425 430
 Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
 435 440 445
 Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
 450 455 460
 Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
 Page 7

465 470 475 480

Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
485 490 495

Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
500 505 510

Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
515 520 525

Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
530 535 540

Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
545 550 555 560

Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
565 570 575

Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
580 585 590

Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp
595 600 605

Thr Glu Pro Phe Gly Ile Ala Leu Thr Leu Phe Ala Val Leu Gly Ile
610 615 620

Phe Leu Thr Ala Phe Val Leu Gly Val Phe Ile Lys Phe Arg Asn Thr
625 630 635 640

Pro Ile Val Lys Ala Thr Asn Arg Glu Leu Ser Tyr Leu Leu Leu Phe
645 650 655

Ser Leu Leu Cys Cys Phe Ser Ser Ser Leu Phe Phe Ile Gly Glu Pro
660 665 670

Gln Asp Trp Thr Cys Arg Leu Arg Gln Pro Ala Phe Gly Ile Ser Phe
675 680 685

Val Leu Cys Ile Ser Cys Ile Leu Val Lys Thr Asn Arg Val Leu Leu
690 695 700

Val Phe Glu Ala Lys Ile Pro Thr Ser Phe His Arg Lys Trp Trp Gly
705 710 715 720

Leu Asn Leu Gln Phe Leu Leu Val Phe Leu Cys Thr Phe Met Gln Ile
725 730 735

Val Ile Cys Val Ile Trp Leu Tyr Thr Ala Pro Pro Ser Ser Tyr Arg
Page 8

740

745

750

Asn Gln Glu Leu Glu Asp Glu Ile Ile Phe Ile Thr Cys His Glu Gly
 755 760 765

Ser Leu Met Ala Leu Gly Phe Leu Ile Gly Tyr Thr Cys Leu Leu Ala
 770 775 780

Ala Ile Cys Phe Phe Phe Ala Phe Lys Ser Arg Lys Leu Pro Glu Asn
 785 790 795 800

Phe Asn Glu Ala Lys Phe Ile Thr Phe Ser Met Leu Ile Phe Phe Ile
 805 810 815

Val Trp Ile Ser Phe Ile Pro Ala Tyr Ala Ser Thr Tyr Gly Lys Phe
 820 825 830

Val Ser Ala Val Glu Val Ile Ala Ile Leu Ala Ala Ser Phe Gly Leu
 835 840 845

Leu Ala Cys Ile Phe Phe Asn Lys Ile Tyr Ile Ile Leu Phe Lys Pro
 850 855 860

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

Phe Lys Val Ala Ala Arg Ala Thr Leu Arg Arg Ser Asn Val Ser Arg
 885 890 895

Lys Arg Ser Ser Ser Leu Gly Gly Ser Thr Gly Ser Thr Pro Ser Ser
 900 905 910

Ser Ile Ser Ser Lys Ser Asn Ser Glu Asp Pro Phe Pro Gln Pro Glu
 915 920 925

Arg Gln Lys Gln Gln Gln Pro Leu Ala Leu Thr Gln Gln Glu Gln Gln
 930 935 940

Gln Gln Pro Leu Thr Leu Pro Gln Gln Gln Arg Ser Gln Gln Gln Pro
 945 950 955 960

Arg Cys Lys Gln Lys Val Ile Phe Gly Ser Gly Thr Val Thr Phe Ser
 965 970 975

Leu Ser Phe Asp Glu Pro Gln Lys Asn Ala Met Ala His Arg Asn Ser
 980 985 990

Thr His Gln Asn Ser Leu Glu Ala Gln Lys Ser Ser Asp Thr Leu Thr
 995 1000 1005

Arg His Gln Pro Leu Leu Pro Leu Gln Cys Gly Glu Thr Asp Leu
 Page 9

1010

1015

1020

Asp Leu Thr Val Gln Glu Thr Gly Leu Gln Gly Pro Val Gly Gly
 1025 1030 1035

Asp Gln Arg Pro Glu Val Glu Asp Pro Glu Glu Leu Ser Pro Ala
 1040 1045 1050

Leu Val Val Ser Ser Ser Gln Ser Phe Val Ile Ser Gly Gly Gly
 1055 1060 1065

Ser Thr Val Thr Glu Asn Val Val Asn Ser
 1070 1075

<210> 3
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <223> primer

<400> 3
 actaatacga ctcactatag ggaccatggc attttatagc tgctgctgg

49

<210> 4
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> primer

<400> 4
 ttatgaattc actacgtttt ctgtaacag

29