

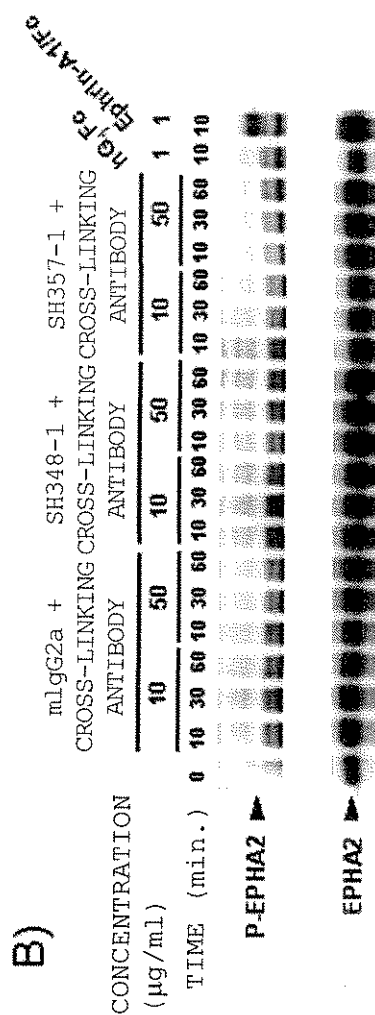
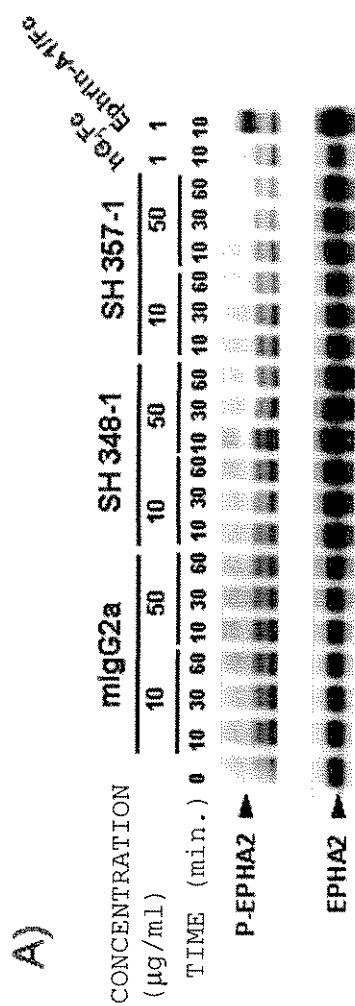


Figure 2

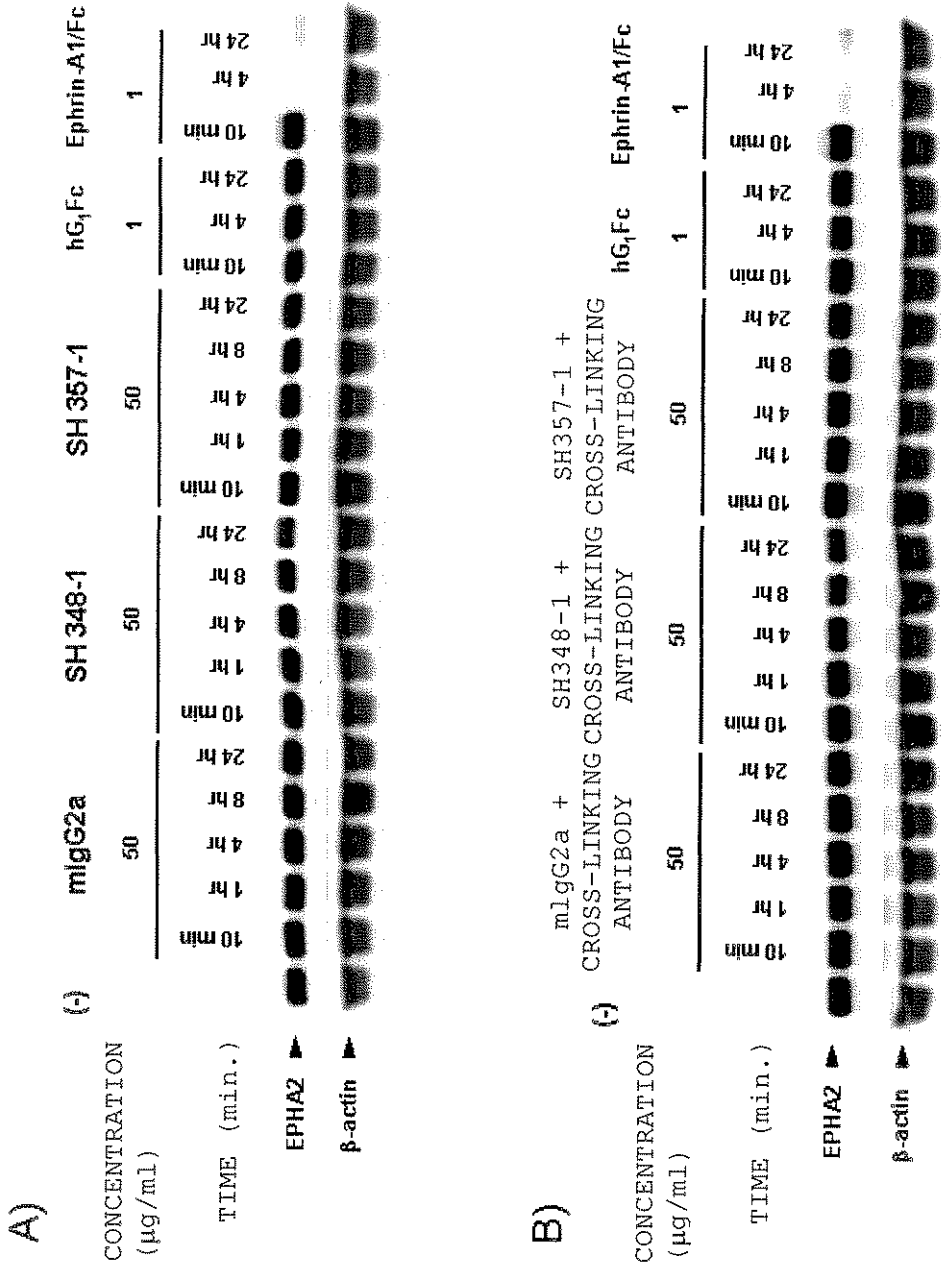


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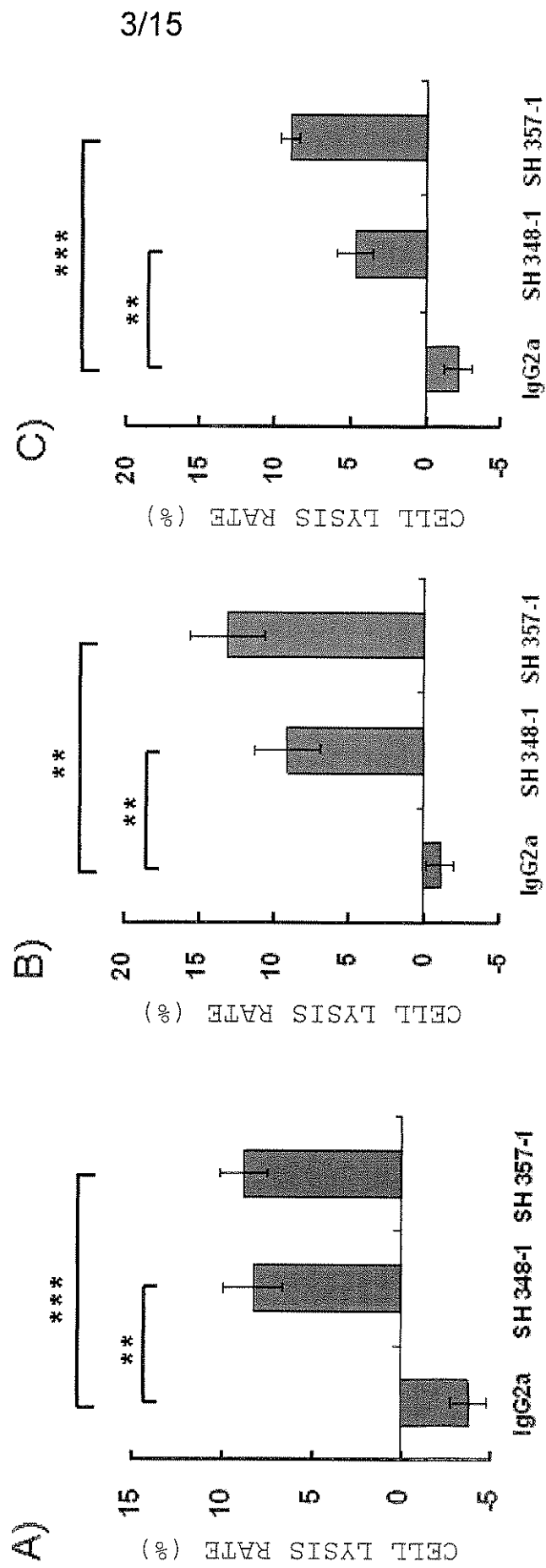


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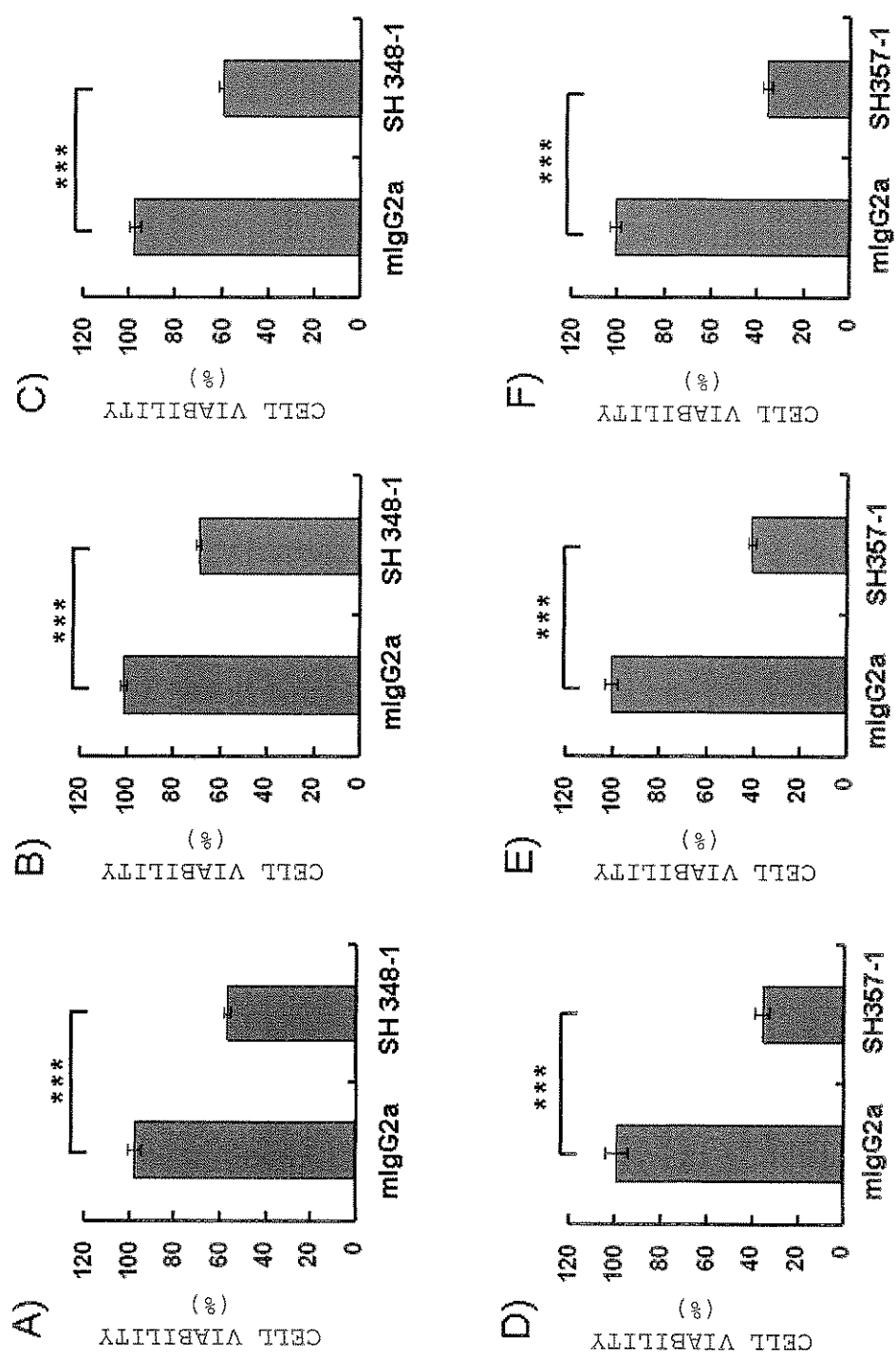


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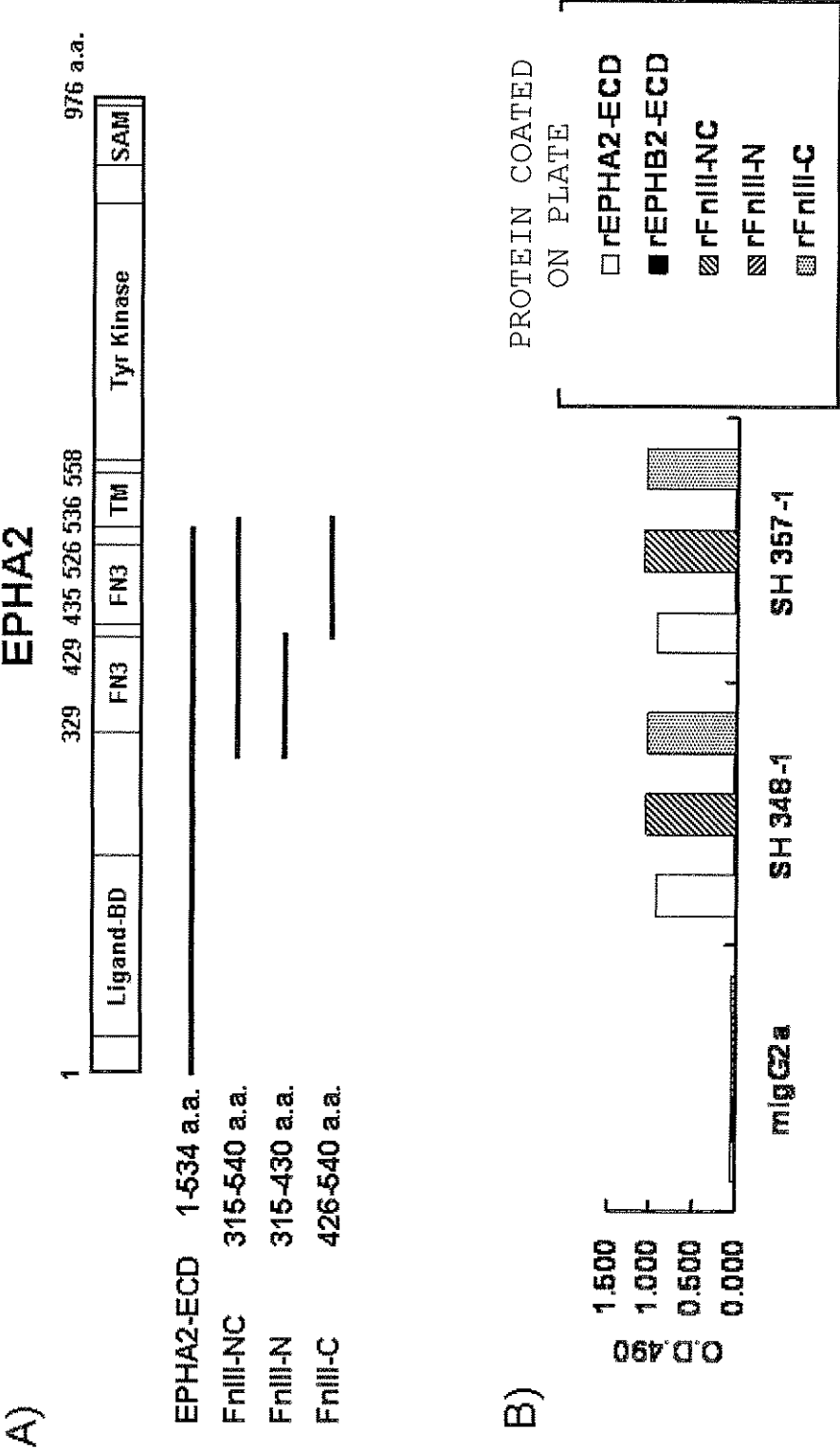


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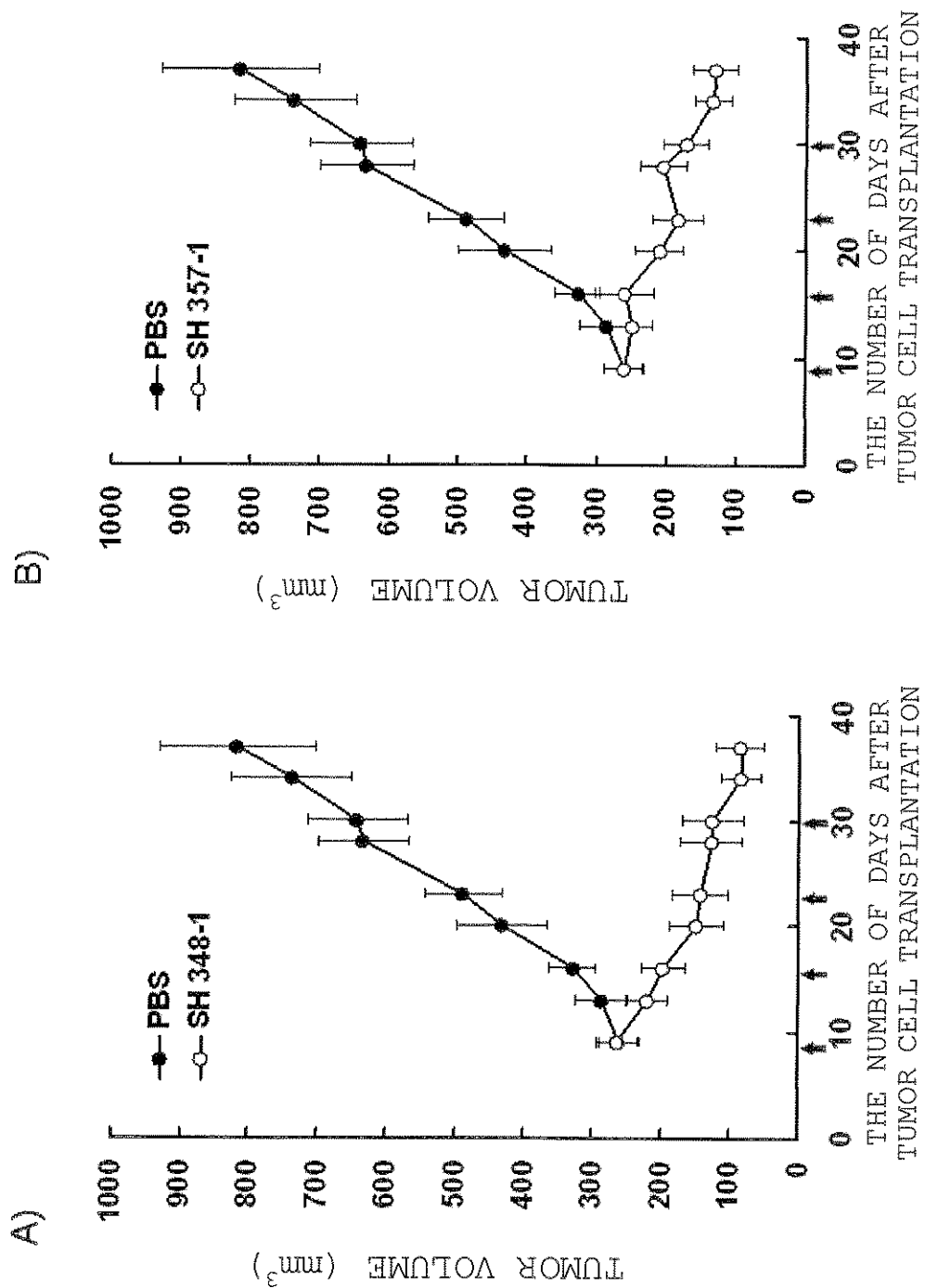


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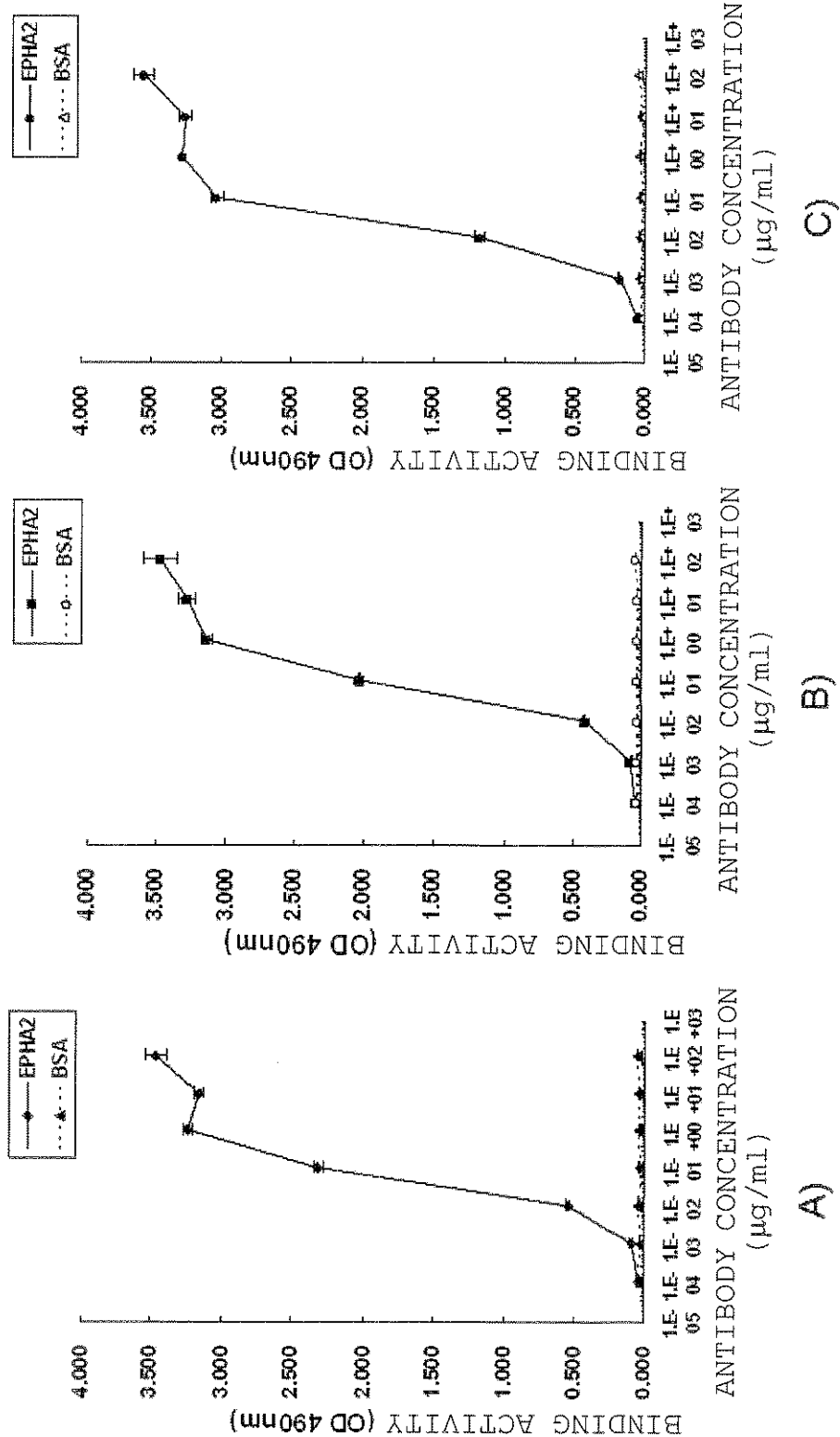


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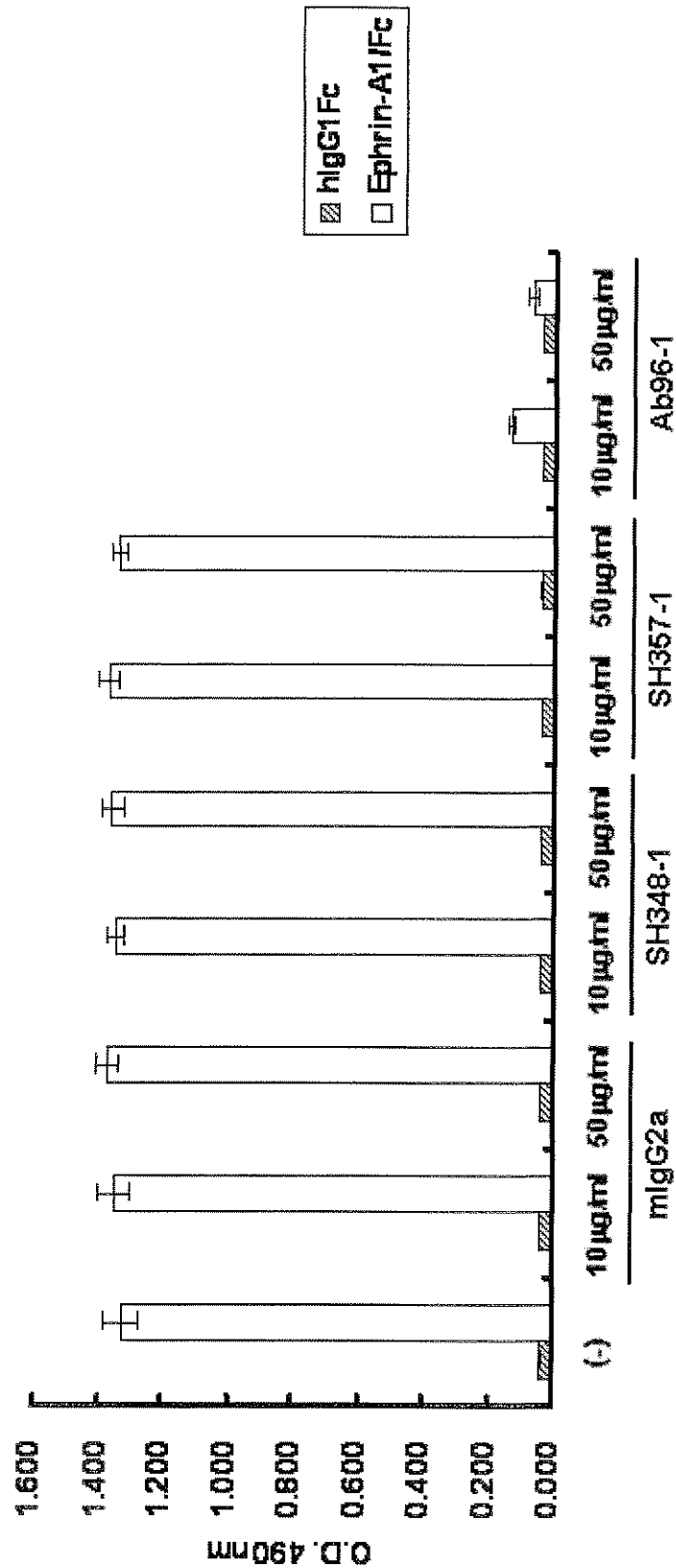


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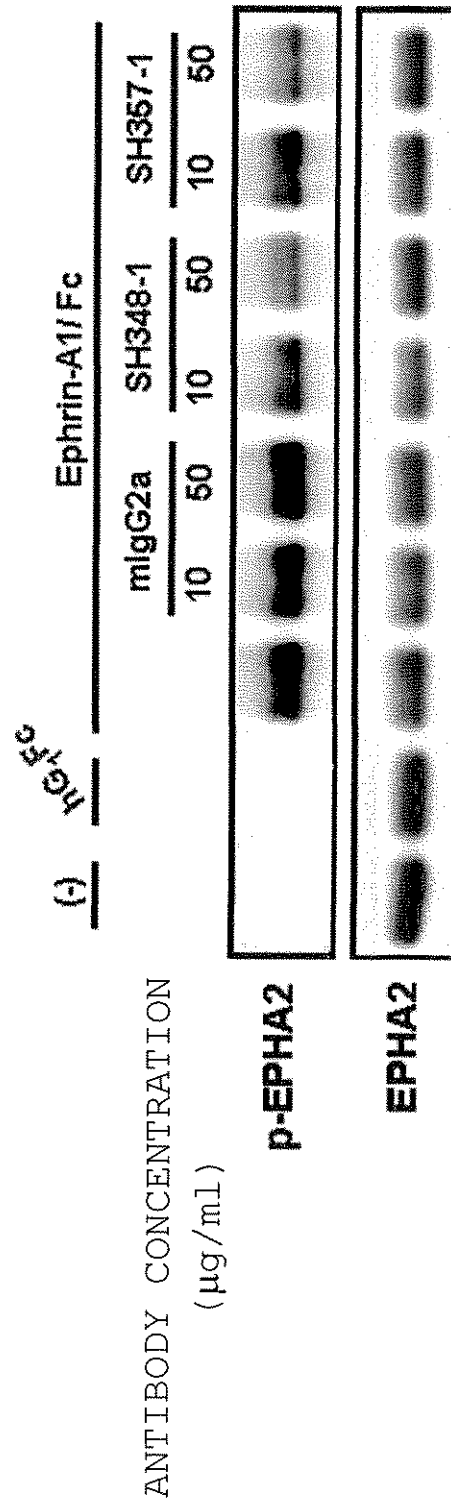


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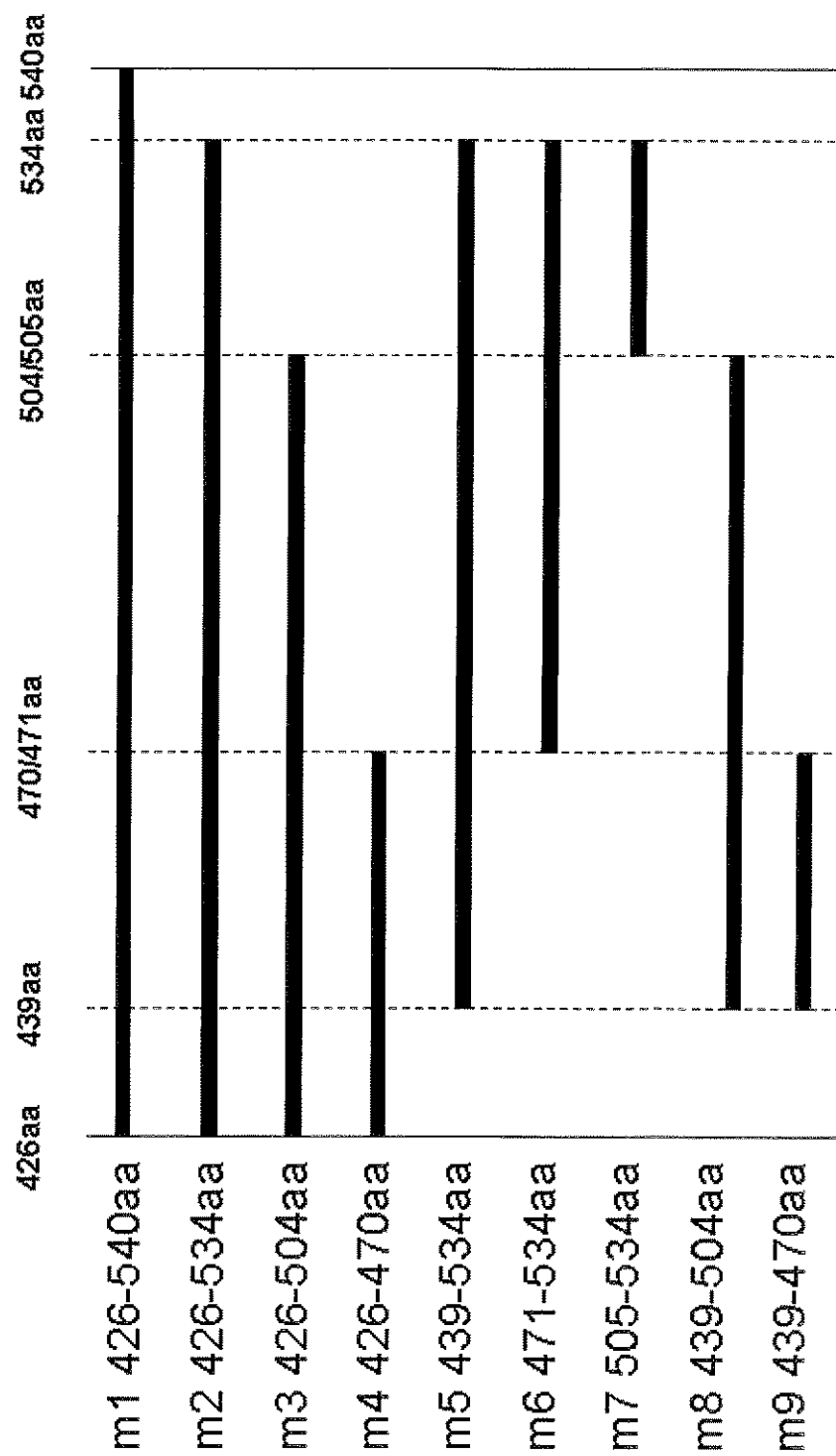


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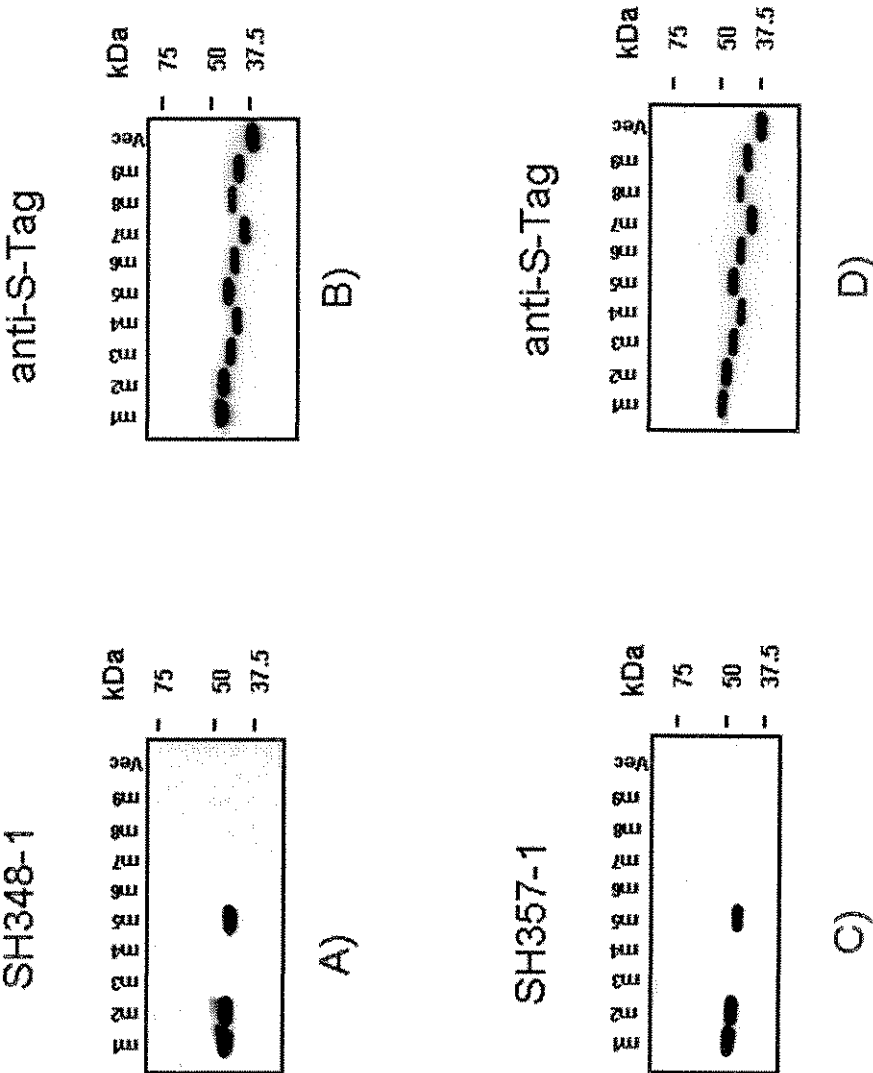


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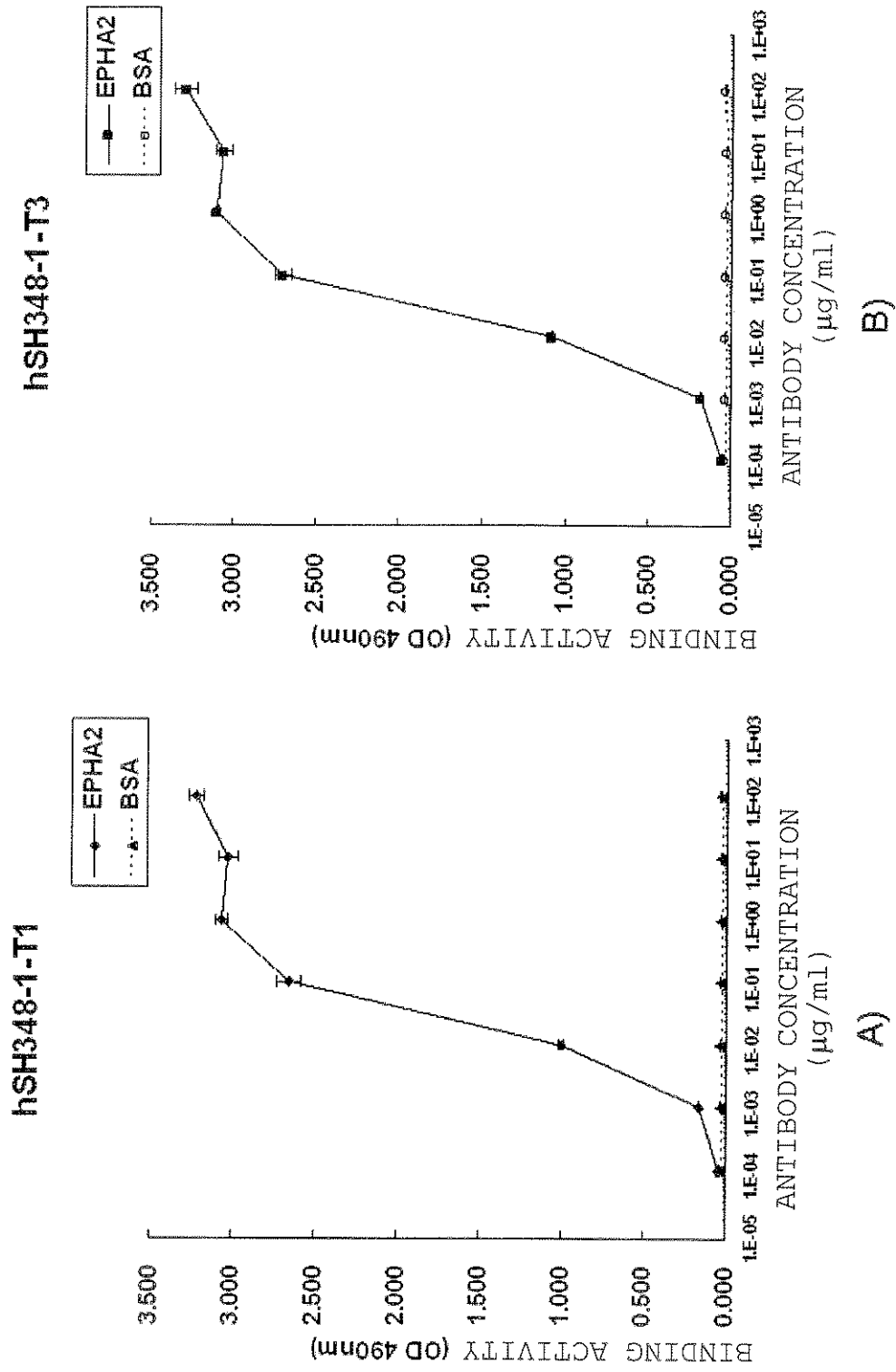


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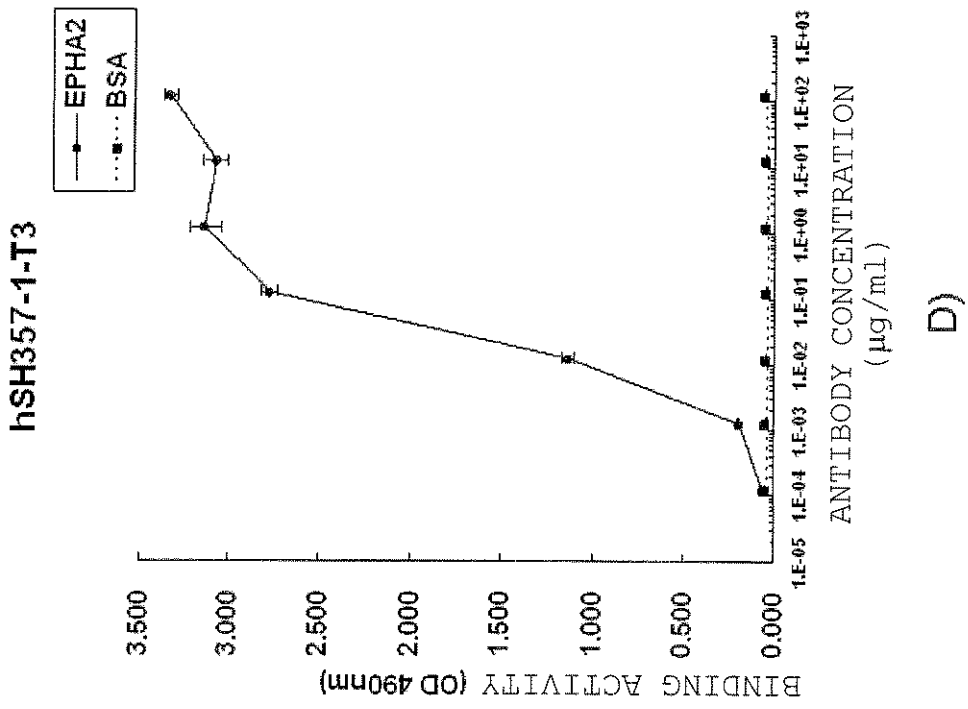
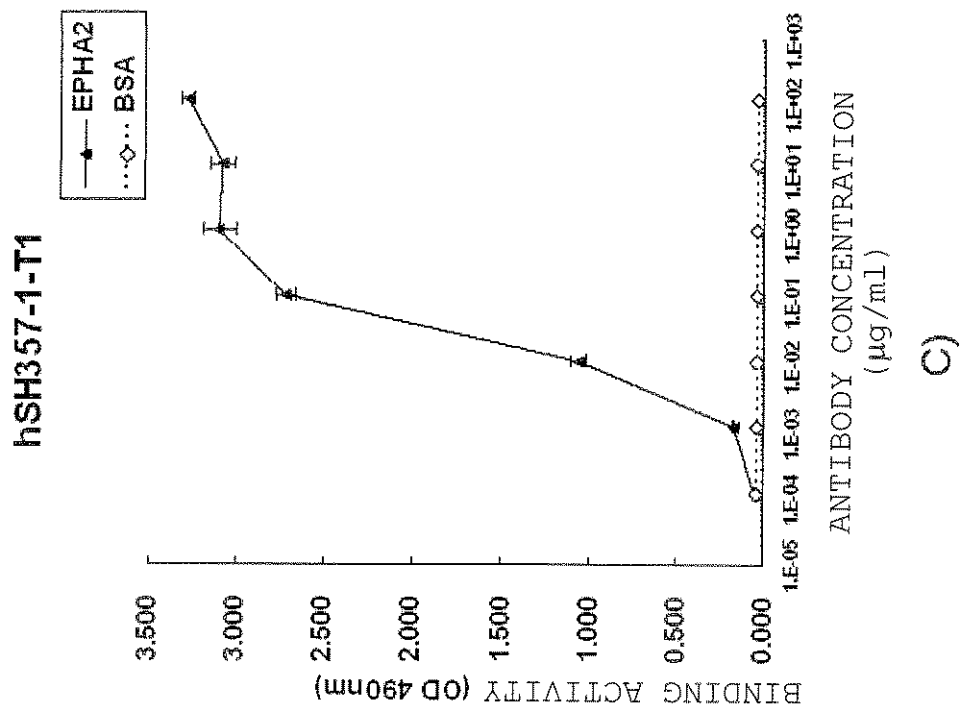


Figure 13

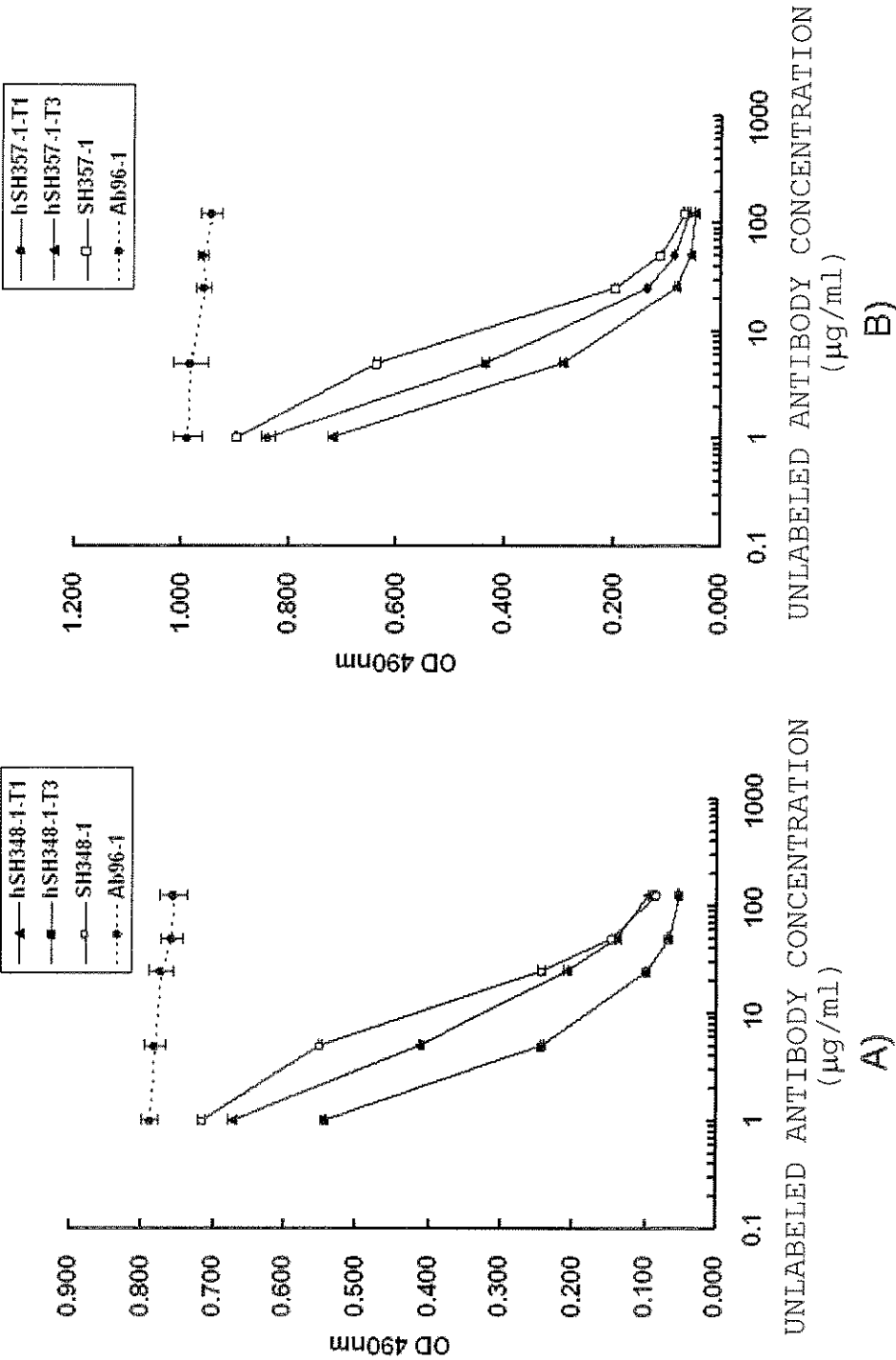
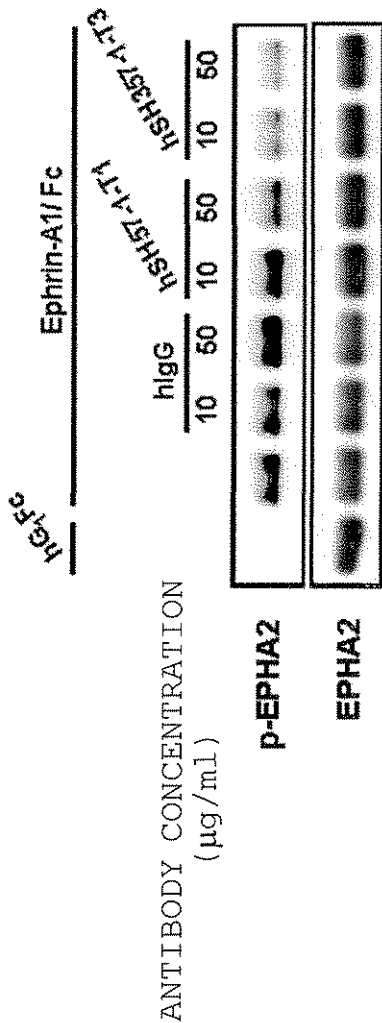
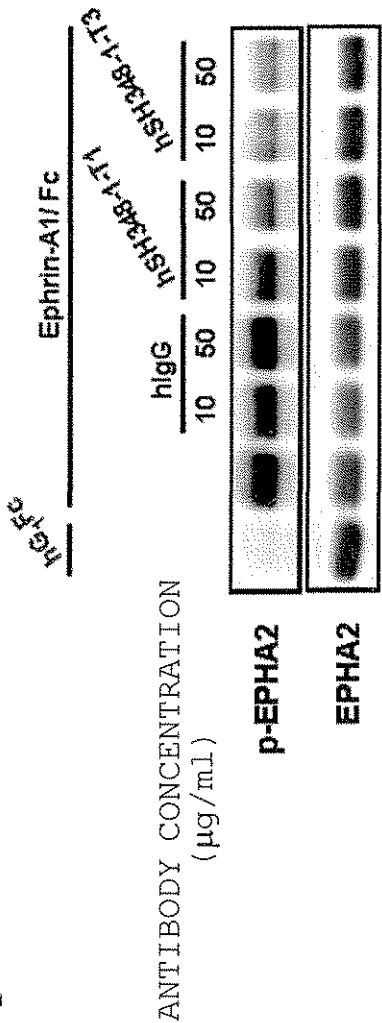


Figure 14



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

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Pro	Cys	Leu	Glu	Cys	Pro	Glu	His	Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala					
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Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly	Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro					
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gcc	gtg	ggc	atg	ggg	gcc	aag	gtg	gag	ctg	cgc	tgg	acg	ccc	cct	cag	1056				
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Cys	Trp	Pro	Glu	Ser	Gly	Glu	Cys	Gly	Pro	Cys	Glu	Ala	Ser	Val	Arg					
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Thr	Thr	Ser	Leu	Ser	Val	Ser	Trp	Ser	Ile	Pro	Pro	Pro	Gln	Gln	Ser	
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Arg	Val	Trp	Lys	Tyr	Glu	Val	Thr	Tyr	Arg	Lys	Lys	Gly	Asp	Ser	Asn	
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Ser	Tyr	Asn	Val	Arg	Arg	Thr	Glu	Gly	Phe	Ser	Val	Thr	Leu	Asp	Asp	
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Pro	Glu	Gly	Ser	Gly	Asn	Leu	Ala	Val	Ile	Gly	Gly	Val	Ala	Val	Gly	
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Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile	
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Val	Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln	
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cac cgt gac ctg gct gcc cgc aac atc ctc gtc aac agc aac ctg gtc	2256						
His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val		740		745		750	
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Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro		755		760		765	
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Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln
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Arg Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu
705 710 715 720

Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
725 730 735

His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
740 745 750

Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
755 760 765

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
770 775 780

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
785 790 795 800

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
805 810 815

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
820 825 830

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
835 840 845

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
850 855 860

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
865 870 875 880

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
885 890 895

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
900 905 910

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
915 920 925

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
930 935 940

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
945 950 955 960

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
965 970 975

<210> 3
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer 1

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ggggacaagt ttgtacaaaa aagcaggctt cggggatcgg accgagagcg agaag

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<210> 4
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer 2

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aac ctc tac tat gcc gag tcg gac ctg gac tac ggc acc aac ttc cag Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln 120 125 130 135	437
aag cgc ctg ttc acc aag att gac acc att gcg ccc gat gag atc acc Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr 140 145 150	485
gtc agc agc gac ttc gag gca cgc cac gtg aag ctg aac gtg gag gag Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu 155 160 165	533
cgc tcc gtg ggg ccg ctc acc cgc aaa ggc ttc tac ctg gcc ttc cag Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln 170 175 180	581
gat atc ggt gcc tgt gtg gca cta ctc tcc gtc cgt gtc tac tac aag Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys 185 190 195	629
aag tgc ccc gag ctg ctg cag ggc ctg gcc cac ttc cct gag acc atc Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile 200 205 210 215	677
gcc ggc tct gat gca cct tcc ctg gcc act gtg gcc ggc acc tgt gtg Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val 220 225 230	725
gac cat gcc gtg gtg cca ccg ggg ggt gaa gag ccc cgt atg cac tgt Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys 235 240 245	773
gca gtg gat ggc gag tgg ctg gtg ccc att ggg cag tgc ctg tgc cag Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln 250 255 260	821
gca ggc tac gag aag gtg gag gat gcc tgc cag gcc tgc tcg cct gga Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly 265 270 275	869
ttt ttt aag ttt gag gca tct gag agc ccc tgc ttg gag tgc cct gag Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu 280 285 290 295	917
cac acg ctg cca tcc cct gag ggt gcc acc tcc tgc gag tgt gag gaa His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu 300 305 310	965
ggc ttc ttc cgg gca cct cag gac cca gcg tcg atg cct tgc aca cga Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg 315 320 325	1013
ccc cct tcc gcc cca cac tac ctc aca gcc gtg ggc atg ggt gcc aag Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys 330 335 340	1061
gtg gag ctg cgc tgg acg ccc cct cag gac agc ggg ggc cgc gag gac Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp 345 350 355	1109

att gtc tac agc gtc acc tgc gaa cag tgc tgg ccc gag tct ggg gaa Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu 360 365 370 375	1157
tgc ggg ccg tgt gag gcc agt gtg cgc tac tgc gag cct cct cac gga Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly 380 385 390	1205
ctg acc cgc acc agt gtg aca gtg agc gac ctg gag ccc cac atg aac Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn 395 400 405	1253
tac acc ttc acc gtg gag gcc cgc aat ggc gtc tca ggc ctg gta acc Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr 410 415 420	1301
agc cgc agc ttc cgt act gcc agt gtg agc atc aac cag aca gag ccc Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro 425 430 435	1349
ccc aag gtg agg ctg gag gcc cgc agc acc acc tgc ctt agc gtc tcc Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser 440 445 450 455	1397
tgg agc atc ccc ccg ccg cag cag agc cga gtg tgg aag tac gag gtc Trp Ser Ile Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val 460 465 470	1445
act tac cgc aag aag gga gac tcc aac agc tac aat gtg cgc cgc acc Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr 475 480 485	1493
gag ggt ttc tcc gtg acc ctg gac gac ctg gcc cca gac acc acc tac Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr 490 495 500	1541
ctg gtc cag gtg cag gca ctg acg cag gag ggc cag ggg gcc gcc agc Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser 505 510 515	1589
aag gtg cac gaa ttc cag acg ctg tcc ccg gag gga tct ggc aac ttg Lys Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu 520 525 530 535	1637
gcg gtg att ggc gcc gtg gct gtc ggt gtg gtc ctg ctt ctg gtg ctg Ala Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu 540 545 550	1685
gca gga gtt ggc ttc ttt atc cac cgc agg agg aag aac cag cgt gcc Ala Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala 555 560 565	1733
cgc cag tcc ccg gag gac gtt tac ttc tcc aag tca gaa caa ctg aag Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys 570 575 580	1781
ccc ctg aag aca tac gtg gac ccc cac aca tat gag gac ccc aac cag Pro Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln 585 590 595	1829
gct gtg ttg aag ttc act acc gag atc cat cca tcc tgt gtc act cgg Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg 600 605 610 615	1877
cag aag gtg atc gga gca gga gag ttt ggg gag gtg tac aag ggc atg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met 620 625 630	1925

ctg aag aca tcc tcg ggg aag aag gag gtg ccg gtg gcc atc aag acg Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr	1973
ctg aaa gcc ggc tac aca gag aag cag cga gtg gac ttc ctc ggc gag Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu	2021
gcc ggc atc atg ggc cag ttc agc cac cac aac atc atc cgc cta gag Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu	2069
ggc gtc atc tcc aaa tac aag ccc atg atg atc atc act gag tac atg Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met	2117
gag aat ggg gcc ctg gac aag ttc ctt cgg gag aag gat ggc gag ttc Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe	2165
agc gtg ctg cag ctg gtg ggc atg ctg cgg ggc atc gca gct ggc atg Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met	2213
aag tac ctg gcc aac atg aac tat gtg cac cgt gac ctg gct gcc cgc Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg	2261
aac atc ctc gtc aac agc aac ctg gtc tgc aag gtg tct gac ttt ggc Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly	2309
ctg tcc cgc gtg ctg gag gac gac ccc gag gcc acc tac acc acc agt Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser	2357
ggc ggc aag atc ccc atc cgc tgg acc gcc ccg gag gcc att tcc tac Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr	2405
cgg aag ttc acc tct gcc agc gac gtg tgg agc ttt ggc att gtc atg Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met	2453
tgg gag gtg atg acc tat ggc gag cgg ccc tac tgg gag ttg tcc aac Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn	2501
cac gag gtg atg aaa gcc atc aat gat ggc ttc cgg ctc ccc aca ccc His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro	2549
atg gac tgc ccc tcc gcc atc tac cag ctc atg atg cag tgc tgg cag Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln	2597
cag gag cgt gcc cgc cgc ccc aag ttc gct gac atc gtc agc atc ctg Gln Glu Arg Ala Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu	2645
gac aag ctc att cgt gcc cct gac tcc ctc aag acc ctg gct gac ttt Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe	2693
gac ccc cgc gtg tct atc cgg ctc ccc agc acg agc ggc tcg gag ggg Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly	2741

gtg ccc ttc cgc acg gtg tcc gag tgg ctg gag tcc atc aag atg cag 2789
 Val Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln
 905 910 915
 cag tat acg gag cac ttc atg gcg gcc gcc tac act gcc atc gag aag 2837
 Gln Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys
 920 925 930 935
 gtg gtg cag atg acc aac gac gac atc aag agg att ggg gtg cgg ctg 2885
 Val Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu
 940 945 950
 ccc ggc cac cag aag cgc atc gcc tac agc ctg ctg gga ctc aag gac 2933
 Pro Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp
 955 960 965
 cag gtg aac act gtg ggg atc ccc atc g 2961
 Gln Val Asn Thr Val Gly Ile Pro Ile
 970 975

<210> 8
 <211> 976
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Synthetic Construct
 <400> 8

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 Ala Leu Ala Ala Ala Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu
 20 25 30
 Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr
 35 40 45
 Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile
 50 55 60
 Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
 65 70 75 80
 Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile
 85 90 95
 Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala
 100 105 110
 Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu
 115 120 125
 Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr
 130 135 140
 Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His

145		150		155		160
Val Lys Leu Asn	Val Glu Glu Arg Ser	Val Gly Pro Leu Thr Arg Lys				
	165	170			175	
Gly Phe Tyr Leu	Ala Phe Gln Asp Ile	Gly Ala Cys Val Ala Leu Leu				
	180	185			190	
Ser Val Arg	Val Tyr Tyr Lys Lys	Cys Pro Glu Leu Leu Gln Gly Leu				
	195	200			205	
Ala His Phe Pro Glu Thr Ile	Ala Gly Ser Asp Ala Pro Ser Leu Ala					
	210	215			220	
Thr Val Ala Gly Thr	Cys Val Asp His Ala Val Val Pro Pro Gly Gly					
	225	230			235	240
Glu Glu Pro Arg	Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro					
	245	250			255	
Ile Gly Gln Cys	Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala					
	260	265			270	
Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser						
	275	280			285	
Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala						
	290	295			300	
Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro						
	305	310			315	320
Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr						
	325	330			335	
Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln						
	340	345			350	
Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln						
	355	360			365	
Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg						
	370	375			380	
Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser						
	385	390			395	400
Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn						
	405	410			415	
Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val						

420 425 430
 Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser
 435 440 445
 Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser
 450 455 460
 Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn
 465 470 475 480
 Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp
 485 490 495
 Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln
 500 505 510
 Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser
 515 520 525
 Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly
 530 535 540
 Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg
 545 550 555 560
 Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
 565 570 575
 Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
 580 585 590
 Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
 595 600 605
 His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
 610 615 620
 Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
 625 630 635 640
 Val Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln
 645 650 655
 Arg Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His
 660 665 670
 His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
 675 680 685
 Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu

690	695	700
Arg Glu Lys Asp Gly 705	Glu Phe Ser Val 710	Leu Gln Leu Val Gly Met Leu 715 720
Arg Gly Ile Ala Ala 725	Gly Met Lys Tyr 730	Leu Ala Asn Met Asn Tyr Val 735
His Arg Asp 740	Leu Ala Ala Arg Asn Ile 745	Leu Val Asn Ser Asn Leu Val 750
Cys Lys Val 755	Ser Asp Phe Gly 760	Leu Ser Arg Val Leu Glu Asp Asp Pro 765
Glu Ala Thr Tyr Thr Thr 770	Ser Gly Gly Lys Ile 775	Pro Ile Arg Trp Thr 780
Ala Pro Glu Ala Ile 785	Ser Tyr Arg Lys Phe 790	Thr Ser Ala Ser Asp Val 795 800
Trp Ser Phe Gly 805	Ile Val Met Trp Glu 810	Val Met Thr Tyr Gly Glu Arg 815
Pro Tyr Trp 820	Glu Leu Ser Asn His 825	Glu Val Met Lys Ala Ile Asn Asp 830
Gly Phe Arg 835	Leu Pro Thr Pro Met 840	Asp Cys Pro Ser Ala Ile Tyr Gln 845
Leu Met Met 850	Gln Cys Trp Gln Gln Glu 855	Arg Ala Arg Arg Pro Lys Phe 860
Ala Asp Ile Val 865	Ser Ile Leu Asp Lys Leu 870	Ile Arg Ala Pro Asp Ser 875 880
Leu Lys Thr Leu 885	Ala Asp Phe Asp Pro 890	Arg Val Ser Ile Arg Leu Pro 895
Ser Thr Ser 900	Gly Ser Glu Gly Val 905	Pro Phe Arg Thr Val Ser Glu Trp 910
Leu Glu Ser 915	Ile Lys Met Gln Gln Tyr Thr 920	Glu His Phe Met Ala Ala 925
Gly Tyr Thr 930	Ala Ile Glu Lys Val Val 935	Gln Met Thr Asn Asp Asp Ile 940
Lys Arg Ile Gly Val 945	Arg Leu Pro Gly His 950	Gln Lys Arg Ile Ala Tyr 955 960
Ser Leu Leu Gly Leu Lys Asp Gln Val 965	Asn Thr Val Gly Ile Pro Ile 970	

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 <213> Artificial Sequence

<220>
 <223> PCR primer 5

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<210> 10
 <211> 30
 <212> DNA
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<220>
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<400> 10
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30

<210> 11
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 11
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43

<210> 12
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 <212> DNA
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<220>
 <223> PCR primer 8

<400> 12
 gtacaagaaa gctgggtgct agccgccaat caccgccaag

40

<210> 13
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<220>
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<400> 13
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40

<210> 14
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 <213> Artificial Sequence

<220>
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 <400> 14
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 <210> 15
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 <220>
 <223> PCR primer 11

 <400> 15
 ggggacaagt ttgtacaaaa aagcaggctt catcgaaggc cgtggg 46

 <210> 16
 <211> 29
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 <220>
 <223> PCR primer 12

 <400> 16
 ggggaccact ttgtacaaga aagctgggt 29

 <210> 17
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 <220>
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 <400> 17
 ggggacaagt ttgtacaaaa aagcaggctt cggccggga agcgcagcc 49

 <210> 18
 <211> 63
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer 14

 <400> 18
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 ctg 63

 <210> 19
 <211> 2961
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1)..(2961)
 <400> 19

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gcc gcc gtg gaa gaa acg cta atg gac tcc act aca gcg act gct gag Ala Ala Val Glu Glu Thr Leu Met Asp Ser Thr Thr Ala Thr Ala Glu 20 25 30	96
ctg ggc tgg atg gtg cat cct cca tca ggg tgg gaa gag gtg agt ggc Leu Gly Trp Met Val His Pro Pro Ser Gly Trp Glu Glu Val Ser Gly 35 40 45	144
tac gat gag aac atg aac acg atc cgc acg tac cag gtg tgc aac gtg Tyr Asp Glu Asn Met Asn Thr Ile Arg Thr Tyr Gln Val Cys Asn Val 50 55 60	192
ttt gag tca agc cag aac aac tgg cta cgg acc aag ttt atc cgg cgc Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr Lys Phe Ile Arg Arg 65 70 75 80	240
cgt ggc gcc cac cgc atc cac gtg gag atg aag ttt tcg gtg cgt gac Arg Gly Ala His Arg Ile His Val Glu Met Lys Phe Ser Val Arg Asp 85 90 95	288
tgc agc agc atc ccc agc gtg cct ggc tcc tgc aag gag acc ttc aac Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys Lys Glu Thr Phe Asn 100 105 110	336
ctc tat tac tat gag gct gac ttt gac tcg gcc acc aag acc ttc ccc Leu Tyr Tyr Tyr Glu Ala Asp Phe Asp Ser Ala Thr Lys Thr Phe Pro 115 120 125	384
aac tgg atg gag aat cca tgg gtg aag gtg gat acc att gca gcc gac Asn Trp Met Glu Asn Pro Trp Val Lys Val Asp Thr Ile Ala Ala Asp 130 135 140	432
gag agc ttc tcc cag gtg gac ctg ggt ggc cgc gtc atg aaa atc aac Glu Ser Phe Ser Gln Val Asp Leu Gly Gly Arg Val Met Lys Ile Asn 145 150 155 160	480
acc gag gtg cgg agc ttc gga cct gtg tcc cgc agc ggc ttc tac ctg Thr Glu Val Arg Ser Phe Gly Pro Val Ser Arg Ser Gly Phe Tyr Leu 165 170 175	528
gcc ttc cag gac tat ggc ggc tgc atg tcc ctc atc gcc gtg cgt gtc Ala Phe Gln Asp Tyr Gly Gly Cys Met Ser Leu Ile Ala Val Arg Val 180 185 190	576
ttc tac cgc aag tgc ccc cgc atc atc cag aat ggc gcc atc ttc cag Phe Tyr Arg Lys Cys Pro Arg Ile Ile Gln Asn Gly Ala Ile Phe Gln 195 200 205	624
gaa acc ctg tcg ggg gct gag agc aca tcg ctg gtg gct gcc cgg ggc Glu Thr Leu Ser Gly Ala Glu Ser Thr Ser Leu Val Ala Ala Arg Gly 210 215 220	672
agc tgc atc gcc aat ggc gaa gag gtg gat gta ccc atc aag ctc tac Ser Cys Ile Ala Asn Ala Glu Glu Val Asp Val Pro Ile Lys Leu Tyr 225 230 235 240	720
tgt aac ggg gac ggc gag tgg ctg gtg ccc atc ggg cgc tgc atg tgc Cys Asn Gly Asp Gly Glu Trp Leu Val Pro Ile Gly Arg Cys Met Cys 245 250 255	768
aaa gca ggc ttc gag gcc gtt gag aat ggc acc gtc tgc cga ggt tgt Lys Ala Gly Phe Glu Ala Val Glu Asn Gly Thr Val Cys Arg Gly Cys 260 265 270	816

cca	tct	ggg	act	ttc	aag	gcc	aac	caa	ggg	gat	gag	gcc	tgt	acc	cac	864
Pro	Ser	Gly	Thr	Phe	Lys	Ala	Asn	Gln	Gly	Asp	Glu	Ala	Cys	Thr	His	
		275					280					285				
tgt	ccc	atc	aac	agc	cgg	acc	act	tct	gaa	ggg	gcc	acc	aac	tgt	gtc	912
Cys	Pro	Ile	Asn	Ser	Arg	Thr	Thr	Ser	Glu	Gly	Ala	Thr	Asn	Cys	Val	
	290					295					300					
tgc	cgc	aat	ggc	tac	tac	aga	gca	gac	ctg	gac	ccc	ctg	gac	atg	ccc	960
Cys	Arg	Asn	Gly	Tyr	Tyr	Arg	Ala	Asp	Leu	Asp	Pro	Leu	Asp	Met	Pro	
305					310					315					320	
tgc	aca	acc	atc	ccc	tcc	gcg	ccc	cag	gct	gtg	att	tcc	agt	gtc	aat	1008
Cys	Thr	Thr	Ile	Pro	Ser	Ala	Pro	Gln	Ala	Val	Ile	Ser	Ser	Val	Asn	
				325					330					335		
gag	acc	tcc	ctc	atg	ctg	gag	tgg	acc	cct	ccc	cgc	gac	tcc	gga	ggc	1056
Glu	Thr	Ser	Leu	Met	Leu	Glu	Trp	Thr	Pro	Pro	Arg	Asp	Ser	Gly	Gly	
			340					345					350			
cga	gag	gac	ctc	gtc	tac	aac	atc	atc	tgc	aag	agc	tgt	ggc	tcg	ggc	1104
Arg	Glu	Asp	Leu	Val	Tyr	Asn	Ile	Ile	Cys	Lys	Ser	Cys	Gly	Ser	Gly	
		355					360					365				
cgg	ggt	gcc	tgc	acc	cgc	tgc	ggg	gac	aat	gta	cag	tac	gca	cca	cgc	1152
Arg	Gly	Ala	Cys	Thr	Arg	Cys	Gly	Asp	Asn	Val	Gln	Tyr	Ala	Pro	Arg	
	370					375					380					
cag	cta	ggc	ctg	acc	gag	cca	cgc	att	tac	atc	agt	gac	ctg	ctg	gcc	1200
Gln	Leu	Gly	Leu	Thr	Glu	Pro	Arg	Ile	Tyr	Ile	Ser	Asp	Leu	Leu	Ala	
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Gln	Ser	Pro	Phe	Ser	Pro	Gln	Phe	Ala	Ser	Val	Asn	Ile	Thr	Thr	Asn	
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Gln	Ala	Ala	Pro	Ser	Ala	Val	Ser	Ile	Met	His	Gln	Val	Ser	Arg	Thr	
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Val	Asp	Ser	Ile	Thr	Leu	Ser	Trp	Ser	Gln	Pro	Asp	Gln	Pro	Asn	Gly	
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Ser Ser Gly Ile Asn Leu Pro Leu Leu Asp Arg Thr Ile Pro Asp Tyr	
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Phe Glu Ser Ser Gln Asn Asn Trp Leu Arg Thr Lys Phe Ile Arg Arg
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 Arg Gly Ala His Arg Ile His Val Glu Met Lys Phe Ser Val Arg Asp
 85 90 95
 Cys Ser Ser Ile Pro Ser Val Pro Gly Ser Cys Lys Glu Thr Phe Asn
 100 105 110
 Leu Tyr Tyr Tyr Glu Ala Asp Phe Asp Ser Ala Thr Lys Thr Phe Pro
 115 120 125
 Asn Trp Met Glu Asn Pro Trp Val Lys Val Asp Thr Ile Ala Ala Asp
 130 135 140
 Glu Ser Phe Ser Gln Val Asp Leu Gly Gly Arg Val Met Lys Ile Asn
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 Thr Glu Val Arg Ser Phe Gly Pro Val Ser Arg Ser Gly Phe Tyr Leu
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 Phe Tyr Arg Lys Cys Pro Arg Ile Ile Gln Asn Gly Ala Ile Phe Gln
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 Ser Cys Ile Ala Asn Ala Glu Glu Val Asp Val Pro Ile Lys Leu Tyr
 225 230 235 240
 Cys Asn Gly Asp Gly Glu Trp Leu Val Pro Ile Gly Arg Cys Met Cys
 245 250 255
 Lys Ala Gly Phe Glu Ala Val Glu Asn Gly Thr Val Cys Arg Gly Cys
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 Pro Ser Gly Thr Phe Lys Ala Asn Gln Gly Asp Glu Ala Cys Thr His
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 Cys Pro Ile Asn Ser Arg Thr Thr Ser Glu Gly Ala Thr Asn Cys Val
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 Cys Arg Asn Gly Tyr Tyr Arg Ala Asp Leu Asp Pro Leu Asp Met Pro
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 325 330 335

Glu Thr Ser Leu Met Leu Glu Trp Thr Pro Pro Arg Asp Ser Gly Gly
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Arg Glu Asp Leu Val Tyr Asn Ile Ile Cys Lys Ser Cys Gly Ser Gly
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Gln Leu Gly Leu Thr Glu Pro Arg Ile Tyr Ile Ser Asp Leu Leu Ala
385 390 395 400

His Thr Gln Tyr Thr Phe Glu Ile Gln Ala Val Asn Gly Val Thr Asp
405 410 415

Gln Ser Pro Phe Ser Pro Gln Phe Ala Ser Val Asn Ile Thr Thr Asn
420 425 430

Gln Ala Ala Pro Ser Ala Val Ser Ile Met His Gln Val Ser Arg Thr
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Val Asp Ser Ile Thr Leu Ser Trp Ser Gln Pro Asp Gln Pro Asn Gly
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Val Ile Leu Asp Tyr Glu Leu Gln Tyr Tyr Glu Lys Glu Leu Ser Glu
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Tyr Asn Ala Thr Ala Ile Lys Ser Pro Thr Asn Thr Val Thr Val Gln
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Gly Leu Lys Ala Gly Ala Ile Tyr Val Phe Gln Val Arg Ala Arg Thr
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Val Ala Gly Tyr Gly Arg Tyr Ser Gly Lys Met Tyr Phe Gln Thr Met
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Thr Glu Ala Glu Tyr Gln Thr Ser Ile Gln Glu Lys Leu Pro Leu Ile
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Ile Gly Ser Ser Ala Ala Gly Leu Val Phe Leu Ile Ala Val Val Val
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Tyr Thr Asp Lys Leu Gln His Tyr Thr Ser Gly His Met Thr Pro Gly
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Met Lys Ile Tyr Ile Asp Pro Phe Thr Tyr Glu Asp Pro Asn Glu Ala
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Lys Leu Pro Gly Lys Arg Glu Ile Phe Val Ala Ile Lys Thr Leu Lys
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Ser Gly Tyr Thr Glu Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
660 665 670
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Val Thr Lys Ser Thr Pro Val Met Ile Ile Thr Glu Phe Met Glu Asn
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740 745 750
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770 775 780
Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr
785 790 795 800
Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met
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Gln Tyr Lys Glu Ser Phe Ala Asn Ala Gly Phe Thr Ser Phe Asp Val
930 935 940

Val Ser Gln Met Met Met Glu Asp Ile Leu Arg Val Gly Val Thr Leu
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 <223> PCR primer KEVR1

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 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
 20 25 30

 tca atg cac tgg gtg aag cag gct cca gga aag ggt tta aag tgg atg 144
 Ser Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

 ggc tgg ata aac acc tac act gga gag cca aca tat gct gat gac ttc 192
 Gly Trp Ile Asn Thr Tyr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
 50 55 60

 aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt 240
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
 65 70 75 80

 ttg cag atc aac aac ctg aaa aat gag gac acg gct aca tat ttc tgt 288
 Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys

85										90					95					
gca	acc	tac	tat	agg	tac	gaa	aga	gac	ttt	gac	tac	tgg	ggc	caa	ggc		336			
Ala	Thr	Tyr	Tyr	Arg	Tyr	Glu	Arg	Asp	Phe	Asp	Tyr	Trp	Gly	Gln	Gly					
			100					105					110							
acc	act	ctc	aca	gtc	tcc	tca	gcc	aaa	aca	aca	gcc	cca	tcg	gtc	tat		384			
Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Lys	Thr	Thr	Ala	Pro	Ser	Val	Tyr					
		115					120					125								
cca	ctg	gcc	cct	gtg	tgt	gga	gat	aca	act	ggc	tcc	tcg	gtg	act	cta		432			
Pro	Leu	Ala	Pro	Val	Cys	Gly	Asp	Thr	Thr	Gly	Ser	Ser	Val	Thr	Leu					
	130					135					140									
gga	tgc	ctg	gtc	aag	ggc	tat	ttc	cct	gag	cca	gtg	acc	ttg	acc	tgg		480			
Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Leu	Thr	Trp					
145					150					155					160					
aac	tct	gga	tcc	ctg	tcc	agt	ggc	gtg	cac	acc	ttc	cca	gct	gtc	ctg		528			
Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu					
				165					170					175						
cag	tct	gac	ctc	tac	acc	ctc	agc	agc	tca	gtg	act	gta	acc	tcg	agc		576			
Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	Thr	Ser	Ser					
			180					185					190							
acc	tgg	ccc	agc	cag	tcc	atc	acc	tgc	aat	gtg	gcc	cac	ccg	gca	agc		624			
Thr	Trp	Pro	Ser	Gln	Ser	Ile	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser					
		195					200					205								
agc	acc	aag	gta	gac	aag	aaa	att	gag	ccc	aga	ggg	ccc	aca	atc	aag		672			
Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Glu	Pro	Arg	Gly	Pro	Thr	Ile	Lys					
	210					215					220									
ccc	tgt	cct	cca	tgc	aaa	tgc	cca	gca	cct	aac	ctc	ttg	ggc	gga	cca		720			
Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Leu	Gly	Gly	Pro					
225					230					235					240					
tcc	gtc	ttc	atc	ttc	cct	cca	aag	atc	aag	gat	gta	ctc	atg	atc	tcc		768			
Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile	Ser					
				245					250					255						
ctg	agc	ccc	ata	gtc	aca	tgt	gtg	gtg	gtg	gat	gtg	agc	gag	gat	gac		816			
Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Glu	Asp	Asp					
			260				265						270							
cca	gat	gtc	cag	atc	agc	tgg	ttt	gtg	aac	aac	gtg	gaa	gta	cac	aca		864			
Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val	Asn	Asn	Val	Glu	Val	His	Thr					
		275					280					285								
gct	cag	aca	caa	acc	cat	aga	gag	gat	tac	aac	agt	act	ctc	cgg	gtg		912			
Ala	Gln	Thr	Gln	Thr	His	Arg	Glu	Asp	Tyr	Asn	Ser	Thr	Leu	Arg	Val					
	290					295					300									
gtc	agt	gcc	ctc	ccc	atc	cag	cac	cag	gac	tgg	atg	agt	ggc	aag	gag		960			
Val	Ser	Ala	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu					
305					310					315					320					
ttc	aaa	tgc	aag	gtc	aac	aac	aaa	gac	ctc	cca	gcg	ccc	atc	gag	aga		1008			
Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg					
				325					330					335						
acc	atc	tca	aaa	ccc	aaa	ggg	tca	gta	aga	gct	cca	cag	gta	tat	gtc		1056			
Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val					
			340				345						350							
ttg	cct	cca	cca	gaa	gaa	gag	atg	act	aag	aaa	cag	gtc	act	ctg	acc		1104			
Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr					

355	360	365	
tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc			1152
Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr			
370	375	380	
aac aac ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg			1200
Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu			
385	390	395	400
gac tct gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag			1248
Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys			
405	410	415	
aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag			1296
Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu			
420	425	430	
ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt			1344
Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly			
435	440	445	
aaa tga			1350
Lys			

<210> 35
 <211> 449
 <212> PRT
 <213> Mus musculus

<400> 35

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
 20 25 30
 Ser Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
 50 55 60
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
 65 70 75 80
 Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95
 Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr
 115 120 125
 Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
 130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser
180 185 190

Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser
195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys
210 215 220

Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
225 230 235 240

Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
245 250 255

Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
260 265 270

Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
275 280 285

Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
290 295 300

Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
305 310 315 320

Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
325 330 335

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

Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
355 360 365

Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
370 375 380

Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
405 410 415

Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
 420 425 430

Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
 435 440 445

Lys

<210> 36
 <211> 660
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(660)

<400> 36
 gat gtt ttg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga 48
 Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15
 gat caa gcc tcc atc tct tgc aga tct agt cag agc att gta cat agt 96
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
 20 25 30
 aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca ggc cag tct 144
 Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca 192
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc agg atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
 65 70 75 80
 agc aga gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
 85 90 95
 tca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336
 Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110
 cgg gct gat gct gca cca act gta tcc atc ttc cca cca tcc agt gag 384
 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 115 120 125
 cag tta aca tct gga ggt gcc tca gtc gtg tgc ttc ttg aac aac ttc 432
 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 130 135 140
 tac ccc aaa gac atc aat gtc aag tgg aag att gat ggc agt gaa cga 480
 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 145 150 155 160
 caa aat ggc gtc ctg aac agt tgg act gat cag gac agc aaa gac agc 528
 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 165 170 175

acc tac agc atg agc agc acc ctc acg ttg acc aag gac gag tat gaa 576
 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 180 185 190

cga cat aac agc tat acc tgt gag gcc act cac aag aca tca act tca 624
 Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 195 200 205

ccc att gtc aag agc ttc aac agg aat gag tgt taa 660
 Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 37
 <211> 219
 <212> PRT
 <213> Mus musculus

<400> 37

Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
 20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
 85 90 95

Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 115 120 125

Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 130 135 140

Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 145 150 155 160

Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 165 170 175

Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 180 185 190

Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 195 200 205

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 210 215

<210> 38
 <211> 1350
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(1350)

<400> 38
 cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag 48
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc ata gac tat 96
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
 20 25 30
 tca atg cac tgg gtg aag cag gct cca gga aag ggt tta aag tgg atg 144
 Ser Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45
 ggc tgg ata aac acc tac act gga gag cca aca tat tct gat gac ttc 192
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe
 50 55 60
 aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc tat 240
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 ttg cag atc agc aac ctc aaa aat gag gac acg gct tca tat ttc tgt 288
 Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Ser Tyr Phe Cys
 85 90 95
 gca acc tac tat agg tac gaa aga gac ttt gac tac tgg ggc caa ggc 336
 Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 acc act ctc aca gtc tcc tca gcc aaa aca aca gcc cca tcg gtc tat 384
 Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr
 115 120 125
 cca ctg gcc cct gtg tgt gga gat aca act ggc tcc tcg gtg act cta 432
 Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
 130 135 140
 gga tgc ctg gtc aag ggt tat ttc cct gag cca gtg acc ttg acc tgg 480
 Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
 145 150 155 160
 aac tct gga tcc ctg tcc agt ggt gtg cac acc ttc cca gct gtc ctg 528
 Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 cag tct gac ctc tac acc ctc agc agc tca gtg act gta acc tcg agc 576
 Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser
 180 185 190

acc tgg ccc agc cag tcc atc acc tgc aat gtg gcc cac ccg gca agc	624
Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser	
195 200 205	
agc acc aag gtg gac aag aaa att gag ccc aga ggg ccc aca atc aag	672
Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys	
210 215 220	
ccc tgt cct cca tgc aaa tgc cca gca cct aac ctc ttg ggt gga cca	720
Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro	
225 230 235 240	
tcc gtc ttc atc ttc cct cca aag atc aag gat gta ctc atg atc tcc	768
Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser	
245 250 255	
ctg agc ccc ata gtc aca tgt gtg gtg gtg gac gtg agc gag gat gac	816
Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp	
260 265 270	
cca gat gtc cag atc agc tgg ttt gtg aac aac gtg gaa gta cac aca	864
Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr	
275 280 285	
gct cag aca caa acc cat aga gag gat tac aac agt act ctc cgg gtg	912
Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val	
290 295 300	
gtc agt gcc ctc ccc atc cag cac cag gac tgg atg agt ggc aag gag	960
Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu	
305 310 315 320	
ttc aaa tgc aag gtc aac aac aaa gac ctc cca gcg ccc atc gag aga	1008
Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg	
325 330 335	
acc atc tca aaa ccc aaa ggg tca gta aga gct cca cag gta tat gtc	1056
Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val	
340 345 350	
ttg cct cca cca gaa gaa gag atg act aag aaa cag gtc act ctg acc	1104
Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr	
355 360 365	
tgc atg gtc aca gac ttc atg cct gaa gac att tac gtg gag tgg acc	1152
Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr	
370 375 380	
aac aac ggg aaa aca gag cta aac tac aag aac act gaa cca gtc ctg	1200
Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu	
385 390 395 400	
gac tct gat ggt tct tac ttc atg tac agc aag ctg aga gtg gaa aag	1248
Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys	
405 410 415	
aag aac tgg gtg gaa aga aat agc tac tcc tgt tca gtg gtc cac gag	1296
Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu	
420 425 430	
ggt ctg cac aat cac cac acg act aag agc ttc tcc cgg act ccg ggt	1344
Gly Leu His Asn His His Thr Lys Ser Phe Ser Arg Thr Pro Gly	
435 440 445	
aaa tga	1350
Lys	

<210> 39
 <211> 449
 <212> PRT
 <213> Mus musculus

<400> 39

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

Thr val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
 20 25 30

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

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

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

Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Ser Tyr Phe Cys
 85 90 95

Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val Tyr
 115 120 125

Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
 130 135 140

Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
 145 150 155 160

Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser Ser
 180 185 190

Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205

Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys
 210 215 220

Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
 225 230 235 240

Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
245 250 255

Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
260 265 270

Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
275 280 285

Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
290 295 300

Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
305 310 315 320

Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
325 330 335

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

Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
355 360 365

Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
370 375 380

Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
385 390 395 400

Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
405 410 415

Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
420 425 430

Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
435 440 445

Lys

<210> 40
<211> 660
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(660)

<400> 40
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Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly	
1 5 10 15	
gat caa gcc tcc atc tct tgc aga tct agt cag agc att gta cat agt	96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser	
20 25 30	
agt gga atc acc tat tta gaa tgg tac ctg cag aaa cca ggc cag tct	144
Ser Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	
cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	
gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile	
65 70 75 80	
agc aga gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt	288
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly	
85 90 95	
tca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa	336
Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
100 105 110	
cgg gct gat gct gca cca act gta tcc atc ttc cca cca tcc agt gag	384
Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu	
115 120 125	
cag tta aca tct gga ggt gcc tca gtc gtg tgc ttc ttg aac aac ttc	432
Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe	
130 135 140	
tac ccc aaa gac atc aat gtc aag tgg aag att gat ggc agt gaa cga	480
Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg	
145 150 155 160	
caa aat ggc gtc ctg aac agt tgg act gat cag gac agc aaa gac agc	528
Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser	
165 170 175	
acc tac agc atg agc agc acc ctc acg ttg acc aag gac gag tat gaa	576
Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu	
180 185 190	
cga cat aac agc tat acc tgt gag gcc act cac aag aca tca act tca	624
Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser	
195 200 205	
ccc att gtc aag agc ttc aac agg aat gag tgt taa	660
Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys	
210 215	

<210> 41
 <211> 219
 <212> PRT
 <213> Mus musculus

<400> 41

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser

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

<210> 42
 <211> 357
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(357)

<400> 42	
cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag	48
Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu	
1 5 10 15	

aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc aca cac tat	96
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr	

	20	25	30	
tca atg cac tgg gtg aag cag gct cca gga aag ggt tta aag tgg atg				144
Ser Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met	35	40	45	
ggc tgg ata aac acc tac act gga gag cca aca tat gct gat gac ttc				192
Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe	50	55	60	
aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt				240
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe	65	70	75	80
ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt				288
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys	85	90	95	
gca acc tac tat agg tac gaa aga gac ttt gac tac tgg ggc caa ggc				336
Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly	100	105	110	
acc act ctc aca gtc tcc tca				357
Thr Thr Leu Thr Val Ser Ser	115			

<210> 43
 <211> 119
 <212> PRT
 <213> Mus musculus

<400> 43

Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr His Tyr
 20 25 30
 Ser Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe
 50 55 60
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe
 65 70 75 80
 Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95
 Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser
 115

<210> 44
 <211> 993

<212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(993)

<400> 44
 gcc aaa aca aca gcc cca tcg gtc tat cca ctg gcc cct gtg tgt gga 48
 Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly
 1 5 10 15
 gat aca act ggc tcc tcg gtg act cta gga tgc ctg gtc aag ggt tat 96
 Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
 20 25 30
 ttc cct gag cca gtg acc ttg acc tgg aac tct gga tcc ctg tcc agt 144
 Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser
 35 40 45
 ggt gtg cac acc ttc cca gct gtc ctg cag tct gac ctc tac acc ctc 192
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 50 55 60
 agc agc tca gtg act gta acc tcg agc acc tgg ccc agc cag tcc atc 240
 Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
 65 70 75 80
 acc tgc aat gtg gcc cac ccg gca agc agc acc aag gta gac aag aaa 288
 Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 85 90 95
 att gag ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa tgc 336
 Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
 100 105 110
 cca gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca 384
 Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
 115 120 125
 aag atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt 432
 Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
 130 135 140
 gtg gtg gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg 480
 Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
 145 150 155 160
 ttt gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga 528
 Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
 165 170 175
 gag gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag 576
 Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
 180 185 190
 cac cag gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac 624
 His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
 195 200 205
 aaa gac ctc cca gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg 672
 Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly
 210 215 220
 tca gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa gag 720
 Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
 225 230 235 240

atg act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc atg 768
Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
245 250 255

cct gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag cta 816
Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
260 265 270

aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac ttc 864
Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe
275 280 285

atg tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga aat 912
Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
290 295 300

agc tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac acg 960
Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
305 310 315 320

act aag agc ttc tcc cgg act ccg ggt aaa tga 993
Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
325 330

<210> 45
<211> 330
<212> PRT
<213> Mus musculus

<400> 45

Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly
1 5 10 15

Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
20 25 30

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

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
50 55 60

Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
65 70 75 80

Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
85 90 95

Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
100 105 110

Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
115 120 125

Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
130 135 140

Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
145 150 155 160

Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
165 170 175

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

His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
195 200 205

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

Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
225 230 235 240

Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
245 250 255

Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
260 265 270

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

Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
290 295 300

Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
305 310 315 320

Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
325 330

<210> 46
<211> 336
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)..(336)

<400> 46
gat gtt ttg atg acc caa agt cca ctc tcc ctg cct gtc agt ctt gga 48
Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15
gat caa gcc tcc atc tct tgc aga tct agt cag agc att gta cat agt 96
Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

aat gga aac acc tat tta gaa tgg tac ctg cag aaa cca ggc cag tct	144
Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser	
35 40 45	
cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca	192
Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro	
50 55 60	
gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc agg atc	240
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile	
65 70 75 80	
agc aga gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt	288
Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly	
85 90 95	
tca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa	336
Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
100 105 110	

<210> 47
 <211> 112
 <212> PRT
 <213> Mus musculus

<400> 47

Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 48
 <211> 324
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(324)

<400> 48	48
cgg gct gat gct gca cca act gta tcc atc ttc cca cca tcc agt gag	

Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	
1				5					10					15		
cag	tta	aca	tct	gga	ggt	gcc	tca	gtc	gtg	tgc	ttc	ttg	aac	aac	ttc	96
Gln	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu	Asn	Asn	Phe	
			20					25					30			
tac	ccc	aaa	gac	atc	aat	gtc	aag	tgg	aag	att	gat	ggc	agt	gaa	cga	144
Tyr	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	Glu	Arg	
		35					40					45				
caa	aat	ggc	gtc	ctg	aac	agt	tgg	act	gat	cag	gac	agc	aaa	gac	agc	192
Gln	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	Asp	Ser	
	50					55					60					
acc	tac	agc	atg	agc	agc	acc	ctc	acg	ttg	acc	aag	gac	gag	tat	gaa	240
Thr	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	Glu	Tyr	Glu	
65					70				75						80	
cga	cat	aac	agc	tat	acc	tgt	gag	gcc	act	cac	aag	aca	tca	act	tca	288
Arg	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr	Ser	Thr	Ser	
				85				90						95		
ccc	att	gtc	aag	agc	ttc	aac	agg	aat	gag	tgt	taa					324
Pro	Ile	Val	Lys	Ser	Phe	Asn	Arg	Asn	Glu	Cys						
			100					105								

<210> 49
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 49

Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	Ser	Ser	Glu	
1				5					10					15		
Gln	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu	Asn	Asn	Phe	
			20					25					30			
Tyr	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	Ser	Glu	Arg	
		35					40					45				
Gln	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	Lys	Asp	Ser	
	50					55					60					
Thr	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	Glu	Tyr	Glu	
65					70				75						80	
Arg	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr	Ser	Thr	Ser	
				85				90						95		
Pro	Ile	Val	Lys	Ser	Phe	Asn	Arg	Asn	Glu	Cys						
			100					105								

<210> 50
 <211> 357
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(357)

<400> 50
 cag atc cag ttg gtg cag tct gga cct gag ctg aag aag cct gga gag 48
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc ata gac tat 96
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
 20 25 30
 tca atg cac tgg gtg aag cag gct cca gga aag ggt tta aag tgg atg 144
 Ser Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45
 ggc tgg ata aac acc tac act gga gag cca aca tat tct gat gac ttc 192
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe
 50 55 60
 aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc tat 240
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 ttg cag atc agc aac ctc aaa aat gag gac acg gct tca tat ttc tgt 288
 Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Ser Tyr Phe Cys
 85 90 95
 gca acc tac tat agg tac gaa aga gac ttt gac tac tgg ggc caa ggc 336
 Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 acc act ctc aca gtc tcc tca 357
 Thr Thr Leu Thr Val Ser Ser
 115

<210> 51
 <211> 119
 <212> PRT
 <213> Mus musculus

<400> 51
 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
 20 25 30
 Ser Met His Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe
 50 55 60
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr
 65 70 75 80
 Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Ser Tyr Phe Cys
 85 90 95

Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser
 115

<210> 52
 <211> 993
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(993)

<400> 52
 gcc aaa aca aca gcc cca tcg gtc tat cca ctg gcc cct gtg tgt gga 48
 Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro Val Cys Gly
 1 5 10 15
 gat aca act ggc tcc tcg gtg act cta gga tgc ctg gtc aag ggt tat 96
 Asp Thr Thr Gly Ser Ser Val Thr Leu Gly Cys Leu Val Lys Gly Tyr
 20 25 30
 ttc cct gag cca gtg acc ttg acc tgg aac tct gga tcc ctg tcc agt 144
 Phe Pro Glu Pro Val Thr Leu Thr Trp Asn Ser Gly Ser Leu Ser Ser
 35 40 45
 ggt gtg cac acc ttc cca gct gtc ctg cag tct gac ctc tac acc ctc 192
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu
 50 55 60
 agc agc tca gtg act gta acc tcg agc acc tgg ccc agc cag tcc atc 240
 Ser Ser Ser Val Thr Val Thr Ser Ser Thr Trp Pro Ser Gln Ser Ile
 65 70 75 80
 acc tgc aat gtg gcc cac ccg gca agc agc acc aag gtg gac aag aaa 288
 Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys
 85 90 95
 att gag ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa tgc 336
 Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
 100 105 110
 cca gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca 384
 Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
 115 120 125
 aag atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt 432
 Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
 130 135 140
 gtg gtg gtg gac gtg agc gag gat gac cca gat gtc cag atc agc tgg 480
 Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
 145 150 155 160
 ttt gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga 528
 Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
 165 170 175
 gag gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag 576
 Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln
 180 185 190

cac	cag	gac	tgg	atg	agt	ggc	aag	gag	ttc	aaa	tgc	aag	gtc	aac	aac	624
His	Gln	Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	
	195						200					205				
aaa	gac	ctc	cca	gcg	ccc	atc	gag	aga	acc	atc	tca	aaa	ccc	aaa	ggg	672
Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	
	210					215					220					
tca	gta	aga	gct	cca	cag	gta	tat	gtc	ttg	cct	cca	cca	gaa	gaa	gag	720
Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	
	225				230					235					240	
atg	act	aag	aaa	cag	gtc	act	ctg	acc	tgc	atg	gtc	aca	gac	ttc	atg	768
Met	Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	
				245					250					255		
cct	gaa	gac	att	tac	gtg	gag	tgg	acc	aac	aac	ggg	aaa	aca	gag	cta	816
Pro	Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	
			260				265						270			
aac	tac	aag	aac	act	gaa	cca	gtc	ctg	gac	tct	gat	ggg	tct	tac	ttc	864
Asn	Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	
		275					280					285				
atg	tac	agc	aag	ctg	aga	gtg	gaa	aag	aag	aac	tgg	gtg	gaa	aga	aat	912
Met	Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	
	290					295					300					
agc	tac	tcc	tgt	tca	gtg	gtc	cac	gag	ggg	ctg	cac	aat	cac	cac	acg	960
Ser	Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	
	305				310					315					320	
act	aag	agc	ttc	tcc	cgg	act	ccg	ggg	aaa	tga						993
Thr	Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys							
				325					330							

<210> 53
 <211> 330
 <212> PRT
 <213> Mus musculus

<400> 53

Ala	Lys	Thr	Thr	Ala	Pro	Ser	Val	Tyr	Pro	Leu	Ala	Pro	Val	Cys	Gly
1				5					10					15	
Asp	Thr	Thr	Gly	Ser	Ser	Val	Thr	Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr
			20					25					30		
Phe	Pro	Glu	Pro	Val	Thr	Leu	Thr	Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser
		35				40						45			
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu
	50					55					60				
Ser	Ser	Ser	Val	Thr	Val	Thr	Ser	Ser	Thr	Trp	Pro	Ser	Gln	Ser	Ile
65					70					75					80
Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys
				85					90					95	

Ile Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys
100 105 110

Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro
115 120 125

Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys
130 135 140

Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp
145 150 155 160

Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg
165 170 175

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

His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn
195 200 205

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

Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu
225 230 235 240

Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met
245 250 255

Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu
260 265 270

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

Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn
290 295 300

Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr
305 310 315 320

Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
325 330

<210> 54
<211> 336
<212> DNA
<213> Mus musculus

<220>

<221> CDS
 <222> (1)..(336)

<400> 54
 gat gtt ttg atg acc caa act cca ctc tcc ctg cct gtc agt ctt gga 48
 Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15
 gat caa gcc tcc atc tct tgc aga tct agt cag agc att gta cat agt 96
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
 20 25 30
 agt gga atc acc tat tta gaa tgg tac ctg cag aaa cca ggc cag tct 144
 Ser Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct ggc gtc cca 192
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc 240
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 agc aga gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt 288
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
 85 90 95
 tca cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 336
 Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 55
 <211> 112
 <212> PRT
 <213> Mus musculus

<400> 55
 Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
 20 25 30
 Ser Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
 85 90 95
 Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 56
 <211> 324
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(324)

<400> 56
 cgg gct gat gct gca cca act gta tcc atc ttc cca cca tcc agt gag 48
 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 1 5 10 15
 cag tta aca tct gga ggt gcc tca gtc gtg tgc ttc ttg aac aac ttc 96
 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 20 25 30
 tac ccc aaa gac atc aat gtc aag tgg aag att gat ggc agt gaa cga 144
 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 35 40 45
 caa aat ggc gtc ctg aac agt tgg act gat cag gac agc aaa gac agc 192
 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 50 55 60
 acc tac agc atg agc agc acc ctc acg ttg acc aag gac gag tat gaa 240
 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 65 70 75 80
 cga cat aac agc tat acc tgt gag gcc act cac aag áca tca act tca 288
 Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser
 85 90 95
 ccc att gtc aag agc ttc aac agg aat gag tgt taa 324
 Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 100 105

<210> 57
 <211> 107
 <212> PRT
 <213> Mus musculus

<400> 57
 Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu
 1 5 10 15
 Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe
 20 25 30
 Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg
 35 40 45
 Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser
 50 55 60
 Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu
 65 70 75 80
 Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser

85

90

95

Pro Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
 100 105

<210> 58
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(30)

<400> 58
 ggg tat acc ttc aca cac tat tca atg cac
 Gly Tyr Thr Phe Thr His Tyr Ser Met His
 1 5 10

30

<210> 59
 <211> 10
 <212> PRT
 <213> Mus musculus

<400> 59

Gly Tyr Thr Phe Thr His Tyr Ser Met His
 1 5 10

<210> 60
 <211> 51
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(51)

<400> 60
 tgg ata aac acc tac act gga gag cca aca tat gct gat gac ttc aag
 Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
 1 5 10 15

48

gga
 Gly

51

<210> 61
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 61

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
 1 5 10 15

Gly

<210> 62
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(30)

<400> 62
 tac tat agg tac gaa aga gac ttt gac tac
 Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

30

<210> 63
 <211> 10
 <212> PRT
 <213> Mus musculus

<400> 63

Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

<210> 64
 <211> 48
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(48)

<400> 64
 aga tct agt cag agc att gta cat agt aat gga aac acc tat tta gaa
 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 1 5 10 15

48

<210> 65
 <211> 16
 <212> PRT
 <213> Mus musculus

<400> 65

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 1 5 10 15

<210> 66
 <211> 21
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(21)

<400> 66
 aaa gtt tcc aac cga ttt tct
 Lys Val Ser Asn Arg Phe Ser

21

1

5

<210> 67
 <211> 7
 <212> PRT
 <213> Mus musculus

<400> 67

Lys Val Ser Asn Arg Phe Ser
 1 5

<210> 68
 <211> 27
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(27)

<400> 68
 ttt caa ggt tca cat gtt ccg tac acg
 Phe Gln Gly Ser His Val Pro Tyr Thr
 1 5

27

<210> 69
 <211> 9
 <212> PRT
 <213> Mus musculus

<400> 69

Phe Gln Gly Ser His Val Pro Tyr Thr
 1 5

<210> 70
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(30)

<400> 70
 ggg tat acc ttc ata gac tat tca atg cac
 Gly Tyr Thr Phe Ile Asp Tyr Ser Met His
 1 5 10

30

<210> 71
 <211> 10
 <212> PRT
 <213> Mus musculus

<400> 71

Gly Tyr Thr Phe Ile Asp Tyr Ser Met His
 1 5 10

<210> 72
 <211> 51
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(51)

<400> 72
 tgg ata aac acc tac act gga gag cca aca tat tct gat gac ttc aag 48
 Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys
 1 5 10 15
 gga 51
 Gly

<210> 73
 <211> 17
 <212> PRT
 <213> Mus musculus

<400> 73

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys
 1 5 10 15
 Gly

<210> 74
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(30)

<400> 74
 tac tat agg tac gaa aga gac ttt gac tac 30
 Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

<210> 75
 <211> 10
 <212> PRT
 <213> Mus musculus

<400> 75

Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

<210> 76
 <211> 48
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(48)

<400> 76
 aga tct agt cag agc att gta cat agt agt gga atc acc tat tta gaa 48
 Arg Ser Ser Gln Ser Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu
 1 5 10 15

<210> 77
 <211> 16
 <212> PRT
 <213> Mus musculus

<400> 77
 Arg Ser Ser Gln Ser Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu
 1 5 10 15

<210> 78
 <211> 21
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(21)

<400> 78
 aaa gtt tcc aac cga ttt tct 21
 Lys Val Ser Asn Arg Phe Ser
 1 5

<210> 79
 <211> 7
 <212> PRT
 <213> Mus musculus

<400> 79
 Lys Val Ser Asn Arg Phe Ser
 1 5

<210> 80
 <211> 27
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(27)

<400> 80
 ttt caa ggt tca cat gtt ccg tac acg 27
 Phe Gln Gly Ser His Val Pro Tyr Thr
 1 5

<210> 81
 <211> 9
 <212> PRT
 <213> Mus musculus

<400> 81

Phe Gln Gly Ser His Val Pro Tyr Thr
1 5

<210> 82

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> primer N1

<400> 82

attaggatcc gagcttccgt actgccagtg tc

32

<210> 83

<211> 28

<212> DNA

<213> Artificial

<220>

<223> primer N2

<400> 83

attaggatcc gccccccaag gtgaggct

28

<210> 84

<211> 34

<212> DNA

<213> Artificial

<220>

<223> primer N3

<400> 84

attaggatcc ggtcacttac cgcaagaagg gaga

34

<210> 85

<211> 32

<212> DNA

<213> Artificial

<220>

<223> primer N4

<400> 85

attaggatcc ggtccaggtg caggcactga cg

32

<210> 86

<211> 31

<212> DNA

<213> Artificial

<220>

<223> primer C1

<400> 86

aattaagctt gccgccaatc accgccaagt t

31

<210> 87

<211> 32
 <212> DNA
 <213> Artificial

 <220>
 <223> primer C2

 <400> 87
 aattaagctt gttgccagat ccctccgggg ac 32

<210> 88
 <211> 29
 <212> DNA
 <213> Artificial

 <220>
 <223> primer C3

 <400> 88
 aattaagctt caggtaggtg gtgtctggg 29

<210> 89
 <211> 30
 <212> DNA
 <213> Artificial

 <220>
 <223> primer C4

 <400> 89
 aattaagctt ctcgtacttc cacactcggc 30

<210> 90
 <211> 720
 <212> DNA
 <213> Artificial

 <220>
 <223> hSH-348-T1L

<220>
 <221> CDS
 <222> (1)..(720)

<220>
 <221> sig_peptide
 <222> (1)..(60)

<400> 90
 atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc 48
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15

ggc gca tat ggc gac ata gtg atg acc cag agc ccc ctg agc ctg ccc 96
 Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro
 20 25 30

gtg acc ccc ggc gag ccc gcc tcc atc agc tgc cgg agc agc cag agc 144
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 35 40 45

atc gtg cac agc aac ggc aac acc tac ctg gag tgg tac ctg cag aag 192
 Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
 50 55 60

ccc ggc cag agc ccc cag ctg ctg atc tac aag gtg agc aac cgg ttc Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe 65 70 75 80	240
agc ggc gtg ccc gac cgg ttc agc ggc agc ggc agc ggc acc gac ttc Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe 85 90 95	288
acc ctg aag atc agc cgg gtg gag gcc gag gac gtg ggc gtg tac tac Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 100 105 110	336
tgc ttc cag ggc tcc cac gtg ccc tac acc ttc ggc cag ggc acc aag Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys 115 120 125	384
gtg gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 130 135 140	432
ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu 145 150 155 160	480
ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp 165 170 175	528
aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 180 185 190	576
agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 195 200 205	624
gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 210 215 220	672
ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt tag Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235	720

<210> 91
 <211> 239
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 91

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

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

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

Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys
115 120 125

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 92
<211> 48
<212> DNA
<213> Artificial

<220>
<223> hSH348-1-T1L CDRL1

<220>
<221> CDS
<222> (1)..(48)

<400> 92
cgg agc agc cag agc atc gtg cac agc aac ggc aac acc tac ctg gag
Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

48

<210> 93

<211> 16
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 93

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
1 5 10 15

<210> 94
<211> 21
<212> DNA
<213> Artificial

<220>
<223> hSH348-1-T1L CDRL2

<220>
<221> CDS
<222> (1)..(21)

<400> 94
aag gtg agc aac cgg ttc agc
Lys Val Ser Asn Arg Phe Ser
1 5

21

<210> 95
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 95

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 96
<211> 24
<212> DNA
<213> Artificial

<220>
<223> hSH348-1-T1L CDRL3

<220>
<221> CDS
<222> (1)..(24)

<400> 96
ttc cag ggc tcc cac gtg ccc tac
Phe Gln Gly Ser His Val Pro Tyr
1 5

24

<210> 97
<211> 8
<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 97

Phe Gln Gly Ser His Val Pro Tyr
1 5

<210> 98

<211> 720

<212> DNA

<213> Artificial

<220>

<223> hSH348-1-T3L

<220>

<221> CDS

<222> (1)..(720)

<220>

<221> sig_peptide

<222> (1)..(60)

<400> 98

atg	gtg	ctg	cag	acc	cag	gtg	ttc	atc	tcc	ctg	ctg	ctg	tgg	atc	tcc	48
Met	Val	Leu	Gln	Thr	Gln	Val	Phe	Ile	Ser	Leu	Leu	Leu	Trp	Ile	Ser	
1			5						10					15		

ggc	gca	tat	ggc	gac	gtg	ctg	atg	acc	cag	agc	ccc	ctg	agc	ctg	ccc	96
Gly	Ala	Tyr	Gly	Asp	Val	Leu	Met	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	
			20					25					30			

gtg	acc	ccc	ggc	gag	ccc	gcc	tcc	atc	agc	tgc	cgg	agc	agc	cag	agc	144
Val	Thr	Pro	Gly	Glu	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	
		35				40						45				

atc	gtg	cac	agc	aac	ggc	aac	acc	tac	ctg	gag	tgg	tac	ctg	cag	aag	192
Ile	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Glu	Trp	Tyr	Leu	Gln	Lys	
	50				55						60					

ccc	ggc	cag	agc	ccc	cag	ctg	ctg	atc	tac	aag	gtg	agc	aac	cgg	ttc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	
65					70					75				80		

agc	ggc	gtg	ccc	gac	cgg	ttc	agc	ggc	agc	ggc	agc	ggc	acc	gac	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
			85					90					95			

acc	ctg	aag	atc	agc	cgg	gtg	gag	gcc	gag	gac	gtg	ggc	gtg	tac	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
			100					105					110			

tgc	ttc	cag	ggc	tcc	cac	gtg	ccc	tac	acc	ttc	ggc	cag	ggc	acc	aag	384
Cys	Phe	Gln	Gly	Ser	His	Val	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
		115					120					125				

gtg	gag	atc	aag	cgt	acg	gtg	gcc	gcc	ccc	tcc	gtg	ttc	atc	ttc	ccc	432
Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
	130					135					140					

ccc	tcc	gac	gag	cag	ctg	aag	tcc	ggc	acc	gcc	tcc	gtg	gtg	tgc	ctg	480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
145					150					155					160	

ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
165 170 175	
aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
180 185 190	
agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
195 200 205	
gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
210 215 220	
ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt tag	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
225 230 235	

<210> 99
 <211> 239
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 99

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

Gly Ala Tyr Gly Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro
20 25 30

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

Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys
115 120 125

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 100
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T3L CDRL1

<220>
 <221> CDS
 <222> (1)..(48)

<400> 100
 cgg agc agc cag agc atc gtg cac agc aac ggc aac acc tac ctg gag
 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 1 5 10 15

48

<210> 101
 <211> 16
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 101

Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 1 5 10 15

<210> 102
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T3L CDRL2

<220>
 <221> CDS

<222> (1)..(21)

<400> 102

aag gtg agc aac cgg ttc agc
Lys Val Ser Asn Arg Phe Ser
1 5

21

<210> 103

<211> 7

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 103

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 104

<211> 24

<212> DNA

<213> Artificial

<220>

<223> hSH348-1-T3L CDRL3

<220>

<221> CDS

<222> (1)..(24)

<400> 104

ttc cag ggc tcc cac gtg ccc tac
Phe Gln Gly Ser His Val Pro Tyr
1 5

24

<210> 105

<211> 8

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 105

Phe Gln Gly Ser His Val Pro Tyr
1 5

<210> 106

<211> 1407

<212> DNA

<213> Artificial

<220>

<223> hSH348-1-T1H

<220>

<221> CDS

<222> (1)..(1407)

<220>
 <221> sig_peptide
 <222> (1)..(57)

 <400> 106
 atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15

 gtg ctg agc cag gtg cag ctg gtg cag agc ggc gcc gag gtg aag aag 96
 Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

 ccc ggc agc agc gtg aag gtg agc tgc aag gcc agc ggc tac acc ttc 144
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

 acc cac tac agc atg cac tgg gtg cgg cag gcc ccc ggc cag ggc ctg 192
 Thr His Tyr Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60

 gag tgg atg ggc tgg atc aac acc tac acc ggc gag ccc acc tac gcc 240
 Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
 65 70 75 80

 gac gac ttc aag ggc cgg gtg acc atc acc gcc gac acc tcc acc tcc 288
 Asp Asp Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
 85 90 95

 acc gcc tac ctg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg 336
 Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

 tac tac tgc gcc acc tac tac cgg tac gag cgg gac ttc gac tac tgg 384
 Tyr Tyr Cys Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp
 115 120 125

 ggc cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca 432
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140

 agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca 480
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160

 gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc 528
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175

 gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc 576
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190

 gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc 624
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205

 gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat 672
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220

 cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct 720
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 225 230 235 240

 tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg 768
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255

ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 260 265 270	816
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 275 280 285	864
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 290 295 300	912
gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 305 310 315 320	960
tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 325 330 335	1008
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 340 345 350	1056
atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 355 360 365	1104
gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val 370 375 380	1152
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val 385 390 395 400	1200
gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 405 410 415	1248
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr 420 425 430	1296
gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val 435 440 445	1344
atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 450 455 460	1392
tct ccc ggc aaa tga Ser Pro Gly Lys 465	1407

<210> 107
 <211> 468
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 107

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr His Tyr Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
 65 70 75 80
 Asp Asp Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
 85 90 95
 Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp
 115 120 125
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

Ser Pro Gly Lys
 465

<210> 108
 <211> 15
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T1H CDRH1

<220>
 <221> CDS
 <222> (1)..(15)

<400> 108
 cac tac agc atg cac
 His Tyr Ser Met His

1 5

<210> 109
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 109

His Tyr Ser Met His
1 5

<210> 110
<211> 51
<212> DNA
<213> Artificial

<220>
<223> hSH348-1-T1H_CDRH2

<220>
<221> CDS
<222> (1)..(51)

<400> 110
tgg atc aac acc tac acc ggc gag ccc acc tac gcc gac gac ttc aag 48
Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
1 5 10 15

ggc 51
Gly

<210> 111
<211> 17
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 111

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
1 5 10 15

Gly

<210> 112
<211> 30
<212> DNA
<213> Artificial

<220>
<223> hSH348-1-T1H_CDRH3

<220>

<221> CDS
 <222> (1)..(30)

<400> 112
 tac tac cgg tac gag cgg gac ttc gac tac
 Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

30

<210> 113
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 113
 Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

<210> 114
 <211> 1407
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T3H

<220>
 <221> CDS
 <222> (1)..(1407)
 <220>
 <221> sig_peptide
 <222> (1)..(57)

<400> 114
 atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15
 gtg ctg agc cag atc cag ctg gtg cag agc ggc gcc gag gtg aag aag 96
 Val Leu Ser Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30
 ccc ggc agc agc gtg aag gtg agc tgc aag gcc agc ggc tac acc ttc 144
 Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 acc cac tac agc atg cac tgg gtg cgg cag gcc ccc ggc cag ggc ctg 192
 Thr His Tyr Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 aag tgg atg ggc tgg atc aac acc tac acc ggc gag ccc acc tac gcc 240
 Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
 65 70 75 80
 gac gac ttc aag ggc cgg ttc gcc ttc agc ctg gac acc tcc acc tcc 288
 Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Thr Ser
 85 90 95
 acc gcc tac ctg gaa ctg agc agc ctg cgg agc gag gac acc gcc gtg 336
 Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110

tac tac tgc gcc acc tac tac cgg tac gag cgg gac ttc gac tac tgg	384
Tyr Tyr Cys Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp	
115 120 125	
ggc cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca	432
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro	
130 135 140	
agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca	480
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr	
145 150 155 160	
gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc	528
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	
165 170 175	
gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc	576
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	
180 185 190	
gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc	624
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	
195 200 205	
gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat	672
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn	
210 215 220	
cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct	720
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser	
225 230 235 240	
tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg	768
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	
245 250 255	
ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	816
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
260 265 270	
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc	864
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	
275 280 285	
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	912
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
290 295 300	
gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg	960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
305 310 315 320	
tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
325 330 335	
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc	1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
340 345 350	
atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag	1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	
355 360 365	
gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc	1152
Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val	
370 375 380	

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg	1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val	
385 390 395 400	
gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct	1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro	
405 410 415	
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc	1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr	
420 425 430	
gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg	1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val	
435 440 445	
atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg	1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu	
450 455 460	
tct ccc ggc aaa tga	1407
Ser Pro Gly Lys	
465	

<210> 115
 <211> 468
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 115

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr His Tyr Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
65 70 75 80

Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
180 185 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
195 200 205

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
210 215 220

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
225 230 235 240

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
245 250 255

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
260 265 270

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
275 280 285

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
355 360 365

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460

Ser Pro Gly Lys
465

<210> 116
<211> 15
<212> DNA
<213> Artificial

<220>
<223> hSH348-1-T3H CDRH1

<220>
<221> CDS
<222> (1)..(15)

<400> 116
cac tac agc atg cac
His Tyr Ser Met His
1 5

15

<210> 117
<211> 5
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 117

His Tyr Ser Met His
1 5

<210> 118
<211> 51
<212> DNA
<213> Artificial

<220>
<223> hSH348-1-T3H CDRH2

<220>
<221> CDS
<222> (1)..(51)

<400> 118
tgg atc aac acc tac acc ggc gag ccc acc tac gcc gac gac ttc aag

48

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
 1 5 10 15

ggc
 Gly

51

<210> 119
 <211> 17
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 119

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Lys
 1 5 10 15

Gly

<210> 120
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T3H CDRH3

<220>
 <221> CDS
 <222> (1)..(30)

<400> 120
 tac tac cgg tac gag cgg gac ttc gac tac
 Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

30

<210> 121
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 121

Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

<210> 122
 <211> 720
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T1L

<220>
 <221> CDS
 <222> (1)..(720)

<220>
 <221> sig_peptide
 <222> (1)..(60)

<400> 122

atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc	48
Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser	
1 5 10 15	
ggc gca tat ggc gac ata gtg atg acc cag agc ccc ctg agc ctg ccc	96
Gly Ala Tyr Gly Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro	
20 25 30	
gtg acc ccc ggc gag ccc gcc agc atc agc tgc cgg agc agc cag agc	144
Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser	
35 40 45	
atc gtg cac agc agc ggc atc acc tac ctg gag tgg tac ctg cag aag	192
Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys	
50 55 60	
ccc ggc cag agc ccc cag ctg ctg atc tac aag gtg agc aac cgg ttc	240
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe	
65 70 75 80	
agc ggc gtg ccc gac cgg ttc agc ggc agc ggc agc ggc acc gac ttc	288
Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe	
85 90 95	
acc ctg aag atc agc cgg gtg gag gcc gag gac gtg ggc gtg tac tac	336
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr	
100 105 110	
tgc ttc cag ggc agc cac gtg ccc tac acc ttc ggc cag ggc acc aag	384
Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys	
115 120 125	
gtg gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc	432
Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro	
130 135 140	
ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg	480
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu	
145 150 155 160	
ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac	528
Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp	
165 170 175	
aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac	576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp	
180 185 190	
agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa	624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys	
195 200 205	
gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag	672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln	
210 215 220	
ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt tag	720
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys	
225 230 235	

<210> 123
 <211> 239
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 123

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

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

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

Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
 50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
 85 90 95

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 105 110

Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 115 120 125

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 124
 <211> 48
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T1L CDRL1

<220>
 <221> CDS
 <222> (1)..(48)

<400> 124
 cgg agc agc cag agc atc gtg cac agc agc ggc atc acc tac ctg gag 48
 Arg Ser Ser Gln Ser Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu
 1 5 10 15

<210> 125
 <211> 16
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 125
 Arg Ser Ser Gln Ser Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu
 1 5 10 15

<210> 126
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T1L CDRL2

<220>
 <221> CDS
 <222> (1)..(21)

<400> 126
 aag gtg agc aac cgg ttc agc 21
 Lys Val Ser Asn Arg Phe Ser
 1 5

<210> 127
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 127
 Lys Val Ser Asn Arg Phe Ser
 1 5

<210> 128
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T1L_CDRL3

<220>
 <221> CDS
 <222> (1)..(24)

<400> 128
 ttc cag ggc agc cac gtg ccc tac
 Phe Gln Gly Ser His Val Pro Tyr
 1 5

24

<210> 129
 <211> 8
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 129
 Phe Gln Gly Ser His Val Pro Tyr
 1 5

<210> 130
 <211> 720
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T3L

<220>
 <221> CDS
 <222> (1)..(720)

<220>
 <221> sig_peptide
 <222> (1)..(60)

<400> 130
 atg gtg ctg cag acc cag gtg ttc atc tcc ctg ctg ctg tgg atc tcc
 Met Val Leu Gln Thr Gln Val Phe Ile Ser Leu Leu Leu Trp Ile Ser
 1 5 10 15 48

ggc gca tat ggc gac gtg ctg atg acc cag agc ccc ctg agc ctg ccc
 Gly Ala Tyr Gly Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro
 20 25 30 96

gtg acc ccc ggc gag ccc gcc agc atc agc tgc cgg agc agc cag agc
 Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
 35 40 45 144

atc gtg cac agc agc ggc atc acc tac ctg gag tgg tac ctg cag aag
 Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
 50 55 60 192

ccc ggc cag agc ccc cag ctg ctg atc tac aag gtg agc aac cgg ttc Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe 65 70 75 80	240
agc ggc gtg ccc gac cgg ttc agc ggc agc ggc agc ggc acc gac ttc Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe 85 90 95	288
acc ctg aag atc agc cgg gtg gag gcc gag gac gtg ggc gtg tac tac Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr 100 105 110	336
tgc ttc cag ggc agc cac gtg ccc tac acc ttc ggc cag ggc acc aag Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys 115 120 125	384
gtg gag atc aag cgt acg gtg gcc gcc ccc tcc gtg ttc atc ttc ccc Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro 130 135 140	432
ccc tcc gac gag cag ctg aag tcc ggc acc gcc tcc gtg gtg tgc ctg Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu 145 150 155 160	480
ctg aat aac ttc tac ccc aga gag gcc aag gtg cag tgg aag gtg gac Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp 165 170 175	528
aac gcc ctg cag tcc ggg aac tcc cag gag agc gtg acc gag cag gac Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp 180 185 190	576
agc aag gac agc acc tac agc ctg agc agc acc ctg acc ctg agc aaa Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys 195 200 205	624
gcc gac tac gag aag cac aag gtg tac gcc tgc gag gtg acc cac cag Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln 210 215 220	672
ggc ctg agc tcc ccc gtc acc aag agc ttc aac agg ggg gag tgt tag Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys 225 230 235	720

<210> 131
 <211> 239
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 131

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

Gly Ala Tyr Gly Asp Val Leu Met Thr Gln Ser Pro Leu Ser Leu Pro
 20 25 30

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

Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
50 55 60

Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
65 70 75 80

Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
85 90 95

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys
115 120 125

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

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

Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
165 170 175

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
180 185 190

Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
195 200 205

Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
210 215 220

Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 132
<211> 48
<212> DNA
<213> Artificial

<220>
<223> hSH357-1-T3L CDRL1

<220>
<221> CDS
<222> (1)..(48)

<400> 132
cgg agc agc cag agc atc gtg cac agc agc ggc atc acc tac ctg gag 48
Arg Ser Ser Gln Ser Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu
1 5 10 15

<210> 133

<211> 16
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 133

Arg Ser Ser Gln Ser Ile Val His Ser Ser Gly Ile Thr Tyr Leu Glu
1 5 10 15

<210> 134
<211> 21
<212> DNA
<213> Artificial

<220>
<223> hSH357-1-T3L CDRL2

<220>
<221> CDS
<222> (1)..(21)

<400> 134
aag gtg agc aac cgg ttc agc
Lys Val Ser Asn Arg Phe Ser
1 5

21

<210> 135
<211> 7
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 135

Lys Val Ser Asn Arg Phe Ser
1 5

<210> 136
<211> 24
<212> DNA
<213> Artificial

<220>
<223> hSH357-1-T3L CDRL3

<220>
<221> CDS
<222> (1)..(24)

<400> 136
ttc cag ggc agc cac gtg ccc tac
Phe Gln Gly Ser His Val Pro Tyr
1 5

24

<210> 137
<211> 8
<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 137

Phe Gln Gly Ser His Val Pro Tyr
1 5

<210> 138

<211> 1407

<212> DNA

<213> Artificial

<220>

<223> hsh357-1-T1H

<220>

<221> CDS

<222> (1)..(1407)

<220>

<221> sig_peptide

<222> (1)..(57)

<400> 138

atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg 48
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

gtg ctg agc cag gtg cag ctg gtg cag tcc ggc gcc gag gtg aag aag 96
Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

ccc ggc gcc tcc gtg aag gtg tcc tgt aag gcc tcc ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

atc gac tac tcc atg cac tgg gtg agg cag gcc ccc ggc cag gcc ctg 192
Ile Asp Tyr Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
50 55 60

gag tgg atg ggc tgg atc aac acc tac acc ggc gag ccc acc tac tcc 240
Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser
65 70 75 80

gac gac ttc aag ggc agg gtg acc atc acc gcc gac acc tcc acc agc 288
Asp Asp Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
85 90 95

acc gcc tac ctg gag ctg tcc tcc ctg agg tcc gag gac acc gcc gtg 336
Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

tac tac tgt gcc acc tac tac agg tac gag agg gac ttc gac tac tgg 384
Tyr Tyr Cys Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp
115 120 125

ggc cag ggc acc ctg gtg acc gtg agc tca gcc tcc acc aag ggc cca 432
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca 480
Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160

gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc	528
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr	
	165
	170
	175
gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc	576
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro	
	180
	185
	190
gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc	624
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr	
	195
	200
	205
gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat	672
Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn	
	210
	215
	220
cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct	720
His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser	
	225
	230
	235
	240
tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg	768
Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu	
	245
	250
	255
ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc	816
Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu	
	260
	265
	270
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc	864
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser	
	275
	280
	285
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag	912
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu	
	290
	295
	300
gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg	960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
	305
	310
	315
	320
tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
	325
	330
	335
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc	1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro	
	340
	345
	350
atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag	1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	
	355
	360
	365
gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc	1152
Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val	
	370
	375
	380
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg	1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val	
	385
	390
	395
	400
gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct	1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro	
	405
	410
	415
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc	1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr	
	420
	425
	430

gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg 1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
435 440 445

atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg 1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
450 455 460

tct ccc ggc aaa tga 1407
Ser Pro Gly Lys
465

<210> 139
<211> 468
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 139

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

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

Glu Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser
65 70 75 80

Asp Asp Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser
85 90 95

Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
130 135 140

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
145 150 155 160

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

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 340 345 350
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 370 375 380
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

Ser Pro Gly Lys
 465

<210> 140
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T1H CDRH1

<220>
 <221> CDS
 <222> (1)..(18)

<400> 140
 atc gac tac tcc atg cac
 Ile Asp Tyr Ser Met His
 1 5

18

<210> 141
 <211> 6
 <212> PRT
 <213> Artificial

<220>
 <223> synthetic Construct

<400> 141

Ile Asp Tyr Ser Met His
 1 5

<210> 142
 <211> 51
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T1H CDRH2

<220>
 <221> CDS
 <222> (1)..(51)

<400> 142
 tgg atc aac acc tac acc ggc gag ccc acc tac tcc gac gac ttc aag
 Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys
 1 5 10 15

48

ggc
 Gly

51

<210> 143
 <211> 17
 <212> PRT
 <213> Artificial

<220>
<223> Synthetic Construct

<400> 143

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys
1 5 10 15

Gly

<210> 144
<211> 30
<212> DNA
<213> Artificial

<220>
<223> hSH357-1-T1H CDRH3

<220>
<221> CDS
<222> (1)..(30)

<400> 144
tac tac agg tac gag agg gac ttc gac tac
Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
1 5 10

30

<210> 145
<211> 10
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 145

Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
1 5 10

<210> 146
<211> 1407
<212> DNA
<213> Artificial

<220>
<223> hSH357-1-T3H

<220>
<221> CDS
<222> (1)..(1407)

<220>
<221> sig_peptide
<222> (1)..(57)

<400> 146
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
1 5 10 15

48

gtg ctg agc cag atc cag ctg gtg cag tcc ggc gcc gag gtg aag aag Val Leu Ser Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys 20 25 30	96
ccc ggc gcc tcc gtg aag gtg tcc tgt aag gcc tcc ggc tac acc ttc Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe 35 40 45	144
atc gac tac tcc atg cac tgg gtg agg cag gcc ccc ggc cag ggc ctg Ile Asp Tyr Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu 50 55 60	192
aag tgg atg ggc tgg atc aac acc tac acc ggc gag ccc acc tac tcc Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser 65 70 75 80	240
gac gac ttc aag ggc agg ttc gcc ttc tcc ctg gac acc tcc acc agc Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Thr Ser 85 90 95	288
acc gcc tac ctg gag ctg tcc tcc ctg agg tcc gag gac acc gcc gtg Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val 100 105 110	336
tac tac tgt gcc acc tac tac agg tac gag agg gac ttc gac tac tgg Tyr Tyr Cys Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp 115 120 125	384
ggc cag ggc acc ctg gtg acg gtg agc tca gcc tcc acc aag ggc cca Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro 130 135 140	432
agc gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct ggc ggc aca Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr 145 150 155 160	480
gcc gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa ccc gtg acc Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr 165 170 175	528
gtg agc tgg aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccc Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro 180 185 190	576
gct gtc ctg cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr 195 200 205	624
gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn 210 215 220	672
cac aag ccc agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser 225 230 235 240	720
tgt gac aaa act cac aca tgc cca ccc tgc cca gca cct gaa ctc ctg Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 245 250 255	768
ggg gga ccc tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu 260 265 270	816
atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser 275 280 285	864

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 290 295 300	912
gtg cat aat gcc aag aca aag ccc cgg gag gag cag tac aac agc acg Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 305 310 315 320	960
tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 325 330 335	1008
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 340 345 350	1056
atc gag aaa acc atc tcc aaa gcc aaa ggc cag ccc cgg gaa cca cag Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 355 360 365	1104
gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val 370 375 380	1152
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val 385 390 395 400	1200
gag tgg gag agc aat ggc cag ccc gag aac aac tac aag acc acc cct Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 405 410 415	1248
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr 420 425 430	1296
gtg gac aag agc agg tgg cag cag ggc aac gtc ttc tca tgc tcc gtg Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val 435 440 445	1344
atg cat gag gct ctg cac aac cac tac acc cag aag agc ctc tcc ctg Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 450 455 460	1392
tct ccc ggc aaa tga Ser Pro Gly Lys 465	1407

<210> 147
 <211> 468
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 147

Met Lys His Leu Trp Phe Phe Leu Leu Val Ala Ala Pro Arg Trp
 1 5 10 15

Val Leu Ser Gln Ile Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 20 25 30

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Ile Asp Tyr Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
 50 55 60
 Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser
 65 70 75 80
 Asp Asp Phe Lys Gly Arg Phe Ala Phe Ser Leu Asp Thr Ser Thr Ser
 85 90 95
 Thr Ala Tyr Leu Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Tyr Cys Ala Thr Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr Trp
 115 120 125
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140
 Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160
 Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175
 Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190
 Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205
 Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
 245 250 255
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 260 265 270
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 275 280 285
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 290 295 300

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 305 310 315 320

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 325 330 335

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 340 345 350

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 355 360 365

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 370 375 380

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 385 390 395 400

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 405 410 415

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 420 425 430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

Ser Pro Gly Lys
 465

<210> 148
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T3H CDRH1

<220>
 <221> CDS
 <222> (1)..(18)

<400> 148
 atc gac tac tcc atg cac
 Ile Asp Tyr Ser Met His
 1 5

18

<210> 149
 <211> 6
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct
 <400> 149

Ile Asp Tyr Ser Met His
 1 5

<210> 150
 <211> 51
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T3H CDRH2

<220>
 <221> CDS
 <222> (1)..(51)

<400> 150
 tgg atc aac acc tac acc ggc gag ccc acc tac tcc gac gac ttc aag 48
 Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys
 1 5 10 15

ggc 51
 Gly

<210> 151
 <211> 17
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct
 <400> 151

Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ser Asp Asp Phe Lys
 1 5 10 15

Gly

<210> 152
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T3H CDRH3

<220>
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 <222> (1)..(30)

<400> 152
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 Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

<210> 153
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 153

Tyr Tyr Arg Tyr Glu Arg Asp Phe Asp Tyr
 1 5 10

<210> 154
 <211> 520
 <212> DNA
 <213> Artificial

<220>
 <223> IgGL constant+signal

<400> 154
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 tgcagaccca ggtgttcac tccctgctgc tgtggatctc cggcgcataat ggcgatatcg 120
 tgatgattaa acgtacggtg gccgccccct ccgtgttcac cttccccccc tccgacgagc 180
 agctgaagtc cggcaccgcc tccgtggtgt gcctgctgaa taactttctac cccagagagg 240
 ccaagggtgca gtggaagggtg gacaacgccc tgcagtccgg gaactcccag gagagcgtga 300
 ccgagcagga cagcaaggac agcacctaca gcctgagcag caccctgacc ctgagcaaag 360
 ccgactacga gaagcacaag gtgtacgcct gcgaggtgac ccaccagggc ctgagctccc 420
 ccgtcaccaa gagcttcaac agggggggagt gttagggggc cgtttaaacg ggtggcatcc 480
 ctgtgacccc tccccagtgc ctctcctggc cctggaagtt 520

<210> 155
 <211> 1140
 <212> DNA
 <213> Artificial

<220>
 <223> IgGH constant+signal

<400> 155
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 gttagctcag ctccaccaa gggcccaagc gtcttcccc tggcaccctc ctccaagagc 180
 acctctggcg gcacagccgc cctgggctgc ctggtcaagg actacttccc cgaaccctgt 240
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 cagtcctcag gactctactc cctcagcagc gtggtgaccg tgccctccag cagcttgggc 360
 acccagacct acatctgcaa cgtgaatcac aagcccagca acaccaaggt ggacaagaga 420
 gttgagccca aatcttgtga caaaactcac acatgcccac cctgcccagc acctgaactc 480

ctgggggggac cctcagtctt cctcttcccc ccaaaaccca aggacaccct catgatctcc	540
cggaccccctg aggtcacatg cgtgggtggtg gacgtgagcc acgaagaccc tgagggtcaag	600
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cagtacaaca gcacgtaccg ggtggtcagc gtcttcaccg tcctgcacca ggactggctg	720
aatggcaagg agtacaagtg caaggtctcc aacaaagccc tcccagcccc catcgagaaa	780
accatctcca aagccaaagg ccagccccgg gaaccacagg tgtacaccct gcccccatcc	840
cgggaggaga tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc	900
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cctcccgtgc tggactccga cggctccttc ttctctaca gcaagctcac cgtggacaag	1020
agcaggtggc agcagggcaa cgtcttctca tgctccgtga tgcatgaggc tctgcacaac	1080
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<210> 156
 <211> 442
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T1L+signal

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caccgacttc accctgaaga tcagccgggt ggaggccgag gacgtgggcg tgtactactg	360
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<210> 157
 <211> 442
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T3L+signal

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gacccccggc gagcccgct ccatcagctg ccggagcagc cagagcatcg tgcacagcaa	180
cggcaacacc tacctggagt ggtacctgca gaagcccggc cagagcccc agctgctgat	240
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caccgacttc accctgaaga tcagccgggt ggaggccgag gacgtgggcg tgtactactg 360
 cttccagggc tcccacgtgc cctacacctt cggccagggc accaagggtg agatcaagcg 420
 tacggtggcc gccccctccg tg 442

<210> 158
 <211> 460
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T1H+signal

<400> 158
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 cagcagcgtg aagggtgagct gcaaggccag cggctacacc ttcacccact acagcatgca 180
 ctgggtgcgg caggcccccg gccagggcct ggagtggatg ggctggatca acacctacac 240
 cggcgagccc acctacgccg acgacttcaa gggccgggtg accatcacccg ccgacacctc 300
 cacctccacc gcctacctgg aactgagcag cctgcgagc gaggacaccg ccgtgtacta 360
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 gaccgtgagc tcagcctcct ccaccaaggg cccctccgtg 460

<210> 159
 <211> 460
 <212> DNA
 <213> Artificial

<220>
 <223> hSH348-1-T3H+signal

<400> 159
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<210> 160
 <211> 442
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T1L+signal

<400> 160

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gacccccggc gagcccccca gcatcagctg ccggagcagc cagagcatcg tgcacagcag	180
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ctacaagggtg agcaaccggt tcagcggcgt gcccgaccgg ttcagcggca gcggcagcgg	300
caccgacttc accctgaaga tcagccgggt ggaggccgag gacgtgggcg tgtactactg	360
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<210> 161
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 <213> Artificial

<220>
 <223> hSH357-1-T3L+signal

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caccgacttc accctgaaga tcagccgggt ggaggccgag gacgtgggcg tgtactactg	360
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<210> 162
 <211> 460
 <212> DNA
 <213> Artificial

<220>
 <223> hSH357-1-T1H+signal

<400> 162	
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cggcgagccc acctactccg acgacttcaa gggcaggggtg accatcaccg ccgacacctc	300
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<220>
 <223> hSH357-1-T3H+signal

<400> 163
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 caccagcacc gcctacctgg agctgtcctc cctgaggtcc gaggacaccg ccgtgtacta 360
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