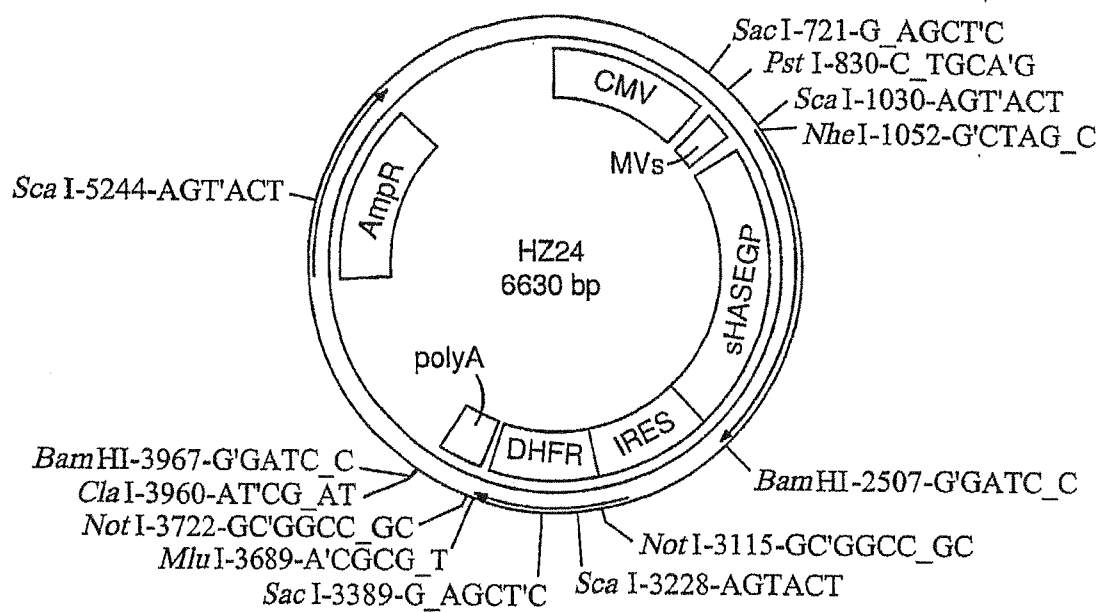




VECTOR MAP of sHASEGP VECTOR HZ24

FIG. 1

SEQUENCE LISTING

<110> HALOZYME, INC.

<120> SOLUBLE GLYCOSAMINOGLYCANASES AND METHODS OF PREPARING
AND USING SOLUBLE GLYCOSAMINOGLYCANASES

<130> SP8913B

<140> US 11/238,171

<141> 2005-09-27

<150> US 11/065,716

<151> 2005-02-23

<160> 53

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 509

<212> PRT

<213> Homo sapiens

<220>

<221> CARBOHYD

<222> 82, 166, 235, 254, 368, 393, 490

<400> 1

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

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145		150		155		160
Lys Asp Val Tyr	Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn					
	165		170		175	
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe						
	180		185		190	
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys						
	195		200		205	
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys						
	210		215		220	
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn						
	225		230		235	
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser						
	245		250		255	
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val						
	260		265		270	
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val						
	275		280		285	
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr						
	290		295		300	
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu						
	305		310		315	
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile						
	325		330		335	
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu						
	340		345		350	
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn						
	355		360		365	
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln						
	370		375		380	
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu						
	385		390		395	
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr						
	405		410		415	
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys						
	420		425		430	
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp						
	435		440		445	
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys						
	450		455		460	
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile						
	465		470		475	
Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val						
	485		490		495	
Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu						
	500		505			

<210> 2
 <211> 35
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr
 35

<210> 3
 <211> 474
 <212> PRT
 <213> Homo sapiens

<400> 3
 Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro Phe Leu Trp
 1 5 10 15
 Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe Asp Glu Pro
 20 25 30
 Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg Ile Asn Ala
 35 40 45
 Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu Gly Tyr Tyr
 50 55 60
 Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly Gly Ile Pro
 65 70 75 80
 Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile
 85 90 95
 Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp
 100 105 110
 Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val
 115 120 125
 Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu
 130 135 140
 Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala
 145 150 155 160
 Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg
 165 170 175
 Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His
 180 185 190
 His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile
 195 200 205
 Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu
 210 215 220
 Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr
 225 230 235 240
 Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile
 245 250 255
 Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val
 260 265 270
 Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr
 275 280 285
 Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp
 290 295 300
 Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp
 305 310 315 320
 Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu
 325 330 335
 Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys
 340 345 350
 Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp
 355 360 365
 Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly
 370 375 380
 Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys
 385 390 395 400
 Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp
 405 410 415
 Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala

	420		425		430										
Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gln	Ile	Phe	Tyr	Asn
	435							440					445		
Ala	Ser	Pro	Ser	Thr	Leu	Ser	Ala	Thr	Met	Phe	Ile	Val	Ser	Ile	Leu
	450						455						460		
Phe	Leu	Ile	Ile	Ser	Ser	Val	Ala	Ser	Leu						
465						470									

<210> 4
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 4

Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro	Phe	Leu	Trp
1				5					10					15	
Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe	Asp	Glu	Pro
		20						25					30		
Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	Ile	Asn	Ala
		35					40					45			
Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	Gly	Tyr	Tyr
	50					55				60					
Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	Gly	Ile	Pro
65					70					75				80	
Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	Lys	Asp	Ile
			85					90						95	
Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	Ile	Asp	Trp
			100					105					110		
Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	Lys	Asp	Val
		115					120					125			
Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	Val	Gln	Leu
	130					135					140				
Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	Glu	Lys	Ala
145				150					155					160	
Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	Leu	Leu	Arg
			165					170					175		
Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	Tyr	Asn	His
		180					185						190		
His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	Val	Glu	Ile
	195						200					205			
Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	Thr	Ala	Leu
	210					215					220				
Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	Ala	Ala	Thr
225					230					235				240	
Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	Ser	Lys	Ile
			245						250					255	
Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	Arg	Ile	Val
		260						265					270		
Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	Leu	Val	Tyr
	275						280					285			
Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	Val	Ile	Trp
	290					295					300				
Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	Leu	Leu	Asp
305				310					315					320	
Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	Val	Thr	Leu
			325						330					335	
Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	Gly	Val	Cys
		340						345					350		
Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	Asn	Pro	Asp

355	360	365
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly		
370	375	380
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys		
385	390	395
Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp Val Lys Asp		400
	405	410
Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys Ile Asp Ala		415
	420	425
Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile Phe Tyr Asn		430
435	440	445

<210> 5
 <211> 482
 <212> PRT
 <213> Homo sapiens

<400> 5

Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys		
1	5	10
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys		15
	20	25
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro		30
	35	40
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe		45
	50	55
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg		60
65	70	75
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu		80
	85	90
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly		95
	100	105
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys		110
	115	120
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val		125
	130	135
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro		140
145	150	155
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn		160
	165	170
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe		175
	180	185
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys		190
	195	200
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys		205
	210	215
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn		220
225	230	235
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser		240
	245	250
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val		255
	260	265
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val		270
	275	280
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr		285
	290	295
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu		300
305	310	315
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile		320

325 330 335
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
 465 470 475 480
 Phe Tyr

<210> 6
 <211> 1530
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1530)
 <223> PH-20 GPI Anchored Hyaluronidase Glycoprotein

<400> 6
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 Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 tca agt gga gta tcc cag ata gtt ttc acc ttc ctt ctg att cca tgt 96
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 tgc ttg act ctg aat ttc aga gca cct cct gtt att cca aat gtg cct 144
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 ttc ctc tgg gcc tgg aat gcc cca agt gaa ttt tgt ctt gga aaa ttt 192
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60
 gat gag cca cta gat atg agc ctc ttc tct ttc ata gga agc ccc cga 240
 Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 65 70 75 80
 ata aac gcc acc ggg caa ggt gtt aca ata ttt tat gtt gat aga ctt 288
 Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 85 90 95
 ggc tac tat cct tac ata gat tca atc aca gga gta act gtg aat gga 336
 Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly

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

340	345	350	
ctc cta gac aat tac atg gag act ata ctg aat cct tac ata atc aac			1104
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn			
355	360	365	
gtc aca cta gca gcc aaa atg tgt agc caa gtg ctt tgc cag gag caa			1152
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln			
370	375	380	
gga gtg tgt ata agg aaa aac tgg aat tca agt gac tat ctt cac ctc			1200
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu			
385	390	395	400
aac cca gat aat ttt gct att caa ctt gag aaa ggt gga aag ttc aca			1248
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr			
405	410	415	
gta cgt gga aaa ccg aca ctt gaa gac ctg gag caa ttt tct gaa aaa			1296
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys			
420	425	430	
ttt tat tgc agc tgt tat agc acc ttg agt tgt aag gag aaa gct gat			1344
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp			
435	440	445	
gta aaa gac act gat gct gtt gat gtg tgt att gct gat ggt gtc tgt			1392
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys			
450	455	460	
ata gat gct ttt cta aaa cct ccc atg gag aca gaa gaa cct caa att			1440
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile			
465	470	475	480
ttc tac aat gct tca ccc tcc aca cta tct gcc aca atg ttc att gtt			1488
Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val			
485	490	495	
agt att ttg ttt ctt atc att tct tct gta gcg agt ttg taa			1530
Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu *			
500	505		

<210> 7
 <211> 509
 <212> PRT
 <213> Homo sapiens

<220>
 <221> CARBOHYD
 <222> 82, 166, 235, 254, 368, 393, 490

<400> 7
 Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45

Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
50 55 60
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65 70 75 80
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
85 90 95
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
100 105 110
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
115 120 125
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
130 135 140
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
145 150 155 160
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
165 170 175
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
180 185 190
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
195 200 205
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
210 215 220
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
225 230 235 240
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
245 250 255
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
260 265 270
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
275 280 285
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
290 295 300
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
305 310 315 320
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
325 330 335
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
340 345 350
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
355 360 365
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
370 375 380
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
385 390 395 400
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
405 410 415
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
420 425 430
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
435 440 445
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
450 455 460
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gln Ile
465 470 475 480
Phe Tyr Asn Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val
485 490 495
Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
500 505

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<210> 8
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer to generate GPI anchor lacking N483
      and terminating at Y482 with BamHI site in the 5'
      end

<400> 8
aattggatcc tcagtagaaa atttgaggtt cttc
34

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer to generate GPI anchor lacking Y482
      and terminating at F481 with BamHI site in the 5'
      end

<400> 9
aattggatcc tcagaaaatt tgaggttctt ctg
33

<210> 10
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer to generate GPI anchor lacking F481
      and terminating at I480 with BamHI site in the 5'
      end

<400> 10
aattggatcc tcaaatttga ggttcttctg tctc
34

<210> 11
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer to generate GPI anchor lacking I480
      and terminating at Q479 with BamHI site in the 5'
      end

<400> 11
aattggatcc tcattgaggt tcttctgtct cc
32

<210> 12
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer to generate GPI anchor lacking Q479
      and terminating at P478 with BamHI site in the 5'

```

```

end

<400> 12
aattggatcc tcaaggttct tctgtctcca tg 32

<210> 13
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse Primer to generate GPI anchor lacking P478
and terminating at E477 with BamHI site in the 5'
end

<400> 13
aattggatcc tcattcttct gtctccatgg g 31

<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward Primer with NheI restriction site at 5'
end

<400> 14
aattgctagc atgggagtg c taaaattcaa gc 32

<210> 15
<211> 1473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1473)
<223> sHASEGPup to P478 and His Tagged

<400> 15
atg gga gtg cta aaa ttc aag cac atc ttt ttc aga agc ttt gtt aaa 48
Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
1 5 10 15

tca agt gga gta tcc cag ata gtt ttc acc ttc ctt ctg att cca tgt 96
Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
20 25 30

tgc ttg act ctg aat ttc aga gca cct cct gtt att cca aat gtg cct 144
Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
35 40 45

ttc ctc tgg gcc tgg aat gcc cca agt gaa ttt tgt ctt gga aaa ttt 192
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
50 55 60

gat gag cca cta gat atg agc ctc ttc tct ttc ata gga agc ccc cga 240
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
65 70 75 80

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ata aac gcc acc ggg caa ggt gtt aca ata ttt tat gtt gat aga ctt	288
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu	
85 90 95	
ggc tac tat cct tac ata gat tca atc aca gga gta act gtg aat gga	336
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly	
100 105 110	
gga atc ccc cag aag att tcc tta caa gac cat ctg gac aaa gct aag	384
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys	
115 120 125	
aaa gac att aca ttt tat atg cca gta gac aat ttg gga atg gct gtt	432
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val	
130 135 140	
att gac tgg gaa gaa tgg aga ccc act tgg gca aga aac tgg aaa cct	480
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro	
145 150 155 160	
aaa gat gtt tac aag aat agg tct att gaa ttg gtt cag caa caa aat	528
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn	
165 170 175	
gta caa ctt agt ctc aca gag gcc act gag aaa gca aaa caa gaa ttt	576
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe	
180 185 190	
gaa aag gca ggg aag gat ttc ctg gta gag act ata aaa ttg gga aaa	624
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys	
195 200 205	
tta ctt cgg cca aat cac ttg tgg ggt tat tat ctt ttt ccg gat tgt	672
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys	
210 215 220	
tac aac cat cac tat aag aaa ccc ggt tac aat gga agt tgc ttc aat	720
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn	
225 230 235 240	
gta gaa ata aaa aga aat gat gat ctc agc tgg ttg tgg aat gaa agc	768
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser	
245 250 255	
act gct ctt tac cca tcc att tat ttg aac act cag cag tct cct gta	816
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val	
260 265 270	
gct gct aca ctc tat gtg cgc aat cga gtt cgg gaa gcc atc aga gtt	864
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val	
275 280 285	
tcc aaa ata cct gat gca aaa agt cca ctt ccg gtt ttt gca tat acc	912
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr	
290 295 300	
cgc ata gtt ttt act gat caa gtt ttg aaa ttc ctt tct caa gat gaa	960
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu	
305 310 315 320	

ctt gtg tat aca ttt ggc gaa act gtt gct ctg ggt gct tct gga att 1008
 Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 325 330 335
 gta ata tgg gga acc ctc agt ata atg cga agt atg aaa tct tgc ttg 1056
 Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 340 345 350
 ctc cta gac aat tac atg gag act ata ctg aat cct tac ata atc aac 1104
 Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 355 360 365
 gtc aca cta gca gcc aaa atg tgt agc caa gtg ctt tgc cag gag caa 1152
 Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 370 375 380
 gga gtg tgt ata agg aaa aac tgg aat tca agt gac tat ctt cac ctc 1200
 Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 385 390 395 400
 aac cca gat aat ttt gct att caa ctt gag aaa ggt gga aag ttc aca 1248
 Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 405 410 415
 gta cgt gga aaa ccg aca ctt gaa gac ctg gag caa ttt tct gaa aaa 1296
 Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 420 425 430
 ttt tat tgc agc tgt tat agc acc ttg agt tgt aag gag aaa gct gat 1344
 Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 435 440 445
 gta aaa gac act gat gct gtt gat gtg tgt att gct gat ggt gtc tgt 1392
 Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 450 455 460
 ata gat gct ttt cta aaa cct ccc atg gag aca gaa gaa cct gga tcc 1440
 Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro Gly Ser
 465 470 475 480
 ggt tct ggt gct cac cat cac cat cac cat taa 1473
 Gly Ser Gly Ala His His His His His His *
 485 490

<210> 16
 <211> 490
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Gly Val Leu Lys Phe Lys His Ile Phe Phe Arg Ser Phe Val Lys
 1 5 10 15
 Ser Ser Gly Val Ser Gln Ile Val Phe Thr Phe Leu Leu Ile Pro Cys
 20 25 30
 Cys Leu Thr Leu Asn Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 35 40 45
 Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 50 55 60

Asp	Glu	Pro	Leu	Asp	Met	Ser	Leu	Phe	Ser	Phe	Ile	Gly	Ser	Pro	Arg	65	70	75	80
Ile	Asn	Ala	Thr	Gly	Gln	Gly	Val	Thr	Ile	Phe	Tyr	Val	Asp	Arg	Leu	85	90	95	
Gly	Tyr	Tyr	Pro	Tyr	Ile	Asp	Ser	Ile	Thr	Gly	Val	Thr	Val	Asn	Gly	100	105	110	
Gly	Ile	Pro	Gln	Lys	Ile	Ser	Leu	Gln	Asp	His	Leu	Asp	Lys	Ala	Lys	115	120	125	
Lys	Asp	Ile	Thr	Phe	Tyr	Met	Pro	Val	Asp	Asn	Leu	Gly	Met	Ala	Val	130	135	140	
Ile	Asp	Trp	Glu	Glu	Trp	Arg	Pro	Thr	Trp	Ala	Arg	Asn	Trp	Lys	Pro	145	150	155	160
Lys	Asp	Val	Tyr	Lys	Asn	Arg	Ser	Ile	Glu	Leu	Val	Gln	Gln	Gln	Asn	165	170	175	
Val	Gln	Leu	Ser	Leu	Thr	Glu	Ala	Thr	Glu	Lys	Ala	Lys	Gln	Glu	Phe	180	185	190	
Glu	Lys	Ala	Gly	Lys	Asp	Phe	Leu	Val	Glu	Thr	Ile	Lys	Leu	Gly	Lys	195	200	205	
Leu	Leu	Arg	Pro	Asn	His	Leu	Trp	Gly	Tyr	Tyr	Leu	Phe	Pro	Asp	Cys	210	215	220	
Tyr	Asn	His	His	Tyr	Lys	Lys	Pro	Gly	Tyr	Asn	Gly	Ser	Cys	Phe	Asn	225	230	235	240
Val	Glu	Ile	Lys	Arg	Asn	Asp	Asp	Leu	Ser	Trp	Leu	Trp	Asn	Glu	Ser	245	250	255	
Thr	Ala	Leu	Tyr	Pro	Ser	Ile	Tyr	Leu	Asn	Thr	Gln	Gln	Ser	Pro	Val	260	265	270	
Ala	Ala	Thr	Leu	Tyr	Val	Arg	Asn	Arg	Val	Arg	Glu	Ala	Ile	Arg	Val	275	280	285	
Ser	Lys	Ile	Pro	Asp	Ala	Lys	Ser	Pro	Leu	Pro	Val	Phe	Ala	Tyr	Thr	290	295	300	
Arg	Ile	Val	Phe	Thr	Asp	Gln	Val	Leu	Lys	Phe	Leu	Ser	Gln	Asp	Glu	305	310	315	320
Leu	Val	Tyr	Thr	Phe	Gly	Glu	Thr	Val	Ala	Leu	Gly	Ala	Ser	Gly	Ile	325	330	335	
Val	Ile	Trp	Gly	Thr	Leu	Ser	Ile	Met	Arg	Ser	Met	Lys	Ser	Cys	Leu	340	345	350	
Leu	Leu	Asp	Asn	Tyr	Met	Glu	Thr	Ile	Leu	Asn	Pro	Tyr	Ile	Ile	Asn	355	360	365	
Val	Thr	Leu	Ala	Ala	Lys	Met	Cys	Ser	Gln	Val	Leu	Cys	Gln	Glu	Gln	370	375	380	
Gly	Val	Cys	Ile	Arg	Lys	Asn	Trp	Asn	Ser	Ser	Asp	Tyr	Leu	His	Leu	385	390	395	400
Asn	Pro	Asp	Asn	Phe	Ala	Ile	Gln	Leu	Glu	Lys	Gly	Gly	Lys	Phe	Thr	405	410	415	
Val	Arg	Gly	Lys	Pro	Thr	Leu	Glu	Asp	Leu	Glu	Gln	Phe	Ser	Glu	Lys	420	425	430	
Phe	Tyr	Cys	Ser	Cys	Tyr	Ser	Thr	Leu	Ser	Cys	Lys	Glu	Lys	Ala	Asp	435	440	445	
Val	Lys	Asp	Thr	Asp	Ala	Val	Asp	Val	Cys	Ile	Ala	Asp	Gly	Val	Cys	450	455	460	
Ile	Asp	Ala	Phe	Leu	Lys	Pro	Pro	Met	Glu	Thr	Glu	Glu	Pro	Gly	Ser	465	470	475	480
Gly	Ser	Gly	Ala	His	His	His	His	His	His	His	His	His	His	His	His	485	490		

<210> 17

<211> 39

<212> DNA

<213> Artificial Sequence

<220>
 <223> SpacerHisFor Primer

 <400> 17
 ataattggat ccggttctgg tgctcaccat caccatcac 39

 <210> 18
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> SpacerHisRev Primer

 <400> 18
 tataattgcg gccgcctaata ggtgatggcg atggcgag 38

 <210> 19
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' REVERSE PRIMER WITHOUT STOP CODON FOR
 GENERATING truncation product HIS-sHASEGP lacking GPI
 anchor and ending at N 483

 <400> 19
 aatggatcca ttgtagaaaa tttgaggttc 30

 <210> 20
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' REVERSE PRIMER WITHOUT STOP CODON FOR
 GENERATING truncation product HIS-sHASEGP lacking GPI
 anchor and ending at Y 482

 <400> 20
 aatggatccg tagaaaattt gaggttcttc 30

 <210> 21
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> 3' REVERSE PRIMER WITHOUT STOP CODON FOR
 GENERATING truncation product HIS-sHASEGP lacking GPI
 anchor and ending at F 481

 <400> 21
 aattggatcc gaaaatttga ggttctctcg 30

 <210> 22
 <211> 30
 <212> DNA

<213> Artificial Sequence

<220>

<223> 3' REVERSE PRIMER WITHOUT STOP CODON FOR
GENERATING truncation product HIS-sHASEGP lacking GPI
anchor and ending at I 480

<400> 22

attggatcca atttgaggtt cttctgtctc

30

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' REVERSE PRIMER WITHOUT STOP CODON FOR
GENERATING truncation product HIS-sHASEGP lacking GPI
anchor and ending at Q 479

<400> 23

aattggatcc ttgaggttct tctgtctcc

29

<210> 24

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' REVERSE PRIMER WITHOUT STOP CODON FOR
GENERATING truncation product HIS-sHASEGP lacking GPI
anchor and ending at P 478

<400> 24

aattggatcc aggttcttct gtctccatg

29

<210> 25

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' REVERSE PRIMER WITHOUT STOP CODON FOR
GENERATING truncation product HIS-sHASEGP lacking GPI
anchor and ending at E 477

<400> 25

aattggatcc ttcttctgtc tccatggg

28

<210> 26

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Reverse primer to amplify sHASEGP deletion mutant
ending at A 467

<400> 26

aattggatcc ctaagcatct atacagacac catcag

36

<210> 27
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse primer to amplify SHASEGP deletion mutant
 ending at A 447

 <400> 27
 aattggatcc ctaagctttc tccttacaac tcaag 35

 <210> 28
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse primer to amplify SHASEGP deletion mutant
 ending at S 430

 <400> 28
 aattggatcc ctaagaaaat tgctccaggt ctcc 34

 <210> 29
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse primer to amplify SHASEGP deletion mutant
 ending at G 413

 <400> 29
 aattggatcc ctatccacct ttctcaagtt gaatag 36

 <210> 30
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse primer to amplify SHASEGP deletion mutant
 ending at S 394

 <400> 30
 aattggatcc ctatgaattc cagtttttcc ttatac 36

 <210> 31
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse primer to amplify SHASEGP deletion mutant
 ending at A 372

 <400> 31
 aattggatcc ctatgctagt gtgacgttga ttatg 35

<210> 32
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Reverse primer to amplify sHASEGP deletion mutant
 ending at S 347

 <400> 32
 aattggatcc ctaacttcgc attatactga ggg 33

 <210> 33
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> LN forward primer for site directed mutagenesis to
 generate sHASEGP fusion with kappa leader with L 36
 as the first sHASEGP amino acid after the kappa
 leader

 <400> 33
 ctgaatttca gagcacctcc tggtattcc 29

 <210> 34
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> FR forward primer for site directed mutagenesis to
 generate sHASEGP fusion with kappa leader with F 38
 as the first sHASEGP amino acid after the kappa
 leader

 <400> 34
 ttcagagcac ctctgttat tccaaatg 28

 <210> 35
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Asp reverse primer for site directed mutagenesis
 to generate sHASEGP fusion with kappa leader with
 Asp as the last Kappa leader amino acid before L
 36 or F 38 of PH-20

 <400> 35
 gtcaccagtg gaacctggaa ccc 23

 <210> 36
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gly reverse primer for site directed mutagenesis
 to generate SHASEGP fusion with kappa leader with
 Gly as the last Kappa leader amino acid before L
 36 or F 38 of PH-20

<400> 36
 accagtggaa cctggaaccc agag 24

<210> 37
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for first fragment of kappa leader

<400> 37
 gagacagaca cactcctgct atgggtactg 30

<210> 38
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer for first fragment of kappa leader

<400> 38
 cccagagcag cagtacccat agcaggagtg 30

<210> 39
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer for second fragment of kappa leader

<400> 39
 ggtactgctg ctctgggttc caggttccac 30

<210> 40
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer for second fragment of kappa leader

<400> 40
 gcgtcaccag tggaacctgg aacccag 27

<210> 41
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nhe Forward primer for kappa leader

<400> 41
 attgctagca tggagacaga cacactcctg 30

 <210> 42
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> EcoR1 reverse primer for kappa leader

 <400> 42
 aattgaattc gtcaccagtg gaacctgg 28

 <210> 43
 <211> 21
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Mouse IgK-chain leader sequence

 <400> 43
 Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15
 Gly Ser Thr Gly Asp
 20

 <210> 44
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> K-leader SPE 1 FORWARD Primer

 <400> 44
 actcactagt gctagcatgg agacagacac 30

 <210> 45
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> K-leader MLU1 REV primer

 <400> 45
 aattacgcgt gaattcgtca ccagtggaac 30

 <210> 46
 <211> 462
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Kappa leader fusion protein with SHASEGP with F 38
 as the first amino acid of the putative mature

secreted sHASEGP (up to P478)

<400> 46

```

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1          5          10          15
Gly Ser Thr Gly Asp Phe Arg Ala Pro Pro Val Ile Pro Asn Val Pro
 20          25          30
Phe Leu Trp Ala Trp Asn Ala Pro Ser Glu Phe Cys Leu Gly Lys Phe
 35          40          45
Asp Glu Pro Leu Asp Met Ser Leu Phe Ser Phe Ile Gly Ser Pro Arg
 50          55          60
Ile Asn Ala Thr Gly Gln Gly Val Thr Ile Phe Tyr Val Asp Arg Leu
 65          70          75          80
Gly Tyr Tyr Pro Tyr Ile Asp Ser Ile Thr Gly Val Thr Val Asn Gly
 85          90          95
Gly Ile Pro Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys
 100          105          110
Lys Asp Ile Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val
 115          120          125
Ile Asp Trp Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro
 130          135          140
Lys Asp Val Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn
 145          150          155          160
Val Gln Leu Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe
 165          170          175
Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys
 180          185          190
Leu Leu Arg Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys
 195          200          205
Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
 210          215          220
Val Glu Ile Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser
 225          230          235          240
Thr Ala Leu Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val
 245          250          255
Ala Ala Thr Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val
 260          265          270
Ser Lys Ile Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr
 275          280          285
Arg Ile Val Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu
 290          295          300
Leu Val Tyr Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile
 305          310          315          320
Val Ile Trp Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu
 325          330          335
Leu Leu Asp Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn
 340          345          350
Val Thr Leu Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln
 355          360          365
Gly Val Cys Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu
 370          375          380
Asn Pro Asp Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr
 385          390          395          400
Val Arg Gly Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys
 405          410          415
Phe Tyr Cys Ser Cys Tyr Ser Thr Leu Ser Cys Lys Glu Lys Ala Asp
 420          425          430
Val Lys Asp Thr Asp Ala Val Asp Val Cys Ile Ala Asp Gly Val Cys
 435          440          445
Ile Asp Ala Phe Leu Lys Pro Pro Met Glu Thr Glu Glu Pro

```

450

455

460

<210> 47

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer BAM REV sHASEGP with GPI anchor up to L
509 including STOP

<400> 47

aattggatcc ctacagaaga aatgataaga aacaaaatac

40

<210> 48

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 48

atgggagtg taaaattcaa gcacatcttt ttcagaagct ttgttaaattc aagtggagta 60
 toccagatag ttttcacett ccttctgatt ccatgttgct tgactctgaa tttcagagca 120
 cctcctgtta ttocaaatgt gcctttcctc tgggcctgga atgccccaaag tgaattttgt 180
 cttggaaaat ttgatgagcc actagatatg agcctcttct ctttcatagg aagccccoga 240
 ataaacgcca cggggcaagg tggtacaata ttttatgttg atagacttgg ctactatcct 300
 tacatagatt caatcacagg agtaactgtg aatggaggaa toccccagaa gatttcctta 360
 caagaccatc tggacaaagc taagaaagac attacatttt atatgccagt agacaatttg 420
 ggaatggctg ttattgactg ggaagaatgg agaccactt gggcaagaaa ctggaaacct 480
 aaagatgttt acaagaatag gtctattgaa ttgggttcagc aacaaaatgt acaacttagt 540
 ctacagagg ccactgagaa agcaaaaaca gaatttgaaa aggcaggga ggatttcctg 600
 gtagagacta taaaattggg aaaattactt cggccaaatc acttgtgggg ttattatctt 660
 ttccggatt gttacaacca tcactataag aaaccgggtt acaatggaag ttgcttcaat 720
 gtagaaaataa aaagaaatga tgatctcagc tgggtgtgga atgaaagcac tgctctttac 780
 ccatccattt atttgaacac tcagcagctc cctgtagctg ctacactcta tgtgcgcaat 840
 cgagttcggg aagccatcag agtttccaaa atacctgatg caaaaagtcc acttcgggtt 900
 tttgcatata ccgcgatagt ttttactgat caagttttga aattcctttc tcaagatgaa 960
 ctttgtgtata catttggcga aactgttgct ctgggtgctt ctggaattgt aatatgggga 1020
 accctcagta taatgccaag tatgaaatct tgcttgctcc tagacaatta catggagact 1080
 atactgaatc cttacataat caacgtcaca ctacagcca aaatgtgtag ocaagtgtt 1140
 tgccaggagc aaggagtgtg tataaggaaa aactggaatt caagtgacta tcttcacctc 1200
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Glu Lys Ala Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys		190
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Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn		220
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<212> DNA

<213> Homo sapiens

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<212> DNA

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