

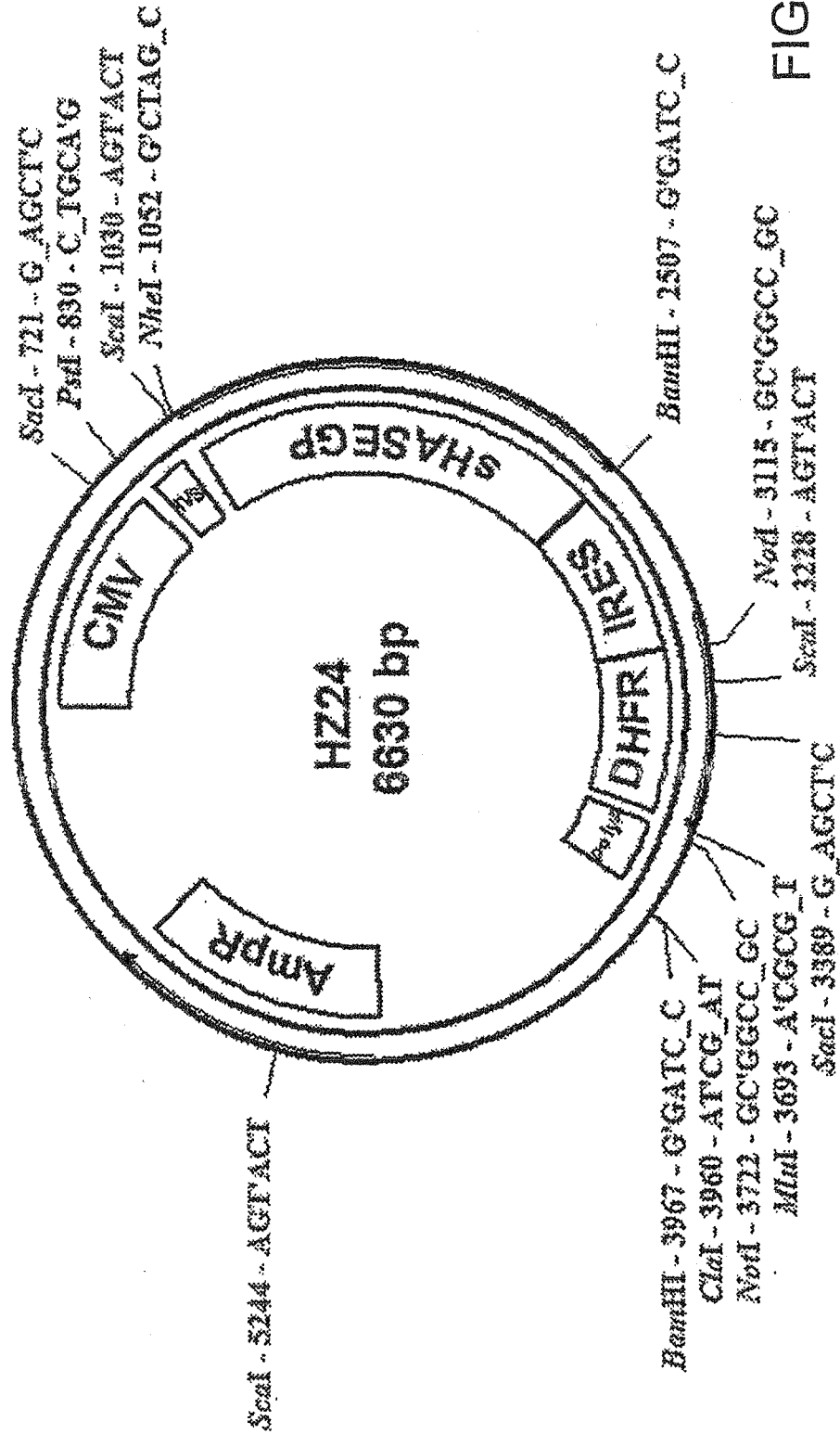


FIG. 1

Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	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

<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
Gln Lys Ile Ser Leu Gln Asp His Leu Asp Lys Ala Lys Lys Asp Ile				80
	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
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
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
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				
	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
 385 390 395 400
 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

<210> 5

<211> 482

<212> PRT

<213> Homo sapiens

<400> 5

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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
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

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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

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	
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 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 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

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<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 atttgagggtt cttc

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34

```

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

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

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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 atgggagtgcc 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	

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						
			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 gccgcctaatt ggtgatggtg atggtgag

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 ttgaggttc 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 ggttcttctg 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 cagttttttcc 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 attataactga 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 tgttattcc

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 ccagtggaaac

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 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									
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									
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

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atggggagtgc taaaattcaa gcacatcttt ttcagaagct ttgttaaadc aagtggagta 60
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cctcctgtta ttccaaatgt gcctttcttc tgggcctgga atgccccaaag tgaattttgt 180
cttggaaaat ttgatgagcc actagatatg agcctcttct ctttcatagg aagccccga 240
ataaacgcc aacgggcaagg tggtacaata ttttatgttg atagacttgg ctactatcct 300
tacatagatt caatcacagg agtaactgtg aatggaggaa tccccagaa gatttcctta 360
caagaccatc tggacaaagc taagaaagac attacatttt atatgccagt agacaatttg 420
ggaatggctg ttattgactg ggaagaatgg agaccactt gggcaagaaa ctggaaacct 480
aaagatgttt acaagaatag gtctattgaa ttggttcagc aacaaaatgt acaacttagt 540
ctcacagagg cactgagaa agcaaaacaa gaatttgaaa aggcagggaa ggatttcctg 600
gtagagacta taaaattggg aaaattactt cggccaaatc acttggtggg ttattatcct 660
tttcoggatt gttacaacca tcactataag aaaccgggtt acaatggaag ttgcttcaat 720

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gtagaaataa aaagaaatga tgatctcagc tggttgtgga atgaaagcac tgctctttac 780
ccatccattt atttgaacac tcagcagctc cctgtagctg ctacactcta tgtgcgcaat 840
cgagttcggg aagccatcag agtttccaaa atacctgatg caaaaagtcc acttccggtt 900
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