

SEQUENCE LISTING

<110> DeliaTroph Pharmaceuticals, Inc.

Frost, Gregory

Kundu, Anirban

Bookbinder, Louis

<120> SOLUBLE HYLAURONIDASE GLYCOPROTEIN (SHASEGP), PROCESS FOR PREPARING THE SAME, USES AND PHARMACEUTICAL COMPOSITIONS COMPRISING THEREOF

<130> DELIA1340WO

<150> US 60/452,360

<151> 2003-03-05

<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

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Cys	Leu	Thr	Leu	Asn	Phe	Arg	Ala	Pro	Pro	Val	Ile	Pro	Asn	Val	Pro
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Phe	Leu	Trp	Ala	Trp	Asn	Ala	Pro	Ser	Glu	Phe	Cys	Leu	Gly	Lys	Phe
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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
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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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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
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 Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
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<210> 2
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 <212> PRT
 <213> Homo sapiens

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 Cys Leu Thr
 35

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

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 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
Thr Phe Tyr Met Pro Val Asp Asn Leu Gly Met Ala Val Ile Asp Trp		95
	100	105
Glu Glu Trp Arg Pro Thr Trp Ala Arg Asn Trp Lys Pro Lys Asp Val		110
	115	120
Tyr Lys Asn Arg Ser Ile Glu Leu Val Gln Gln Gln Asn Val Gln Leu		125
	130	135
Ser Leu Thr Glu Ala Thr Glu Lys Ala Lys Gln Glu Phe Glu Lys Ala		140
145	150	155
Gly Lys Asp Phe Leu Val Glu Thr Ile Lys Leu Gly Lys Leu Leu Arg		160
	165	170
Pro Asn His Leu Trp Gly Tyr Tyr Leu Phe Pro Asp Cys Tyr Asn His		175
	180	185
His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn Val Glu Ile		190
	195	200
Lys Arg Asn Asp Asp Leu Ser Trp Leu Trp Asn Glu Ser Thr Ala Leu		205
	210	215
Tyr Pro Ser Ile Tyr Leu Asn Thr Gln Gln Ser Pro Val Ala Ala Thr		220
225	230	235
Leu Tyr Val Arg Asn Arg Val Arg Glu Ala Ile Arg Val Ser Lys Ile		240
	245	250
Pro Asp Ala Lys Ser Pro Leu Pro Val Phe Ala Tyr Thr Arg Ile Val		255
	260	265
Phe Thr Asp Gln Val Leu Lys Phe Leu Ser Gln Asp Glu Leu Val Tyr		270
	275	280
Thr Phe Gly Glu Thr Val Ala Leu Gly Ala Ser Gly Ile Val Ile Trp		285
	290	295
Gly Thr Leu Ser Ile Met Arg Ser Met Lys Ser Cys Leu Leu Leu Asp		300
305	310	315
Asn Tyr Met Glu Thr Ile Leu Asn Pro Tyr Ile Ile Asn Val Thr Leu		320
	325	330
Ala Ala Lys Met Cys Ser Gln Val Leu Cys Gln Glu Gln Gly Val Cys		335
	340	345
Ile Arg Lys Asn Trp Asn Ser Ser Asp Tyr Leu His Leu Asn Pro Asp		350
	355	360
Asn Phe Ala Ile Gln Leu Glu Lys Gly Gly Lys Phe Thr Val Arg Gly		365
	370	375
Lys Pro Thr Leu Glu Asp Leu Glu Gln Phe Ser Glu Lys Phe Tyr Cys		380
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
Ala Ser Pro Ser Thr Leu Ser Ala Thr Met Phe Ile Val Ser Ile Leu		445
	450	455
Phe Leu Ile Ile Ser Ser Val Ala Ser Leu		460
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
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 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

Met	Gly	Val	Leu	Lys	Phe	Lys	His	Ile	Phe	Phe	Arg	Ser	Phe	Val	Lys
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			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
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 Phe Tyr

<210> 6

<211> 1530

<212> DNA

<213> Homo sapiens

<220>

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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

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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

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 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

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 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
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 <212> PRT
 <213> Homo sapiens

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

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 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

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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
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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
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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
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Ser Ile Leu Phe Leu Ile Ile Ser Ser Val Ala Ser Leu
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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	
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 oca 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
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 Gly Ser		
465	470	475
Gly Ser Gly Ala His His His His His His		480
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 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 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 gggttcttctg

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 cttc

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 gaattcgta 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 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

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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

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<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 ttgttaaatac aagtggagta 60
tcccagatag ttttcacctt ccttctgatt ccatgttgct tgactctgaa tttcagagca 120
cctcctgtta ttccaaatgt gcctttcctc tgggcctgga atgccccaaag tgaattttgt 180
cttggaataat ttgatgagcc actagatatg agcctcttct ctttcatagg aagccccga 240
ataaacgccca cgggcaagg tgttacaata 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 agcaaaaaca gaatttgaaa aggcaaggaa ggatttcctg 600
gtagagacta taaaattggg aaaattactt cggccaaatc acttgtgggg ttattatctt 660
tttccggatt gttacaacca tcactataag aaaccgggtt acaatggaag ttgcttcaat 720

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gtagaaataa aaagaaatga tgatctcagc tgggttggtga atgaaagcac tgctctttac 780
ccatccattt atttgaacac tcagcagctc cctgtagctg ctacactcta tgtgcgcaat 840
cgagttcggg aagccatcag agttttccaaa atacctgatg caaaaagtcc acttccggtt 900
tttgcataata cccgcatagt ttttactgat caagttttga aattcctttc tcaagatgaa 960
cttgtgtata catttggcga aactgttgct ctgggtgctt ctggaattgt aatatgggga 1020
accctcagta taatgcgaag tatgaaatct tgcttgctcc tagacaatta catggagact 1080
atactgaatc cttacataat caacgtcaca ctagcagcca aaatgtgtag ccaagtgtt 1140
tgccaggagc aaggagtgtg tataaggaaa aactggaatt caagtgacta tcttcacctc 1200
aaccagata attttgctat tcaacttgag aaaggtggaa agttcacagt acgtggaaaa 1260
ccgacacttg aagacctgga gcaattttct gaaaaatttt attgcagctg ttatagcacc 1320
ttgagttgta aggagaaagc tgatgtaaaa gacactgatg ctgttgatgt gtgtattgct 1380
gatggtgtct gtatagatgc ttttctaaaa cctcccatgg agacagaaga acctcaaatt 1440
ttctactaa 1449

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<210> 49

<211> 467

<212> PRT

<213> Homo sapiens

<400> 49

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Tyr Asn His His Tyr Lys Lys Pro Gly Tyr Asn Gly Ser Cys Phe Asn
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