

SEQUENCE LISTING

<110> Hangzhou Sumgen Biotech Co., Ltd.
Sumgen Mab (Beijing) Biotech Co., Ltd.

<120> FUSION PROTEIN AND USE THEREOF

<130> 0070-PA-014SG

<160> 78

<170> PatentIn version 3.5

<210> 1

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> LCDR1 of SG003

<400> 1

Arg	Ala	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ala	Phe	Ser	Tyr	Val	His
1				5					10					15

<210> 2

<211> 7

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<223> LCDR2 of SG003

<400> 2

Leu	Ala	Ser	Asn	Leu	Glu	Ser
1				5		

<210> 3

<211> 9

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<220>

<223> LCDR3 of SG003

<400> 3

His His Ser Arg Glu Leu Pro Phe Thr
1 5

<210> 4
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<213> Artificial Sequence

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<223> HCDR1 of SG003

<400> 4

Leu Tyr Trp Met Asn
1 5

<210> 5
<211> 17
<212> PRT
<213> Artificial Sequence

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<223> HCDR2 of SG003

<400> 5

Lys Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu Lys
1 5 10 15

Asp

<210> 6
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3 of SG003

<400> 6

Leu Trp Ile Ala Thr Gly Gly Phe Asp Tyr
1 5 10

<210> 7
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of SG003

<400> 7

Glu Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

Ala Phe Ser Tyr Val His Trp Tyr Gln Gln Lys Ser Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

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

Pro Val Glu Ser Glu Asp Val Ala Thr Tyr Tyr Cys His His Ser Arg
85 90 95

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

<210> 8
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of SG003

<400> 8

Gln Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

[illegible]

accttcggca gcggcaccaa gctggagatc aag

333

<210> 10

<211> 357

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid encoding VH ofSG003

<400> 10

cagggtgcagc tgctggagag cggcggcggc ctggtgcagc ctggcggcag cctgaagctg 60

agctgcgtgg ccagcggctt cgacttcagc ctgtactgga tgaactgggt gaggcaggcc 120

cctggcaagg gcctggagtg gatcggcaag atcaaccctg acagcagcac catcaactac 180

acccctagcc tgaaggacaa gttcttcatc agcagggaca acgccaagaa caccctgtac 240

ctgcagatga ccaaggtgag gagcgaggac accgccctgt actactgcgc caggctgtgg 300

atgccaccg gcggcttcga ctactggggc cagggcacca ccctgaccgt gagcagc 357

<210> 11

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Light chain of SG003

<400> 11

Glu Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
20 25 30

Ala Phe Ser Tyr Val His Trp Tyr Gln Gln Lys Ser Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

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

Pro Val Glu Ser Glu Asp Val Ala Thr Tyr Tyr Cys His His Ser Arg
85 90 95

Glu Leu Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
100 105 110

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

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
165 170 175

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215

<210> 12

<211> 657

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid encoding light chain of SG003

<400> 12

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

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid encoding heavy chain of SG003

<400> 14
caggtgcagc tgctggagag cggcggcggc ctggtgcagc ctggcggcag cctgaagctg 60
agctgcgtgg ccagcggctt cgacttcagc ctgtactgga tgaactgggt gaggcaggcc 120
cctggcaagg gcctggagtg gatcggcaag atcaaccctg acagcagcac catcaactac 180
acccttagcc tgaaggacaa gttcttcatc agcagggaca acgccaagaa caccctgtac 240
ctgcagatga ccaaggtgag gagcggaggac accgccctgt actactgcgc caggctgtgg 300
atcgccaccg gcggcttcga ctactggggc cagggcacca ccctgaccgt gagcagcgct 360
agcaccaagg gcccacgtgt cttccccctg gcaccctcct ccaagagcac ctctgggggc 420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg 480
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga 540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac 600
atctgcaacg tgaatcaca gcccagcaac accaaggtgg acaagaaagt tgagcccaaa 660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg 720
tcagtcttcc tcttcccccc aaaacccaag gacaccctca tgatctccccg gacccctgag 780
gtcacgtgcg tgggtggtgga cgtgagccac gaagaccccg aggtcaagtt caactggtac 840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc 900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag 960
tacaagtgca aggtctccaa caaagccctc ccagcccca tcgagaaaac catctccaaa 1020
gccaaagggc agccccgaga accacaggtg tacaccctgc ccccatccccg ggatgagctg 1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1200
gactccgacg gtccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1260

caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1320
aagagcctct ccctgtctcc gggtaaatga 1350

<210> 15
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Binding epitope of CD38 protein

<400> 15

Ser Thr Phe Gly Ser Val Glu Val His Asn Leu Gln Pro Glu Lys Val
1 5 10 15

Gln Thr Leu Glu Ala Trp
20

<210> 16
<211> 218
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutant light chain 1 of SG003

<400> 16

Glu Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Gln Arg Ala Ser Ile Ser Cys Arg Ala Ser Asn Ser Val Ser Ser Ser
20 25 30

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

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Ile Gln Ser Gly Val Pro Ala
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile His

65		70		75		80
Pro Val Glu Ser	Glu Asp Val Ala Thr Tyr Tyr Cys His His Ser Arg					
	85		90			95
Gln Leu Pro Ser Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg						
	100		105			110
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln						
	115		120			125
Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr						
	130		135			140
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser						
145		150		155		160
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr						
	165		170			175
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys						
	180		185			190
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro						
	195		200			205
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys						
	210		215			

<210> 17
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant heavy chain 1 of SG003

<400> 17

Gln Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys

405

410

415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 18

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant light chain 2 of SG003

<400> 18

Glu Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Ser Ser Val Ser Ser Ser
 20 25 30

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

Lys Leu Leu Ile Tyr Leu Ala Ser Asp Leu Gln Ser Gly Val Pro Ala
 50 55 60

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

Pro Val Glu Ser Glu Asp Val Ala Thr Tyr Tyr Cys His His Ser Arg
 85 90 95

Glu Leu Pro Tyr Ser Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg

100

105

110

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

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

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 19
 <211> 449
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Mutant heavy chain 2 of SG003

<400> 19

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

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Asp Phe Ser Leu Tyr
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile

35

40

45

Gly Lys Ile Ser Pro Asn Ser Ser Thr Ile Asn Tyr Ser Pro Ser Leu
 50 55 60

Lys Asp Lys Phe Phe Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Thr Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95

Ala Arg Leu Tyr Ile Ala Ser Gly Gly Phe Asp Tyr Trp Gly Gln Gly
 100 105 110

Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

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

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

435

440

445

Lys

<210> 20

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant light chain 3 of SG003

<400> 20

Glu Ile Val Met Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Asn Ser Val Ser Thr Ser
20 25 30

Ala Phe Ser Tyr Val His Trp Tyr Gln Gln Lys Ser Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
50 55 60

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

Pro Val Glu Ser Glu Asp Val Ala Thr Tyr Tyr Cys His His Ser Arg
85 90 95

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

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

Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr

130

135

140

Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
 145 150 155 160

Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
 165 170 175

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

His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 195 200 205

Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 21

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Mutant heavy chain 3 of SG003

<400> 21

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

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Asp Phe Ser Leu Tyr
 20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45

Gly Lys Ile Ser Pro Asp Ser Ser Ser Leu Asn Tyr Thr Pro Ser Val
 50 55 60

Lys Asp Lys Phe Phe Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr

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

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

Lys

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

<220>
<223> LCDR1 of C6G12

<400> 22

Arg	Ser	Ser	Arg	Ser	Leu	Leu	His	Ser	Asn	Gly	Phe	Thr	Tyr	Leu	Tyr
1				5					10					15	

<210> 23
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR2 of C6G12

<400> 23

Gln	Met	Ser	Asn	Leu	Ala	Ser
1				5		

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3 of C6G12

<400> 24

Gly	Gln	Asn	Leu	Glu	Leu	Pro	Leu	Thr
1				5				

<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1 of C6G12

<400> 25

Ser Gly Tyr Tyr Trp Asn
1 5

<210> 26
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 of C6G12

<400> 26

Tyr Arg Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu Lys Asn
1 5 10 15

<210> 27
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR3 of C6G12

<400> 27

Gly Trp Leu Leu His Tyr Thr Met Asp Tyr
1 5 10

<210> 28
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> VL of C6G12

<400> 28

Glu Leu Val Met Thr Gln Ser Pro Phe Ser Asn Ala Val Thr Leu Gly
1 5 10 15

Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Arg Ser Leu Leu His Ser
20 25 30

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

Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
50 55 60

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

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

Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

<210> 29
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> VH of C6G12

<400> 29

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Phe Ser Ile Ser Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Arg Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Leu Leu His Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser
115

<210> 30
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid ancoding VL of C6G12

<400> 30
gagctcgtga tgacacagtc tccattctcc aatgcagtc ctcttggaac atcagcttcc 60
atctcctgca ggtctagtag gagtctccta catagtaatg gcttcactta tttgtattgg 120
tatctgcaga agccaggcca gtctcctcag ctcttgattt atcagatgtc caaccttgcc 180
tcaggagtcc cagacagggt cagtagcagt gggtcaggaa ctgatttcac actgagaatc 240
agcagagtgg aggctgagga tgtgggtgtt tattactgtg gtcaaaatct agagcttccg 300
ctcacgttcg gtgctgggac caagctggag ctgaaa 336

<210> 31
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid ancoding VH of C6G12

<400> 31
caggtgcagc tgaagcagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc 60
acctgttctg tcaactggctt ctccatcagc agtgggttatt actggaactg gatccggcag 120
tttccaggaa acaaactgga atggatgggc tacagaagct acgacgggtc caataactac 180

aacccatctc tcaaaaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc	240
ctgaagttga attctgtgac aactgaggac acagctacat attactgtgc aagaggatgg	300
ttactgcatt atactatgga ctactgggggt caaggaacct cagtcaccgt ctcctca	357

<210> 32
 <211> 219
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain of C6G12

<400> 32

Glu	Leu	Val	Met	Thr	Gln	Ser	Pro	Phe	Ser	Asn	Ala	Val	Thr	Leu	Gly
1				5					10					15	

Thr	Ser	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Arg	Ser	Leu	Leu	His	Ser
			20					25					30		

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

Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro
	50					55					60				

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

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

Leu	Glu	Leu	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
			100					105					110		

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

Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

130

135

140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 145 150 155 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 165 170 175

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

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 195 200 205

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 210 215

<210> 33
 <211> 660
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid ancoding light chain of C6G12

<400> 33
 gagctcgtga tgacacagtc tccattctcc aatgcagtca ctcttggAAC atcagcttcc 60
 atctcctgca ggtctagtag gAgctccta catagtaatg gcttcactta tttgtattgg 120
 tatctgcaga agccaggcca gtctcctcag ctcttgattt atcagatgtc caaccttgcc 180
 tcaggagtcc cagacaggtt cagtagcagt gggtcaggaa ctgatttcac actgagaatc 240
 agcagagtgg aggctgagga tgtgggtgtt tattactgtg gtcaaaatct agagcttccg 300
 ctcacgttcg gtgctgggac caagctggag ctgaaacgta cggtggctgc accatctgtc 360
 ttcaccttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg 420
 ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa 480
 tcgggtaact cccaggagag tgTcacagag caggacagca aggacagcac ctacagcctc 540

agcagcaccc tgacgctgag caaagcagac tacgagaaac acaaagtcta cgcctgcgaa 600

gtcacccatc agggcctgag ctcgcccgtc acaaagagct tcaacagggg agagtgttag 660

<210> 34

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain of C6G12

<400> 34

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Phe Ser Ile Ser Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Arg Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Leu Leu His Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr

340

345

350

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys

<210> 35

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleic acid ancoding heavy chain of C6G12

<400> 35

caggtgcagc tgaagcagtc aggacctggc ctcgtgaaac cttctcagtc tctgtctctc 60

acctgttctg tcaactggctt ctccatcagc agtggttatt actggaactg gatccggcag 120

tttccaggaa acaaactgga atggatgggc tacagaagct acgacgggtc caataactac 180

aaccatctc tcaaaaatcg aatctccatc actcgtgaca catctaagaa ccagtttttc 240

ctgaagttga attctgtgac aactgaggac acagctacat attactgtgc aagaggatgg 300

ttactgcatt atactatgga ctactgggggt caaggaacct cagtcaccgt ctcctcagct	360
agcaccaagg gcccacggt cttccccctg gcaccctcct ccaagagcac ctctgggggc	420
acagcggccc tgggctgcct ggtcaaggac tacttccccg aaccggtgac ggtgtcgtgg	480
aactcaggcg ccctgaccag cggcgtgcac accttccccg ctgtcctaca gtcctcagga	540
ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttggggcac ccagacctac	600
atctgcaacg tgaatcaciaa gcccagcaac accaagggtgg acaagaaaagt tgagcccaaa	660
tcttgtgaca aaactcacac atgcccaccg tgcccagcac ctgaactcct ggggggaccg	720
tcagtcttcc tcttcccccc aaaaccaag gacaccctca tgatctcccg gaccctgag	780
gtcacgtgcg tgggtggtgga cgtgagccac gaagaccccg aggtcaagtt caactggtac	840
gtggacggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gtacaacagc	900
acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgaa tggcaaggag	960
tacaagtgca aggtctccaa caaagccctc ccagcccca tcgagaaaac catctccaaa	1020
gccaaagggc agccccgaga accacagggtg tacaccctgc ccccatcccg ggatgagctg	1080
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc	1140
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg	1200
gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag	1260
caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag	1320
aagagcctct ccctgtctcc gggtaaatga	1350

<210> 36
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LCDR1 of SG701

<400> 36

Arg	Ala	Ser	Gln	Gly	Ile	Ser	Ser	Trp	Leu	Ala
1				5				10		

<210> 37
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR2 of SG701

<400> 37

Asp Ala Ser Asn Leu Glu Ala
1 5

<210> 38
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> LCDR3 of SG701

<400> 38

Gln Gln Tyr Gly Asp Phe Pro Leu Thr
1 5

<210> 39
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR1 of SG701

<400> 39

Asn Asn Tyr Ile His
1 5

<210> 40
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> HCDR2 of SG701

<400> 40

Met Ile Asn Pro Ser Gly Gly Ser Thr Thr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 41

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> HCDR3 of SG701

<400> 41

Ala Ala Leu Ser Tyr Tyr Ser Ile Val Thr Ala Lys Asp Tyr Gly Met
1 5 10 15

Asp Val

<210> 42

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> VL of SG701

<400> 42

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

Asp Arg Val Asn Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Ala Gly Val Pro Ser Arg Phe Arg Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Thr Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Gly Asp Phe Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 43

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> VH of SG701

<400> 43

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

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

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Leu Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 44
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid ancoding VL of SG701

<400> 44
gacatccagc tgacccagag ccctagcagc gtgagcgcca gcgtgggcga cagggtgaac 60
atcacctgca gggccagcca gggcatcagc agctggctgg cctggtacca gcagaagcct 120
ggcaaggccc ctaagctgct gatctacgac gccagcaacc tggaggccgg cgtgcctagc 180
aggttcaggg gcagcggcag cggcaccgac ttcaccttca ccatcaccag cctgcagcct 240
gaggacatcg ccacctactt ctgccagcag tacggcgact tccctctgac cttcggccag 300
ggcaccaagc tggagatcaa g 321

<210> 45
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid ancoding VH of SG701

<400> 45
caggtgcagc tggcgcagag cggcgccgag gtgaagaagc ctggcgccag cgtgaagggtg 60
agctgcaagg ccagcggcta caccttcacc aacaactaca tccactgggt gaggcaggcc 120
cctggccagg gcctggagtg gatgggcatg atcaacccta gcggcggcag caccacctac 180
gcccagaagt tccagggcag gctgaccatg accaggggaca ccagcaccag caccgtgtac 240
atggacctga gcagcctgag gagcgaggac accgccgtgt actactgcgc cagggccgcc 300

ctgagctact acagcatcgt gaccgccaag gactacggca tggacgtgtg gggccagggc 360
 accaccgtga ccgtgagcag c 381

<210> 46
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light tchain of SG701

<400> 46

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

Asp Arg Val Asn Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Leu Glu Ala Gly Val Pro Ser Arg Phe Arg Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Thr Ser Leu Gln Pro
 65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Gly Asp Phe Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 47
 <211> 645
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleic acid ancoding light chain of SG701

<400> 47
 gacatccagc tgacccagag ccctagcagc gtgagcgcca gcgtgggcga cagggtgaac 60
 atcacctgca gggccagcca gggcatcagc agctggctgg cctggtacca gcagaagcct 120
 ggcaaggccc ctaagctgct gatctacgac gccagcaacc tggaggccgg cgtgcctagc 180
 aggttcaggg gcagcggcag cggcaccgac ttcaccttca ccatcaccag cctgcagcct 240
 gaggacatcg ccacctactt ctgccagcag tacggcgact tccctctgac cttcggccag 300
 ggcaccaagc tggagatcaa gcgtacggtg gctgcaccat ctgtcttcat cttcccgcc 360
 tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420
 cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480
 gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540
 ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gttag

645

<210> 48

<211> 457

<212> PRT

<213> Artificial Sequence

<220>

<223> Heavy chain of SG701

<400> 48

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

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

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Leu Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
115 120 125

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

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe

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

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
355 360 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
370 375 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
385 390 395 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
405 410 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
420 425 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys
450 455

<210> 49
<211> 1374
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid ancoding heavy chain of SG701

<400> 49
caggtgcagc tgggtgcagag cggcgccgag gtgaagaagc ctggcgccag cgtgaagggtg 60
agctgcaagg ccagcggcta caccttcacc aacaactaca tccactgggt gaggcaggcc 120
cctggccagg gcctggagtg gatgggcatg atcaacccta gcggcggcag caccacctac 180
gcccagaagt tccagggcag gctgaccatg accagggaca ccagcaccag caccgtgtac 240
atggacctga gcagcctgag gagcgaggac accgccgtgt actactgcgc cagggccgcc 300
ctgagctact acagcatcgt gaccgccaag gactacggca tggacgtgtg gggccagggc 360

accaccgtga ccgtgagcag cgctagcacc aaggggcccat cggtcttccc cctggcaccc	420
tcctccaaga gcacctctgg gggcacagcg gccctgggct gcctgggtcaa ggactacttc	480
cccgaaccgg tgacgggtgtc gtggaactca ggcgccctga ccagcggcgt gcacaccttc	540
ccggctgtcc tacagtcttc aggactctac tccctcagca gcgtgggtgac cgtgccctcc	600
agcagcttgg gcacccagac ctacatctgc aacgtgaatc acaagcccag caacaccaag	660
gtggacaaga aagttgagcc caaatcttgt gacaaaaactc acacatgccc accgtgccc	720
gcacctgaac tcctgggggg accgtcagtc ttctcttcc ccccaaaacc caaggacacc	780
ctcatgatct cccggacccc tgaggtcacg tgcgtgggtg tggacgtgag ccacgaagac	840
cccgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag	900
ccgcggggagg agcagtacaa cagcacgtac cgtgtgggtca gcgtcctcac cgtcctgcac	960
caggactggc tgaatggcaa ggagtacaag tgcaagggtct ccaacaaagc cctcccagcc	1020
cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagaaccaca ggtgtacacc	1080
ctgcccccat cccgggatga gctgaccaag aaccagggtca gcctgacctg cctgggtcaaa	1140
ggcttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac	1200
tacaagacca cgcctcccggt gctggactcc gacggctcct tcttcctcta cagcaagctc	1260
accgtggaca agagcagggtg gcagcagggg aacgtcttct catgctccgt gatgcatgag	1320
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa atga	1374

<210> 50
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Truncated domain of human SIRP¹ variant 1

<400> 50

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly

20

25

30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
 35 40 45

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
 50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
 65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
 100 105 110

Arg Ala Lys Pro Ser
 115

<210> 51
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M1

<400> 51

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
 20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Ile Leu Ile Tyr
 35 40 45

Asn Gln Lys Lys Gly His Phe Pro Arg Val Thr Thr Leu Ser Asp Ser

50

55

60

Thr Arg Arg Gly Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
 65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 85 90 95

Pro Asp Asp Leu Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
 100 105 110

Arg Ala Lys Pro Ser
 115

<210> 52
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M5

<400> 52

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Val Pro Val Gly
 20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Asn Leu Ile Tyr
 35 40 45

Asn Ser Arg His Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
 50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
 65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser

85

90

95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
 100 105 110

Arg Ala Lys Pro Ser
 115

<210> 53
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M12

<400> 53

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Phe Pro Ile Gly
 20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
 35 40 45

Asn Gln Arg Lys Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
 50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
 65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 85 90 95

Pro Asp Asp Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
 100 105 110

Arg Ala Lys Pro Ser

115

<210> 54
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M35

<400> 54

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Gln Leu Ile Tyr
35 40 45

Asn Gln Lys Asp Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Asn Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 55
<211> 117
<212> PRT
<213> Artificial Sequence

<220>

<223> M37

<400> 55

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Lys Leu Ile Tyr
35 40 45

Asn Gln Arg Asp Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
50 55 60

Thr Lys Arg Gly Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 56

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> M41

<400> 56

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Val Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg His Leu Ile Tyr
35 40 45

Asn Arg Arg His Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Ser Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 57
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M57

<400> 57

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Ile Leu Ile Tyr
35 40 45

Asn Gly Lys Arg Gly His Phe Pro Arg Val Thr Thr Leu Ser Asp Thr
50 55 60

Thr Lys Arg Gly Asn Met Asp Phe Ser Ile Ser Ile Arg Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Arg Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 58
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M67

<400> 58

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Met Leu Ile Tyr
35 40 45

Asn Gly Arg Asp Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Leu Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 59
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M81

<400> 59

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
35 40 45

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 60
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M82

<400> 60

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Phe Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
35 40 45

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser His Ser
50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile His Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Ser Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 61
<211> 117
<212> PRT

<213> Artificial Sequence

<220>

<223> M84

<400> 61

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Phe Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
35 40 45

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser His Ser
50 55 60

Thr Arg Arg Asn Asn Met Asp Phe Ser Ile Arg Ile His Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Ser Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 62

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> M91

<400> 62

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly

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

<210> 63
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M99

<400> 63

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Ile Pro Val Gly	20	25	30
---	----	----	----

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Lys Leu Ile Tyr

35

40

45

Asn Gln Lys Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Ser
 50 55 60

Thr Lys Arg Lys Asn Met Asp Phe Ser Ile Arg Ile His Asn Ile Thr
 65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
 85 90 95

Pro Asp Asp Leu Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
 100 105 110

Arg Ala Lys Pro Ser
 115

<210> 64
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M102

<400> 64

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
 20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Glu Leu Ile Tyr
 35 40 45

Asn Gly Lys Gly Gly His Phe Pro Arg Val Thr Thr Val Ser Arg Ser
 50 55 60

Thr Lys Arg Asp Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr

65		70		75		80									
Pro	Ala	Asp	Ala	Gly	Thr	Tyr	Tyr	Cys	Val	Lys	Phe	Arg	Lys	Gly	Ser
				85					90					95	

Pro	Asp	Asp	Ile	Glu	Phe	Lys	Ser	Gly	Ala	Gly	Thr	Glu	Leu	Ser	Val
			100					105					110		

Arg	Ala	Lys	Pro	Ser
		115		

<210> 65
 <211> 117
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> M111

<400> 65

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

Glu	Thr	Ala	Thr	Leu	Arg	Cys	Thr	Ala	Thr	Ser	Leu	Leu	Pro	Val	Gly
			20					25					30		

Pro	Ile	Gln	Trp	Phe	Arg	Gly	Ala	Gly	Pro	Gly	Arg	Arg	Leu	Ile	Tyr
		35					40					45			

Asn	Asn	Arg	Gly	Gly	His	Phe	Pro	Arg	Val	Thr	Thr	Leu	Ser	Glu	Thr
	50					55					60				

Thr	Arg	Arg	Asp	Asn	Met	Asp	Phe	Ser	Ile	Arg	Ile	Gly	Asn	Ile	Thr
65					70					75				80	

Pro	Ala	Asp	Ala	Gly	Thr	Tyr	Tyr	Cys	Val	Lys	Phe	Arg	Lys	Gly	Ser
				85					90					95	

Pro	Asp	Asp	Leu	Glu	Phe	Lys	Ser	Gly	Ala	Gly	Thr	Glu	Leu	Ser	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Arg Ala Lys Pro Ser
115

<210> 66
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M122

<400> 66

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Val Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Asn Leu Ile Tyr
35 40 45

Asn Ser Arg His Gly His Phe Pro Arg Val Thr Thr Ala Ser Asp Leu
50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 67

<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M126

<400> 67

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Val Pro Ile Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu Ile Tyr
35 40 45

Asn Gln Arg Asp Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Thr
50 55 60

Thr Arg Arg Glu Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 68
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M130

<400> 68

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Val Leu Ile Tyr
35 40 45

Asn Gln Arg Glu Gly His Phe Pro Arg Val Thr Thr Val Ser Glu Ser
50 55 60

Thr Arg Arg Asp Asn Met Asp Phe Ser Ile Arg Ile Arg Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 69
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M135

<400> 69

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Val Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Leu Leu Ile Tyr
35 40 45

Asn Gly Lys Gly Gly His Phe Pro Arg Val Thr Thr Leu Ser Glu Thr
50 55 60

Thr Arg Arg Gly Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 70
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> M145

<400> 70

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Ile Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Asn Leu Ile Tyr
35 40 45

Asn Gly Lys Gly Gly His Phe Pro Arg Val Thr Thr Val Ser Asp Leu
50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Arg Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Val Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser
115

<210> 71
<211> 233
<212> PRT
<213> Artificial Sequence

<220>
<223> IgG1-FC

<400> 71

Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
115 120 125

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
130 135 140

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145 150 155 160

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 72
<211> 350
<212> PRT
<213> Artificial Sequence

<220>
<223> SS002M91

<400> 72

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

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
20 25 30

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Gln Leu Ile Tyr
35 40 45

Asn Gln Lys Asp Gly His Phe Pro Arg Val Thr Thr Ala Ser Asp Leu
50 55 60

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Asn Ile Gly Asn Ile Thr
65 70 75 80

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
85 90 95

Pro Asp Asp Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
100 105 110

Arg Ala Lys Pro Ser Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr
115 120 125

Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
130 135 140

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
145 150 155 160

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
165 170 175

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
180 185 190

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
195 200 205

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys

210

215

220

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 225 230 235 240

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 245 250 255

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 260 265 270

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 275 280 285

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
 290 295 300

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
 305 310 315 320

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
 325 330 335

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 340 345 350

<210> 73

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker 1

<400> 73

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10

<210> 74

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Linker 2

<400> 74

Gly Gly Gly Ser Ala Ala Ala
1 5

<210> 75
<211> 576
<212> PRT
<213> Artificial Sequence

<220>
<223> The second polypeptide chain of SG3847L1

<400> 75

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

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Asp Phe Ser Leu Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Lys Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
50 55 60

Lys Asp Lys Phe Phe Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Thr Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

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

Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu

305		310		315		320									
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys
				325					330					335	
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
			340					345					350		
Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
		355					360					365			
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
	370					375					380				
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
385					390					395					400
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys
				405					410					415	
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
			420					425					430		
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
		435					440					445			
Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Gln	Val	Ile
	450					455					460				
Gln	Pro	Asp	Lys	Ser	Val	Leu	Val	Ala	Ala	Gly	Glu	Thr	Ala	Thr	Leu
465					470					475					480
Arg	Cys	Thr	Ala	Thr	Ser	Leu	Leu	Pro	Val	Gly	Pro	Ile	Gln	Trp	Phe
				485					490					495	
Arg	Gly	Ala	Gly	Pro	Gly	Arg	Gln	Leu	Ile	Tyr	Asn	Gln	Lys	Asp	Gly
			500					505					510		

His Phe Pro Arg Val Thr Thr Ala Ser Asp Leu Thr Lys Arg Asn Asn
515 520 525

Met Asp Phe Ser Ile Asn Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly
530 535 540

Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser Pro Asp Asp Ile Glu
545 550 555 560

Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser
565 570 575

<210> 76
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> The second polypeptide chain of SG3847L2

<400> 76

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

Ser Leu Lys Leu Ser Cys Val Ala Ser Gly Phe Asp Phe Ser Leu Tyr
20 25 30

Trp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Lys Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
50 55 60

Lys Asp Lys Phe Phe Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Thr Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

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

Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val

290

295

300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys Gly Gly Gly Ser Ala Ala Ala Glu Leu Gln Val Ile Gln Pro Asp
 450 455 460

Lys Ser Val Leu Val Ala Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr
 465 470 475 480

Ala Thr Ser Leu Leu Pro Val Gly Pro Ile Gln Trp Phe Arg Gly Ala
 485 490 495

Gly Pro Gly Arg Gln Leu Ile Tyr Asn Gln Lys Asp Gly His Phe Pro
500 505 510

Arg Val Thr Thr Ala Ser Asp Leu Thr Lys Arg Asn Asn Met Asp Phe
515 520 525

Ser Ile Asn Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr
530 535 540

Cys Val Lys Phe Arg Lys Gly Ser Pro Asp Asp Ile Glu Phe Lys Ser
545 550 555 560

Gly Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser
565 570

<210> 77
<211> 573
<212> PRT
<213> Artificial Sequence

<220>
<223> The second polypeptide chain of SGAXL47

<400> 77

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

Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Phe Ser Ile Ser Ser Gly
20 25 30

Tyr Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Arg Ser Tyr Asp Gly Ser Asn Asn Tyr Asn Pro Ser Leu
50 55 60

Lys Asn Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Lys Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Gly Trp Leu Leu His Tyr Thr Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

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

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

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

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225 230 235 240

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

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn

275

280

285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

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

Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

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

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 435 440 445

Lys Gly Gly Gly Ser Ala Ala Ala Glu Leu Gln Val Ile Gln Pro Asp
 450 455 460

Lys Ser Val Leu Val Ala Ala Gly Glu Thr Ala Thr Leu Arg Cys Thr
 465 470 475 480

Ala Thr Ser Leu Leu Pro Val Gly Pro Ile Gln Trp Phe Arg Gly Ala
485 490 495

Gly Pro Gly Arg Gln Leu Ile Tyr Asn Gln Lys Asp Gly His Phe Pro
500 505 510

Arg Val Thr Thr Ala Ser Asp Leu Thr Lys Arg Asn Asn Met Asp Phe
515 520 525

Ser Ile Asn Ile Gly Asn Ile Thr Pro Ala Asp Ala Gly Thr Tyr Tyr
530 535 540

Cys Val Lys Phe Arg Lys Gly Ser Pro Asp Asp Ile Glu Phe Lys Ser
545 550 555 560

Gly Ala Gly Thr Glu Leu Ser Val Arg Ala Lys Pro Ser
565 570

<210> 78

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> The second polypeptide chain of SGTrop247

<400> 78

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

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

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asn Pro Ser Gly Gly Ser Thr Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Leu Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Asp Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala
115 120 125

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

Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
180 185 190

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

Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys
210 215 220

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

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
245 250 255

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val

260

265

270

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 275 280 285

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 290 295 300

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 305 310 315 320

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 325 330 335

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 340 345 350

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 355 360 365

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 370 375 380

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 385 390 395 400

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 405 410 415

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 420 425 430

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 435 440 445

Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Ser Ala Ala Ala
 450 455 460

Glu Leu Gln Val Ile Gln Pro Asp Lys Ser Val Leu Val Ala Ala Gly
465 470 475 480

Glu Thr Ala Thr Leu Arg Cys Thr Ala Thr Ser Leu Leu Pro Val Gly
485 490 495

Pro Ile Gln Trp Phe Arg Gly Ala Gly Pro Gly Arg Gln Leu Ile Tyr
500 505 510

Asn Gln Lys Asp Gly His Phe Pro Arg Val Thr Thr Ala Ser Asp Leu
515 520 525

Thr Lys Arg Asn Asn Met Asp Phe Ser Ile Asn Ile Gly Asn Ile Thr
530 535 540

Pro Ala Asp Ala Gly Thr Tyr Tyr Cys Val Lys Phe Arg Lys Gly Ser
545 550 555 560

Pro Asp Asp Ile Glu Phe Lys Ser Gly Ala Gly Thr Glu Leu Ser Val
565 570 575

Arg Ala Lys Pro Ser
580