

Sequence Listing

<110> PROGEN CO., LTD.

<120> RECOMBINANT EXTRACELLULAR DOMAIN OF IgE Fc RECEPTOR SUBUNIT ALPHA,
PHARMACEUTICAL
COMPOSITION COMPRISING SAME AND METHOD FOR PREPARING SAME

<130> PCB812140PRG/PCT

<150> KR 10-2018-0002248
<151> 2018-01-08

<160> 22

<170> KopatentIn 2.0

<210> 1
<211> 180
<212> PRT
<213> Artificial Sequence

<220>
<223> FcεRI1 ECD

<400> 1
Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
1 5 10 15
Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
20 25 30
Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu
35 40 45
Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
50 55 60
Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
65 70 75 80
Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
85 90 95
Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
100 105 110
Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
115 120 125

Sequence Listing

Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
130 135 140

Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
145 150 155 160

Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys
165 170 175

Tyr Trp Leu Gln
180

<210> 2
<211> 215
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified Fc

<400> 2
Ser His Thr Gln Pro Leu Gly Val Phe Leu Phe Pro Pro Lys Pro Lys
1 5 10 15

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
20 25 30

Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp
35 40 45

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

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
65 70 75 80

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu
85 90 95

Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
100 105 110

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys
115 120 125

Sequence Listing

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
130 135 140

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
145 150 155 160

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
165 170 175

Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser
180 185 190

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

Leu Ser Leu Ser Leu Gly Lys
210 215

<210> 3
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> IgD hinge variant

<400> 3
Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Gly Ser Lys Glu Lys
1 5 10 15

Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu Cys Pro
20 25 30

<210> 4
<211> 49
<212> PRT
<213> Artificial Sequence

<220>
<223> IgD hinge variant

<400> 4
Ala Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro
1 5 10 15

Sequence Listing

Ala Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Gly Ser
20 25 30

Lys Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu Cys
35 40 45

Pro

<210> 5
<211> 540
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotides sequence of FcεRI1 ECD

<400> 5
gtgccccaga agcccaaggt gagcctgaac cctccctgga acagaatctt caagggcgag 60
aacgtgaccc tgacctgcaa cggcaacaac ttcttcgagg tgagcagcac caagtgggtc 120
cacaatggca gcctgagcga ggagaccaac agctccctga acatcgtgaa cgccaagttc 180
gaggacagcg gcgagtacaa gtgccagcac cagcagggtga acgagagcga gcccgtgtac 240
ctggagggtgt tcagcgactg gctgctgctg caggccagcg ccgagggtggt gatggagggc 300
cagccccctgt tcctgagatg ccacggctgg agaaactggg acgtgtacaa ggtgatctac 360
tacaaggatg gcgaggccct gaagtactgg tacgagaacc acaacatctc catcaccaac 420
gccaccgtgg aggacagcgg cacctactac tgcacaggca aggtgtggca gctggactac 480
gagagcgagc ccctgaacat caccgtgatc aaggctccca gagagaagta ctggctgcag 540
540

<210> 6
<211> 561
<212> DNA
<213> Artificial Sequence

<220>

Sequence Listing

<223> nucleotides sequence of modified Fc

<400> 6
 tgcgtggtcg tggatgtgag ccaggaagat cccgaagtgc agttcaactg gtacgtggat 60
 ggcgtggaag tgcacaacgc caagaccaag cccagagaag agcagttcaa ctccacctac 120
 agagtgggtga gcggtctgac cgtgctgcac caggactggc tgaacggcaa ggagtacaag 180
 tgcaagggtgt ccaacaaagg cctgcccagc tccatcgaga agaccatcag caaagccaaa 240
 ggccagccca gagaacccca ggtgtacacc ctgcctccca gccaggaaga gatgaccaag 300
 aaccagggtgt ccctgacctg cctggtgaaa ggcttctacc ccagcgacat cgccgtggag 360
 tgggaaagca acggccagcc cgagaacaat tacaagacaa cccctcccgt gctggatagc 420
 gatggcagct tctttctgta cagcagactg accgtggaca agagcagatg gcaggaaggc 480
 aacgtgttca gctgcagcgt gatgcacgaa gccctgcaca accactacac ccagaagagc 540
 ctgtccctga gcctgggcaa g 561

<210> 7
 <211> 174
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotides sequence of IgD hinge variant

<400> 7
 aggaacaccg gcagaggagg cgaggaaaag aaaggaagca aggagaagga ggagcaggag 60
 gaaagagaaa ccaagacccc cgagtgcacc agccacaccc agcccctggg cgtgttcctg 120
 ttccccccca agcccaagga caccctgatg atcagcagaa cccccgaggt gacc 174

<210> 8
 <211> 231
 <212> DNA
 <213> Artificial Sequence

<220>

Sequence Listing

<223> nucleotides sequence of IgD hinge variant

<400> 8
 gccccagcccc aggccgaggg cagcctggct aaggccacca cagctcccgc caccaccagg 60
 aacaccggca gaggaggcga ggaaaagaaa ggaagcaagg agaaggagga gcaggaggaa 120
 agagaaacca agacccccga gtgcccagc cacaccagc ccctgggcgt gttcctgttc 180
 ccccccaagc ccaaggacac cctgatgatc agcagaacct ccgaggtgac c 231

<210> 9
 <211> 25
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> signal peptide

<400> 9
 Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser His Ala
 20 25

<210> 10
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> nucleotides sequence of signal peptide

<400> 10
 atggacgcca tgctgagagg cctgtgctgt gtgctgctgc tgtgcggcgc cgtgttcgtg 60
 tcccctagcc acgcc 75

<210> 11
 <211> 450
 <212> PRT

Sequence Listing

<213> Artificial Sequence

<220>

<223> FceRIa ECD-hinge-Fc2

<400> 11

Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser His Ala Val Pro Gln Lys Pro Lys Val
20 25 30

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

Leu Thr Cys Asn Gly Asn Asn Phe Phe Glu Val Ser Ser Thr Lys Trp
50 55 60

Phe His Asn Gly Ser Leu Ser Glu Glu Thr Asn Ser Ser Leu Asn Ile
65 70 75 80

Val Asn Ala Lys Phe Glu Asp Ser Gly Glu Tyr Lys Cys Gln His Gln
85 90 95

Gln Val Asn Glu Ser Glu Pro Val Tyr Leu Glu Val Phe Ser Asp Trp
100 105 110

Leu Leu Leu Gln Ala Ser Ala Glu Val Val Met Glu Gly Gln Pro Leu
115 120 125

Phe Leu Arg Cys His Gly Trp Arg Asn Trp Asp Val Tyr Lys Val Ile
130 135 140

Tyr Tyr Lys Asp Gly Glu Ala Leu Lys Tyr Trp Tyr Glu Asn His Asn
145 150 155 160

Ile Ser Ile Thr Asn Ala Thr Val Glu Asp Ser Gly Thr Tyr Tyr Cys
165 170 175

Thr Gly Lys Val Trp Gln Leu Asp Tyr Glu Ser Glu Pro Leu Asn Ile
180 185 190

Thr Val Ile Lys Ala Pro Arg Glu Lys Tyr Trp Leu Gln Arg Asn Thr
195 200 205

Gly Arg Gly Gly Glu Glu Lys Lys Gly Ser Lys Glu Lys Glu Glu Gln
210 215 220

Sequence Listing

Glu	Glu	Arg	Glu	Thr	Lys	Thr	Pro	Glu	Cys	Pro	Ser	His	Thr	Gln	Pro	225	230	235	240
Leu	Gly	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	245	250	255	
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	260	265	270	
Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	275	280	285	
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	290	295	300	
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	305	310	315	320
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	325	330	335	
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	340	345	350	
Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	355	360	365	
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	370	375	380	
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	385	390	395	400
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	405	410	415	
Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	420	425	430	
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	435	440	445	
Gly	Lys															450			

<210> 12

Sequence Listing

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<223> nucleotides sequence of FcεRIα ECD-hinge-Fc2

<400> 12

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tcccctagcc acgccgtgcc ccagaagccc aagggtgagcc tgaaccctcc ctggaacaga      120
atcttcaagg gcgagaacgt gaccctgacc tgcaacggca acaacttctt cgagggtgagc      180
agcaccaagt ggttccacaa tggcagcctg agcgaggaga ccaacagctc cctgaacatc      240
gtgaacgcca agttcgagga cagcggcgag tacaagtgcc agcaccagca ggtgaacgag      300
agcgagcccc tgtacctgga ggtgttcagc gactggctgc tgctgcaggc cagcgccgag      360
gtggtgatgg agggccagcc cctgttcctg agatgccacg gctggagaaa ctgggacgtg      420
tacaaggatga tctactacaa ggatggcgag gccctgaagt actggtacga gaaccacaac      480
atctccatca ccaacgccac cgtggaggac agcggcacct actactgcac aggcaagggtg      540
tggcagctgg actacgagag cgagcccctg aacatcaccg tgatcaaggc tcccagagag      600
aagtactggc tgcagaggaa caccggcaga ggaggcgagg aaaagaaagg aagcaaggag      660
aaggaggagc aggaggaaa agaaaccaag acccccagagt gcccagcca caccagccc      720
ctgggcgtgt tcctgttccc cccaagccc aaggacaccc tgatgatcag cagaaccccc      780
gaggtgacct gcgtggtcgt ggatgtgagc caggaagatc ccgaagtgca gttcaactgg      840
tacgtggatg gcgtggaagt gcacaacgcc aagaccaagc ccagagaaga gcagttcaac      900
tccacctaca gagtgggtgag cgtgctgacc gtgctgcacc aggactggct gaacggcaag      960
gagtacaagt gcaagggtgtc caacaaaggc ctgcccagct ccatcgagaa gaccatcagc     1020
aaagccaaaag gccagcccag agaaccccag gtgtacaccc tgccctcccag ccaggaagag     1080
atgaccaaga accagggtgtc cctgacctgc ctggtgaaag gcttctaccc cagcgacatc     1140
gccgtggagt gggaaagcaa cggccagccc gagaacaatt acaagacaac ccctcccgtg     1200

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Sequence Listing

ctggatagcg atggcagctt ctttctgtac agcagactga ccgtggacaa gagcagatgg 1260
caggaaggca acgtgttcag ctgcagcgtg atgcacgaag ccctgcacaa ccactacacc 1320
cagaagagcc tgtccctgag cctgggcaag 1350

<210> 13
<211> 469
<212> PRT
<213> Artificial Sequence

<220>
<223> FceRIa ECD-hinge-Fc3

<400> 13
Met Asp Ala Met Leu Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15
Ala Val Phe Val Ser Pro Ser His Ala Val Pro Gln Lys Pro Lys Val
20 25 30
Ser Leu Asn Pro Pro Trp Asn Arg Ile Phe Lys Gly Glu Asn Val Thr
35 40 45
Leu Thr Cys Asn Gly Asn Asn Phe Phe Glu Val Ser Ser Thr Lys Trp
50 55 60
Phe His Asn Gly Ser Leu Ser Glu Glu Thr Asn Ser Ser Leu Asn Ile
65 70 75 80
Val Asn Ala Lys Phe Glu Asp Ser Gly Glu Tyr Lys Cys Gln His Gln
85 90 95
Gln Val Asn Glu Ser Glu Pro Val Tyr Leu Glu Val Phe Ser Asp Trp
100 105 110
Leu Leu Leu Gln Ala Ser Ala Glu Val Val Met Glu Gly Gln Pro Leu
115 120 125
Phe Leu Arg Cys His Gly Trp Arg Asn Trp Asp Val Tyr Lys Val Ile
130 135 140
Tyr Tyr Lys Asp Gly Glu Ala Leu Lys Tyr Trp Tyr Glu Asn His Asn
145 150 155 160

Sequence Listing

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

Sequence Listing

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
420 425 430

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

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

Leu Ser Leu Gly Lys
465

<210> 14
<211> 1407
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotides sequence of FcεRIα ECD-hinge-Fc3

<400> 14
atggacgcca tgctgagagg cctgtgctgt gtgctgctgc tgtgcggcgc cgtgttcgtg 60
tcccctagcc acgccgtgcc ccagaagccc aagggtgagcc tgaaccctcc ctggaacaga 120
atcttcaagg gcgagaacgt gaccctgacc tgcaacggca acaacttctt cgagggtgagc 180
agcaccaagt ggttccacaa tggcagcctg agcgaggaga ccaacagctc cctgaacatc 240
gtgaacgcca agttcgagga cagcggcgag tacaagtgcc agcaccagca ggtgaacgag 300
agcgagccccg tgtacctgga ggtgttcagc gactggctgc tgctgcaggc cagcgccgag 360
gtggtgatgg agggccagcc cctgttcctg agatgccacg gctggagaaa ctgggacgtg 420
tacaaggtga tctactacaa ggatggcgag gccctgaagt actggtacga gaaccacaac 480
atctccatca ccaacgccac cgtggaggac agcggcacct actactgcac aggcaagggtg 540
tggcagctgg actacgagag cgagcccctg aacatcaccg tgatcaaggc tcccagagag 600
aagtactggc tgcaggccca gccccaggcc gagggcagcc tggctaaggc caccacagct 660
cccgccacca ccaggaacac cggcagagga ggcgaggaaa agaaaggaag caaggagaag 720
gaggagcagg aggaaagaga aaccaagacc cccgagtgcc ccagccacac ccagcccctg 780

Sequence Listing

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ggcgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagcag aacccccgag      840
gtgacctgcg tggtcgtgga tgtgagccag gaagatcccc aagtgcagtt caactggtac      900
gtggatggcg tggaagtgca caacgccaag accaagccca gagaagagca gttcaactcc      960
acctacagag tggtgagcgt gctgaccgtg ctgcaccagg actggctgaa cggcaaggag     1020
tacaagtgca aggtgtccaa caaaggcctg cccagctcca tcgagaagac catcagcaaa     1080
gccaaaggcc agcccagaga accccagggtg tacaccctgc ctcccagcca ggaagagatg     1140
accaagaacc aggtgtccct gacctgcctg gtgaaaggct tctaccccag cgacatcgcc     1200
gtggagtggg aaagcaacgg ccagcccagag aacaattaca agacaacccc tcccgtgctg     1260
gatagcgatg gcagcttctt tctgtacagc agactgaccg tggacaagag cagatggcag     1320
gaaggcaacg tgttcagctg cagcgtgatg cacgaagccc tgcacaacca ctacaccag     1380
aagagcctgt ccctgagcct gggcaag                                           1407

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<210>      15
<211>     406
<212>      PRT
<213>      Artificial Sequence

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<220>
<223>      human a-2,6 sialic acid transferase

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<400>      15
Met Ile His Thr Asn Leu Lys Lys Lys Phe Ser Cys Cys Val Leu Val
  1             5             10            15

Phe Leu Leu Phe Ala Val Ile Cys Val Trp Lys Glu Lys Lys Lys Gly
      20             25            30

Ser Tyr Tyr Asp Ser Phe Lys Leu Gln Thr Lys Glu Phe Gln Val Leu
      35             40            45

Lys Ser Leu Gly Lys Leu Ala Met Gly Ser Asp Ser Gln Ser Val Ser
      50             55            60

Ser Ser Ser Thr Gln Asp Pro His Arg Gly Arg Gln Thr Leu Gly Ser
      65             70            75            80

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Sequence Listing

Leu Arg Gly Leu Ala Lys Ala Lys Pro Glu Ala Ser Phe Gln Val Trp
 85 90 95
 Asn Lys Asp Ser Ser Ser Lys Asn Leu Ile Pro Arg Leu Gln Lys Ile
 100 105 110
 Trp Lys Asn Tyr Leu Ser Met Asn Lys Tyr Lys Val Ser Tyr Lys Gly
 115 120 125
 Pro Gly Pro Gly Ile Lys Phe Ser Ala Glu Ala Leu Arg Cys His Leu
 130 135 140
 Arg Asp His Val Asn Val Ser Met Val Glu Val Thr Asp Phe Pro Phe
 145 150 155 160
 Asn Thr Ser Glu Trp Glu Gly Tyr Leu Pro Lys Glu Ser Ile Arg Thr
 165 170 175
 Lys Ala Gly Pro Trp Gly Arg Cys Ala Val Val Ser Ser Ala Gly Ser
 180 185 190
 Leu Lys Ser Ser Gln Leu Gly Arg Glu Ile Asp Asp His Asp Ala Val
 195 200 205
 Leu Arg Phe Asn Gly Ala Pro Thr Ala Asn Phe Gln Gln Asp Val Gly
 210 215 220
 Thr Lys Thr Thr Ile Arg Leu Met Asn Ser Gln Leu Val Thr Thr Glu
 225 230 235 240
 Lys Arg Phe Leu Lys Asp Ser Leu Tyr Asn Glu Gly Ile Leu Ile Val
 245 250 255
 Trp Asp Pro Ser Val Tyr His Ser Asp Ile Pro Lys Trp Tyr Gln Asn
 260 265 270
 Pro Asp Tyr Asn Phe Phe Asn Asn Tyr Lys Thr Tyr Arg Lys Leu His
 275 280 285
 Pro Asn Gln Pro Phe Tyr Ile Leu Lys Pro Gln Met Pro Trp Glu Leu
 290 295 300
 Trp Asp Ile Leu Gln Glu Ile Ser Pro Glu Glu Ile Gln Pro Asn Pro
 305 310 315 320
 Pro Ser Ser Gly Met Leu Gly Ile Ile Ile Met Met Thr Leu Cys Asp
 325 330 335

Sequence Listing

Gln Val Asp Ile Tyr Glu Phe Leu Pro Ser Lys Arg Lys Thr Asp Val
340 345 350

Cys Tyr Tyr Tyr Gln Lys Phe Phe Asp Ser Ala Cys Thr Met Gly Ala
355 360 365

Tyr His Pro Leu Leu Tyr Glu Lys Asn Leu Val Lys His Leu Asn Gln
370 375 380

Gly Thr Asp Glu Asp Ile Tyr Leu Leu Gly Lys Ala Thr Leu Pro Gly
385 390 395 400

Phe Arg Thr Ile His Cys
405

<210> 16
<211> 1218
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotides sequence of human a-2,6 sialic acid transferase

<400> 16
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gccgtgatct gcggtgtggaa ggagaagaag aaaggcagct actacgacag cttcaagctg 120
cagaccaagg agttccaggt gctgaagagc ctgggcaagc tggccatggg cagcgacagc 180
cagagcgtgt ccagctcctc caccacaggat cccacacagag gcagacagac cctgggcagc 240
ctgagaggcc tggccaaggc caagcccagag gccagcttcc aggtgtggaa caaggacagc 300
agcagcaaga acctgatccc cagactgcag aagatctgga agaactacct gagcatgaac 360
aagtacaagg tgagctacaa aggacccgga cccggcatca agttcagcgc cgaggccctg 420
aggtgccacc tgagagacca cgtgaacgtg agcatgggtgg aagtgaccga cttccccttc 480
aacaccagcg agtgggaagg ctacctgccc aaggagagca tcaggaccaa ggctggcccc 540
tggggcagat gcgccgtggt gagcagcgtt ggcagcctga agagctccca gctgggcaga 600
gagatcgacg accacgatgc cgtgctgagg ttcaatggcg ctcccaccgc caacttccag 660

Sequence Listing

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caggacgtgg gcaccaagac cacaatccgg ctgatgaaca gccagctggt gacaaccgag      720
aagcgggttcc tgaaggacag cctgtacaac gagggcatcc tgatcgtgtg ggatcccagc      780
gtgtaccaca gcgacatccc caagtgggtac cagaatcccg actacaactt cttcaacaac      840
tacaagacct atagaaagct gcacccaac cagcccttct acatcctgaa gcccagatg      900
ccctggggagc tgtgggacat cctgcaggag atcagccctg aagagatcca gccaaccct      960
ccctccagcg gcatgctggg cattatcatc atgatgaccc tgtgcgacca ggtggacatc     1020
tacgagttcc tgcccagcaa gagaaagacc gacgtgtgct actactatca gaagttcttc     1080
gacagcgctt gcaccatggg cgcctaccac cccctgctgt acgagaagaa cctggtgaag     1140
cacctgaacc agggcaccga cgaggacatc tacctgctgg gcaaagccac cctgcccggc     1200
ttcagaacca tccactgc                                     1218

```

```

<210>      17
<211>      30
<212>      PRT
<213>      Artificial Sequence

```

```

<220>
<223>      IgD hinge variant

```

```

<400>      17
Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Xaa Xaa Lys Glu Lys
  1             5             10             15

Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu Cys Pro
          20             25             30

```

```

<210>      18
<211>      49
<212>      PRT
<213>      Artificial Sequence

```

```

<220>
<223>      IgD hinge variant

```

Sequence Listing

<400> 18
 Ala Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys Ala Thr Thr Ala Pro
 1 5 10 15
 Ala Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Xaa Xaa
 20 25 30
 Lys Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu Cys
 35 40 45

Pro

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

<220>
 <223> IgD hinge

<400> 19
 Arg Asn Thr Gly Arg Gly Gly Glu Glu Lys Lys Lys Glu Lys Glu Lys
 1 5 10 15
 Glu Glu Gln Glu Glu Arg Glu Thr Lys Thr Pro Glu Cys Pro
 20 25 30

<210> 20
 <211> 425
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FceRIa ECD-hinge-Fc1

<400> 20
 Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
 1 5 10 15
 Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
 20 25 30
 Glu Val Ser Ser Thr Lys Trp Phe His Asn Gly Ser Leu Ser Glu Glu

Sequence Listing

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

Sequence Listing

290

295

300

Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
305 310 315 320

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
325 330 335

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
340 345 350

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
355 360 365

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
370 375 380

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
385 390 395 400

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
405 410 415

Lys Ser Leu Ser Leu Ser Leu Gly Lys
420 425

<210> 21
<211> 425
<212> PRT
<213> Artificial Sequence

<220>
<223> FceRIa ECD-hinge-Fc2

<400> 21
Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
1 5 10 15

Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
20 25 30

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

Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
50 55 60

Sequence Listing_SP020-017.txt

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

Sequence Listing

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
325 330 335

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
340 345 350

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
355 360 365

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
370 375 380

Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
385 390 395 400

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
405 410 415

Lys Ser Leu Ser Leu Ser Leu Gly Lys
420 425

<210> 22
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> FceRIa ECD-hinge-Fc3

<400> 22
Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
1 5 10 15

Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
20 25 30

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

Thr Asn Ser Ser Leu Asn Ile Val Asn Ala Lys Phe Glu Asp Ser Gly
50 55 60

Glu Tyr Lys Cys Gln His Gln Gln Val Asn Glu Ser Glu Pro Val Tyr
65 70 75 80

Sequence Listing

Leu Glu Val Phe Ser Asp Trp Leu Leu Leu Gln Ala Ser Ala Glu Val
 85 90 95
 Val Met Glu Gly Gln Pro Leu Phe Leu Arg Cys His Gly Trp Arg Asn
 100 105 110
 Trp Asp Val Tyr Lys Val Ile Tyr Tyr Lys Asp Gly Glu Ala Leu Lys
 115 120 125
 Tyr Trp Tyr Glu Asn His Asn Ile Ser Ile Thr Asn Ala Thr Val Glu
 130 135 140
 Asp Ser Gly Thr Tyr Tyr Cys Thr Gly Lys Val Trp Gln Leu Asp Tyr
 145 150 155 160
 Glu Ser Glu Pro Leu Asn Ile Thr Val Ile Lys Ala Pro Arg Glu Lys
 165 170 175
 Tyr Trp Leu Gln Ala Gln Pro Gln Ala Glu Gly Ser Leu Ala Lys Ala
 180 185 190
 Thr Thr Ala Pro Ala Thr Thr Arg Asn Thr Gly Arg Gly Gly Glu Glu
 195 200 205
 Lys Lys Gly Ser Lys Glu Lys Glu Glu Gln Glu Glu Arg Glu Thr Lys
 210 215 220
 Thr Pro Glu Cys Pro Ser His Thr Gln Pro Leu Gly Val Phe Leu Phe
 225 230 235 240
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320
 Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
 325 330 335

Sequence Listing

Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
			340					345						350	
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		355					360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
	370					375					380				
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385					390					395					400
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
				405					410					415	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
		420						425					430		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys				
		435					440								