

<110> GI Innovation, Inc.

<120> FORMULATION FOR FUSION PROTEIN COMPRISING EXTRACELLULAR DOMAIN OF IgE
Fc RECEPTOR SUBUNIT ALPHA

<130> SP022-001-GII-PCT

<150> KR 10-2021-0030501

<151> 2021-03-09

<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

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

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
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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

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 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 caagtggttc 120
 cacaatggca gcctgagcga ggagaccaac agctccctga acatcgtgaa cgccaagttc 180
 gaggacagcg gcgagtacaa gtgccagcac cagcaggtga acgagagcga gcccggtgtac 240
 ctggaggtgt tcagcgactg gctgctgctg caggccagcg ccgaggtggt gatggagggc 300
 cagcccctgt 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>
 <223> nucleotides sequence of modified Fc

<400> 6
 tgcgtggtcg tggatgtgag ccaggaagat cccgaagtgc agttcaactg gtacgtggat 60
 ggcgtggaag tgcacaacgc caagaccaag cccagagaag agcagttcaa ctccacctac 120
 agagtggatga gcgtgctgac cgtgctgcac caggactggc tgaacggcaa ggagtacaag 180
 tgcaagggtgt ccaacaaagg cctgcccagc tccatcgaga agaccatcag caaagccaaa 240
 ggccagccca gagaacccca ggtgtacacc ctgcctccca gccaggaaga gatgaccaag 300
 aaccaggtgt 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 cgagtgtccc agccacaccc agcccctggg cgtgttcctg 120
 ttcccccca agcccaagga caccctgatg atcagcagaa cccccgaggt gacc 174

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

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

<400> 8
 gccagcccc aggccgaggg cagcctggct aaggccacca cagctccgc caccaccagg 60
 aacaccggca gaggaggcga ggaaaagaaa ggaagcaagg agaaggagga gcaggaggaa 120
 agagaaacca agacccccga gtgccccagc cacaccacgc 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
 <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
 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
<211> 1350
<212> DNA
<213> Artificial Sequence

<220>
<223> nucleotides sequence of FcεRIα ECD-hinge-Fc2

<400> 12
atggacgcca tgctgagagg cctgtgctgt gtgctgctgc tgtgcggcgc cgtgttcgtg 60
tcccctagcc acgccgtgcc ccagaagccc aaggtgagcc tgaaccctcc ctggaacaga 120
atcttcaagg gcgagaacgt gaccctgacc tgcaacggca acaacttctt cgaggtgagc 180
agcaccaagt ggttcacaa tggcagcctg agcgaggaga ccaacagctc cctgaacatc 240
gtgaacgcca agttcgagga cagcggcgag tacaagtgcc agcaccagca ggtgaacgag 300
agcgagcccg 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 tgcaagaggaa caccggcaga ggaggcgagg aaaagaaagg aagcaaggag 660
aaggaggagc aggaggaaag agaaaccaag acccccagat gccccagcca caccagccc 720
ctgggcgtgt tcctgttccc cccaagccc aaggacaccc tgatgatcag cagaaccccc 780
gaggtgacct gcgtggctgt ggatgtgagc caggaagatc ccgaagtgc gttcaactgg 840
tacgtggatg gcgtggaagt gcacaacgcc aagaccaagc ccagagaaga gcagttcaac 900
tccacctaca gagtgggtgag cgtgctgacc gtgctgcacc aggactggct gaacggcaag 960
gagtacaagt gcaagggtgtc caacaaaggc ctgcccagct ccatcgagaa gaccatcagc 1020
aaagccaaag gccagcccag agaaccacag gtgtacaccc tgccctcccag ccaggaagag 1080
atgaccaaga accagggtgtc cctgacctgc ctggtgaaag gcttctaccc cagcgacatc 1140
gccgtggagt gggaaagcaa cggccagccc gagaacaatt acaagacaac ccctcccgtg 1200

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
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		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		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		400
Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr				
	405		410	415
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 aaggtgagcc tgaaccctcc ctggaacaga 120
 atcttcaagg gcgagaacgt gaccctgacc tgcaacggca acaacttctt cgaggtgagc 180
 agcaccaagt ggttccacaa tggcagcctg agcgaggaga ccaacagctc cctgaacatc 240
 gtgaacgcca agttcgagga cagcggcgag tacaagtgcc agcaccagca ggtgaacgag 300
 agcgagcccg 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
 ggcgtgttcc tgttcccccc caagcccaag gacaccctga tgatcagcag aacccccgag 840
 gtgacctgcg tggtcgtgga tgtgagccag gaagatcccg 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 tggtcagctg cagcgtgatg cacgaagccc tgcacaacca ctacacccag 1380
aagagcctgt ccctgagcct gggcaag 1407

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

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

<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
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
 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
 atgatccaca ccaacctgaa gaagaagttc agctgctgcg tgctggtggt cctgctgttc 60
 gccgtgatct gcgtgtggaa ggagaagaag aaaggcagct actacgacag cttcaagctg 120

cagaccaagg agttccaggt gctgaagagc ctgggcaagc tggccatggg cagcgacagc	180
cagagcgtgt ccagctcctc caccaggat cccacagag gcagacagac cctgggcagc	240
ctgagaggcc tggccaaggc caagcccag ggcagcttcc aggtgtggaa caaggacagc	300
agcagcaaga acctgatccc cagactgcag aagatctgga agaactacct gagcatgaac	360
aagtacaagg tgagctacaa aggacccgga cccggcatca agttcagcgc cgaggccctg	420
aggtgccacc tgagagacca cgtgaacgtg agcatggtgg aagtgaccga cttccccttc	480
aacaccagcg agtgggaagg ctacctgccc aaggagagca tcaggaccaa ggctggcccc	540
tggggcagat gcgccgtggt gagcagcgtt ggcagcctga agagctccca gctgggcaga	600
gagatcgacg accacgatgc cgtgctgagg ttcaatggcg ctcccaccgc caacttccag	660
caggacgtgg gcaccaagac cacaatccgg ctgatgaaca gccagctggt gacaaccgag	720
aagcggttcc tgaaggacag cctgtacaac gagggcatcc tgatcgtgtg ggatcccagc	780
gtgtaccaca gcgacatccc caagtggtag cagaatcccg actacaactt cttcaacaac	840
tacaagacct atagaaagct gcacccaac cagcccttct acatcctgaa gccccagatg	900
ccctgggagc tgtgggacat cctgcaggag atcagccctg aagagatcca gcccaaccct	960
ccctccagcg gcatgctggg cattatcatc atgatgacct tgtgcgacca ggtggacatc	1020
tacgagttcc tgcccagcaa gagaaagacc gacgtgtgct actactatca gaagttcttc	1080
gacagcgcct gcacatggg 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

<220>
 <221> VARIANT
 <222> (12)
 <223> Xaa is selected from the group consisting of Lys and Gly.

<220>
 <221> VARIANT
 <222> (13)
 <223> Xaa is selected from the group consisting of Glu, Gly and Ser.

<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

<220>
 <221> VARIANT
 <222> (31)
 <223> Xaa is selected from the group consisting of Lys and Gly.

<220>
 <221> VARIANT
 <222> (32)
 <223> Xaa is selected from the group consisting of Glu, Gly or Ser.

<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
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

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 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
 225 230 235 240
 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
 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

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 <212> PRT
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<220>

<223> FceRIa ECD-hinge-Fc2

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Val Pro Gln Lys Pro Lys Val Ser Leu Asn Pro Pro Trp Asn Arg Ile
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Phe Lys Gly Glu Asn Val Thr Leu Thr Cys Asn Gly Asn Asn Phe Phe
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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

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
 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

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 <211> 444
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<220>
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 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

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Glu	Tyr	Lys	Cys	Gln	His	Gln	Gln	Val	Asn	Glu	Ser	Glu	Pro	Val	Tyr		
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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		
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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		
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Glu	Ser	Glu	Pro	Leu	Asn	Ile	Thr	Val	Ile	Lys	Ala	Pro	Arg	Glu	Lys		
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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			
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				
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										