Sequence Listing

<110> PROGEN CO., LTD.
GI INNOVATION, INC.

<120> COMPOSITION COMPRISING PROBIOTICS AND IGE-BINDING POLYPEPTIDE AND USE THEREOF

<130> PCB812127GEE/PCT

<150> KR 10-2018-0004421
<151> 2018-01-12

<160> 22

<170> KopatentIn 2.0

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

<220>
<223> FCeRI1 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

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 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 FCeRI1 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 gcccgtgtac 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

agagtggtga gcgtgctgac cgtgctgcac caggactggc tgaacggcaa ggagtacaag 180

tgcaaggtgt 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 cgagtgcccc agccacaccc agcccctggg cgtgttcctg 120

ttccccccca 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
gcccagcccc aggccgaggg cagcctggct aaggccacca cagctcccgc caccaccagg 60

aacaccggca gaggaggcga ggaaaagaaa ggaagcaagg agaaggagga gcaggaggaa 120

agagaaacca agacccccga gtgccccagc cacacccagc ccctgggcgt gttcctgttc 180

ccccccaagc ccaaggacac cctgatgatc agcagaaccc 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
```

```
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 FceRIa 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 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 aggcaaggtg 540

tggcagctgg actacgagag cgagcccctg aacatcaccg tgatcaaggc tcccagagag 600

aagtactggc tgcagaggaa caccggcaga ggaggcgagg aaaagaaagg aagcaaggag 660

aaggaggagc aggaggaaag agaaaccaag acccccgagt gccccagcca cacccagccc 720

ctgggcgtgt tcctgttccc ccccaagccc aaggacaccc tgatgatcag cagaacccca 780

gaggtgacct gcgtggtcgt ggatgtgagc caggaagatc ccgaagtgca gttcaactgg 840

tacgtggatg gcgtggaagt gcacaacgcc aagaccaagc ccagagaaga gcagttcaac 900

tccacctaca gagtggtgag cgtgctgacc gtgctgcacc aggactggct gaacggcaag 960

gagtacaagt gcaaggtgtc caacaaaggc ctgcccagct ccatcgagaa gaccatcagc 1020

aaagccaaag gccagcccag agaaccccag gtgtacaccc tgcctcccag ccaggaagag 1080

atgaccaaga accaggtgtc 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                 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
```

```
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 FceRIa ECD-hinge-Fc3

<400> 14

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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 aggcaaggtg        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 accccaggtg tacaccctgc ctcccagcca ggaagagatg 1140

accaagaacc aggtgtccct gacctgcctg gtgaaaggct tctaccccag cgacatcgcc 1200

gtggagtggg aaagcaacgg ccagcccgag aacaattaca agacaacccc tcccgtgctg 1260

gatagcgatg gcagcttctt tctgtacagc agactgaccg tggacaagag cagatggcag 1320

gaaggcaacg tgttcagctg 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

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atgatccaca ccaacctgaa gaagaagttc agctgctgcg tgctggtgtt cctgctgttc         60

gccgtgatct gcgtgtggaa ggagaagaag aaaggcagct actacgacag cttcaagctg        120

cagaccaagg agttccaggt gctgaagagc ctgggcaagc tggccatggg cagcgacagc        180

cagagcgtgt ccagctcctc cacccaggat ccccacagag gcagacagac cctgggcagc        240

ctgagaggcc tggccaaggc caagcccgag gccagcttcc 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 gagcagcgct ggcagcctga agagctccca gctgggcaga        600

gagatcgacg accacgatgc cgtgctgagg ttcaatggcg ctcccaccgc caacttccag        660
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caggacgtgg gcaccaagac cacaatccgg ctgatgaaca gccagctggt gacaaccgag 720

aagcggttcc tgaaggacag cctgtacaac gagggcatcc tgatcgtgtg ggatcccagc 780

gtgtaccaca gcgacatccc caagtggtac cagaatcccg actacaactt cttcaacaac 840

tacaagacct atagaaagct gcaccccaac cagcccttct acatcctgaa gccccagatg 900

ccctgggagc tgtgggacat cctgcaggag atcagccctg aagagatcca gcccaaccct 960

ccctccagcg gcatgctggg cattatcatc atgatgaccc tgtgcgacca ggtggacatc 1020

tacgagttcc tgcccagcaa gagaaagacc gacgtgtgct actactatca gaagttcttc 1080

gacagcgcct 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

<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

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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

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         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
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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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<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

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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
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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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<213>    Artificial Sequence

<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
     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 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                 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
```