SEQUENCE LISTING

<110> Université Catholique de Louvain
LUCAS Sophie

<120> ANTI-GARP PROTEIN AND USES THEREOF

<130> CV - 285/PCT

<160> 52

<170> BiSSAP 1.3

<210> 1
<211> 662
<212> PRT
<213> Homo sapiens

<400> 1

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Val Ser Cys Gln Val Leu Gly Leu Leu Gln Val Pro Ser Val Leu Pro
        35                  40                  45
Pro Asp Thr Glu Thr Leu Asp Leu Ser Gly Asn Gln Leu Arg Ser Ile
    50                  55                  60
Leu Ala Ser Pro Leu Gly Phe Tyr Thr Ala Leu Arg His Leu Asp Leu
65                  70                  75                  80
Ser Thr Asn Glu Ile Ser Phe Leu Gln Pro Gly Ala Phe Gln Ala Leu
                85                  90                  95
Thr His Leu Glu His Leu Ser Leu Ala His Asn Arg Leu Ala Met Ala
            100                 105                 110
Thr Ala Leu Ser Ala Gly Gly Leu Gly Pro Leu Pro Arg Val Thr Ser
        115                 120                 125
Leu Asp Leu Ser Gly Asn Ser Leu Tyr Ser Gly Leu Leu Glu Arg Leu
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Leu Gly Glu Ala Pro Ser Leu His Thr Leu Ser Leu Ala Glu Asn Ser
145                 150                 155                 160
Leu Thr Arg Leu Thr Arg His Thr Phe Arg Asp Met Pro Ala Leu Glu
                165                 170                 175
Gln Leu Asp Leu His Ser Asn Val Leu Met Asp Ile Glu Asp Gly Ala
            180                 185                 190
Phe Glu Gly Leu Pro Arg Leu Thr His Leu Asn Leu Ser Arg Asn Ser
        195                 200                 205
Leu Thr Cys Ile Ser Asp Phe Ser Leu Gln Gln Leu Arg Val Leu Asp
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Leu Ser Cys Asn Ser Ile Glu Ala Phe Gln Thr Ala Ser Gln Pro Gln
225                 230                 235                 240
Ala Glu Phe Gln Leu Thr Trp Leu Asp Leu Arg Glu Asn Lys Leu Leu
                245                 250                 255
His Phe Pro Asp Leu Ala Ala Leu Pro Arg Leu Ile Tyr Leu Asn Leu
            260                 265                 270
Ser Asn Asn Leu Ile Arg Leu Pro Thr Gly Pro Pro Gln Asp Ser Lys
        275                 280                 285
Gly Ile His Ala Pro Ser Glu Gly Trp Ser Ala Leu Pro Leu Ser Ala
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Pro Ser Gly Asn Ala Ser Gly Arg Pro Leu Ser Gln Leu Leu Asn Leu
305                 310                 315                 320
Asp Leu Ser Tyr Asn Glu Ile Glu Leu Ile Pro Asp Ser Phe Leu Glu
                325                 330                 335
His Leu Thr Ser Leu Cys Phe Leu Asn Leu Ser Arg Asn Cys Leu Arg
            340                 345                 350
Thr Phe Glu Ala Arg Arg Leu Gly Ser Leu Pro Cys Leu Met Leu Leu
        355                 360                 365
Asp Leu Ser His Asn Ala Leu Glu Thr Leu Glu Leu Gly Ala Arg Ala
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Leu Gly Ser Leu Arg Thr Leu Leu Leu Gln Gly Asn Ala Leu Arg Asp
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Pro Ser Gly Cys Val Ala Phe Ser Gly Ile Thr Ser Leu Arg Ser Leu
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Ser Leu Val Asp Asn Glu Ile Glu Leu Leu Arg Ala Gly Ala Phe Leu
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His Thr Pro Leu Thr Glu Leu Asp Leu Ser Ser Asn Pro Gly Leu Glu
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Val Ala Thr Gly Ala Leu Gly Gly Leu Glu Ala Ser Leu Glu Val Leu
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Ala Leu Gln Gly Asn Gly Leu Met Val Leu Gln Val Asp Leu Pro Cys
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Phe Ile Cys Leu Lys Arg Leu Asn Leu Ala Glu Asn Arg Leu Ser His
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Leu Pro Ala Trp Thr Gln Ala Val Ser Leu Glu Val Leu Asp Leu Arg
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Gly Asn Gly Trp Leu Ala Ala Gln Leu His Gln Gly Arg Val Asp Val
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Asp Ala Thr Gln Asp Leu Ile Cys Arg Phe Ser Ser Gln Glu Glu Val
595 600 605
Ser Leu Ser His Val Arg Pro Glu Asp Cys Glu Lys Gly Gly Leu Lys
610 615 620
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<223> VH-CDR1

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<212> PRT
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<220>
<223> VH-CDR2

<400> 3
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<210> 4
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<213> Artificial Sequence

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<223> VH-CDR3

<400> 4
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<210> 5
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<212> PRT
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<220>
<223> VL-CDR1

<400> 5
Lys Ala Ser Asp His Ile Lys Asn Trp Leu Ala
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<210> 6
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<220>
<223> VL-CDR2

<400> 6
Gly Ala Thr Ser Leu Glu Ala
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<220>
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Gln Gln Tyr Trp Ser Thr Pro Trp Thr
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<220>
<223> heavy chain variable region

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Met Ala Val Leu Ala Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
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Ile Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala
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Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45
Thr Gly Tyr Gly Ile Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
50 55 60
Glu Trp Leu Gly Met Ile Trp Ser Asp Gly Ser Thr Asp Tyr Asn Ser
65 70 75 80
Val Leu Thr Ser Arg Leu Arg Ile Ser Lys Asp Asn Ser Asn Ser Gln
85 90 95
Val Phe Leu Lys Met Asn Ser Leu Gln Val Asp Asp Thr Ala Arg Tyr
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Tyr Cys Ala Arg Asp Arg Asn Tyr Tyr Asp Tyr Asp Gly Ala Met Asp
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Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser

130 135 140

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<212> PRT
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<220>
<223> light chain variable region

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Met Lys Phe Pro Ser Gln Leu Leu Leu Phe Leu Leu Phe Arg Ile Thr
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Gly Ile Ile Cys Asp Ile Gln Val Thr Gln Ser Ser Ser Tyr Leu Ser
20 25 30
Val Ser Leu Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Asp His
35 40 45
Ile Lys Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Ile Ala Pro
50 55 60
Arg Leu Leu Val Ser Gly Ala Thr Ser Leu Glu Ala Gly Val Pro Ser
65 70 75 80
Arg Phe Ser Gly Ser Gly Ser Gly Lys Asn Phe Thr Leu Ser Ile Thr
85 90 95
Ser Leu Gln Thr Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp
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Ser Thr Pro Trp Thr Phe Gly Gly Gly Thr Thr Leu Glu Ile Arg
115 120 125

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<212> DNA
<213> Artificial Sequence

<220>
<223> heavy chain variable region

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tgcaccgtct cagggttctc attaaccggc tatggtataa actgggttcg ccagcctcca 180

ggaaagggtc tggagtggct gggaatgata tggagtgatg gaagcacaga ctataattca 240

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atgaacagtc tgcaagttga tgacacagcc aggtactatt gtgccagaga tcgaaactac 360

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<212> DNA
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<223> light chain variable region

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attacttgca aggcaagtga ccacattaaa aattggttag cctggtatca gcagaaacca 180

ggaattgctc ctaggctctt agtttctggt gcaaccagtt tggaagctgg ggttccttca 240

agattcagtg gcagtggatc tggaaagaat ttcactctca gcattaccag tcttcagact 300

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<213> Artificial Sequence

<220>
<223> conformational epitope

<400> 12
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Ala Gly Gly Leu Gly Pro Leu Pro Arg Val Thr Ser Leu Asp Leu Ser
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Gly Asn Ser Leu Tyr Ser Gly Leu Leu
35 40

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<220>
<223> VH-CDR1 LHG-10

<400> 13
Ser Tyr Tyr Ile Asp
1 5

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<223> VH-CDR2 LHG-10

<400> 14
Arg Ile Asp Pro Glu Asp Gly Gly Thr Lys Tyr Ala Gln Lys Phe Gln
1 5 10 15
Gly

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<212> PRT
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<220>
<223> VH-CDR3 LHG-10

<400> 15
Asn Glu Trp Glu Thr Val Val Val Gly Asp Leu Met Tyr Glu Tyr Glu
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Tyr

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<220>
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<223> X is Y or F

<400> 16
Gln Ala Ser Gln Xaa Ile Xaa Ser Xaa Leu Ala
1 5 10

<210> 17
<211> 7
<212> PRT
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<220>
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<222> 1
<223> X is S or T

<220>
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<222> 2
<223> X is A or T

<220>
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<223> X is R or I

<220>
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<222> 5
<223> X is L or P

<220>
<221> SITE
<222> 6
<223> X is Q or K

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Xaa Xaa Ser Xaa Xaa Xaa Thr
1 5

<210> 18
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-CDR3 LHG-10

<220>
<221> SITE
<222> 4
<223> X is D, A, Y or V

<220>
<221> SITE
<222> 6
<223> X is A, L or V

<220>
<221> SITE
<222> 8
<223> X is V or P

<400> 18
Gln Gln Tyr Xaa Ser Xaa Pro Xaa Thr
1 5

<210> 19
<211> 11
<212> PRT
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<220>
<223> VL-CDR1 LHG-10

<400> 19
Gln Ala Ser Gln Ser Ile Ser Ser Tyr Leu Ala
1 5 10

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<211> 7
<212> PRT
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<220>
<223> VL-CDR2 LHG10

<400> 20
Gly Ala Ser Arg Leu Gln Thr
1 5

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<211> 9
<212> PRT
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<220>
<223> VL-CDR3 LHG10

<400> 21
Gln Gln Tyr Asp Ser Leu Pro Val Thr
1 5

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<211> 11
<212> PRT
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<220>
<223> VL-CDR1 LHG10.3

<400> 22
Gln Ala Ser Gln Ser Ile Val Ser Tyr Leu Ala
1 5 10

<210> 23

<211> 7
<212> PRT
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<220>
<223> VL-CDR2 LHG10.3

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1 5

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<220>
<223> VL-CDR3 LHG10.3

<400> 24
Gln Gln Tyr Ala Ser Ala Pro Val Thr
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<212> PRT
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<220>
<223> VL-CDR1 LHG10.4

<400> 25
Gln Ala Ser Gln Ser Ile Ser Ser Tyr Leu Ala
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<210> 26
<211> 7
<212> PRT
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<220>
<223> VL-CDR2 LHG10.4

<400> 26
Gly Thr Ser Arg Leu Lys Thr
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<211> 9
<212> PRT
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<220>
<223> VL-CDR3 LHG10.4

<400> 27
Gln Gln Tyr Tyr Ser Ala Pro Val Thr
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<210> 28
<211> 11
<212> PRT
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<220>
<223> VL-CDR1 LHG10.5

<400> 28

Gln Ala Ser Gln Thr Ile Ser Ser Phe Leu Ala
1 5 10

<210> 29
<211> 7
<212> PRT
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<220>
<223> VL-CDR2 LHG10.5

<400> 29
Arg Ala Ser Ile Pro Gln Thr
1 5

<210> 30
<211> 9
<212> PRT
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<220>
<223> VL-CDR3 LHG10.5

<400> 30
Gln Gln Tyr Val Ser Ala Pro Pro Thr
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<210> 31
<211> 11
<212> PRT
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<220>
<223> VL-CDR1 LHG10.6

<400> 31
Gln Ala Ser Gln Ser Ile Ser Ser Tyr Leu Ala
1 5 10

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

<220>
<223> VL-CDR2 LHG10.6

<400> 32
Gly Ala Ser Arg Leu Lys Thr
1 5

<210> 33
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> VL-CDR3 LHG10.6

<400> 33
Gln Gln Tyr Ala Ser Val Pro Val Thr
1 5

<210> 34
<211> 126
<212> PRT
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<400> 34
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Arg Phe Thr Ser Tyr
20 25 30
Tyr Ile Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45
Gly Arg Ile Asp Pro Glu Asp Gly Gly Thr Lys Tyr Ala Gln Lys Phe
50 55 60
Gln Gly Arg Val Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80
Val Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Arg Asn Glu Trp Glu Thr Val Val Val Gly Asp Leu Met Tyr Glu
100 105 110
Tyr Glu Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
115 120 125

<210> 35
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<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region of sequence LHG10

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

<210> 36
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region of sequence of LHG10.3

<400> 36
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Val Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Gly Ala Ser Arg Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Ser Phe Thr Leu Thr Ile Ser Gly Leu Glu Ala
65 70 75 80
Glu Asp Ala Gly Thr Tyr Tyr Cys Gln Gln Tyr Ala Ser Ala Pro Val
85 90 95
Thr Phe Gly Gln Gly Thr Gly Val Glu Leu Lys
100 105

<210> 37
<211> 107
<212> PRT
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<220>
<223> Light chain variable region of sequence of LHG10.4

<400> 37
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu Leu Ile
35 40 45
Tyr Gly Thr Ser Arg Leu Lys Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Ser Phe Thr Leu Thr Ile Ser Gly Leu Glu Ala
65 70 75 80
Glu Asp Ala Gly Thr Tyr Tyr Cys Gln Gln Tyr Tyr Ser Ala Pro Val
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Leu Lys
100 105

<210> 38
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Light chain variable region of sequence of LHG10.5

<400> 38
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Pro Ser Leu Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Thr Ile Ser Ser Phe
20 25 30
Leu Ala Trp Tyr His Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
35 40 45
Tyr Arg Ala Ser Ile Pro Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Ser Phe Thr Leu Thr Ile Gly Gly Leu Glu Ala
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Glu Asp Ala Gly Thr Tyr Tyr Cys Gln Gln Tyr Val Ser Ala Pro Pro
85 90 95
Thr Phe Gly Gln Gly Thr Lys Val Glu Leu Lys
100 105

<210> 39
<211> 107
<212> PRT
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<220>
<223> Light chain variable region of sequence of LHG10.6

<400> 39
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
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Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Asn Ile Leu Ile
35 40 45
Tyr Gly Ala Ser Arg Leu Lys Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Ser Phe Thr Leu Thr Ile Ser Gly Leu Glu Ala
65 70 75 80

Glu Asp Ala Gly Thr Tyr Tyr Cys Gln Gln Tyr Ala Ser Val Pro Val
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Thr Phe Gly Gln Gly Thr Lys Val Glu Leu Lys
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<400> 40
Glu Ala Ala Glu Asn Leu Tyr Phe Gln Gly Ala Ala Trp Ser His Pro
1 5 10 15
Gln Phe Glu Lys Gly Ala Ala Trp Ser His Pro Gln Phe Glu Lys Gly
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Ala Ala Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ala
35 40 45

<210> 41
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<212> RNA
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<210> 42
<211> 2188
<212> RNA
<213> Macaca fascicularis

<220>
<223> cynomolgus TGF β1

<400> 42
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<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> cyno TGFB S1

<400> 43
cgcctccccc atgccgccct ccg 23

<210> 44
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> cyno TGFB Sens 2

<400> 44
acaattcctg gcgatacctc 20

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> cyno TGFB Anti-Sens 1

<400> 45
ctcaaccact gccgcacaac 20

<210> 46
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> cyno TGFB Anti-Sens 2

<400> 46
tcagctgcat ttgcaggagc 20

<210> 47
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<223> human IgG1; Fc region of LHG-10

<400> 47

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

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
210 215 220
Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 48
<211> 330
<212> PRT
<213> Artificial Sequence

<220>
<223> Heavy chain constant domain of LHG-10

<220>
<221> SITE
<222> 297
<223> wherein X is N or Q

<400> 48
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15
Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30
Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45
Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60
Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80
Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110
Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140
Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
165 170 175
Glu Gln Tyr Xaa Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
180 185 190
His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
195 200 205
Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
210 215 220
Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225 230 235 240
Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
245 250 255
Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
260 265 270
Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
275 280 285
Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
290 295 300
Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305 310 315 320
Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
325 330

<210> 49
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

<223> Light chain constant domain of LHG-10

<400> 49
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1 5 10 15
Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
20 25 30
Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
35 40 45
Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
50 55 60
Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65 70 75 80
Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
85 90 95
Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
100 105

<210> 50
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> heavy chain variable region

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

<210> 51
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> light chain variable region

<400> 51
Asp Ile Gln Val Thr Gln Ser Ser Ser Tyr Leu Ser Val Ser Leu Gly
1 5 10 15
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Asp His Ile Lys Asn Trp
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Pro Gly Ile Ala Pro Arg Leu Leu Val
35 40 45
Ser Gly Ala Thr Ser Leu Glu Ala Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Lys Asn Phe Thr Leu Ser Ile Thr Ser Leu Gln Thr
65 70 75 80
Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr Pro Trp
85 90 95
Thr Phe Gly Gly Gly Thr Thr Leu Glu Ile Arg
100 105

<210> 52
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> VH-CDR1

<400> 52
Gly Tyr Gly Ile Asn
1 5