SEQUENCE LISTING

<110> Lonza Biologics PLC
<120> Expression vectors comprising chimeric cytomegalovirus promoter and enhancer sequences

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<140> not assigned yet
<141> 2013-09-23

<150> EP12185728.8
<151> 2012-09-24

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Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
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tac ggc cct ccc tgc ccc agc tgt ccc gcc cca gag ttc ctg ggc gga  3200
Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Glu Leu Gly Gly
                220                 225                 230
ccc tca gtg ttt ctg ttc cca ccc aag ccc aag gat acc ctg atg atc  3248
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
            235                 240                 245
agc cgg acc cct gaa gtg acc tgc gtg gtg gtg gat gtg agc cag gag  3296
Ser Arg Thr Pro Glu val Thr Cys Val Val Val Asp Val Ser Gln Glu
        250                 255                 260
gac ccc gaa gtc cag ttc aat tgg tac gtg gac ggc gtg gaa gtg cac  3344
Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
    265                 270                 275
aac gcc aag acc aag ccc aga gag gag cag ttc aac agc acc tac cgc  3392
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
280                 285                 290                 295
gtg gtg tct gtg ctg acc gtg ctg cac cag gat tgg ctg aac ggc aaa  3440
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
                300                 305                 310
gag tac aag tgc aag gtc tcc aac aag ggc ctg cct agc agc atc gag  3488
Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
            315                 320                 325
aaa acc atc agc aag gcc aag ggc cag cca cgc gag ccc cag gtg tac  3536
Lys Thr Ile Ser Lys Ala lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
        330                 335                 340
acc ctg ccc ccc agc caa gag gag atg acc aag aac cag gtg tcc ctg  3584
Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
    345                 350                 355
acc tgt ctg gtg aag ggc ttc tac ccc agc gac atc gcc gtg gag tgg  3632
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
360                 365                 370                 375
gag agc aac ggc cag ccc gag aac aac tac aag acc acc ccc cct gtg  3680
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr pro Pro Val
                380                 385                 390
ctg gac agc gat ggc agc ttc ttc ctg tac tca cgg ctg acc gtg gat  3728
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
            395                 400                 405
aag agc aga tgg caa gag ggc aat gtc ttt agc tgc agc gtg atg cac  3776
Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
        410                 415                 420
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gag gcc ctg cac aat cct aca ccc aga aga gcc tga gcctgtcc                3820
Glu Ala Leu His Asn Pro Thr Pro Arg Arg Ala Xaa
    425                 430
cctgggcaag tgatagtcgc gaattgatca taatcagcca taccacattt gtagaggttt       3880
tacttgcttt aaaaaacctc ccacacctcc ccctgaacct gaaacataaa atgaatgcaa       3940
ttgttgttgt taacttgttt attgcagctt ataatggtta caaataaagc aatagcatca       4000
caaatttcac aaataaagca ttttttttcac tgcattctag ttgtggtttg tccaaactca      4060
tcaatgtatc ttatcatgtc tggatcagct tgagcagctg tggaatgtgt gtcagttagg       4120
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gtcagcaacc aggtgtggaa agtccccagg ctccccagca ggcagaagta tgcaaagcat       4240
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gacgctcaag tcagaggtgg cgaaacccga caggactata aagataccag gcgtttcccc       4600
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ctctgctgaa gccagttacc ttcggaaaaa gagttggtag ctcttgatcc ggcaaacaaa       5020
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cacgttaagg gattttggtc atgagattat caaaaaggat cttcacctag atccttttaa       5200
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gtgctgcaat gataccgcga gacccacgct caccggctcc agatttatca gcaataaacc       5440
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cgcgcacatt tccccgaaaa gtgccacctg acgtctaaga aaccattatt atcatgacat       6280
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tgagtcaata gggactttcc attgggtttt gcccagtaca aaaggtcaat agggggtgag       6640
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ttttccagcc aatttaatta aaacgccatg tactttccca ccattgacgt caatgggcta       6760
ttgaaactaa tgcaacgtga cctttaaacg gtactttccc atagctgatt aatgggaaag       6820
taccgttctc gagccaatac acgtcaatgg gaagtgaaag ggcagccaaa acgtaacacc       6880
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gtagaacgca gcctcaggac ctccatagaa gacaccggga ccgatccagc ctccgcggcc       7060
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ttattgacca ttattgacca ctcccctatt ggtgacgata ctttccatta ctaatccata       7300
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taacagtgga ggccagactt aggcacagca cgatgcccac caccaccagt gtgccgcaca       7660
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acgcatttgg aagacttaag gcagcggcag aagaagatgc aggcagctga gttgttgtgt 7780
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tctgagcagt actcgttgct gccgcgcgcg ccaccagaca taatagctga cagactaaca 7900
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<210> 3
<211> 492
<212> DNA
<213> artificial sequence

<220>
<223> fragment of the mCMV IE1 promoter sequence

<400> 3

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aatcaacagg aaagtcccat tggagccaag tacactgagt caatagggac tttccattgg 120
gttttgccca gtacaaaagg tcaatagggg gtgagtcaat gggtttttcc cattattggc 180
acgtacataa ggtcaatagg ggtgagtcat tgggtttttc cagccaattt aattaaaacg 240
ccatgtactt tcccaccatt gacgtcaatg ggctattgaa actaatgcaa cgtgaccttt 300
aaacggtact ttcccatagc tgattaatgg gaaagtaccg ttctcgagcc aatacacgtc 360
aatgggaagt gaaagggcag ccaaaacgta acaccgcccc ggttttcccc tggaaattcc 420
atattggcac gcattctatt ggctgagctg cgttctacgt gggtataaga ggcgcgacca 480
gcgtcggtac cg 492

<210> 4
<211> 102
<212> DNA
<213> artificial sequence

<220>
<223> fragment of the mCMV IE1 promoter sequence ("core promoter")

<400> 4

acaccgcccc ggttttcccc tggaaattcc atattggcac gcattctatt ggctgagctg 60
cgttctacgt gggtataaga ggcgcgacca gcgtcggtac cg 102

<210> 5
<211> 117
<212> DNA
<213> artificial sequence

<220>
<223> fragment of the hCMV IE1 promoter sequence ("core promoter")

<400> 5

gcaccaaaat caacgggact ttccaaaatg tcgtaacaac tccgccccat tgacgcaaat 60
gggcggtagg cgtgtacggt gggaggtcta tataagcaga gctcgtttag tgaaccg 117

<210> 6
<211> 452
<212> DNA
<213> artificial sequence

<220>
<223> fragment of the sCMV IE1 enhancer sequence

<400> 6

gaccatagcc aattcaatat ggcgtatatg gactcatgcc aattcaatat ggtggatctg 60
gacctgtgcc aattcaatat ggcgtatatg gactcgtgcc aattcaatat ggtggatctg 120
gaccccagcc aattcaatat ggcggacttg gcaccatgcc aattcaatat ggcggacctg 180
gcactgtgcc aactggggag gggtctactt ggcacggtgc caagtttgag gaggggtctt 240
ggccctgtgc caagtccgcc atattgaatt ggcatggtgc caataatggc ggccatattg 300

gctatatgcc aggatcaata tataggcaat atccaatatg gccctatgcc aatatggcta 360
ttggccaggt tcaatactat gtattggccc tatgccatat agtattccat atatgggttt 420
tcctattgac gtagatagcc cctcccaatg gg 452

<210> 7
<211> 1074
<212> DNA
<213> artificial sequence

<220>
<223> chimeric 5'-untranslated regulatory sequence ("construct 1")

<220>
<221> enhancer
<222> (1)...(582)
<223> fragment of hCMV IE1 and mCMV IE1 enhancer sequence

<220>
<221> promoter
<222> (583)...(1074)
<223> fragment of mCMV IE1 promoter sequence

<400> 7

ctgcagtgaa taataaaatg tgtgtttgtc cgaaatacgc gttttgagat ttctgtcgcc 60
gactaaattc atgtcgcgcg atagtggtgt ttatcgccga tagagatggc gatattggaa 120
aaatcgatat ttgaaaatat ggcatattga aaatgtcgcc gatgtgagtt tctgtgtaac 180
tgatatcgcc atttttccaa aagtgatttt tgggcatacg cgatatctgg cgatagcgct 240
tatatcgttt acgggggatg gcgatagacg actttggtga cttgggcgat tctgtgtgtc 300
gcaaatatcg cagtttcgat ataggtgaca gacgatatga ggctatatcg ccgatagagg 360
cgacatcaag ctggcacatg gccaatgcat atcgatctat acattgaatc aatattggcc 420
attagccata ttattcattg gttatatagc ataaatcaat attggctatt ggccattgca 480
tacgttgtat ccatatcata atatgtacat ttatattggc tcatgtccaa cattaccgcc 540
atgttgacat tgattattga ctagttatta atagtaatca attactgagt cattagggac 600
tttccaatgg gttttgccca gtacataagg tcaatagggg tgaatcaaca ggaaagtccc 660
attggagcca agtacactga gtcaataggg actttccatt gggttttgcc cagtacaaaa 720
ggtcaatagg gggtgagtca atgggttttt cccattattg gcacgtacat aaggtcaata 780
ggggtgagtc attgggtttt tccagccaat ttaattaaaa cgccatgtac tttcccacca 840
ttgacgtcaa tgggctattg aaactaatgc aacgtgacct ttaaacggta ctttcccata 900
gctgattaat gggaaagtac cgttctcgag ccaatacacg tcaatgggaa gtgaaagggc 960
agccaaaacg taacaccgcc ccggttttcc cctggaaatt ccatattggc acgcattcta 1020
ttggctgagc tgcgttctac gtgggtataa gaggcgcgac cagcgtcggt accg 1074

<210> 8
<211> 1128
<212> DNA
<213> artificial sequence

<220>
<223> chimeric 5'-untranslated regulatory sequence ("construct 2")

<220>
<221> enhancer
<222> (1)...(1026)
<223> fragment of hCMV IE1 enhancer sequence

<220>
<221> promoter
<222> (1027)...(1128)
<223> fragment of mCMV IE1 promoter sequence ("core promoter")

<400> 8

ctgcagtgaa taataaaatg tgtgtttgtc cgaaatacgc gttttgagat ttctgtcgcc 60
gactaaattc atgtcgcgcg atagtggtgt ttatcgccga tagagatggc gatattggaa 120
aaatcgatat ttgaaaatat ggcatattga aaatgtcgcc gatgtgagtt tctgtgtaac 180
tgatatcgcc atttttccaa aagtgatttt tgggcatacg cgatatctgg cgatagcgct 240
tatatcgttt acgggggatg gcgatagacg actttggtga cttgggcgat tctgtgtgtc 300

gcaaatatcg cagtttcgat ataggtgaca gacgatatga ggctatatcg ccgatagagg 360
cgacatcaag ctggcacatg gccaatgcat atcgatctat acattgaatc aatattggcc 420
attagccata ttattcattg gttatatagc ataaatcaat attggctatt ggccattgca 480
tacgttgtat ccatatcata atatgtacat ttatattggc tcatgtccaa cattaccgcc 540
atgttgacat tgattattga ctagttatta atagtaatca attacggggt cattagttca 600
tagcccatat atggagttcc gcgttacata acttacggta aatggcccgc ctggctgacc 660
gcccaacgac ccccgcccat tgacgtcaat aatgacgtat gttcccatag taacgccaat 720
agggactttc cattgacgtc aatgggtgga gtatttacgg taaactgccc acttggcagt 780
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cgcctggcat tatgcccagt acatgacctt atgggacttt cctacttggc agtacatcta 900
cgtattagtc atcgctatta ccatggtgat gcggttttgg cagtacatca atgggcgtgg 960
atagcggttt gactcacggg gatttccaag tctccacccc attgacgtca atgggagttt 1020
gttttgacac cgccccggtt ttcccctgga aattccatat tggcacgcat tctattggct 1080
gagctgcgtt ctacgtgggt ataagaggcg cgaccagcgt cggtaccg 1128

<210> 9
<211> 509
<212> DNA
<213> artificial sequence

<220>
<223> chimeric 5'-untranslated regulatory sequence ("construct 3")

<220>
<221> enhancer
<222> (1)...(407)
<223> fragment of hCMV IE1 enhancer sequence

<220>
<221> promoter
<222> (408)...(509)
<223> fragment of mCMV IE1 promoter sequence ("core promoter")

<400> 9

cgcgttacat aacttacggt aaatggcccg cctggctgac cgcccaacga cccccgccca 60
ttgacgtcaa taatgacgta tgttcccata gtaacgccaa tagggacttt ccattgacgt 120
caatgggtgg agtatttacg gtaaactgcc cacttggcag tacatcaagt gtatcatatg 180
ccaagtacgc cccctattga cgtcaatgac ggtaaatggc ccgcctggca ttatgcccag 240
tacatgacct tatgggactt tcctacttgg cagtacatct acgtattagt catcgctatt 300
accatggtga tgcggttttg gcagtacatc aatgggcgtg gatagcggtt tgactcacgg 360
ggatttccaa gtctccaccc cattgacgtc aatgggagtt tgttttgaca ccgccccggt 420
tttcccctgg aaattccata ttggcacgca ttctattggc tgagctgcgt tctacgtggg 480
tataagaggc gcgaccagcg tcggtaccg 509

<210> 10
<211> 961
<212> DNA
<213> artificial sequence

<220>
<223> chimeric 5'-untranslated regulatory sequence ("construct 4")

<220>
<221> enhancer
<222> (1)...(452)
<223> fragment of sCMV IE1 enhancer sequence

<220>
<221> enhancer
<222> (453)...(859)
<223> fragment of hCMV IE1 enhancer sequence

<220>
<221> promoter
<222> (860)...(961)
<223> fragment of mCMV IE1 promoter sequence ("core promoter")

<400> 10

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gacctgtgcc aattcaatat ggcgtatatg gactcgtgcc aattcaatat ggtggatctg 120
gaccccagcc aattcaatat ggcggacttg gcaccatgcc aattcaatat ggcggacctg 180
gcactgtgcc aactggggag gggtctactt ggcacggtgc caagtttgag gaggggtctt 240
ggccctgtgc caagtccgcc atattgaatt ggcatggtgc caataatggc ggccatattg 300
gctatatgcc aggatcaata tataggcaat atccaatatg gccctatgcc aatatggcta 360
ttggccaggt tcaatactat gtattggccc tatgccatat agtattccat atatgggttt 420
tcctattgac gtagatagcc cctcccaatg ggcgcgttac ataacttacg gtaaatggcc 480
cgcctggctg accgcccaac gacccccgcc cattgacgtc aataatgacg tatgttccca 540
tagtaacgcc aatagggact ttccattgac gtcaatgggt ggagtattta cggtaaactg 600
cccacttggc agtacatcaa gtgtatcata tgccaagtac gccccctatt gacgtcaatg 660
acggtaaatg gcccgcctgg cattatgccc agtacatgac cttatgggac tttcctactt 720
ggcagtacat ctacgtatta gtcatcgcta ttaccatggt gatgcggttt tggcagtaca 780
tcaatgggcg tggatagcgg tttgactcac ggggatttcc aagtctccac cccattgacg 840
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g 961

<210> 11
<211> 909
<212> DNA
<213> artificial sequence

<220>
<223> chimeric 5'-untranslated regulatory sequence ("construct 5")

<220>
<221> enhancer
<222> (1)...(807)
<223> fragment of sCMV IE1 enhancer sequence

<220>
<221> promoter
<222> (808)...(909)
<223> fragment of mCMV IE1 promoter sequence ("core promoter")

<400> 11

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gacctgtgcc aattcaatat ggcgtatatg gactcgtgcc aattcaatat ggtggatctg 120
gaccccagcc aattcaatat ggcggacttg gcaccatgcc aattcaatat ggcggacctg 180
gcactgtgcc aactggggag gggtctactt ggcacggtgc caagtttgag gaggggtctt 240
ggccctgtgc caagtccgcc atattgaatt ggcatggtgc caataatggc ggccatattg 300
gctatatgcc aggatcaata tataggcaat atccaatatg gccctatgcc aatatggcta 360
ttggccaggt tcaatactat gtattggccc tatgccatat agtattccat atatgggttt 420
tcctattgac gtagatagcc cctcccaatg ggcggtccca tataccatat atggggcttc 480
ctaataccgc ccatagccac tcccccattg acgtcaatgg tctctatata tggtctttcc 540
tattgacgtc atatgggcgg tcctattgac gtatatggcg cctcccccat tgacgtcaat 600
tacggtaaat ggcccgcctg gctcaatgcc cattgacgtc aataggacca cccaccattg 660
acgtcaatgg gatggctcat tgcccattca tatccgttct cacgcccccct attgacgtca 720
atgacggtaa atggcccact tggcagtaca tcaatatcta ttaatagtaa cttggcaagt 780
acattactat tggaagtacg ccagggtaca ccgccccggt tttcccctgg aaattccata 840
ttggcacgca ttctattggc tgagctgcgt tctacgtggg tataagaggc gcgaccagcg 900
tcggtaccg 909

<210> 12
<211> 976
<212> DNA
<213> artificial sequence

<220>
<223> chimeric 5'-untranslated regulatory sequence ("construct 6")

<220>
<221> enhancer
<222> (1)...(452)

<223> fragment of sCMV IE1 enhancer sequence

<220>
<221> enhancer
<222> (453)…(859)
<223> fragment of hCMV IE1 enhancer sequence

<220>
<221> promoter
<222> (860)...(976)
<223> fragment of hCMV IE1 promoter sequence ("core promoter")

<400> 12
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gaccccagcc aattcaatat ggcggacttg gcaccatgcc aattcaatat ggcggacctg 180
gcactgtgcc aactggggag gggtctactt ggcacggtgc caagtttgag gaggggtctt 240
ggccctgtgc caagtccgcc atattgaatt ggcatggtgc caataatggc ggccatattg 300
gctatatgcc aggatcaata tataggcaat atccaatatg gccctatgcc aatatggcta 360
ttggccaggt tcaatactat gtattggccc tatgccatat agtattccat atatgggttt 420
tcctattgac gtagatagcc cctcccaatg ggcgcgttac ataacttacg gtaaatggcc 480
cgcctggctg accgcccaac gacccccgcc cattgacgtc aataatgacg tatgttccca 540
tagtaacgcc aatagggact ttccattgac gtcaatgggt ggagtattta cggtaaactg 600
cccacttggc agtacatcaa gtgtatcata tgccaagtac gccccctatt gacgtcaatg 660
acggtaaatg gcccgcctgg cattatgccc agtacatgac cttatgggac tttcctactt 720
ggcagtacat ctacgtatta gtcatcgcta ttaccatggt gatgcggttt tggcagtaca 780
tcaatgggcg tggatagcgg tttgactcac ggggatttcc aagtctccac cccattgacg 840
tcaatgggag tttgttttgg caccaaaatc aacgggactt tccaaaatgt cgtaacaact 900
ccgccccatt gacgcaaatg ggcggtaggc gtgtacggtg ggaggtctat ataagcagag 960
ctcgtttagt gaaccg 976

<210> 13
<211> 924
<212> DNA
<213> artificial sequence

<220>
<223> chimeric 5'-untranslated regulatory sequence ("construct 7")

<220>
<221> enhancer
<222> (1)...(807)
<223> fragment of sCMV IE1 enhancer sequence

<220>
<221> promoter
<222> (808)...(924)
<223> fragment of hCMV IE1 promoter sequence ("core promoter")

<400> 13
gaccatagcc aattcaatat ggcgtatatg gactcatgcc aattcaatat ggtggatctg 60
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gaccccagcc aattcaatat ggcggacttg gcaccatgcc aattcaatat ggcggacctg 180
gcactgtgcc aactggggag gggtctactt ggcacggtgc caagtttgag gaggggtctt 240
ggccctgtgc caagtccgcc atattgaatt ggcatggtgc caataatggc ggccatattg 300
gctatatgcc aggatcaata tataggcaat atccaatatg gccctatgcc aatatggcta 360
ttggccaggt tcaatactat gtattggccc tatgccatat agtattccat atatgggttt 420
tcctattgac gtagatagcc cctcccaatg ggcggtccca tataccatat atggggcttc 480
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tacggtaaat ggcccgcctg gctcaatgcc cattgacgtc aataggacca cccaccattg 660
acgtcaatgg gatggctcat tgcccattca tatccgttct cacgcccccct attgacgtca 720
atgacggtaa atggcccact tggcagtaca tcaatatcta ttaatagtaa cttggcaagt 780
acattactat tggaagtacg ccagggtgca ccaaaatcaa cgggactttc caaaatgtcg 840
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<210> 14

<211> 214
<212> PRT
<213> artificial sequence

<220>
<223> optimized cB72.3 kappa light chain

<400> 14

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Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ser Val Ser Val Gly
1               5                  10                  15
Asp Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Asn
            20                  25                  30
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45
Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80
Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro Tyr
                85                  90                  95
Thr Phe Gly Gly Gly Thr Arg Leu Glu Ile Lys Arg Thr Val Ala Ala
            100                 105                 110
Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
        115                 120                 125
Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
    130                 135                 140
Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145                 150                 155                 160
Asp Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
                165                 170                 175
Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
            180                 185                 190
Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
        195                 200                 205
Phe Asn Arg Gly Glu Cys
    210
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<210> 15
<211> 434
<212> PRT
<213> artificial sequence

<220>
<223> optimized cB72.3 gamma-4 heavy chain

<400> 15

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

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```
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
                165                 170                 175
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
            180                 185                 190
Lys Thr Tyr Thr cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val
        195                 200                 205
Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro
    210                 215                 220
Ala Pro Glu Glu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
225                 230                 235                 240
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu val Thr Cys Val
                245                 250                 255
Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
            260                 265                 270
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
        275                 280                 285
Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
    290                 295                 300
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
305                 310                 315                 320
Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
                325                 330                 335
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met
            340                 345                 350
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
        355                 360                 365
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
    370                 375                 380
Tyr Lys Thr Thr pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
385                 390                 395                 400
Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val
                405                 410                 415
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn Pro Thr Pro Arg
            420                 425                 430
Arg Ala
```