SEQUENCE LISTING

<110> VACCINEX, INC.

<120> FUSION PROTEINS TO FACILITATE SELECTION OF CELLS INFECTED WITH SPECIFIC IMMUNOGLOBULIN GENE RECOMBINANT VACCINIA VIRUS

<130> 1843.071PCO2/EJH/BNC

<140> To Be Assigned
<141> Herewith

<150> US 13/844,388
<151> 2013-03-15

<150> US 61/732,776
<151> 2012-12-03

<150> US 61/639,046
<151> 2012-04-26

<160> 32

<170> PatentIn version 3.5

<210> 1
<211> 1416
<212> DNA
<213> Artificial sequence

<220>
<223> pJEM1 transfer plasmid

<400> 1
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atcataaatt ccatgggatg gagctgtatc atcctcttct tggtagcaac agctacaggc 120

gcgcactccg agatccagct ggtgcagagc ggccctgagc tgaagcagcc tggcgagacc 180

gtgaggatca gctgcaaggc cagcggctac accttcacca actacggcat gaactgggtg 240

aagcaggccc ctggcaaggg cctgaagtgg atgggctgga tcaacaccta caccggcgag 300

cctacctacg ccgccgactt caagaggagg ttcaccttca gcctggagac cagcgccagc 360

accgcctacc tgcagatcag caacctgaag aacgacgaca ccgccaccta cttctgcgcc 420

aagtaccctc actactacgg cagcagccac tggtacttcg acgtgtgggg cgccggcacc 480

acggtcaccg tctcctcagc ctccaccaag ggcccatcgg tcttcccccct ggcaccctcc 540

tccaagagca cctctggggg cacagcggcc ctgggctgcc tggtcaagga ctacttcccc 600

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gctgtcctac agtcctcagg actctactcc ctcagcagcg tcgtgaccgt gccctccagc 720

agcttgggca cccagaccta catctgcaac gtgaatcaca agcccagcaa caccaaggtg 780

gacaagaaag ttacatcaac tacaaatgac actgataaag tagattatga agaatactcc 840

acagagttga ttgtaaatac agatagtgaa tcgactatag acataatact atctggatct 900

acacattcac cggaaactag ttctaagaaa cctgattata tagataattc taattgctcg 960

tcggtattcg aaatcgcgac tccggaacca attactgata atgtagaaga tcatacagac 1020

accgtcacat acactagtga tagcattaat acagtaagtg catcatctgg agaatccaca 1080

acagacgaga ctccggaacc aattactgat aaagaagatc atacagttac agacactgtc 1140

tcatacacta cagtaagtac atcatctgga attgtcacta ctaaatcaac caccgatgat 1200

gcggatcttt atgatacgta caatgataat gatacagtac caccaactac tgtaggcggt 1260

agtacaacct ctattagcaa ttataaaacc aaggactttg tagaaatatt tggtattacc 1320

gcattaatta tattgtcggc cgtggcaatt ttctgtatta catattatat atataataaa 1380

cgttcacgta aatacaaaac agagaacaaa gtctag 1416

<210> 2
<211> 446
<212> DNA
<213> Artificial sequence

<220>
<223> pVKE transfer plasmid

<400> 2
ggccaaaaat tgaaaaacta gatctattta ttgcacgcgg ccgcccatgg gatggagctg 60

tatcatcctc ttcttggtag caacagctac aggcgtgcac ttgactcgag atcaaacgaa 120

ctgtggctgc accatctgtc ttcatcttcc cgccatctga tgagcagttg aaatctggaa 180

ctgcctctgt tgtgtgcctg ctgaataact tctatcccag agaggccaaa gtacagtgga 240

aggtggataa cgccctccaa tcgggtaact cccaggagag tgtcacagag caggacagca 300

aggacagcac ctacagcctc agcagcaccc tgacgctgag caaagcagac tacgagaaac 360

acaaagtcta cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc acaaagagct 420

tcaacagggg agagtgttag gtcgac 446

<210> 3
<211> 455
<212> DNA
<213> Artificial sequence

<220>
<223> pVLE transfer plasmid

<400> 3
ggccaaaaat tgaaaaacta gatctattta ttgcacgcgg ccgcccatgg gatggagctg 60

tatcatcctc ttcttggtag caacagctac aggcgtgcac ttgactcgag aagcttaccg 120

tcctacgaac tgtggctgca ccatctgtct tcatcttccc gccatctgat gagcagttga 180

aatctggaac tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga gaggccaaag 240

tacagtggaa ggtggataac gccctccaat cgggtaactc ccaggagagt gtcacagagc 300

aggacagcaa ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact 360

acgagaaaca caaagtctac gcctgcgaag tcacccatca gggcctgagc tcgcccgtca 420

caaagagctt caacagggga gagtgttagg tcgac 455

<210> 4

<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> 5' primer huC?1-5B:

<400> 4
attaggatcc ggtcaccgtc tcctcagcc 29

<210> 5
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> 3' primer huC?1-3S:

<400> 5
attagtcgac tcatttaccg gagacaggga gag 33

<210> 6
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<223> CH1(F):

<400> 6
caagggaccc tggtcaccgt ctcctcagcc tcc 33

<210> 7
<211> 25
<212> DNA
<213> Artificial sequence

<220>
<223> CH1(R):

<400> 7
aactttcttg tccaccttgg tgttg 25

<210> 8
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> A56R(F):

<400> 8
caacaccaag gtggacaaga aagttacatc aactacaaat gacactgata g 51

<210> 9
<211> 40
<212> DNA
<213> Artificial sequence

<220>
<223> A56R(R):

<400> 9

tatagtcgac ctagactttg ttctctgttt tgtatttacg 40

<210> 10
<211> 1266
<212> DNA
<213> Artificial sequence

<220>
<223> VH (H2124)-CH1-A56R Fab Product Fusion Protein

<400> 10
caggtgcagc tgcagcagtg gggcgcagga ctgctgaagc ctagcgagac cctgtccctc 60

acctgcgctg tctatggcta ctccatcacc agcggctatt tctggaactg gatccgccag 120

cccccaggga aggggctgga gtggattggg tacatcagct acgacggcag cagcaactcc 180

aacccatctc tcaaaaatag ggtcacaatc agcagagaca cctccaagaa ccagttctcc 240

ctgaagctga gctctgtgac cgccgccgac accgctgtgt attactgtgc cagaggaact 300

accgggtttg cttactgggg ccaagggacc ctggtcaccg tctcctcagc ctccaccaag 360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tcgtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttacatcaac tacaaatgac 660

actgataaag tagattatga agaatactcc acagagttga ttgtaaatac agatagtgaa 720

tcgactatag acataatact atctggatct acacattcac cggaaactag ttctaagaaa 780

cctgattata tagataattc taattgctcg tcggtattcg aaatcgcgac tccggaacca 840

attactgata atgtagaaga tcatacagac accgtcacat acactagtga tagcattaat 900

acagtaagtg catcatctgg agaatccaca acagacgaga ctccggaacc aattactgat 960

aaagaagatc atacagttac agacactgtc tcatacacta cagtaagtac atcatctgga 1020

attgtcacta ctaaatcaac caccgatgat gcggatcttt atgatacgta caatgataat 1080

gatacagtac caccaactac tgtaggcggt agtacaacct ctattagcaa ttataaaacc 1140

aaggactttg tagaaatatt tggtattacc gcattaatta tattgtcggc cgtggcaatt 1200

ttctgtatta catattatat atataataaa cgttcacgta aatacaaaac agagaacaaa 1260

gtctag 1266

<210> 11
<211> 421
<212> PRT
<213> Artificial sequence

<220>
<223> VH (H2124)-CH1-A56R Fab Product Fusion Protein

<400> 11

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu

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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Tyr Ser Ile Thr Ser Gly
            20                  25                  30

Tyr Phe Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
        35                  40                  45

Ile Gly Tyr Ile Ser Tyr Asp Gly Ser Ser Asn Ser Asn Pro Ser Leu
    50                  55                  60

Lys Asn Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65                  70                  75                  80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Thr Thr Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
        115                 120                 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
    130                 135                 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145                 150                 155                 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
                165                 170                 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
            180                 185                 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
        195                 200                 205

Lys Val Asp Lys Lys Val Thr Ser Thr Thr Asn Asp Thr Asp Lys Val
    210                 215                 220

Asp Tyr Glu Glu Tyr Ser Thr Glu Leu Ile Val Asn Thr Asp Ser Glu
225                 230                 235                 240

Ser Thr Ile Asp Ile Ile Leu Ser Gly Ser Thr His Ser Pro Glu Thr
                245                 250                 255

Ser Ser Lys Lys Pro Asp Tyr Ile Asp Asn Ser Asn Cys Ser Ser Val
            260                 265                 270

Phe Glu Ile Ala Thr Pro Glu Pro Ile Thr Asp Asn Val Glu Asp His
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275 280 285

Thr Asp Thr Val Thr Tyr Thr Ser Asp Ser Ile Asn Thr Val Ser Ala
290 295 300

Ser Ser Gly Glu Ser Thr Thr Asp Glu Thr Pro Glu Pro Ile Thr Asp
305 310 315 320

Lys Glu Asp His Thr Val Thr Asp Thr Val Ser Tyr Thr Thr Val Ser
325 330 335

Thr Ser Ser Gly Ile Val Thr Thr Lys Ser Thr Thr Asp Asp Ala Asp
340 345 350

Leu Tyr Asp Thr Tyr Asn Asp Asn Asp Thr Val Pro Pro Thr Thr Val
355 360 365

Gly Gly Ser Thr Thr Ser Ile Ser Asn Tyr Lys Thr Lys Asp Phe Val
370 375 380

Glu Ile Phe Gly Ile Thr Ala Leu Ile Ile Leu Ser Ala Val Ala Ile
385 390 395 400

Phe Cys Ile Thr Tyr Tyr Ile Tyr Asn Lys Arg Ser Arg Lys Tyr Lys
405 410 415

Thr Glu Asn Lys Val
420

<210> 12
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Sense VH 3 primer

<400> 12
aatatgcgcg cactccgagg tgcagctggt ggagtctgg 39

<210> 13
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<223> Sense VH 3a primer

<400> 13
aatatgcgcg cactccgagg tgcagctgtt ggagtctgg 39

<210> 14
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Antisense JH 1 primer

<400> 14
gagacggtga ccagggtgcc ctggcccca 29

<210> 15
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Antisense JH 2 primer

<400> 15
gagacggtga ccagggtgcc acggcccca 29

<210> 16
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Antisense JH 3 primer

<400> 16
gagacggtga ccattgtccc ttggcccca 29

<210> 17
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Antisense JH 4/5 primer

<400> 17
gagacggtga ccagggttcc ctggcccca 29

<210> 18
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> Antisense JH 6 primer

<400> 18
gagacggtga ccgtggtccc ttggcccca 29

<210> 19
<211> 113
<212> PRT
<213> Artificial sequence

<220>
<223> variable heavy chain

<400> 19

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Thr Asp Tyr
            20                  25                  30

Tyr Leu Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Leu
        35                  40                  45

Ser Tyr Ile Ser Ser Tyr Ser Arg Tyr Thr Asn Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Thr Arg Asn Ser Ile Tyr
65                  70                  75                  80

Leu Gln Met Asn Asn Leu Arg Val Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ala Gly Ser Tyr Tyr Gly Tyr Trp Gly Gln Gly Thr Leu Val
            100                 105                 110

Thr
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<210> 20
<211> 121
<212> PRT
<213> Artificial sequence

<220>
<223> Her2 B10 clone

<400> 20

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Phe Val Gln Pro Gly Gly
1               5                   10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Asn Asn Tyr
            20                  25                  30

Ala Leu Ser Trp Val Arg Gln Ala Pro Gly Arg Gly Leu Lys Trp Val
        35                  40                  45

Ser Ala Ile Ser Pro Asp Gly Asp Tyr Ile Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Ile Phe Ser Arg Asp Asn Ser Arg Asn Met Leu Ser
65                  70                  75                  80

Leu Gln Met Thr Ser Leu Gly Ala Glu Asp Thr Ala Leu Tyr Tyr Cys
                85                  90                  95

Ala Arg Gln Asn Asn Val Arg Asp Gly Ala Val Ala Gly Pro Leu Asp
            100                 105                 110

His Trp Gly Gln Gly Thr Leu Val Thr
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115 120

<210> 21
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> A56R(F2)

<400> 21
caacaccaag gtggacaaga aagttaccac cgatgatgcg gatctttatg a 51

<210> 22
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> CH1 (R2):

<400> 22
acaaaagtat tggtaatcgt gtcataactt tcttgtccac cttggtgttg 50

<210> 23
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> A56R(R2):

<400> 23
tcataaagat ccgcatcatc ggtggtttta cccggagaca gggagaggct c 51

<210> 24
<211> 51
<212> DNA
<213> Artificial sequence

<220>
<223> A56R(F3):

<400> 24
gagcctctcc ctgtctccgg gtaaaaccac cgatgatgcg gatctttatg a 51

<210> 25
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> A56R(R3):

<400> 25
tatcagtgtc atttgtagtt gatgttttac ccggagacag ggagaggctc 50

<210> 26
<211> 50
<212> DNA
<213> Artificial sequence

<220>
<223> A56R (F4):

<400> 26
gagcctctcc ctgtctccgg gtaaaacatc aactacaaat gacactgata 50

<210> 27
<211> 1566
<212> DNA
<213> Artificial sequence

<220>
<223> VH (H2124)-IgG-A56R TR Construct

<400> 27
caggtgcagc tgcagcagtg gggcgcagga ctgctgaagc ctagcgagac cctgtccctc 60

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cccccaggga aggggctgga gtggattggg tacatcagct acgacggcag cagcaactcc 180

aacccatctc tcaaaaatag ggtcacaatc agcagagaca cctccaagaa ccagttctcc 240

ctgaagctga gctctgtgac cgccgccgac accgctgtgt attactgtgc cagaggaact 300

accgggtttg cttactgggg ccaagggacc ctggtcaccg tctcctcagc ctccaccaag 360

ggcccatcgg tcttcccccc ggcaccctcc tccaagagca cctctggggg cacagcggcc 420

ctgggctgcc tggtcaagga ctacttcccc gaaccggtga cggtgtcgtg gaactcaggc 480

gccctgacca gcggcgtgca caccttcccg gctgtcctac agtcctcagg actctactcc 540

ctcagcagcg tcgtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720

ctcttccccc caaaacccaa ggacaccctc atgatctccc ggacccctga ggtcacatgc 780

gtggtggtgg acgtgagcca cgaagaccct gaggtcaagt tcaactggta cgtggacggc 840

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caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

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ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacgca gaagagcctc 1320

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aaggactttg tagaaatatt tggtattacc gcattaatta tattgtcggc cgtggcaatt 1500

ttctgtatta catattatat atataataaa cgttcacgta aatacaaaac agagaacaaa 1560

gtctag 1566

<210> 28
<211> 521
<212> PRT
<213> Artificial sequence

<220>
<223> VH (H2124)-IgG-A56R TR Construct

<400> 28

Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys Pro Ser Glu
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Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Tyr Ser Ile Thr Ser Gly
20 25 30

Tyr Phe Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Ser Tyr Asp Gly Ser Ser Asn Ser Asn Pro Ser Leu
50 55 60

Lys Asn Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Thr Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
165 170 175

Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
180 185 190

Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
195 200 205

Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
210 215 220

```
Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
225                 230                 235                 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
                245                 250                 255

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
            260                 265                 270

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
        275                 280                 285

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
    290                 295                 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
                325                 330                 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
            340                 345                 350

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
        355                 360                 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
    370                 375                 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
                405                 410                 415

Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
            420                 425                 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Thr Thr
        435                 440                 445

Asp Asp Ala Asp Leu Tyr Asp Thr Tyr Asn Asp Asn Asp Thr Val Pro
    450                 455                 460

Pro Thr Thr Val Gly Gly Ser Thr Thr Ser Ile Ser Asn Tyr Lys Thr
465                 470                 475                 480

Lys Asp Phe Val Glu Ile Phe Gly Ile Thr Ala Leu Ile Ile Leu Ser
                485                 490                 495
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Ala Val Ala Ile Phe Cys Ile Thr Tyr Tyr Ile Tyr Asn Lys Arg Ser
500 505 510

Arg Lys Tyr Lys Thr Glu Asn Lys Val
515 520

<210> 29
<211> 1962
<212> DNA
<213> Artificial sequence

<220>
<223> VH (H2124)-IgG-A56R FL Construct

<400> 29
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acctgcgctg tctatggcta ctccatcacc agcggctatt tctggaactg gatccgccag 120

cccccaggga aggggctgga gtggattggg tacatcagct acgacggcag cagcaactcc 180

aacccatctc tcaaaaatag ggtcacaatc agcagagaca cctccaagaa ccagttctcc 240

ctgaagctga gctctgtgac cgccgccgac accgctgtgt attactgtgc cagaggaact 300

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ctcagcagcg tcgtgaccgt gccctccagc agcttgggca cccagaccta catctgcaac 600

gtgaatcaca agcccagcaa caccaaggtg gacaagaaag ttgagcccaa atcttgtgac 660

aaaactcaca catgcccacc gtgcccagca cctgaactcc tgggggggacc gtcagtcttc 720

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caggtcagcc tgacctgcct ggtcaaaggc ttctatccca gcgacatcgc cgtggagtgg 1140

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac 1200

ggctccttct tcctctacag caagctcacc gtggacaaga gcaggtggca gcaggggaac 1260

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tccctgtctc cgggtaaaac atcaactaca aatgacactg ataaagtaga ttatgaagaa 1380

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Tyr Phe Trp Asn Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp
35 40 45

Ile Gly Tyr Ile Ser Tyr Asp Gly Ser Ser Asn Ser Asn Pro Ser Leu
50 55 60

Lys Asn Arg Val Thr Ile Ser Arg Asp Thr Ser Lys Asn Gln Phe Ser
65 70 75 80

Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Thr Thr Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val
100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
115 120 125

Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu
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Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
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Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser

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Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr
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Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
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Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
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Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
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Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
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Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
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Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
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Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305                 310                 315                 320

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
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Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
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Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
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Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
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Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385                 390                 395                 400

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
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Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
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Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Thr Ser
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Leu Ile Val Asn Thr Asp Ser Glu Ser Thr Ile Asp Ile Ile Leu Ser
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Gly Ser Thr His Ser Pro Glu Thr Ser Ser Lys Lys Pro Asp Tyr Ile
485 490 495

Asp Asn Ser Asn Cys Ser Ser Val Phe Glu Ile Ala Thr Pro Glu Pro
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Ile Thr Asp Asn Val Glu Asp His Thr Asp Thr Val Thr Tyr Thr Ser
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Asp Ser Ile Asn Thr Val Ser Ala Ser Ser Gly Glu Ser Thr Thr Asp
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Glu Thr Pro Glu Pro Ile Thr Asp Lys Glu Asp His Thr Val Thr Asp
545 550 555 560

Thr Val Ser Tyr Thr Thr Val Ser Thr Ser Ser Gly Ile Val Thr Thr
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Lys Ser Thr Thr Asp Asp Ala Asp Leu Tyr Asp Thr Tyr Asn Asp Asn
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Asp Thr Val Pro Pro Thr Thr Val Gly Gly Ser Thr Thr Ser Ile Ser
595 600 605

Asn Tyr Lys Thr Lys Asp Phe Val Glu Ile Phe Gly Ile Thr Ala Leu
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