SEQUENCE LISTING

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<120> COMPOSITIONS AND METHODS RELATED TO ENGINEERED Fc CONSTRUCTS

<130> 50937-012WO3

<150> US 62/081,923
<151> 2014-11-19

<150> US 61/987,863
<151> 2014-05-04

<160> 46

<170> PatentIn version 3.5

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Gly Gly Ser Gly
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Ser Gly Gly Gly
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Gly Ser Gly Ser
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Gly Ser Gly Ser Gly Ser
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<400> 6

Gly Ser Gly Ser Gly Ser Gly Ser
1 5

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Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser
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Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly
Ser
1 5 10

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Gly Gly Ser Gly Gly Ser
1 5

<210> 10
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Ser
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Gly Gly Ser Gly
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Gly Gly Ser Gly
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Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
Gly
1 5 10

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<400> 16

Gly Gly Gly Gly Ser
1 5

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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
Gly Gly Gly Ser
1 5 10
15

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Gly Glu Asn Leu Tyr Phe Gln Ser Gly Gly
1 5 10

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<400> 19

Ser Ala Cys Tyr Cys Glu Leu Ser
1 5

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<400> 20

Arg Ser Ile Ala Thr
1 5

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<400> 21

Arg Pro Ala Cys Lys Ile Pro Asn Asp Leu Lys
Gln Lys Val Met Asn
1 5 10
15

His

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<220>
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<400> 22

Gly Gly Ser Ala Gly Gly Ser Gly Ser Gly Ser
Ser Gly Gly Ser Ser
1 5 10
15

Gly Ala Ser Gly Thr Gly Thr Ala Gly Gly Thr
Gly Ser Gly Ser Gly
20 25
30

Thr Gly Ser Gly
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<400> 23

Ala Ala Ala Asn Ser Ser Ile Asp Leu Ile Ser
Val Pro Val Asp Ser
1 5 10
15

Arg

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<400> 24

Gly Gly Ser Gly Gly Gly Ser Glu Gly Gly Gly
Ser Glu Gly Gly Gly
1 5 10
15

Ser Glu Gly Gly Gly Ser Glu Gly Gly Gly Ser
Glu Gly Gly Gly Ser
20 25
30

Gly Gly Gly Ser
35

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Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly
Ser
1 5 10

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<400> 26

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly
Gly Ser Gly Gly Gly
1 5 10
15

Ser Gly Gly Gly
20

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<400> 27

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
Gly Gly Gly Ser Gly
1 5 10
15

Gly Ser

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<220>
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<400> 28

Asp Ile Cys Leu Pro Arg Trp Gly Cys Leu Trp
1 5 10

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<211> 681
<212> DNA
<213> Homo sapiens

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gccggacccc cgaagtgacc 120

tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga
agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg
aacagtacaa cagcacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc
tgaacggcaa agaatacaag 300

tgcaaagtct ccaacaaggc cctgcctgcc cccatcgaga
aaaccatcag caaggccaag 360

ggccagcccc gcgagcccca ggtgtacaca ctgcccccca
gccgggacga gctgaccaag 420

aaccaggtgt ccctgacctg cctggtgaaa ggcttctacc
ccagcgatat cgccgtggaa 480

tgggagagca acggccagcc cgagaacaac tacaagacca
ccccccctgt gctggacagc 540

gacggctcat tcttcctgta cagcaagctg accgtggaca
agagccggtg gcagcagggc 600

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ctgagcctga gccccggcaa g
681

<210> 30
<211> 227
<212> PRT
<213> Homo sapiens

<400> 30

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
Pro Glu Leu Leu Gly
1 5 10
15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
Lys Asp Thr Leu Met
20 25
30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
Val Asp Val Ser His
35 40
45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
Tyr Asn Ser Thr Tyr
65 70 75
80

Arg Val Val Ser Val Leu Thr Val Leu His Gln
Asp Trp Leu Asn Gly
85 90
95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
Leu Pro Ala Pro Ile
100 105
110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
Arg Glu Pro Gln Val
115 120
125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
Lys Asn Gln Val Ser
130 135
140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
Asp Ile Ala Val Glu
145 150 155
160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
Lys Thr Thr Pro Pro
165 170
175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
Ser Lys Leu Thr Val
180 185
190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
Ser Cys Ser Val Met
195 200
205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys
Ser Leu Ser Leu Ser
210 215
220

Pro Gly Lys
225

<210> 31
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<212> DNA
<213> Artificial Sequence

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agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg
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Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
Pro Glu Leu Leu Gly
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15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
Lys Asp Thr Leu Met
20 25
30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
Val Asp Val Ser His
35 40
45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
Tyr Asn Ser Thr Tyr
65 70 75
80

Arg Val Val Ser Val Leu Thr Val Leu His Gln
Asp Trp Leu Asn Gly
85 90
95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
Leu Pro Ala Pro Ile
100 105
110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
Arg Glu Pro Gln Val
115 120
125

Tyr Thr Leu Pro Pro Cys Arg Asp Glu Leu Thr
Lys Asn Gln Val Ser
130 135
140

Leu Trp Cys Leu Val Lys Gly Phe Tyr Pro Ser
Asp Ile Ala Val Glu
145 150 155
160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
Lys Thr Thr Pro Pro
165 170
175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
Ser Lys Leu Thr Val
180 185
190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
Ser Cys Ser Val Met
195 200
205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys
Ser Leu Ser Leu Ser
210 215
220

Pro Gly Lys
225

<210> 33
<211> 681
<212> DNA
<213> Artificial Sequence

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gccggacccc cgaagtgacc 120

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agttcaattg gtacgtggac 180

ggcgtggaag tgcacaacgc caagaccaag cccagagagg
aacagtacaa cagcacctac 240

cgggtggtgt ccgtgctgac cgtgctgcac caggactggc
tgaacggcaa agaatacaag 300

tgcaaagtct ccaacaaggc cctgcctgcc cccatcgaga
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agagccggtg gcagcagggc 600

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accactacac ccagaagtcc 660

ctgagcctga gccccggcaa g
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<210> 34
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<220>
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<400> 34

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
Pro Glu Leu Leu Gly
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15

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
Lys Asp Thr Leu Met
20 25
30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
Val Asp Val Ser His
35 40
45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
Tyr Asn Ser Thr Tyr
65 70 75
80

Arg Val Val Ser Val Leu Thr Val Leu His Gln
Asp Trp Leu Asn Gly
85 90
95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
Leu Pro Ala Pro Ile
100 105
110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
Arg Glu Pro Gln Val
115 120
125

Cys Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
Lys Asn Gln Val Ser
130 135
140

Leu Ser Cys Ala Val Lys Gly Phe Tyr Pro Ser
Asp Ile Ala Val Glu
145 150 155
160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
Lys Thr Thr Pro Pro
165 170
175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Val
Ser Lys Leu Thr Val
180 185
190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
Ser Cys Ser Val Met
195 200
205

His Glu Ala Leu His Asn His Tyr Thr Gln Lys
Ser Leu Ser Leu Ser
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Pro Gly Lys
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<223> Synthetic Construct

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gccggacccc cgaagtgacc 120

tgcgtggtgg tggacgtgtc ccacgaggac cctgaagtga
agttcaattg gtacgtggac 180

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tgaacggcaa agaatacaag 300

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aaccaggtgt ccctgacctg cctggtgaaa ggcttctacc
ccagcgatat cgccgtggaa 480

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ccccccctgt gctggacagc 540

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agagccggtg gcagcagggc 600

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accactacac ccagaagtcc 660

ctgagcctga gccccggcaa g
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Pro Glu Leu Leu Gly
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Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
Lys Asp Thr Leu Met
20 25
30

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
Val Asp Val Ser His
35 40
45

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
Asp Gly Val Glu Val
50 55 60

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
Tyr Asn Ser Thr Tyr
65 70 75
80

Arg Val Val Ser Val Leu Thr Val Leu His Gln
Asp Trp Leu Asn Gly
85 90
95

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
Leu Pro Ala Pro Ile
100 105
110

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
Arg Glu Pro Gln Val
115 120
125

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
Lys Asn Gln Val Ser
130 135
140

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
Asp Ile Ala Val Glu
145 150 155
160

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
Lys Thr Thr Pro Pro
165 170
175

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
Ser Lys Leu Thr Val
180 185
190

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
Ser Cys Ser Val Met
195 200
205