

SEQUENCE LISTING

<110> Affinity Biosciences Pty Ltd

<120> Cytoplasmic expression of Fabs

<130> P94572.PCT

<150> AU 2013900572

<151> 2013-02-20

<160> 89

<170> PatentIn version 3.5

<210> 1

<211> 456

<212> DNA

<213> Homo sapiens

<400> 1

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| tcttttcgcac agtaatatatac ggccgtgtcc tcggctctca ggctgttcat ttgcagatac | 60 |
| agcgtgtttct tgggaattgtc tctggagatg gtgaaccggc ccttcacgga gtctgcgtag | 120 |
| tatgtgctac caccactacc actaatagct gagaccact ccagcccctt ccctggagcc | 180 |
| tggcggaccc agctcatggc atagctgcta aagggtgaatc cagaggctgc acaggagagt | 240 |
| ctcagggacc ccccaggctg taccaagcct cccccagact ccaacagctg cacctcacac | 300 |
| tggacacctg caaacaacaaa gaaaccctgg tcagaaactg ccacacgtat ccactgtttc | 360 |
| tctcactctt atccattcac actcaatttt tctattttctc catgaattac cttttaaaat | 420 |
| agccacaaga aaaagccagc tcagcccaaa ctccat | 456 |

<210> 2

<211> 296

<212> DNA

<213> Homo sapiens

<400> 2

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| gaggtgcagc tggttgagtc tgggggagggc ttggtacagc ctgggggggc cctgagactc | 60 |
| tctgtgcag cctctggatt caccttttagc agctatgcc tgagctgggt ccgccaggct | 120 |

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ccaggggaagg ggctggagtg ggtctcagct attagtggta gtggtggtag cacatactac      180
gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat      240
ctgcaaataga acagcctgag agccgaggac acggccgtat attactgtgc gaaaga      296

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<210> 3

<211> 98

<212> PRT

<213> Homo sapiens

<400> 3

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

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<210> 4

<211> 481

<212> DNA

<213> Homo sapiens

<400> 4

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atgaccctgc tgcaggtgga tgggctcggc ggggctgaaa tccccccaca cagtgtcat      60
gtgtctcacac tgccttaggg ctctttcatc cctggatctg tgtccaggcc aggcacgtgg      120
gaagatttac ttggagttca gctcctcagt ttcaagcctt ttctctcccg ttttctctcc      180
tgtaggatcc gtggcctcct atgagctgac tcagccaccc tcagtgtccg tgtccccagg      240
acagacagcc agcatcacct gctctggaga taaattgggg gataaatatg cttgctggta      300

```

```

tcagcagaag ccaggccagt cccctgtgct ggtcatctat caagatagca agcggccctc 360
agggatccct gagcgattct ctggctccaa ctctgggaac acagccactc tgaccatcag 420
cgggacccag gctatggatg aggctgacta ttactgtcag gcgtgggaca gcagcactgc 480
a 481

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<210> 5

<211> 285

<212> DNA

<213> Homo sapiens

<400> 5

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acctgctctg gagataaatt gggggataaa tatgcttgct ggtatcagca gaagccaggc 120
cagtcacctg tgctggatcat ctatcaagat agcaagcggc cctcagggat ccctgagcga 180
ttctctggct ccaactctgg gaacacagcc actctgacca tcagcgggac ccaggctatg 240
gatgaggctg actattactg tcaggcgtgg gacagcagca ctgca 285

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<210> 6

<211> 95

<212> PRT

<213> Homo sapiens

<400> 6

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

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<210> 7

<211> 781

<212> DNA

<213> Homo sapiens

<400> 7

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| atggcctgga ccgttctcct cctcggcctc ctctctcact gcacagggtga tccccccagg | 60 |
| gtctcaccaa cctgcccagc ccaagggttc tgggtccagc gtgtccttga ttctgagctc | 120 |
| aggaggggccc ttctgttgtt gggcaggatg ctcatgaccc tgctgcaggg tgggaggctg | 180 |
| gtggggctga actccccca aactgtgctc aaaggcttgt gagagcctga gggactgcac | 240 |
| ctgccaggag agagtagtga gttttcagtt caaagtctcc atacaacagg aaagtcattg | 300 |
| gccactgggg ctggggctga ttgcagggga taccctgagg gttcacagac tctctggagc | 360 |
| ttgtctggga cagcagggca agggatttca taagaagcat ctttcacctg caagccaacc | 420 |
| tctctcttat ttatttattt atttatttat ttatttattt atttattttt atctttgcag | 480 |
| gctctgtgac ctctatgtg ctgactcagc caccctcggg gtcagtggcc ccaggacaga | 540 |
| cggccaggat tacctgtggg ggaaacaaca ttggaagtaa aagtgtgcac tggtagcagc | 600 |
| agaagccagg ccaggcccct gtgctggtcg tctatgatga tagcgaccgg ccctcaggga | 660 |
| tccctgagcg attctctggc tccaactctg ggaacacggc caccctgacc atcagcaggg | 720 |
| togaagccgg ggatgaggcc gactattact gtcagggtgtg ggatagtagt agtgatcatc | 780 |
| c | 781 |

<210> 8

<211> 290

<212> DNA

<213> Homo sapiens

<400> 8

| | |
|--|-----|
| tcctatgtgc tgactcagcc accctcgggtg tcagtggccc caggacagac ggccaggatt | 60 |
| acctgtgggg gaaacaacat tggaagtaaa agtgtgcact ggtaccagca gaagccaggc | 120 |
| caggccccctg tgctgggtcg ctatgatgat agcgaccggc cctcagggat ccctgagcga | 180 |
| ttctctgggt ccaactctgg gaacacggcc accctgacca tcagcagggt cgaagccggg | 240 |
| gatgaggccg actattactg tcagggtgtg gatagtagta gtgatcatcc | 290 |

<210> 9

<211> 97

<212> PRT

<213> Homo sapiens

<400> 9

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

Pro

<210> 10

<211> 478

<212> DNA

<213> homo sapiens

<400> 10

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|------------|------------|------------|------------|------------|-------------|-----|
| atggcctggg | ctccactact | tctcaccctc | ctcgctcact | gcacaggtgg | ctgcctgcaa | 60 |
| ggaattcagg | gagcgttcct | ggatgtcacc | tgggctgatg | atctgttcct | cctgcctggg | 120 |
| aaccagtctt | catctctccc | cactgatctc | tgtgttgctc | tcttcttgca | ggttcttggg | 180 |
| ccaattttat | gctgactcag | ccccactctg | tgtcggagtc | tccggggaag | acggtaacca | 240 |
| tctcctgcac | cggcagcagt | ggcagcattg | ccagcaacta | tgtgcagtgg | taccagcagc | 300 |
| gcccgggcag | tgccccacc | actgtgatct | atgaggataa | ccaaagaccc | tctgggggtcc | 360 |
| ctgatcggtt | ctctggctcc | atcgacagct | cctccaactc | tgctccctc | accatctctg | 420 |
| gactgaagac | tgaggacgag | gctgactact | actgtcagtc | ttatgatagc | agcaatca | 478 |

<210> 11

<211> 296

<212> DNA

<213> Homo sapiens

<400> 11

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aattttatgc tgactcagcc ccactctgtg tcggagtctc cggggaagac ggtaaccatc      60
tcttgcaccg gcagcagtgg cagcattgcc agcaactatg tgcagtggta ccagcagcgc      120
ccgggcagtg cccccaccac tgtgatctat gaggataacc aaagaccctc tggggtcctt      180
gatcggttct ctggctccat cgacagctcc tccaactctg cctccctcac catctctgga      240
ctgaagactg aggacgaggc tgactactac tgtcagtcctt atgatagcag caatca      296

```

<210> 12

<211> 98

<212> PRT

<213> Homo sapiens

<400> 12

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

```

<210> 13

<211> 462

<212> DNA

<213> homo sapiens

<400> 13

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atgacctgct cccctctcct cctcaccctt ctcattcact gcacaggtgc ccagacacag      60
ggtcagggga ggggtccagg aagcccatga ggccctgctt tctccttctc tctctagacc    120
aagaatcacc gtgtctgtgt ctctcctgct tccaggggtcc tgggcccagt ctgtgttgac    180
gcagccgccc tcagtgtctg cggccccagg acagaaggtc accatctcct gctctggaag    240
cagctccaac attggaata attatgtatc ctggtaccag cagctcccag gaacagcccc    300
caaactcctc atttatgaca ataataagcg accctcaggg attcctgacc gattctctgg    360
ctccaagtct ggcacgtcag ccaccctggg catcaccgga ctccagactg gggacgaggc    420
cgattattac tgcggaacat gggatagcag cctgagtgtc gg                        462

```

<210> 14

<211> 296

<212> DNA

<213> Homo sapiens

<400> 14

```

cagtctgtgt tgacgcagcc gccctcagtg tctgcggccc caggacagaa ggtcaccatc      60
tcttgctctg gaagcagctc caacattggg aataattatg tatcctggta ccagcagctc    120
ccaggaacag cccccaaact cctcattht gacaataata agcgaccctc agggattcct    180
gaccgattct ctggctccaa gtctggcacg tcagccaccc tgggcatcac cggactccag    240
actggggacg aggccgatta ttactgcgga acatgggata gcagcctgag tgctgg      296

```

<210> 15

<211> 99

<212> PRT

<213> Homo sapiens

<400> 15

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Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
1           5           10           15
Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
           20           25           30
Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
           35           40           45
Ile Tyr Asp Asn Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser
           50           55           60

```

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80
Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Thr Trp Asp Ser Ser Leu
85 90 95
Ser Ala Gly

```
<210> 16
<211> 466
<212> DNA
<213> homo sapiens
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| | | | | | | | |
|------------|------------|------------|------------|------------|-------------|--|-----|
| <400> | 16 | | | | | | |
| atggcctggg | ctcctctcct | cctcactctc | ctcgctcact | gcacaggtga | ctggatacag | | 60 |
| gtccagggga | ggggcccttg | gaagcctatg | gattcttgct | ttctcctggt | gtctctagaa | | 120 |
| gccgaataat | gatgcctgtg | tctctcccac | ttccagggtc | ctggggccag | tctgtgctga | | 180 |
| cgcagccgcc | ctcagtgtct | ggggccccag | ggcagagggg | caccatctcc | tgcactggga | | 240 |
| gcagctccaa | catcggggca | ggttatgatg | tacactggta | ccagcagctt | ccaggaacag | | 300 |
| ccccaaaact | cctcatctat | ggtaacagca | atcggccttc | aggggtccct | gaccgattct | | 360 |
| ctgggtccaa | gtctggcacc | tcagcctccc | tggccatcac | tgggctccag | gctgagggatg | | 420 |
| aggctgatta | ttactgccag | tcctatgaca | gcagcctgag | tgggttc | | | 466 |

| | |
|-------|--------------|
| <210> | 17 |
| <211> | 299 |
| <212> | DNA |
| <213> | Homo sapiens |

[illegible]

| | |
|-----------------------|-----|
| $\langle 210 \rangle$ | 18 |
| $\langle 211 \rangle$ | 100 |

<212> PRT

<213> Homo sapiens

<400> 18

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

<210> 19

<211> 468

<212> DNA

<213> homo sapiens

<400> 19

atggccagct tccctctcct cctcaccctc ctcaactcact gtgcagggtga caggatgggg 60
 accaagaaaag gggccctggg aagcccatgg ggccctgctt tctcctcttg tctccttttg 120
 tctcttggtca atcaccatgt ctgtgtctct ctcaacttcca gggtcctggg ccaggtctgt 180
 gctgactcag ccaccctcag cgtctgggac ccccgggcag agggtcacca tctcttggtc 240
 tggaagcagc tccaacatcg gaagtaatac tgtaaactgg taccagcagc tcccaggaac 300
 ggcccccaaa ctctcatct atagtaataa tcagcgcccc tcaggggtcc ctgaccgatt 360
 ctctgggtcc aagtctggca cctcagcctc cctggccatc agtgggctcc agtctgagga 420
 tgaggctgat tattactgtg cagcatggga tgacagcctg aatggtcc 468

<210> 20

<211> 296

<212> DNA

<213> Homo sapiens

<400> 20

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cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc      60
tcttgttctg gaagcagctc caacatcgga agtaatactg taaactggta ccagcagctc      120
ccaggaacgg cccccaaact cctcatctat agtaataatc agcggccctc aggggtccct      180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccag      240
tctgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgaa tgggcc      296

```

<210> 21

<211> 99

<212> PRT

<213> Homo sapiens

<400> 21

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

```

<210> 22

<211> 468

<212> DNA

<213> homo sapiens

<400> 22

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atggccggct tccctctcct cctcaccctc ctcactcact gtgcagggtga caggatgggg      60
accaagagag gggccctggg aagcccatgg ggccctgctt tctcctcttg tctcctttcg      120
tctcttgtca atcaccatgt ctgtgtctct ctcacttcca gggtcctggg cccagtctgt      180
gctgactcag ccaccctcag cgtctgggac ccccgggcag agggtcacca tctcttggtc      240
tggaagcagc tccaacatcg gaagtaatta tgtatactgg taccagcagc tcccaggaac      300
ggcccccaaa ctctcatct atagtaataa tcagcgcccc tcaggggtcc ctgaccgatt      360
ctctggctcc aagtctggca cctcagcctc cctggccatc agtgggctcc ggtccgagga      420
tgaggctgat tattactgtg cagcatggga tgacagcctg agtgggtcc      468

```

<210> 23

<211> 296

<212> DNA

<213> Homo sapiens

<400> 23

```

cagtctgtgc tgactcagcc accctcagcg tctgggaccc ccgggcagag ggtcaccatc      60
tcttgttctg gaagcagctc caacatcgga agtaattatg tatactggta ccagcagctc      120
ccaggaacgg cccccaaact cctcatctat agtaataatc agcgggcctc aggggtccct      180
gaccgattct ctggctccaa gtctggcacc tcagcctccc tggccatcag tgggctccgg      240
tccgaggatg aggctgatta ttactgtgca gcatgggatg acagcctgag tgggtcc      296

```

<210> 24

<211> 99

<212> PRT

<213> Homo sapiens

<400> 24

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Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1           5           10           15
Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
          20           25           30
Tyr Val Tyr Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
          35           40           45
Ile Tyr Ser Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
          50           55           60

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[illegible]

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<210> 25
<211> 493
<212> DNA
<213> homo sapiens
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| | | | | | | | |
|------------|------------|------------|------------|-------------|------------|--|-----|
| <400> | 25 | | | | | | |
| atggcctgga | cccctctctg | gctcactctc | ctcactcttt | gcatagggtgc | tgcctcccag | | 60 |
| ggctcaacc | catattatca | tgctagctgt | gccaacctgg | ccctgagctt | cggctcaaca | | 120 |
| cagggagtag | tgtagggtgt | gggactctag | gcgtgaaacc | cttatcctca | cctcttctgt | | 180 |
| cctcttttgc | aggttctgtg | gtttcttctg | agctgactca | ggaccctgct | gtgtctgtgg | | 240 |
| ccttgggaca | gacagtcagg | atcacatgcc | aaggagacag | cctcagaagc | tattatgcaa | | 300 |
| gctggtacca | gcagaagcca | ggacaggccc | ctgtacttgt | catctatggt | aaaaacaacc | | 360 |
| ggccctcagg | gatcccagac | cgattctctg | gctccagctc | aggaaacaca | gcttccttga | | 420 |
| ccatcactgg | ggctcaggcg | gaagatgagg | ctgactatta | ctgtaactcc | cgggacagca | | 480 |
| gtggtaacca | tct | | | | | | 493 |

```
<210> 26
<211> 290
<212> DNA
<213> Homo sapiens
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| | |
|--|-----|
| <400> | 26 |
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| acatgccaaag gagacagcct cagaagctat tatgcaagct ggtaccagca gaagccagga | 120 |
| caggcccctg tactttgtcat ctatggtaaa aacaaccggc cctcagggat ccagaccga | 180 |
| ttctctggct ccagctcagg aaacacagct tccttgacca tcactggggc tcaggcgga | 240 |
| gatgaggctg actattactg taactccggg gacagcagt gtaacctct | 290 |

<210> 27

<211> 97

<212> PRT

<213> Homo sapiens

<400> 27

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

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<210> 28

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Variant Sequence 1

<220>

<221> VARIANT

<222> (1)..(3)

<223> X is any amino acid other than Trp, Gln, Lys, Glu, Met

<220>

<221> VARIANT

<222> (6)..(8)

<223> X is any amino acid other than Trp, Gln, Lys, Glu, Met

<400> 28

Xaa Xaa Xaa Gly Gly Xaa Xaa Xaa

1 5

<210> 29

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR Variant Sequence

<220>

<221> VARIANT

<222> (1)..(3)

<223> X is any amino acid other than Trp, Gln, Lys, Glu, Met

<220>

<221> VARIANT

<222> (5)..(7)

<223> X is any amino acid other than Trp, Gln, Lys, Glu, Met

<400> 29

Xaa Xaa Xaa Gly Xaa Xaa Xaa

1 5

<210> 30

<211> 11

<212> PRT

<213> Homo sapiens

<400> 30

Val Phe Gly Thr Gly Thr Lys Val Thr Val Ser

1 5 10

<210> 31

<211> 11

<212> PRT

<213> Homo sapiens

<400> 31

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Ser

1 5 10

<210> 32

<211> 11

<212> PRT

<213> Homo sapiens

<400> 32

Val Phe Gly Gly Gly Thr Lys Leu Thr Val Ser

1 5 10

<210> 33

<211> 11

<212> PRT

<213> Homo sapiens

<400> 33

Val Phe Gly Gly Gly Thr Gln Leu Ile Ile Ser

1 5 10

<210> 34

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<213> Homo sapiens

<400> 34

Val Phe Gly Glu Gly Thr Glu Leu Thr Val Ser

1 5 10

<210> 35

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Val Phe Gly Ser Gly Thr Lys Val Thr Val Ser
1 5 10

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<400> 36
Val Phe Gly Gly Gly Thr Gln Leu Thr Ala Ser
1 5 10

<210> 37
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<400> 37
Val Phe Gly Thr Gly Thr Lys Leu Ile Ile Ser
1 5 10

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<223> n is a, c, g, or t

<400> 38

gacgagggtc tgagacgaga ccgtcacttt cgtaccggtg ccgaacacca cagtannann 60

anntccgccca nnannanngt cccacgcctg acagtaatag tcagc 105

<210> 39

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<213> Homo sapiens

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<223> X is any amino acid other than Trp, Gln, Lys, Glu, Met

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<222> (15)..(17)

<223> X is any amino acid other than Trp, Gln, Lys, Glu, Met

<400> 39

Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Xaa Xaa Xaa Gly Gly Xaa Xaa

1 5 10 15

Xaa Thr Val Val Phe Gly Thr Gly Thr Lys Val Thr Val Ser Ser

20 25 30

<210> 40

<211> 105

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<222> (83)..(84)

<223> n is a, c, g, or t

<400> 40

gatcagggtc tgagacccgc tgctcacggt aaccatggta ccttgacccc aaatatcaaa 60

cgcannanna nngccannan nanntttcgc acagtagtaa acagc 105

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<211> 25

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<222> (11)..(13)

<223> X is any amino acid other than Trp, Gln, Lys, Glu, Met

<400> 41

Val Tyr Tyr Cys Ala Lys Xaa Xaa Xaa Gly Xaa Xaa Xaa Ala Phe Asp

1 5 10 15

Ile Trp Gly Gln Gly Thr Met Val Thr

20

25

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<222> (724)..(725)

<223> n is a, c, g, or t

<400> 42

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| atgggagacg gtcagtctgt gctgactcag ccaccctcag tgtccgtgtc cccaggacag | 60 |
| acagccagca tcacctgctc tggagataaa ttgggggata aatatgcttg ctggtatcag | 120 |
| cagaagccag gccagtcccc tgtgctgggtc atctatcaag atagcaagcg gccctcaggg | 180 |
| atccctgagc gattctcttg ctccaactct gggaacacag ccactctgac catcagcggg | 240 |
| accagggcta tggatgaggc tgactattac tgtcaggcgt gggacnntnn tnntggaggt | 300 |

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nntnntnnta ctgtggtggt cggcacgggc accaagctca tcatttcgtc tcagaccggt      360
ggttcttggtg gtggtggttc tggcggcggc ggctccggtg gtggtggatc cgaagtccaa      420
ctgctggagt cggcgggtgg cctggtgcag ccagggtggca gcctgcgctt gagctgcgcc      480
gcatccggtt ttactttcag cagctacgcg atgtcgtggg tgcgccaggc accgggcaag      540
ggcctggagt gggtcagcgc catcagcggg agcggcgggt ctacgtatta tgcggacagc      600
gtcaaggggc gtttcaccat cagccgtgac aattccaaaa acaccctgta cttgcagatg      660
aacagcttgc gtgcggaaga tacggctggt tactactgtg cgaaanntnn tnntggannt      720
nntnntgcct ttgatatttg gggcaagggt accatgggta ccgtgagcag c              771

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<210> 43

<211> 257

<212> PRT

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<222> (240)..(242)

<223> Xaa can be any naturally occurring amino acid

<400> 43

Met Gly Asp Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val

1

5

10

15

Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly
 20 25 30
 Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
 35 40 45
 Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
 50 55 60
 Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
 65 70 75 80
 Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Xaa
 85 90 95
 Xaa Xaa Gly Gly Xaa Xaa Xaa Thr Val Val Phe Gly Thr Gly Thr Lys
 100 105 110
 Val Thr Val Ser Ser Gln Thr Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser
 130 135 140
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
 145 150 155 160
 Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln
 165 170 175
 Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly
 180 185 190
 Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 195 200 205
 Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
 210 215 220
 Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Xaa Xaa Xaa Gly Xaa
 225 230 235 240
 Xaa Xaa Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
 245 250 255
 Ser

<210> 44

<211> 361

<212> DNA

<213> Homo sapiens

<400> 44

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atgggagacg gtcagtctgt gctgactcag ccaccctcag tgtccgtgtc cccaggacag      60
acagccagca tcacctgctc tggagataaa ttgggggata aatatgcttg ctggtatcag      120
cagaagccag gccagtcccc tgtgctgggtc atctatcaag atagcaagcg gccctcaggg      180
atccctgagc gattctctgg ctccaactct gggaacacag ccactctgac catcagcggg      240
acccaggcta tggatgaggc tgactattac tgtcaggcgt gggactgaga cctagacggt      300
ctctgcgttt gatatttggg gtcaaggtag catggttacc gtgagcagct cgtctcagac      360
c                                                                    361

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<210> 45

<211> 396

<212> DNA

<213> Homo sapiens

<400> 45

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actgtggtgt tcggcaccgg tacgaaagtg actgtctcat ctgagaccgg tggttctggt      60
ggtggtggtt ctggcggcgg cggtccggt ggtggtggat ccgaagtcca actgctggag      120
tcggcggttg gcctggtgca gccagggtggc agcctgcgcc tgagctgcgc cgcattccgt      180
tttactttca gcagctacgc gatgtcgtgg gtgcgccagg caccgggcaa gggcctggag      240
tggttcagcg ccatcagcgg tagcggcggg tctacgtatt atgcggacag cgtcaagggc      300
cgttttacca tcagccgtga caattccaaa aacaccctgt acttgcagat gaacagcttg      360
cgtgcggaag atacggctgt ttactactgt gcgaaa                          396

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<210> 46

<211> 8

<212> PRT

<213> Homo sapiens

<400> 46

Pro Phe Gly Gly Gly Gly Tyr Val

1

5

<210> 47

<211> 7

<212> PRT

<213> Homo sapiens

<400> 47

Pro Pro His Gly Ala Pro Ala

1 5

<210> 48

<211> 8

<212> PRT

<213> Homo sapiens

<400> 48

Leu Cys Ile Gly Gly Val Ala Ser

1 5

<210> 49

<211> 7

<212> PRT

<213> Homo sapiens

<400> 49

His Asn Ser Gly Asn Asn Phe

1 5

<210> 50

<211> 8

<212> PRT

<213> Homo sapiens

<400> 50

Phe Val Ser Gly Gly Ile Ser Thr

1 5

<210> 51

<211> 7

<212> PRT

<213> Homo sapiens

<400> 51

Phe Asn Phe Gly Asn Ala Tyr

1 5

<210> 52

<211> 8

<212> PRT

<213> Homo sapiens

<400> 52

Ile Asn Ser Gly Gly Ala Ser Phe

1 5

<210> 53

<211> 7

<212> PRT

<213> Homo sapiens

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<400> 53

Xaa Xaa Xaa Gly Thr Asn Tyr

1 5

<210> 54

<211> 8

<212> PRT

<213> Homo sapiens

<400> 54

Ser Arg Ala Gly Gly Cys Asn Gly

1 5

<210> 55

<211> 7

<212> PRT

<213> Homo sapiens

<400> 55

Phe Asp Tyr Gly His Cys Ile

1 5

<210> 56

<211> 8

<212> PRT

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<400> 56

Thr Asn Arg Gly Gly Val Cys Ala

1 5

<210> 57

<211> 7

<212> PRT

<213> Homo sapiens

<400> 57

Thr Ala Ala Gly Val Pro Phe

1 5

<210> 58

<211> 8

<212> PRT

<213> Homo sapiens

<400> 58

Phe Ser Thr Gly Gly Cys Ala Phe

1 5

<210> 59

<211> 7

<212> PRT

<213> Homo sapiens

<400> 59

Ala Ile Cys Gly Ala Thr Ala

1 5

<210> 60

<211> 8

<212> PRT

<213> Homo sapiens

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<222> (2)..(2)

<223> Xaa can be any naturally occurring amino acid

<400> 60

Phe Xaa Gly Gly Gly Asp Gly Thr

1 5

<210> 61

<211> 7

<212> PRT

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<400> 61

Pro Tyr Arg Gly Ser Phe Phe

1 5

<210> 62

<211> 8

<212> PRT

<213> Homo sapiens

<400> 62

Ile Ile Pro Gly Gly Leu Tyr Ala

1 5

<210> 63

<211> 7

<212> PRT

<213> Homo sapiens

<400> 63

Pro Val Ile Gly Ser Asn Thr

1 5

<210> 64

<211> 266

<212> PRT

<213> Homo sapiens

<400> 64

Met Gly Asp Gly Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val

1 5 10 15

Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly

20 25 30

Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val

35 40 45

Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg

50 55 60

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly

65 70 75 80

Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Phe

85 90 95

Asn Leu Gly Gly Cys Gly Asp Thr Val Val Phe Gly Thr Gly Thr Lys

100 105 110

Val Thr Val Ser Ser Gln Thr Gly Gly Ser Gly Gly Gly Gly Ser Gly
 115 120 125
 Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser
 130 135 140
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala
 145 150 155 160
 Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln
 165 170 175
 Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly
 180 185 190
 Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser
 195 200 205
 Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg
 210 215 220
 Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys His Ile Asp Gly Pro
 225 230 235 240
 Val Ala Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
 245 250 255
 Ser Ser Ser Gln Thr Ser Ile Leu Val Ala
 260 265

<210> 65

<211> 89

<212> PRT

<213> Homo sapiens

<400> 65

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln
 1 5 10 15
 Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp Lys Tyr Ala
 20 25 30
 Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu Val Ile Tyr
 35 40 45
 Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
 50 55 60
 Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Met

65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ala

85

<210> 66

<211> 93

<212> PRT

<213> Homo sapiens

<400> 66

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

<210> 67

<211> 93

<212> PRT

<213> Homo sapiens

<400> 67

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asp | Gly | Gln | Ser | Val | Leu | Thr | Gln | Pro | Pro | Ser | Val | Ser | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Pro | Gly | Gln | Thr | Ala | Ser | Ile | Thr | Cys | Ser | Gly | Asp | Lys | Leu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asp | Lys | Tyr | Ala | Cys | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ser | Pro | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Val | Ile | Tyr | Gln | Asp | Ser | Lys | Arg | Pro | Ser | Gly | Ile | Pro | Glu | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |

Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
65 70 75 80
Thr Gln Ala Met Asp Glu Ala His Tyr Tyr Cys Gln Thr
85 90

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<210> 68
<211> 93
<212> PRT
<213> Homo sapiens
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|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| <400> | 68 | | | | | | | | | | | | | | | |
| Met | Gly | Asp | Gly | Gln | Ser | Val | Leu | Thr | Gln | Pro | Pro | Ser | Val | Ser | Val | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Ser | Pro | Gly | Gln | Thr | Ala | Thr | Ile | Thr | Cys | Ser | Gly | Asp | Lys | Leu | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Asp | Lys | Phe | Ala | Cys | Trp | Tyr | Gln | Gln | Lys | Pro | Gly | Gln | Ser | Pro | Val | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Leu | Val | Ile | Tyr | Gln | Asp | Tyr | Gln | Arg | Pro | Ser | Gly | Ile | Pro | Glu | Arg | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Phe | Ser | Gly | Ser | Asn | Ser | Gly | Asn | Thr | Ala | Thr | Leu | Thr | Ile | Ser | Gly | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Thr | Gln | Val | Met | Asp | Glu | Ala | Asp | Tyr | Tyr | Cys | Gln | Ala | | | | |
| | | | | 85 | | | | | 90 | | | | | | | |

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<210> 69
<211> 87
<212> PRT
<213> Homo sapiens
<220>
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<223> Xaa can be any naturally occurring amino acid
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<220>  
<221>  misc_feature  
<222>  (61)..(61)
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<223> Xaa can be any naturally occurring amino acid

<400> 69

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Met Gly Asp Gly Gln Ser Val Leu Thr Gln Pro Pro Ala Val Ser Val
1           5           10           15
Ala Pro Glu Lys Thr Ala Thr Ile Ala Cys Gly Gly Asn Arg Ile Gly
           20           25           30
Ser Lys Ser Val His Trp Tyr Gln Xaa Lys Pro Gly Gln Ala Pro Val
           35           40           45
Leu Val Ile Tyr Asn Asp Asn Asp Arg Pro Ser Gly Xaa Pro Glu Arg
           50           55           60
Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Arg
65           70           75           80
Val Glu Val Gly Asp Glu Ala
           85

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<210> 70

<211> 87

<212> PRT

<213> Homo sapiens

<400> 70

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

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<210> 71

<211> 83

<212> PRT

<213> Homo sapiens

<400> 71

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

<210> 72

<211> 87

<212> PRT

<213> Homo sapiens

<400> 72

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

<210> 73

<211> 95

<212> PRT

<213> Homo sapiens

<400> 73

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

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<210> 74

<211> 99

<212> PRT

<213> Homo sapiens

<400> 74

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Met Gly Asp Gly Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu
1           5           10           15
Ser Pro Gly Lys Thr Val Thr Ile Pro Cys Thr Gly Ser Ser Gly Ser
          20           25           30
Ile Ala Ser Asn Tyr Val Gln Trp Tyr Gln Gln Arg Pro Gly Ser Ala
          35           40           45
Pro Thr Thr Val Ile Tyr Glu Asp Lys Gln Lys Pro Ser Gly Val Pro
          50           55           60
Asp Arg Phe Ser Gly Ser Ile Asp Ser Ser Ser Asn Ser Ala Ser Leu
65           70           75           80

```

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

| | |
|-------|--------------|
| <210> | 75 |
| <211> | 99 |
| <212> | PRT |
| <213> | Homo sapiens |

[illegible]

| | |
|-------|--------------|
| <210> | 76 |
| <211> | 99 |
| <212> | PRT |
| <213> | Homo sapiens |

<400> 76

Met Gly Asp Gly Asn Phe Met Leu Thr Gln Pro His Ser Val Ser Glu
1 5 10 15

Ser Pro Gly Lys Thr Val Thr Ile Ser Cys Thr Gly Arg Ser Gly Ser
20 25 30

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

<210> 77
 <211> 106
 <212> PRT
 <213> Homo sapiens

<400> 77
 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
 1 5 10 15
 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
 20 25 30
 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
 35 40 45
 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
 50 55 60
 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
 65 70 75 80
 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
 85 90 95
 Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
 100 105

<210> 78
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 78

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
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 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
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 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 Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro
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<210> 79

<211> 1403

<212> DNA

<213> Artificial Sequence

<220>

<223> Fab polynucleotide sequence

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<222> (286)..(291)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (295)..(300)

<223> n is a, c, g, or t

<220>

<221> misc_feature
 <222> (996)..(1004)
 <223> n is a, c, g, or t

<220>

<221> misc_feature
 <222> (1008)..(1016)
 <223> n is a, c, g, or t

<400> 79

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| actgcttcca tcacctgtag cggcgataag ctgggtgaca agtatgcgtg ttggtatcag | 120 |
| cagaaaccgg gtcaaagccc ggttctggtc atctaccaag atagcaagcg tccgtcgggt | 180 |
| atcccggagc gtttttagcgg cagcaattcc ggtaatacgg cgaccctgac catctccggc | 240 |
| acgcaggcta tggatgaggc agactactat tgccaggcgt gggatnnnnn nggtnnnnnn | 300 |
| accgtggtct ttggcacggg taccaaagtt accgttctgg gccagccgaa agcagcgccg | 360 |
| agcgtgacgc tgttcccggc gtccagcgaa gaactgcaag cgaacaaagc gacgctgggtg | 420 |
| tgctgatta gcgactttta tccagggtgcc gtcaccgtcg cgtggaaagc ggacagctcc | 480 |
| ccagtcaaag cgggcgttga aaccacgacc ccgagcaagc agtctaacaa caaatacgcg | 540 |
| gcctctagct acttgctcct gaccccgga caatggaaga gccaccgcag ctacagctgt | 600 |
| caggtcaccc atgagggtag caccgtggaa aagacgggtg cacctaccga gtgtagcgat | 660 |
| tacaaggacg acgacgataa ggagaatacc tgatgggtag cgagggtcag ctgctggaat | 720 |
| ccggtggtgg cttggtgcaa ccggtggtt cgttgcgtct gagctgtgcc gccagcggtt | 780 |
| tcacctttag cagctatgca atgtcctggg tgcgccaaag gcctggtaag ggcttgaggt | 840 |
| gggtgtctgc aattagcggg agcggcggtg gcacctatta cgccgatagc gtcaagggtc | 900 |
| gcttcactat tagccgtgat aacagcaaaa acacgctgta tctgcaaatg aattccctgc | 960 |
| gtgcagagga cacggcggtc tactactgcg caaaannnnn nnnnggtnnn nnnnnngcat | 1020 |
| tcgacatttg gggccagggt accatggtta ccgttagcag cgccagcacg aagggcccgga | 1080 |
| gcgttttccc gctggcgccg tgcagccgta gcacgtctgg cgttacggct gctctgggct | 1140 |
| gcctgggttaa ggactatttc ccggagccgg ttaccgtgag ctggaactct ggtgcgctga | 1200 |
| ctagcggtgt ccataccttt ccggccgtgc tgcagagcag cggctctgtac agcctgtcta | 1260 |
| gcgttgctcac cgttcctagc tctagcctgg gcactcagac gtacacctgc aatgttaatc | 1320 |
| acaaaccgag caataccaag gtcgataaga aagttgagcc gaaaagctgt tcgtctcaga | 1380 |
| cccaccacca tcatcaccac taa | 1403 |

<210> 80

<211> 466
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Amino acid sequence of Fab

<220>

<221> misc_feature

<222> (96)..(97)

<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

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<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature

<222> (332)..(334)

<223> Xaa can be any naturally occurring amino acid

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<221> misc_feature

<222> (336)..(338)

<223> Xaa can be any naturally occurring amino acid

<400> 80

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Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly
          20           25           30
Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
          35           40           45
Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg

```


| | | | | | |
|---|-----|-----|-----|-----|-----|
| 50 | | 55 | | 60 | |
| Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly | | | | | |
| 65 | | 70 | | 75 | 80 |
| Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Xaa | | | | | |
| | 85 | | 90 | | 95 |
| Xaa Gly Xaa Xaa Thr Val Val Phe Gly Thr Gly Thr Lys Val Thr Val | | | | | |
| | 100 | | 105 | | 110 |
| Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser | | | | | |
| | 115 | | 120 | | 125 |
| Ser Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser | | | | | |
| | 130 | | 135 | | 140 |
| Asp Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser | | | | | |
| 145 | | 150 | | 155 | 160 |
| Pro Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn | | | | | |
| | 165 | | 170 | | 175 |
| Asn Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp | | | | | |
| | 180 | | 185 | | 190 |
| Lys Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr | | | | | |
| | 195 | | 200 | | 205 |
| Val Glu Lys Thr Val Ala Pro Thr Glu Cys Ser Asp Tyr Lys Asp Asp | | | | | |
| | 210 | | 215 | | 220 |
| Asp Asp Lys Glu Asn Thr Met Gly Ser Glu Val Gln Leu Leu Glu Ser | | | | | |
| 225 | | 230 | | 235 | 240 |
| Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala | | | | | |
| | 245 | | 250 | | 255 |
| Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser Trp Val Arg Gln | | | | | |
| | 260 | | 265 | | 270 |
| Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Ser Gly | | | | | |
| | 275 | | 280 | | 285 |
| Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser | | | | | |
| | 290 | | 295 | | 300 |
| Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg | | | | | |
| 305 | | 310 | | 315 | 320 |
| Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Xaa Xaa Xaa Gly Xaa | | | | | |
| | 325 | | 330 | | 335 |
| Xaa Xaa Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser | | | | | |

340 345 350
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser
 355 360 365
 Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 370 375 380
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 385 390 395 400
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 405 410 415
 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 420 425 430
 Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
 435 440 445
 Lys Lys Val Glu Pro Lys Ser Cys Ser Ser Gln Thr His His His His
 450 455 460
 His His
 465

<210> 81
 <211> 233
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fab

<400> 81

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 Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val
 35 40 45
 Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg
 50 55 60

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Phe | Ser | Gly | Ser | Asn | Ser | Gly | Asn | Thr | Ala | Thr | Leu | Thr | Ile | Ser | Gly | |
| 65 | | | | 70 | | | | 75 | | | | 80 | | | | |
| Thr | Gln | Ala | Met | Asp | Glu | Ala | Asp | Tyr | Tyr | Cys | Gln | Ala | Trp | Asp | Phe | |
| 85 | | | | 90 | | | | 95 | | | | | | | | |
| Asn | Leu | Gly | Gly | Cys | Gly | Asp | Thr | Val | Val | Phe | Gly | Thr | Gly | Thr | Lys | |
| 100 | | | | 105 | | | | 110 | | | | | | | | |
| Val | Thr | Val | Leu | Gly | Gln | Pro | Lys | Ala | Ala | Pro | Ser | Val | Thr | Leu | Phe | |
| 115 | | | | 120 | | | | 125 | | | | | | | | |
| Pro | Pro | Ser | Ser | Glu | Glu | Leu | Gln | Ala | Asn | Lys | Ala | Thr | Leu | Val | Cys | |
| 130 | | | | 135 | | | | 140 | | | | | | | | |
| Leu | Ile | Ser | Asp | Phe | Tyr | Pro | Gly | Ala | Val | Thr | Val | Ala | Trp | Lys | Ala | |
| 145 | | | | 150 | | | | 155 | | | | 160 | | | | |
| Asp | Ser | Ser | Pro | Val | Lys | Ala | Gly | Val | Glu | Thr | Thr | Thr | Pro | Ser | Lys | |
| 165 | | | | 170 | | | | 175 | | | | | | | | |
| Gln | Ser | Asn | Asn | Lys | Tyr | Ala | Ala | Ser | Ser | Tyr | Leu | Ser | Leu | Thr | Pro | |
| 180 | | | | 185 | | | | 190 | | | | | | | | |
| Glu | Gln | Trp | Lys | Ser | His | Arg | Ser | Tyr | Ser | Cys | Gln | Val | Thr | His | Glu | |
| 195 | | | | 200 | | | | 205 | | | | | | | | |
| Gly | Ser | Thr | Val | Glu | Lys | Thr | Val | Ala | Pro | Thr | Glu | Cys | Ser | Asp | Tyr | |
| 210 | | | | 215 | | | | 220 | | | | | | | | |
| Lys | Asp | Asp | Asp | Asp | Lys | Glu | Asn | Thr | | | | | | | | |
| 225 | | | | 230 | | | | | | | | | | | | |

<210> 82

<211> 236

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> VH domain linked to IGHG3 CH1

<400> 82

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Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 20 | | 25 | | 30 | | | | | | | | | | |
| Ser | Ser | Tyr | Ala | Met | Ser | Trp | Val | Arg | Gln | Ala | Pro | Gly | Lys | Gly | Leu |
| | 35 | | 40 | | 45 | | | | | | | | | | |
| Glu | Trp | Val | Ser | Ala | Ile | Ser | Gly | Ser | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala |
| | 50 | | 55 | | 60 | | | | | | | | | | |
| Asp | Ser | Val | Lys | Gly | Arg | Phe | Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Asn |
| 65 | | | 70 | | 75 | | | | | | | | | 80 | |
| Thr | Leu | Tyr | Leu | Gln | Met | Asn | Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val |
| | | | 85 | | 90 | | | | | | | | | 95 | |
| Tyr | Tyr | Cys | Ala | Lys | His | Ile | Asp | Gly | Pro | Val | Ala | Ala | Phe | Asp | Ile |
| | 100 | | 105 | | 110 | | | | | | | | | | |
| Trp | Gly | Gln | Gly | Thr | Met | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys | Gly |
| | 115 | | 120 | | 125 | | | | | | | | | | |
| Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Cys | Ser | Arg | Ser | Thr | Ser | Gly | Gly |
| | 130 | | 135 | | 140 | | | | | | | | | | |
| Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val |
| 145 | | | 150 | | 155 | | | | | | | | | 160 | |
| Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe |
| | | | 165 | | 170 | | | | | | | | | 175 | |
| Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val |
| | 180 | | 185 | | 190 | | | | | | | | | | |
| Thr | Val | Pro | Ser | Ser | Ser | Leu | Gly | Thr | Gln | Thr | Tyr | Thr | Cys | Asn | Val |
| | 195 | | 200 | | 205 | | | | | | | | | | |
| Asn | His | Lys | Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys | Lys | Val | Glu | Pro | Lys |
| | 210 | | 215 | | 220 | | | | | | | | | | |
| Ser | Cys | Ser | Ser | Gln | Thr | His | His | His | His | His | His | | | | |
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<210> 83

<211> 1412

<212> DNA

<213> Artificial Sequence

<220>

<223> anti-mAG1 Fab polynucleotide sequence

<400> 83

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cagaaaccgg gtcaaagccc ggttctggtc atctaccaag atagcaagcg tccgtcgggt      180
atccccgagc gtttttagcgg cagcaattcc ggtaatacgg cgaccctgac catctccggc      240
acgcaggcta tggatgaggc agactactat tgccaggcgt gggatttcaa cctgggtggt      300
tgcggtgata ccgtggtctt tggcacgggt accaaagtta ccgttctggg ccagccgaaa      360
gcagcgccga gcgtgacgct gttcccgcgg tccagcgaag aactgcaagc gaacaaagcg      420
acgctggtgt gcctgattag cgacttttat ccagggtgccg tcaccgtcgc gtggaaagcg      480
gacagctccc cagtcaaagc gggcgttgaa accacgaccc cgagcaagca gtctaacaac      540
aaatacgcgg cctctagcta cttgtccctg accccggaac aatggaagag ccaccgcagc      600
tacagctgtc aggtcaccca tgagggtagc accgtggaaa agacggtggc acctaccgag      660
tgtagcgtat acaaggacga cgacgataag gagaatacct gatgggtagc gaggtgcagc      720
tgctggaatc cgggtggtggc ttggtgcaac cgggtggttc gttgcgtctg agctgtgccg      780
ccagcggttt caccttttagc agctatgcaa tgtcctgggt gcgccaagcg cctggtaagg      840
gcttggaagt ggtgtctgca attagcggta gcggcggtag cacctattac gccgatagcg      900
tcaagggtcg cttcactatt agccgtgata acagcaaaaa cacgtgttat ctgcaaatga      960
attccctgcg tgcagaggac acggcgggtc actactgcgc aaaacacatc gatggtccgg     1020
tggcggcatt cgacatttgg ggccagggtta ccatggttac cgttagcagc gccagcacga     1080
agggcccgag cgttttcccg ctggcgccgt gcagccgtag cacgtctggc ggtacggctg     1140
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gtgcgctgac tagcgggtgt catacctttc cggccgtgct gcagagcagc ggtctgtaca     1260
gcctgtctag cgttgtcacc gttcctagct ctagcctggg cactcagacg tacacctgca     1320
atgttaaatca caaaccgagc aataccaagg tcgataagaa agttgagccg aaaagctggt     1380
cgtctcagac ccaccaccat catcaccact aa                                     1412

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<210> 84

<211> 919

<212> PRT

<213> Artificial Sequence

<220>

<223> anti-mAG1 Fab::PG::SNAP::DBP fusion

<400> 84

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

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Ser | Gly | Gly | Ser | Thr | Tyr | Tyr | Ala | Asp | Ser | Val | Lys | Gly | Arg | Phe |
| 290 | | | | | | 295 | | | | | 300 | | | | |
| Thr | Ile | Ser | Arg | Asp | Asn | Ser | Lys | Asn | Thr | Leu | Tyr | Leu | Gln | Met | Asn |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ser | Leu | Arg | Ala | Glu | Asp | Thr | Ala | Val | Tyr | Tyr | Cys | Ala | Lys | His | Ile |
| | | | | 325 | | | | | | 330 | | | | 335 | |
| Asp | Gly | Pro | Val | Ala | Ala | Phe | Asp | Ile | Trp | Gly | Gln | Gly | Thr | Met | Val |
| | | | 340 | | | | | | 345 | | | | | 350 | |
| Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys | Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Pro | Cys | Ser | Arg | Ser | Thr | Ser | Gly | Gly | Thr | Ala | Ala | Leu | Gly | Cys | Leu |
| | 370 | | | | | 375 | | | | | | 380 | | | |
| Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro | Val | Thr | Val | Ser | Trp | Asn | Ser | Gly |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ala | Leu | Thr | Ser | Gly | Val | His | Thr | Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser |
| | | | | 405 | | | | | | 410 | | | | 415 | |
| Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val | Val | Thr | Val | Pro | Ser | Ser | Ser | Leu |
| | | | 420 | | | | | | 425 | | | | 430 | | |
| Gly | Thr | Gln | Thr | Tyr | Thr | Cys | Asn | Val | Asn | His | Lys | Pro | Ser | Asn | Thr |
| | 435 | | | | | | 440 | | | | | | 445 | | |
| Lys | Val | Asp | Lys | Lys | Val | Glu | Pro | Lys | Ser | Cys | Ser | Ser | Gln | Thr | Ser |
| | 450 | | | | | 455 | | | | | | | 460 | | |
| Leu | Ile | Glu | Val | Glu | Lys | Pro | Leu | Tyr | Gly | Val | Glu | Val | Phe | Val | Gly |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Glu | Thr | Ala | His | Phe | Glu | Ile | Glu | Leu | Ser | Glu | Pro | Asp | Val | His | Gly |
| | | | | 485 | | | | | | 490 | | | | 495 | |
| Gln | Trp | Lys | Leu | Lys | Gly | Gln | Pro | Leu | Thr | Ala | Ser | Pro | Asp | Cys | Glu |
| | | | 500 | | | | | | 505 | | | | | 510 | |
| Ile | Ile | Glu | Asp | Gly | Lys | Lys | His | Ile | Leu | Ile | Leu | His | Asn | Cys | Gln |
| | | 515 | | | | | 520 | | | | | | 525 | | |
| Leu | Gly | Met | Thr | Gly | Glu | Val | Ser | Phe | Gln | Ala | Ala | Asn | Ala | Lys | Ser |
| | 530 | | | | | | 535 | | | | | | 540 | | |
| Ala | Ala | Asn | Leu | Lys | Val | Lys | Glu | Leu | Asn | Ser | Ser | Ser | Gln | Thr | Ser |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Gly | Thr | Arg | His | His | Asn | Ser | His | Asn | Ser | Ser | Gly | Thr | Asn | Ser | Pro |
| | | | | 565 | | | | | | 570 | | | | 575 | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Val | Leu | Arg | Lys | Gly | Asp | Arg | Gly | Asp | Glu | Val | Cys | Gln | Leu | | | | |
| | | | | | | | | | | | | | | | | 580 | 585 | 590 | |
| Gln | Thr | Leu | Leu | Asn | Leu | Cys | Gly | Tyr | Asp | Val | Gly | Lys | Pro | Asp | Gly | | | | |
| | | | | | | | | | | | | | | | | 595 | 600 | 605 | |
| Ile | Phe | Gly | Asn | Asn | Thr | Phe | Asn | Gln | Val | Val | Lys | Phe | Gln | Lys | Asp | | | | |
| | | | | | | | | | | | | | | | | 610 | 615 | 620 | |
| Asn | Cys | Leu | Asp | Ser | Asp | Gly | Ile | Val | Gly | Lys | Asn | Thr | Trp | Ala | Glu | | | | |
| | | | | | | | | | | | | | | | | 625 | 630 | 635 | 640 |
| Leu | Phe | Ser | Lys | Tyr | Ser | Pro | Pro | Ser | Met | Asp | Lys | Asp | Cys | Glu | Met | | | | |
| | | | | | | | | | | | | | | | | 645 | 650 | 655 | |
| Lys | Arg | Thr | Thr | Leu | Asp | Ser | Pro | Leu | Gly | Lys | Leu | Glu | Leu | Ser | Gly | | | | |
| | | | | | | | | | | | | | | | | 660 | 665 | 670 | |
| Cys | Glu | Gln | Gly | Leu | His | Glu | Ile | Lys | Leu | Leu | Gly | Lys | Gly | Thr | Ser | | | | |
| | | | | | | | | | | | | | | | | 675 | 680 | 685 | |
| Ala | Ala | Asp | Ala | Val | Glu | Val | Pro | Ala | Pro | Ala | Ala | Val | Leu | Gly | Gly | | | | |
| | | | | | | | | | | | | | | | | 690 | 695 | 700 | |
| Pro | Glu | Pro | Leu | Met | Gln | Ala | Thr | Ala | Trp | Leu | Asn | Ala | Tyr | Phe | His | | | | |
| | | | | | | | | | | | | | | | | 705 | 710 | 715 | 720 |
| Gln | Pro | Glu | Ala | Ile | Glu | Glu | Phe | Pro | Val | Pro | Ala | Leu | His | His | Pro | | | | |
| | | | | | | | | | | | | | | | | 725 | 730 | 735 | |
| Val | Phe | Gln | Gln | Glu | Ser | Phe | Thr | Arg | Gln | Val | Leu | Trp | Lys | Leu | Leu | | | | |
| | | | | | | | | | | | | | | | | 740 | 745 | 750 | |
| Lys | Val | Val | Lys | Phe | Gly | Glu | Val | Ile | Ser | Tyr | Gln | Gln | Leu | Ala | Ala | | | | |
| | | | | | | | | | | | | | | | | 755 | 760 | 765 | |
| Leu | Ala | Gly | Asn | Pro | Ala | Ala | Thr | Ala | Ala | Val | Lys | Thr | Ala | Leu | Ser | | | | |
| | | | | | | | | | | | | | | | | 770 | 775 | 780 | |
| Gly | Asn | Pro | Val | Pro | Ile | Leu | Ile | Pro | Cys | His | Arg | Val | Val | Ser | Ser | | | | |
| | | | | | | | | | | | | | | | | 785 | 790 | 795 | 800 |
| Ser | Gly | Ala | Val | Gly | Gly | Tyr | Glu | Gly | Gly | Leu | Ala | Val | Lys | Glu | Trp | | | | |
| | | | | | | | | | | | | | | | | 805 | 810 | 815 | |
| Leu | Leu | Ala | His | Glu | Gly | His | Arg | Leu | Gly | Lys | Pro | Gly | Leu | Gly | Pro | | | | |
| | | | | | | | | | | | | | | | | 820 | 825 | 830 | |
| Ala | Gly | Asn | Ser | Gly | Lys | Gly | Ala | Val | Asn | Ile | Asn | Ala | Ala | Ser | Gln | | | | |
| | | | | | | | | | | | | | | | | 835 | 840 | 845 | |
| Gln | Glu | Leu | Glu | Ala | Leu | Pro | Gly | Ile | Gly | Pro | Ala | Lys | Ala | Lys | Ala | | | | |
| | | | | | | | | | | | | | | | | 850 | 855 | 860 | |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Ile | Ala | Glu | Tyr | Arg | Ala | Gln | Asn | Gly | Ala | Phe | Lys | Ser | Val | Asp | Asp | | | | |
| 865 | | | | | 870 | | | | | 875 | | | | | 880 | | | | |
| Leu | Ile | Lys | Val | Lys | Gly | Ile | Gly | Pro | Ala | Val | Leu | Ala | Lys | Leu | Lys | | | | |
| | | | | | 885 | | | | | 890 | | | | | 895 | | | | |
| Asp | Gln | Ala | Ser | Val | Gly | Ala | Pro | Ala | Pro | Lys | Gly | Pro | Ala | Lys | Pro | | | | |
| | | | | | 900 | | | | | 905 | | | | | 910 | | | | |
| Val | Leu | Pro | Ala | Val | Lys | Lys | | | | | | | | | | | | | |
| | | | | | 915 | | | | | | | | | | | | | | |

| | |
|-----------------------|---------------------|
| $\langle 210 \rangle$ | 85 |
| $\langle 211 \rangle$ | 8 |
| $\langle 212 \rangle$ | PRT |
| $\langle 213 \rangle$ | Artificial Sequence |

<220>
<223> FLAG epitope

<400> 85
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

| | |
|-------|---------------------|
| <210> | 86 |
| <211> | 20 |
| <212> | PRT |
| <213> | Artificial Sequence |

<220>

<223> VL CDR3 + J region sequence

```
<400> 86
Ser Ser Arg Asn Thr Val Val Phe Gly Thr Gly Thr Lys Val Thr Val
1          5          10          15
Ser Ser Gln Thr
          20
```

<210> 87

<211> 1892

<212> DNA

<213> Artificial Sequence

<220>

<223> IGLV6-57/IGHV3-23::CaM Fab sequence

<400> 87

| | |
|--|------|
| tctagaatgg gagacggtaa ttttatgctg actcagcccc actctgtgtc ggagtctccg | 60 |
| gggaagacgg taaccatctc ctgcacccgc agcagtggca gcattgccag caactatgtg | 120 |
| cagtgggtacc agcagcgccc gggcagtgcc cccaccactg tgatctatga ggataaccaa | 180 |
| agaccctctg ggggtccctga tcggttctct gggtccatcg acagctcctc caactctgcc | 240 |
| tccttcacca tctctggact gaagactgag gacgaggctg actactactg tcagtcttat | 300 |
| gattcatcgc gcaacaccgt ggtctttggc acgggtacca aagttaccgt tctgggccag | 360 |
| ccgaaagcag cgccgagcgt gacgctgttc ccgccgtcca gcgaagaact gcaagcgaac | 420 |
| aaagcgacgc tgggtgtgcct gattagcgac ttttatccag gtgccgtcac cgtcgcgtgg | 480 |
| aaagcggaca gctccccagt caaagcgggc gttgaaacca cgaccccgag caagcagtct | 540 |
| aacaacaaat acgcggcctc tagctacttg tccctgaccc cggaacaatg gaagagccac | 600 |
| cgcagctaca gctgtcaggt caccatgag ggtagcaccg tggaaaagac ggtggcacct | 660 |
| accgagtgtg gcgattacaa ggacgacgac gataaggaga atacctgatg ggtagcgagg | 720 |
| tgcagctgct ggaatccggt ggtggccttg tgcaaccggg tggttcgttg cgtctgagct | 780 |
| gtgccgccag cggtttcacc tttagcagct atgcaatgtc ctgggtgcgc caagcgctg | 840 |
| gtaagggctt ggagtgggtg tctgcaatta gcggtagcgg cggtagcacc tattacgccg | 900 |
| atagcgtcaa gggtcgcttc actattagcc gtgataacag caaaaacacg ctgtatctgc | 960 |
| aatgaattc cctgcgtgca gaggacacgg cggctacta ctgcgcaaaa cacatcgatg | 1020 |
| gtccggtggc ggcattcgac atttggggcc agggtagcat ggttaccgtt agcagcgcca | 1080 |
| gcacgaaggg cccgagcgtt ttcccgtgg cgccgtgcag ccgtagcacg tctggcggta | 1140 |
| cggctgctct gggctgcctg gttaaggact atttcccga gccggttacc gtgagctgga | 1200 |
| actctggtgc gctgactagc ggtgtccata cttttccggc cgtgctgcag agcagcggtc | 1260 |
| tgtacagcct gtctagcgtt gtcaccgttc ctagctctag cctgggcact cagacgtaca | 1320 |
| cctgcaatgt taatcacaaa ccgagcaata ccaaggtcga taagaaagt gagccgaaaa | 1380 |
| gctgttcgag ctcgtctcag accagcgcgg accaactgac cgaagaacaa atcgcggagt | 1440 |
| tcaaagaagc gttctccctg ttgacaaaag atggcgatgg tacgattacc accaaagaac | 1500 |
| tgggcaccgt tatgcgcagc ctgggccaga atccgacgga ggcggagctg caggacatga | 1560 |
| ttaacgaggt tgacgcggat ggtaacggca ccattgactt tccggagttt ttgacgatga | 1620 |
| tggcacgtaa gatgaaggat actgatagcg aagaagagat ccgtgaggca tttcgtgtgt | 1680 |

```

tcgataagga tggtaatggt tacatcagcg ccgcagaact gcgccacgtg atgacgaatc 1740
tgggtgagaa gctgaccgac gaagaggtcg atgagatgat tcgtgaggcc gacatcgacg 1800
gtgacgggtca ggtcaactat gaagagttcg ttcaaatgat gaccgctggt tccaacagtg 1860
attacaagga cgatgatgac aaataagaat tc 1892

```

<210> 88

<211> 392

<212> PRT

<213> Artificial Sequence

<220>

<223> Fab heavy chain::Calmodulin fusion

<400> 88

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Met Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
1           5           10           15
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
           20           25           30
Ser Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
           35           40           45
Glu Trp Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala
           50           55           60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
65           70           75           80
Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
           85           90           95
Tyr Tyr Cys Ala Lys His Ile Asp Gly Pro Val Ala Ala Phe Asp Ile
           100          105          110
Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly
           115          120          125
Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly
           130          135          140
Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145          150          155          160
Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
           165          170          175

```

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 180 185 190
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val
 195 200 205
 Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys
 210 215 220
 Ser Cys Ser Ser Ser Ser Gln Thr Ser Ala Asp Gln Leu Thr Glu Glu
 225 230 235 240
 Gln Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly
 245 250 255
 Asp Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu
 260 265 270
 Gly Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val
 275 280 285
 Asp Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu Phe Leu Thr Met
 290 295 300
 Met Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu
 305 310 315 320
 Ala Phe Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala
 325 330 335
 Glu Leu Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu
 340 345 350
 Glu Val Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Asp Gly Gln
 355 360 365
 Val Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala Gly Ser Asn Ser
 370 375 380
 Asp Tyr Lys Asp Asp Asp Asp Lys
 385 390

<210> 89

<211> 149

<212> PRT

<213> Artificial Sequence

<220>

<223> gpD::CBP fusion

<400> 89

```

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

```