

HB01P012W0 Sequence Listing\_ST25  
SEQUENCE LISTING

<110> Humabs BioMed SA, Bellinzona, Switzerland

<120> ULTRA-POTENT NEUTRALIZATION OF CYTOKINES BY MULTISPECIFIC  
ANTIBODIES AND USES THEREOF

<130> HB01P012W0

<140> PCT/EP2015/000879

<141> 2015-04-29

<160> 190

<170> PatentIn version 3.5

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA7 CDRH1 aa

<400> 1

Gly Phe Thr Val Ser Thr Asn Tyr  
1 5

<210> 2

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA7 CDRH2 aa

<400> 2

Leu Tyr Ala Gly Gly Val Thr  
1 5

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA7 CDRH3 aa

HB01P012WO Sequence Listing\_ST25

<400> 3

Ala Lys His Tyr Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser  
1 5 10 15

<210> 4

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA7 CDRL1 aa

<400> 4

Gln Ser Val Phe Tyr Thr Ser Lys Asn Lys Asn Tyr  
1 5 10

<210> 5

<400> 5

000

<210> 6

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA7 CDRL2 long aa

<400> 6

Leu Ile Tyr Trp Ala Ser Thr Arg Glu  
1 5

<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA7 CDRL3 aa

<400> 7

Gln Gln Tyr Tyr Ser Thr Pro Phe Thr  
1 5

# HB01P012W0 Sequence Listing\_ST25

```

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> GCA7 CDRH1 nuc varS1

<400> 8
ggattcaccg tcagtaccaa ctac
24

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> GCA7 CDRH1 nuc varS2

<400> 9
gggtttactg tgtctacaaa ctac
24

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> GCA7 CDRH1 nuc varN1

<400> 10
ggctttactg tctctacaaa ctac
24

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> GCA7 CDRH1 nuc varC1

<400> 11
ggcttcaccg tgtcaacaaa ctac
24

<210> 12
<211> 24
<212> DNA

```

# HB01P012WO Sequence Listing\_ST25

<213> Artificial Sequence

<220>

<223> GCA7 CDRH1 nuc varC2

<400> 12

gggtttaccg tctctacaaa ctac

24

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRH2 nuc varS1

<400> 13

ctttatgccg gaggtgtcac a

21

<210> 14

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRH2 nuc varS2/N1/C2

<400> 14

ctgtacgctg gcgggggtgac c

21

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRH2 nuc varC1

<400> 15

ctgtacgccg gaggcgtgac t

21

<210> 16

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRH3 nuc varS1

# HB01P012W0 Sequence Listing\_ST25

<400> 16  
gcgaaacact atgattcggg atattctacc atagatcact ttgactcc 48

<210> 17  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA7 CDRH3 nuc varS2

<400> 17  
gccaaacact atgatagtgg gtactccact attgaccatt ttgactct 48

<210> 18  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA7 CDRH3 nuc varN1

<400> 18  
gccaaacact atgatagtgg gtatagcaca atcgaccatt ttgacagc 48

<210> 19  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA7 CDRH3 nuc varC1

<400> 19  
gcaaaacact acgattctgg gtatagtaca attgaccatt ttgattct 48

<210> 20  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA7 CDRH3 nuc varC2

<400> 20  
gccaaacact atgatagtgg gtacagtacc attgaccatt tcgatagc 48

# HB01P012WO Sequence Listing\_ST25

<210> 21  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> GCA7 CDRL1 nuc varS1  
  
 <400> 21  
 cagagtgttt tctacacctc caaaaataaa aactac 36  
  
 <210> 22  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> GCA7 CDRL1 nuc varS2  
  
 <400> 22  
 cagtccgtct tctacaccag taagaacaaa aactat 36  
  
 <210> 23  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> GCA7 CDRL1 nuc varN1  
  
 <400> 23  
 cagagcgtgt tctacaccag taagaacaaa aactat 36  
  
 <210> 24  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> GCA7 CDRL1 nuc varC1  
  
 <400> 24  
 cagtccgtgt tctacacttc taagaacaaa aactat 36  
  
 <210> 25  
 <211> 36  
 <212> DNA

HB01P012WO Sequence Listing\_ST25

<213> Artificial Sequence

<220>

<223> GCA7 CDRL1 nuc varC2

<400> 25

cagagtgtct tctacaccag taagaacaaa aactat

36

<210> 26

<400> 26

000

<210> 27

<400> 27

000

<210> 28

<400> 28

000

<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRL2 long nuc varS1

<400> 29

ctcatttact gggcatctac ccgggag

27

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRL2 long nuc varS2/N1/C2

<400> 30

ctgatctact gggctagcac tagagag

27

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

# HB01P012WO Sequence Listing\_ST25

<220>

<223> GCA7 CDRL2 long nuc varC1

<400> 31

ctgatctact gggcctcaac ccgagag

27

<210> 32

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRL3 nuc varS1

<400> 32

cagcaatatt atagtacccc ttctact

27

<210> 33

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRL3 nuc varS2

<400> 33

cagcagtatt attctacccc cttcaca

27

<210> 34

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRL3 nuc varN1

<400> 34

cagcagtatt acagcacccc attcaca

27

<210> 35

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 CDRL3 nuc varC1



# HB01P012W0 Sequence Listing\_ST25

<400> 35  
cagcagtact atagcactcc attcacc 27

<210> 36  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA7 CDRL3 nuc varC2

<400> 36  
cagcagtatt attcaacacc cttcaca 27

<210> 37  
<211> 122  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> GCA7 heavy chain variable domain (VH) aa

<400> 37

Gly Val Gln Leu Val Gln 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 Val Ser Thr Asn  
20 25 30

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

Ser Ile Leu Tyr Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys  
50 55 60

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

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

Lys His Tyr Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp  
100 105 110

# HB01P012W0 Sequence Listing\_ST25

Gly Gln Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> 38  
<211> 113  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> GCA7 light chain variable domain (VL) aa

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Val Ala Val Ser Leu Gly  
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Phe Tyr Thr  
20 25 30

Ser Lys Asn Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln  
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val  
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
65 70 75 80

Ile Ser Ser Leu Arg Pro Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln  
85 90 95

Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile  
100 105 110

Lys

<210> 39  
<211> 366  
<212> DNA  
<213> Artificial Sequence

# HB01P012W0 Sequence Listing\_ST25

<220>

<223> GCA7 heavy chain variable domain (VH) nuc varS1

<400> 39

```

ggggtgcaac tgggtgcagtc tgggggaggc ttggtccagc cggggggggtc cctgagactc      60
tcctgtgcag cctctggatt caccgtcagt accaactaca tgagctgggt ccgccaggct      120
ccagggaagg ggctggagtg ggtctcaatt ctttatgccg gaggtgtcac aagggtacgca      180
gactccgtga agaccagatt caccatctcc agagacaatt ccaagaacac tctctttctt      240
caaatgaacg ccctgagcgc cgaggacacg gctatatatt actgtgcgaa acactatgat      300
tcgggatatt ctacataga tcactttgac tcctggggcc aggggaaccct ggtcaccgtc      360
tcctca                                         366
    
```

<210> 40

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 heavy chain variable domain (VH) nuc varS2

<400> 40

```

ggcgtgcagc tgggtgcagag cggcggcggc ctggtgcagc ctggagggtc actgagactg      60
tcatgcgcag caagcgggtt tactgtgtct acaaactaca tgtcttgggt gaggcaggca      120
cctggaaagg gactggagtg ggtctcaatc ctgtacgctg gcgggggtgac ccggtatgca      180
gacagcgtca agacccggtt cacaattagc agagataact ccaaaaatac tctgtttctg      240
cagatgaatg ccctgtccgc tgaagacacc gcaatctact attgcgcaa acactatgat      300
agtgggtact ccactattga ccattttgac tcttgggggc aggggactct ggtgactgtc      360
tcttca                                         366
    
```

<210> 41

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA7 heavy chain variable domain (VH) nuc varN1

# HB01P012W0 Sequence Listing\_ST25

```

<400> 41
ggcgtccagc tgggtgcagag cggaggggggc ctggtgcagc ctggcgggtc cctgagactg      60
agttgtgccg caagtggctt tactgtctct acaaactaca tgtcttgggt gaggcaggca      120
cctggaaagg gactggagtg ggtctcaatc ctgtacgctg gcggggtgac ccggtatgca      180
gacagcgtca agacccggtt cacaattagc agagataact ccaaaaatac tctgtttctg      240
cagatgaatg ccctgtccgc tgaagacacc gcaatctact attgcgcaa acactatgat      300
agtgggtata gcacaatcga ccattttgac agctggggac agggaactct ggtgacagtc      360
tcatca                                          366

```

```

<210> 42
<211> 366
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GCA7 heavy chain variable domain (VH) nuc varC1

```

```

<400> 42
ggagtgcagc tgggtccagag cggaggagga ctggtgcagc caggagggtc actgaggctg      60
agctgcgcag cttccggctt caccgtgtca acaaactaca tgagctgggt ccgccaggca      120
cctgggaagg gactggagtg ggtgtccatc ctgtacgccg gaggcgtgac tcgatatgct      180
gactctgtca agactcgggt caccatctct agagataaca gtaagaacac cctgtttctg      240
cagatgaatg cactgagtgc cgaagacaca gctatctact attgtgcaa acactacgat      300
tctgggtata gtacaattga ccattttgat tcttggggcc aggggacact ggtgactgtc      360
agctcc                                          366

```

```

<210> 43
<211> 366
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GCA7 heavy chain variable domain (VH) nuc varC2

```

```

<400> 43
ggcgtgcagc tgggtccagag cggaggcgga ctggtccagc ccggcggatc actgagactg      60
tcatgtgccg caagcgggtt taccgtctct acaaactaca tgtcttgggt gaggcaggca      120

```

# HB01P012WO Sequence Listing\_ST25

```

cctggaaagg gactggagtg ggtctcaatc ctgtacgctg gcgggggtgac ccggtatgca      180
gacagcgtca agacccgggt cacaattagc agagataact ccaaaaatac tctgtttctg      240
cagatgaatg ccctgtccgc tgaagacacc gcaatctact attgcgcaa acactatgat      300
agtgggtaca gtaccattga ccatttcgat agctgggggc aggggactct ggtgaccgtc      360
tcatca                                          366

```

```

<210> 44
<211> 339
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GCA7 light chain variable domain (VL) nuc varS1

```

```

<400> 44
gacatccaga tgaccagtc tccagactcc gtggctgtgt ctctgggcga gagggccacc      60
atcaactgca agtccagcca gagtgttttc tacacctcca aaaataaaaa ctacttagct      120
tggttccagc agaaaccagg acagcctcct aaactgctca ttactgggc atctaccgg      180
gagtccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc      240
atcagcagcc tgcggcctga agatgtggca gtttattact gtcagcaata ttatagtacc      300
cctttcactt tcggccctgg gaccaaagtg gatatcaaa                                339

```

```

<210> 45
<211> 339
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GCA7 light chain variable domain (VL) nuc varS2

```

```

<400> 45
gacattcaga tgaccagag tcctgacagc gtggccgtct cactggggga aagggtact      60
atcaattgta aaagttcaca gtccgtcttc tacaccagta agaacaaaaa ctatctggcc      120
tggtttcagc agaagccagg ccagccccct aaactgctga tctactgggc tagcactaga      180
gagtctggag tgccagacag attctctggc agtgggtcag gaaccgactt caccctgaca      240
attagctccc tgaggccccga agacgtggcc gtctattatt gtcagcagta ttattctacc      300

```

# HB01P012WO Sequence Listing\_ST25

cccttcacat tcggacctgg gactaaagtg gatatcaaa 339

<210> 46  
<211> 339  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA7 light chain variable domain (VL) nuc varN1

<400> 46  
gacattcaga tgacccagag tcctgattcc gtggctgtct cactggggga gcgagcaact 60  
attaactgca agtcttcaca gagcgtgttc tacaccagta agaacaaaaa ctatctggcc 120  
tggtttcagc agaagccagg ccagccccct aaactgctga tctactgggc tagcactaga 180  
gagtctggag tgccagacag attctctggc agtgggtcag gaaccgactt caccctgaca 240  
attagctccc tgaggcccga agacgtggcc gtctactatt gtcagcagta ttacagcacc 300  
ccattcacat tcggccctgg aaccaaagtg gatattaag 339

<210> 47  
<211> 339  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA7 light chain variable domain (VL) nuc varC1

<400> 47  
gacatccaga tgactcagtc tcccgatagt gtggccgtct ccctggggga gagggctaca 60  
attaactgca agagctccca gtccgtgttc tacacttcta agaacaaaaa ctatctggca 120  
tggtttcagc agaagcctgg acagccccct aaactgctga tctactgggc ctcaaccga 180  
gagagcggag tcccagacag attctcaggc agcgggtccg gaacagattt taccctgaca 240  
atttctagtc tgcggcctga agacgtggct gtctactatt gtcagcagta ctatagcact 300  
ccattcacct ttggccccgg gacaaaggtg gatatcaaa 339

<210> 48  
<211> 339  
<212> DNA  
<213> Artificial Sequence

# HB01P012WO Sequence Listing\_ST25

<220>

<223> GCA7 light chain variable domain (VL) nuc varC2

<400> 48

gatattcaga tgacccagag tcctgattcc gtcgctgtct cactgggaga aagggcaacc	60
attaactgta aaagctcaca gagtgtcttc tacaccagta agaacaaaaa ctatctggcc	120
tggtttcagc agaagccagg ccagccccct aaactgctga tctactgggc tagcactaga	180
gagtctggag tgccagacag attctctggc agtgggtcag gaaccgactt caccctgaca	240
attagctccc tgaggcccga agacgtggcc gtctactatt gtcagcagta ttattcaaca	300
cccttcacat tcggaccagg aacaaaagtg gatattaag	339

<210> 49

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA21 CDRH1 aa

<400> 49

Gly	Phe	Thr	Phe	Ser	Asn	Tyr	Pro
1				5			

<210> 50

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA21 CDRH2 aa

<400> 50

Ile	Leu	Pro	Asp	Gly	Asn	Arg	Lys
1				5			

<210> 51

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

HB01P012WO Sequence Listing\_ST25

<223> GCA21 CDRH3 aa

<400> 51

Thr	Arg	Asp	Gly	Thr	Tyr	Tyr	Ser	Asn	Gly	Gly	Val	Tyr	Gln	Thr	Tyr
1				5					10					15	

Arg	Arg	Phe	Phe	Asp	Phe
				20	

<210> 52

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA21 CDRL1 aa

<400> 52

Gln	Asn	Ile	Leu	Asn	Trp
1				5	

<210> 53

<400> 53

000

<210> 54

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA21 CDRL2 long aa

<400> 54

Leu	Ile	Tyr	Lys	Ala	Ser	Asp	Leu	Gln
1				5				

<210> 55

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA21 CDRL3 aa



# HB01P012WO Sequence Listing\_ST25

<400> 55

Gln His Tyr Asn Ser Tyr Pro Leu Thr  
1 5

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA21 CDRH1 nuc

<400> 56

ggattcacct tttcgaacta tcct

24

<210> 57

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA21 CDRH2 nuc

<400> 57

attttacctg atgggaacag aaaa

24

<210> 58

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA21 CDRH3 nuc

<400> 58

acgagagatg gcacgtatta ctctaattgg ggtgtttatc agacatatcg aaggttcttc

60

gatttc

66

<210> 59

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> GCA21 CDRL1 nuc

# HB01P012WO Sequence Listing\_ST25

<400> 59  
cagaatatcc ttaattgg 18

<210> 60

<400> 60  
000

<210> 61  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA21 CDRL2 long nuc

<400> 61  
ctgatata aggctctga ttacaa 27

<210> 62  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA21 CDRL3 nuc

<400> 62  
cagcattata atagttatcc tctcact 27

<210> 63  
<211> 129  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> GCA21 heavy chain variable domain (VH) aa

<400> 63

Gln Val Gln Leu Met Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
1 5 10 15

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

# HB01P012W0 Sequence Listing\_ST25

Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Ile Ile Leu Pro Asp Gly Asn Arg Lys Asn Tyr Gly Arg Ser Val  
 50 55 60

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

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

Thr Arg Asp Gly Thr Tyr Tyr Ser Asn Gly Gly Val Tyr Gln Thr Tyr  
 100 105 110

Arg Arg Phe Phe Asp Phe Trp Gly Arg Gly Thr Leu Val Thr Val Ser  
 115 120 125

Ser

<210> 64  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCA21 light chain variable domain (VL) aa

<400> 64

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Thr Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Leu Asn Trp  
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Asn Leu Leu Ile  
 35 40 45

Tyr Lys Ala Ser Asp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

# HB01P012W0 Sequence Listing\_ST25

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Asn Ser Tyr Pro Leu  
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys  
100 105

<210> 65  
<211> 387  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA21 heavy chain variable domain (VH) nuc

<400> 65  
caggtgcaat tgatggagtc tgggggagggc gtgggtccagc ctgggagggtc cctgcgactc 60  
tcattgcagtg ccttttgatt caccttttcg aactatccta tgcactgggt cgcagggt 120  
ccaggcaagg gacttgagtg ggtggctatc attttacctg atgggaacag aaaaaactat 180  
ggaagggtccg tgacggggccg attcaccatc tccagagaca attccaacaa cagcctttat 240  
ttgcaaatga acaacctgac gactgaggac acggctatgt actattgtac gagagatggc 300  
acgtattact ctaatgggtg tgtttatcag acatatcgaa ggttcttcga tttctggggc 360  
cgtggcacc cttggtcaccgt ctctca 387

<210> 66  
<211> 321  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA21 light chain variable domain (VL) nuc

<400> 66  
gacatccaga tgacccagtc tccttcacc ctgtctacat ctgtgggaga cagagtcacc 60  
atcacttgcc gggccagtca gaatatcctt aattgggttg cctgggtatca acagaaacca 120  
gggaacgccc ctaacctcct gatataaag gcgtctgatt tacaaagtgg ggtcccctca 180

# HB01P012WO Sequence Listing\_ST25

```

agattcagcg gcagtgggtc tgggacagaa ttcactctca ccatcagcag cctgcagcct      240
gatgattttg caacttatta ctgccagcat tataatagtt atcctctcac tttcggcgga      300
gggaccaagg tggaaatcaa a                                                  321

```

```

<210> 67
<211> 8
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> GCB59 CDRH1 aa

```

```

<400> 67

```

```

Gly Leu Ser Phe Ser Ser Ser Gly
1           5

```

```

<210> 68
<211> 8
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> GCB59 CDRH2 aa

```

```

<400> 68

```

```

Ile Ser Gly Ser Gln Asn Tyr Lys
1           5

```

```

<210> 69
<211> 18
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> GCB59 CDRH3 aa

```

```

<400> 69

```

```

Val Gly Gly Phe Pro Tyr Trp Leu Pro Pro Ser Asp Phe Ser Gly Phe
1           5              10              15

```

```

His Val

```

# HB01P012W0 Sequence Listing\_ST25

<210> 70  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCB59 CDRL1 aa

<400> 70

Asn Ile Gly Ser Lys Ser  
 1 5

<210> 71

<400> 71  
 000

<210> 72  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCB59 CDRL2 long aa

<400> 72

Val Val Tyr Ala Asp Asn Asp Arg Pro  
 1 5

<210> 73  
 <211> 11  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCB59 CDRL3 aa

<400> 73

Gln Val Trp Asp Gly Asn Thr Asp His Val Val  
 1 5 10

<210> 74  
 <211> 24  
 <212> DNA

# HB01P012W0 Sequence Listing\_ST25

<213> Artificial Sequence

<220>

<223> GCB59 CDRH1 nuc varS1

<400> 74

ggattgtcct tcagtagttc aggc

24

<210> 75

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> GCB59 CDRH1 nuc varN1/N2

<400> 75

ggcctgtcct tcagctcctc tggc

24

<210> 76

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> GCB59 CDRH1 nuc varC1

<400> 76

gggctgagct tcagctcctc tgga

24

<210> 77

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> GCB59 CDRH2 nuc var S1

<400> 77

attagtggta gtcagaacta caaa

24

<210> 78

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> GCB59 CDRH2 nuc varN1/N2

# HB01P012WO Sequence Listing\_ST25

<400> 78  
attagcgggt cccagaatta caag 24

<210> 79  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCB59 CDRH2 nuc varC1

<400> 79  
atttctggca gtcagaatta caag 24

<210> 80  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCB59 CDRH3 nuc varS1

<400> 80  
gtgggagggt tcccctattg gttacccccg agcgacttct ccggtttcca tgtc 54

<210> 81  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCB59 CDRH3 nuc varN1/N2

<400> 81  
gtcggcgggt tcccctattg gctgcctcca agcgactttt cagggtttca tgtc 54

<210> 82  
<211> 54  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCB59 CDRH3 nuc varC1

<400> 82  
gtcgggggat tcccctattg gctgccccct tccgatttct ctggctttca cgtg 54



# HB01P012WO Sequence Listing\_ST25

<210>	83	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	GCB59 CDRL1 nuc varS1	
<400>	83	
	aacattggaa gtaaaaagt	18
<210>	84	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	GCB59 CDRL1 nuc varN1/N2	
<400>	84	
	aacatcggca gcaagagc	18
<210>	85	
<211>	18	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	GCB59 CDRL1 nuc varC1	
<400>	85	
	aacatcgggt ctaagagt	18
<210>	86	
<400>	86	
	000	
<210>	87	
<400>	87	
	000	
<210>	88	
<400>	88	
	000	

# HB01P012WO Sequence Listing\_ST25

<210> 89  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> GCB59 CDRL2 long nuc varS1  
  
 <400> 89  
 gtcgtctatg ctgataacga caggccc 27  
  
 <210> 90  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> GCB59 CDRL2 long nuc varN1/N2  
  
 <400> 90  
 gtggtctatg ctgacaacga tcggccc 27  
  
 <210> 91  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> GCB59 CDRL2 long nuc varC1  
  
 <400> 91  
 gtggtctatg ccgacaatga tcggcca 27  
  
 <210> 92  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> GCB59 CDRL3 nuc var S1  
  
 <400> 92  
 cagggtgtggg atggtaatac tgatcatgtg gtc 33  
  
 <210> 93  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

# HB01P012WO Sequence Listing\_ST25

<220>

<223> GCB59 CDRL3 nuc var N1/N2

<400> 93

caggtctggg atgggaatac tgaccacgtc gtc

33

<210> 94

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> GCB59 CDRL3 nuc varC1

<400> 94

caggtctggg acgggaacac agatcatgtg gtc

33

<210> 95

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> GCB59 heavy chain variable domain (VH) aa

<400> 95

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	Val	Lys	Ala	Gly	Gly
1				5					10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Leu	Ser	Phe	Ser	Ser	Ser
			20						25					30	

Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
		35					40					45			

Ser	Ser	Ile	Ser	Gly	Ser	Gln	Asn	Tyr	Lys	Tyr	Tyr	Ala	Asp	Ser	Val
		50				55					60				

Lys	Gly	Arg	Phe	Val	Val	Ser	Arg	Asp	Asn	Ala	Arg	Asn	Phe	Leu	Tyr
65					70					75				80	

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

# HB01P012W0 Sequence Listing\_ST25

Val Gly Gly Phe Pro Tyr Trp Leu Pro Pro Ser Asp Phe Ser Gly Phe  
100 105 110

His Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser  
115 120 125

<210> 96  
<211> 108  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> GCB59 light chain variable domain (VL) aa

<400> 96

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln  
1 5 10 15

Thr Ala Ser Leu Thr Cys Gly Gly Thr Asn Ile Gly Ser Lys Ser Val  
20 25 30

His Trp Tyr Gln Gln Lys Ala Gly Gln Ala Pro Val Leu Val Val Tyr  
35 40 45

Ala Asp Asn Asp Arg Pro Ser Gly Val 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 Glu  
65 70 75 80

Asp Glu Ser Asp Tyr Phe Cys Gln Val Trp Asp Gly Asn Thr Asp His  
85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
100 105

<210> 97  
<211> 375  
<212> DNA  
<213> Artificial Sequence

# HB01P012WO Sequence Listing\_ST25

<220>

<223> GCB59 heavy chain variable domain (VH) nuc varS1

<400> 97

gagggtacaat tgggtggagtc tgggggagac ctggtcaagg cggggggggtc cctgagactc	60
tcctgtgccg tctctggatt gtccttcagt agttcaggca tgaattgggt ccgccaggct	120
ccagggaagg ggctggagtg gatctcatcg attagtggta gtcagaacta caaatactat	180
gcagactcag tgaagggccg attcgtcgtc tccagagaca acgcccgcaa ctttctatat	240
ctgcaaattgg acagcctgag ggccgaggat acggctgtgt atttttgtgt gggaggtttc	300
ccctattgggt taccctcgag cgacttctcc ggtttccatg tctggggcca agggaccacg	360
gtcaccgtct cctca	375

<210> 98

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> GCB59 heavy chain variable domain (VH) nuc var N1

<400> 98

gagggtgcagc tgggtggaaag cggaggggat ctggtgaaag caggagggag cctgagactg	60
tcatgcgccg tgagcgggct gtcattcagc tcctctggca tgaactgggt gcgacaggct	120
cctggaaagg gactggagtg gatcagttca attagcgggt cccagaatta caagtactat	180
gcagactctg tcaaaggaag gttcgtggtc agccgggata acgccagaaa ttttctgtat	240
ctgcagatgg acagcctgcg cgccgaagat accgccgtgt acttctgcgt cggcgggttt	300
ccctattggc tgcctccaag cgatttcagc ggatttcatg tctgggggca gggaactaca	360
gtgaccgtct catca	375

<210> 99

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> GCB59 heavy chain variable domain (VH) nuc var N2

# HB01P012W0 Sequence Listing\_ST25

```

<400> 99
gaggtgcagc tgggtggaaag tggggggcgat ctgggtcaaag ccggagggtc tctgcgactg      60
tcttgtgctg tgagcggcct gtccttcagc tcctctggca tgaactgggt gcgacaggct      120
cctggaaagg gactggagtg gatcagttca attagcgggt cccagaatta caagtactat      180
gcagactctg tcaaaggaag gttcgtggtc agccgggata acgccagaaa ttttctgtat      240
ctgcagatgg acagcctgcg cgccgaagat accgccgtgt acttctgcgt cggcggggtt      300
ccctattggc tgcctccaag cgacttttca gggtttcatg tctgggggca gggaactacc      360
gtgaccgtct catct                                                         375

```

```

<210> 100
<211> 375
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GCB59 heavy chain variable domain (VH) nuc varC1

```

```

<400> 100
gaggtgcagc tggtcgaatc tggcgggggac ctgggtgaagg caggaggcag tctgaggctg      60
tcatgcgccg tctcagggtg gagcttcagc tcctctggaa tgaactgggt gcgccaggca      120
ccaggcaaag gactggagtg gatcagttca atttctggca gtcagaatta caagtactat      180
gctgacagtg tgaaagggcg attcgtggtc tcccgggata acgcaagaaa ttttctgtat      240
ctgcagatgg acagcctgag agccgaagat actgctgtgt acttctgtgt cgggggattt      300
ccctattggc tgcccccttc cgattttctt ggctttcacg tgtggggaca gggcaccaca      360
gtgaccgtca gctcc                                                         375

```

```

<210> 101
<211> 324
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GCB59 light chain variable domain (VL) nuc varS1

```

```

<400> 101
tcatatgtgc tgactcaacc accctcggtg tcagtggccc caggacagac ggccagtcta      60
acctgtgggg gaactaacat tggaagtaaa agtgttcatt ggtaccagca aaaggcaggc      120

```

# HB01P012WO Sequence Listing\_ST25

```

cagggcccctg tgttggtcgt ctatgctgat aacgacaggc cctcaggggt ccctgagcga      180
ttctctggct ccaactctgg gaacacggcc accctgacca tcagcaggggt cgaggccgag      240
gatgagtccg actatctctg tcaggtgtgg gatggtaata ctgatcatgt ggtcttcggc      300
ggagggacca agctgaccgt cctg                                              324

```

```

<210> 102
<211> 324
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GCB59 light chain variable domain (VL) nuc var N1

```

```

<400> 102
tcctacgtcc tgaccagcc acctagcgtg agcgtcgac cagggcagac agcttcactg      60
acttgccggag gcacaaacat tggcagcaag agcgtgcact ggtaccagca gaaagccgga      120
caggctcccg tcctggtggt ctatgctgac aacgatcggc cctctggcgt gcctgaaaga      180
ttcagcggct ccaactctgg gaataccgca acactgacca tcagtaggggt cgaggccgaa      240
gacgagtcag attacttttg ccaggtgtgg gacggcaata ctgacatgt cgtgttcggc      300
ggcgggacca aactgactgt gctg                                              324

```

```

<210> 103
<211> 324
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> GCB59 light chain variable domain (VL) nuc var N2

```

```

<400> 103
tcctacgtcc tgactcagcc acctagcgtg tccgtcgac ctgggcagac agcatcactg      60
acttgccggg gaaccaacat cggcagcaag agcgtgcact ggtaccagca gaaagccgga      120
caggctcccg tcctggtggt ctatgctgac aacgatcggc cctctggcgt gcctgaaaga      180
ttcagcggct ccaactctgg gaataccgca acactgacca tcagtaggggt cgaggccgaa      240
gacgagtcag attacttttg ccaggtctgg gatgggaata ctgaccacgt cgtcttcgga      300
ggcgggaacca aactgactgt cctg                                              324

```

# HB01P012W0 Sequence Listing\_ST25

<210> 104  
 <211> 324  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCB59 light chain variable domain (VL) nuc varC1

<400> 104  
 tcctacgtgc tgactcagcc acctagcgtg tccgtcgcac ctggacagac tgccagcctg 60  
 acctgcggag gaacaaacat cgggtctaag agtgtgcact ggtaccagca gaaagccgga 120  
 caggctcccg tcctggtggt ctatgccgac aatgatcggc catctggcgt gcccgaaaga 180  
 ttctcaggaa gcaactccgg caataccgct aactgacta tttctagggt ggaggcagaa 240  
 gacgagagtg attatttctg tcaggctctgg gacgggaaca cagatcatgt ggtctttgga 300  
 ggcgggacca agctgacagt gctg 324

<210> 105  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRH1 aa

<400> 105

Gly Tyr Val Phe Thr Ser Tyr Tyr  
 1 5

<210> 106  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRH2 aa

<400> 106

Ile Ser Pro Gly Asp Val Asn Thr  
 1 5



HB01P012WO Sequence Listing\_ST25

<210> 107  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRH3 aa

<400> 107

Ala	Arg	Gly	Pro	Arg	Ser	Lys	Pro	Pro	Tyr	Leu	Tyr	Phe	Ala	Leu	Asp
1				5					10					15	

Val

<210> 108  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRL1 aa

<400> 108

Gln	Ser	Val	Ser	Ser	Ser	Leu
1			5			

<210> 109

<400> 109  
 000

<210> 110  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRL2 long aa

<400> 110

Leu	Ile	Tyr	Gly	Ala	Ser	Asn	Arg	Ala
1				5				

<210> 111

# HB01P012WO Sequence Listing\_ST25

<211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRL3 aa

<400> 111

Gln His Tyr Gly Ser Arg Val Thr  
 1 5

<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRH1 nuc varS1

<400> 112  
 ggatacgtgt tcacctctta ctat 24

<210> 113  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRH1 nuc varS2

<400> 113  
 ggatacgtct ttacctctta ctat 24

<210> 114  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCE536 CDRH1 nuc varN1/C1

<400> 114  
 ggatacgtct tcacctctta ctat 24

<210> 115  
 <211> 24  
 <212> DNA

HB01P012W0 Sequence Listing\_ST25

<213> Artificial Sequence

<220>

<223> GCE536 CDRH2 nuc varS1/S2/N1/C1

<400> 115

atctctcccg gagacgtgaa cact

24

<210> 116

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> GCE536 CDRH3 nuc varS1

<400> 116

gctagggggc cccgcagcaa gcctccttat ctgtattttg ctctggatgt g

51

<210> 117

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> GCE536 CDRH3 nuc varS2

<400> 117

gctagggggc cccgcagcaa gcctccttat ctgtacttcg ctctggatgt c

51

<210> 118

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> GCE536 CDRH3 nuc varN1/C1

<400> 118

gctagggggc cccgcagcaa gcctccttat ctgtattttc ctctggatgt c

51

<210> 119

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> GCE536 CDRL1 nuc varS1

# HB01P012WO Sequence Listing\_ST25

<400> 119  
cagagtgtca gcagcagcct c 21

<210> 120  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCE536 CDRL1 nuc varS2

<400> 120  
cagtctgtga gctcctctct g 21

<210> 121  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCE536 CDRL1 nuc varN1/C1

<400> 121  
cagtccgtga gctcctctct g 21

<210> 122

<400> 122  
000

<210> 123

<400> 123  
000

<210> 124  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCE536 CDRL2 long nuc varS1

<400> 124  
ctcatctacg gtgcatccaa tagggcc 27

<210> 125

# HB01P012W0 Sequence Listing\_ST25

```

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> GCE536 CDRL2 long nuc varS2/N1/C1

<400> 125
ctgatctatg ggcctccaa ccgcgct
27

<210> 126
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> GCE536 CDRL3 nuc varS1

<400> 126
cagcactatg gctcacgggt cact
24

<210> 127
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> GCE536 CDRL3 nuc varS2

<400> 127
cagcactatg gcagcagggt cact
24

<210> 128
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> GCE536 CDRL3 nuc varN1

<400> 128
cagcattatg ggtcacgggt cact
24

<210> 129
<211> 24
<212> DNA
<213> Artificial Sequence

```

# HB01P012W0 Sequence Listing\_ST25

<220>

<223> GCE536 CDRL3 nuc varC1

<400> 129

cagcattatg gaagcagggt cacc

24

<210> 130

<211> 124

<212> PRT

<213> Artificial Sequence

<220>

<223> GCE536 heavy chain variable domain (VH) aa

<400> 130

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

Ser	Val	Lys	Val	Ser	Cys	Lys	Ser	Ser	Gly	Tyr	Val	Phe	Thr	Ser	Tyr
			20					25					30		

Tyr	Leu	Val	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			

Ala	Thr	Ile	Ser	Pro	Gly	Asp	Val	Asn	Thr	Ser	Tyr	Glu	Gln	Arg	Phe
	50					55					60				

Gln	Gly	Arg	Val	Thr	Val	Thr	Thr	Asp	Ala	Ser	Thr	Asn	Thr	Val	Asp
65					70					75				80	

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

Ala	Arg	Gly	Pro	Arg	Ser	Lys	Pro	Pro	Tyr	Leu	Tyr	Phe	Ala	Leu	Asp
			100					105					110		

Val	Trp	Gly	Gln	Gly	Thr	Ala	Val	Thr	Val	Ser	Ser
		115					120				

<210> 131

<211> 107

<212> PRT

# HB01P012WO Sequence Listing\_ST25

<213> Artificial Sequence

<220>

<223> GCE536 light chain variable domain (VL) aa

<400> 131

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly  
1 5 10 15

Glu Thr Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser  
20 25 30

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

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Arg Gly Arg Phe Ser  
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu  
65 70 75 80

Pro Glu Asp Phe Val Leu Tyr Tyr Cys Gln His Tyr Gly Ser Arg Val  
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
100 105

<210> 132

<211> 372

<212> DNA

<213> Artificial Sequence

<220>

<223> GCE536 heavy chain variable domain (VH) nuc varS1

<400> 132

cagctgcagc tgggtccagtc aggcacagag gtcaaaaagc caggagcatc agtgaaggtg 60

tcttgtaagt catcaggata cgtgttcacc tcttactatc tgggtgtgggt ccggcaggca 120

ccaggacagg gactggagtg gatggccaca atctctcccg gagacgtgaa cactagttac 180

gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat 240

# HB01P012WO Sequence Listing\_ST25

atggagctgc ggagcctgag atccgaagat acagccgtct actattgcgc tagggggccc 300  
 cgcagcaagc ctccttatct gtattttgct ctggatgtgt gggggcaggg gaccgctgtc 360  
 accgtgtcaa gc 372

<210> 133  
 <211> 372  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCE536 heavy chain variable domain (VH) nuc varS2

<400> 133  
 cagctgcagc tgggtccagtc aggcacagaa gtcaaaaaac ccggcgcaag cgtgaaggtc 60  
 tcatgtaa at catcaggata cgtctttacc tcttactatc tgggtgtgggt ccggcaggca 120  
 ccaggacagg gactggagtg gatggccaca atctctccc gagacgtgaa cactagttac 180  
 gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat 240  
 atggagctgc ggagcctgag atccgaagat acagccgtct actattgcgc tagggggccc 300  
 cgcagcaagc ctccttatct gtacttcgct ctggatgtct gggggcaggg gaccgccgtc 360  
 accgtctcaa gc 372

<210> 134  
 <211> 372  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCE536 heavy chain variable domain (VH) nuc varN1

<400> 134  
 cagctgcagc tgggtccagag cggcacagag gtgaaaaagc caggagcatc agtcaaagt 60  
 tcttgtaagt catcaggata cgtcttcacc tcttactatc tgggtgtgggt ccggcaggca 120  
 ccaggacagg gactggagtg gatggccaca atctctccc gagacgtgaa cactagttac 180  
 gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat 240  
 atggagctgc ggagcctgag atccgaagat acagccgtct actattgcgc tagggggccc 300  
 cgcagcaagc ctccttatct gtatttcgct ctggatgtct gggggcaggg aacagcagtc 360



## HB01P012WO Sequence Listing\_ST25

accgtctctt ct 372

<210> 135  
 <211> 372  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCE536 heavy chain variable domain (VH) nuc varC1

<400> 135  
 cagctgcagc tgggtccagag cggaaccgaa gtgaagaaac ccggcgcaag cgtcaaagtc 60  
 tcatgcaaat caagcggata cgtcttcacc tcttactatc tgggtgtgggt ccggcaggca 120  
 ccaggacagg gactggagtg gatggccaca atctctcccg gagacgtgaa cactagttac 180  
 gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat 240  
 atggagctgc ggagcctgag atccgaagat acagccgtct actattgcgc tagggggccc 300  
 cgcagcaagc ctccttatct gtatttcgct ctggatgtct gggggcaggg aacagcagtc 360  
 accgtctcaa gc 372

<210> 136  
 <211> 322  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCE536 light chain variable domain (VL) nuc varS1

<400> 136  
 gaaattgtgt tgacgcagtc tcctggcacc ctgtctttgt ctccagggga aacagccatc 60  
 ctctcctgca gggccagtca gagtgtcagc agcagcctct tagcctggta ccagcaaaaa 120  
 cctggccagg ctcccaggct cctcatctac ggtgcatcca atagggccac tggcatcaga 180  
 ggcaggttta gtggcagtgg gtctgggaca gacttcactc tcaccatcag tagattggag 240  
 cctgaagatt ttgtacttta ttactgtcag cactatggct cacgggtcac ttttggccag 300  
 gggaccaagc tggagatcaa ac 322

<210> 137  
 <211> 321  
 <212> DNA

HB01P012WO Sequence Listing\_ST25

<213> Artificial Sequence

<220>

<223> GCE536 light chain variable domain (VL) nuc varS2

<400> 137

gaaatcgtgc tgaccagtc tcctggaact ctgtctctgt cacctggcga aaccgcaatc	60
ctgtcctgta gggcaagtca gtctgtgagc tcctctctgc tggcatggta ccagcagaag	120
cccggacagg cccctaggct gctgatctat ggcgctcca accgcgtac tggcattcgg	180
gggagattca gtggctcagg gagcggaacc gactttaccc tgacaatcag ccggctggag	240
cccgaagatt tcgtgctgta ttactgtcag cactatggca gcagggtcac ttttgggcag	300
gggactaaac tggagattaa a	321

<210> 138

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> GCE536 light chain variable domain (VL) nuc varN1

<400> 138

gaaatcgtcc tgaccagtc acctggcacc ctgagtctga gtcctggcga aacagcaatc	60
ctgtcttgtc gggcttcaca gtccgtgagc tcctctctgc tggcatggta ccagcagaag	120
cccggacagg cccctaggct gctgatctat ggcgctcca accgcgtac tggcattcgg	180
gggagattca gtggctcagg gagcggaacc gactttaccc tgacaatcag ccggctggag	240
cccgaagatt tcgtgctgta ctactgtcag cattatgggt cacgggtcac ttttgggcag	300
gggactaaac tggaaatcaa g	321

<210> 139

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> GCE536 light chain variable domain (VL) nuc varC1

<400> 139

gagattgtcc tgaccagtc acctggcacc ctgagcctga gtcctggaga gaccgctatt	60
--	----

HB01P012WO Sequence Listing\_ST25

ctgtcttgtc gggcatcaca gtccgtgagc tcctctctgc tggcatggta ccagcagaag 120  
 cccggacagg cccctaggct gctgatctat ggcgctcca accgcgtac tggcattcgg 180  
 gggagattca gtggctcagg gagcggaacc gactttaccc tgacaatcag ccggctggag 240  
 cccgaagatt tcgtgctgta ctattgtcag cattatggaa gcagggtcac cttcggacag 300  
 ggaactaaac tggaaatcaa g 321

<210> 140  
 <211> 330  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IgG1 CH1-CH2-CH3 aa

<400> 140

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys  
 1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr  
 20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser  
 35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser  
 50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr  
 65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys  
 85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
 100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro  
 115 120 125

# HB01P012W0 Sequence Listing\_ST25

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
145 150 155 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu  
165 170 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
180 185 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
195 200 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
210 215 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
225 230 235 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
245 250 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
260 265 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
275 280 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn  
290 295 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr  
305 310 315 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
325 330

# HB01P012W0 Sequence Listing\_ST25

<210> 141  
 <211> 107  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IgG CK aa

<400> 141

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu  
 1 5 10 15

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe  
 20 25 30

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln  
 35 40 45

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser  
 50 55 60

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu  
 65 70 75 80

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser  
 85 90 95

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 100 105

<210> 142  
 <211> 106  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> IgG CL aa

<400> 142

Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser  
 1 5 10 15

# HB01P012W0 Sequence Listing\_ST25

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> 143  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Short linker aa

<400> 143

Gly Gly Gly Gly Ser  
1 5

<210> 144  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Long linker aa

<400> 144

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

# HB01P012WO Sequence Listing\_ST25

<210> 145  
<211> 990  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> IgG1 CH1-CH2-CH3 nucl varS1

<400> 145  
gcgtcgacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 60  
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaacctgt gacggctctcg 120  
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 180  
ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 240  
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc 300  
aaatcttggt acaaaaactca cacatgcccc ccgtgcccag cacctgaact cctggggggga 360  
ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccctt 420  
gaggtcacat gcgtgggtgg ggacgtgagc cacgaggatc ctgagggtcaa gttcaactgg 480  
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 540  
agcacgtacc gtgtggtcag cgtcctcacc gtcctgcacc aggactggct gaatggcaag 600  
gagtacaagt gcaagggtct caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 660  
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggaggag 720  
atgaccaaga accagggtcag cctgacctgc ctgggtcaaag gcttctatcc cagcgacatc 780  
gccgtggagt gggagagcaa tgggcagccg gagaacaact acaagaccac gcctcccgtg 840  
ctggactccg acggctcctt cttcctctat agcaagctca ccgtggacaa gagcagggtgg 900  
cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 960  
cagaagagcc tctccctgtc cccgggtaaa 990

<210> 146  
<211> 990  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> IgG1 CH1-CH2-CH3 nucl varS2

# HB01P012WO Sequence Listing\_ST25

```

<400> 146
gcgtcgacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg      60
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaacctgt gacggtctcg      120
tggaactcag gcgccctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca      180
ggactctact ccctcagcag cgtgggtgacc gtgccctcca gcagcttggg caccagacc      240
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagag agttgagccc      300
aaatcttgtg aaaaaactca cacatgcca ccgtgccag cacctgaact cctgggggga      360
ccgtcagtct tcctcttccc ccaaaaaccc aaggacaccc tcatgatctc ccggaccctt      420
gaggtcacat gcgtggtggt ggacgtgagc cagcaggatc ctgaagtcaa gttcaactgg      480
tacgtggatg gcgtcgaggt gcataatgcc aagacaaaac cccgggagga acagtacaac      540
tcaacttata gagtctgag cgtcctgacc gtgctgcatc aggactggct gaacggcaaa      600
gaatacaagt gcaaagtgtc taataaggcc ctgcctgctc caatcgagaa aacaattagc      660
aaggcaaaag ggcagcccag ggaacctcag gtgtacactc tgcctccaag ccgcgaggaa      720
atgaccaaga accaggtctc cctgacatgt ctggtgaaag gattctatcc tagtgacatt      780
gccgtggagt gggaatcaaa tggccagcca gagaacaatt acaagaccac acccctgtg      840
ctggactctg atgggagttt ctttctgtat tccaagctga ccgtggataa atctagatgg      900
cagcagggaa atgtctttag ctgttccgtg atgcatgagg cactgcacaa ccattacacc      960
cagaaatcac tgtcactgtc cccaggaaaa      990

```

```

<210> 147
<211> 321
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> IgG CK nucl

```

```

<400> 147
cgtacgggtgg ctgcaccatc tgtcttcac ttcccggcat ctgatgagca gttgaaatct      60
ggaactgcct ctgttgtgtg cctgctgaat aacttctatc ccagagaggc caaagtacag      120
tggaagggtgg ataacgccct ccaatcgggt aactcccagg agagtgtcac agagcaggac      180

```



# HB01P012W0 Sequence Listing\_ST25

agcaaggaca gcacctacag cctcagcagc accctgacgc tgagcaaagc agactacgag 240

aaacacaaag tctacgcctg cgaagtcacc catcagggcc tgagctcgcc cgtcacaaag 300

agcttcaaca ggggagagtg t 321

<210> 148

<211> 318

<212> DNA

<213> Artificial Sequence

<220>

<223> IgG CL nucl

<400> 148

ggtcagccca aggctgcccc ctcggtcact ctgttccgc cctcctctga ggagcttcaa 60

gccaacaagg ccacactggg gtgtctcata agtgacttct acccgggagc cgtgacagtg 120

gcttggaag cagatagcag ccccgtaag gcgggagtg agaccaccac accctccaaa 180

caaagcaaca acaagtacgc ggccagcagc tatctgagcc tgacgcctga gcagtggaag 240

tcccacagaa gctacagctg ccaggtcacg catgaaggga gcaccgtgga gaagacagtg 300

gcccctacag aatgttca 318

<210> 149

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Short linker nucl

<400> 149

ggcgggggag gctct 15

<210> 150

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Long linker nucl

<400> 150

ggcgggggag gctctggggg aggcgggagt ggaggcgggg gatca 45

# HB01P012W0 Sequence Listing\_ST25

<210> 151  
 <211> 967  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Ts1GC1 heavy chain aa

<400> 151

Gln Val Gln Leu Met Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg  
 1 5 10 15

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

Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ala Ile Ile Leu Pro Asp Gly Asn Arg Lys Asn Tyr Gly Arg Ser Val  
 50 55 60

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

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

Thr Arg Asp Gly Thr Tyr Tyr Ser Asn Gly Gly Val Tyr Gln Thr Tyr  
 100 105 110

Arg Arg Phe Phe Asp Phe Trp Gly Arg Gly Thr Leu Val Thr Val Ser  
 115 120 125

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
 130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
 145 150 155 160

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr

HB01P012WO Sequence Listing\_ST25

165 170 175

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
180 185 190

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
210 215 220

Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro  
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
290 295 300

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
305 310 315 320

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
355 360 365

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

# HB01P012W0 Sequence Listing\_ST25

370

375

380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
405 410 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser  
450 455 460

Gly Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
465 470 475 480

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Thr Asn  
485 490 495

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
500 505 510

Ser Ile Leu Tyr Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys  
515 520 525

Thr Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu  
530 535 540

Gln Met Asn Ala Leu Ser Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala  
545 550 555 560

Lys His Tyr Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp  
565 570 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

HB01P012W0 Sequence Listing\_ST25

580

585

590

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser  
595 600 605

Pro Asp Ser Val Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys  
610 615 620

Lys Ser Ser Gln Ser Val Phe Tyr Thr Ser Lys Asn Lys Asn Tyr Leu  
625 630 635 640

Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr  
645 650 655

Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
660 665 670

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro Glu  
675 680 685

Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr  
690 695 700

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Gly Gly Gly Gly Ser Glu  
705 710 715 720

Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Ala Gly Gly Ser  
725 730 735

Leu Arg Leu Ser Cys Ala Val Ser Gly Leu Ser Phe Ser Ser Ser Gly  
740 745 750

Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Ser  
755 760 765

Ser Ile Ser Gly Ser Gln Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys  
770 775 780

Gly Arg Phe Val Val Ser Arg Asp Asn Ala Arg Asn Phe Leu Tyr Leu

HB01P012WO Sequence Listing\_ST25

785 790 795 800

Gln Met Asp Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys Val  
805 810 815

Gly Gly Phe Pro Tyr Trp Leu Pro Pro Ser Asp Phe Ser Gly Phe His  
820 825 830

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly  
835 840 845

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr  
850 855 860

Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala Ser Leu Thr  
865 870 875 880

Cys Gly Gly Thr Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln Gln  
885 890 895

Lys Ala Gly Gln Ala Pro Val Leu Val Val Tyr Ala Asp Asn Asp Arg  
900 905 910

Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr  
915 920 925

Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Glu Ser Asp Tyr  
930 935 940

Phe Cys Gln Val Trp Asp Gly Asn Thr Asp His Val Val Phe Gly Gly  
945 950 955 960

Gly Thr Lys Leu Thr Val Leu  
965

<210> 152  
<211> 2901  
<212> DNA  
<213> Artificial Sequence

## HB01P012W0 Sequence Listing\_ST25

&lt;220&gt;

&lt;223&gt; Ts1GC1 heavy chain nucl

&lt;400&gt; 152

caggtgcaat tgatggagtc tgggggaggc gtggtccagc ctgggaggtc cctgcgactc	60
tcatgcagtg cctttggatt caccttttcg aactatccta tgcactgggt ccgccaggct	120
ccaggcaagg gacttgagtg ggtggctatc attttacctg atgggaacag aaaaaactat	180
ggaagggtccg tgacgggccg attcaccatc tccagagaca attccaacaa cagcctttat	240
ttgcaaatga acaacctgac gactgaggac acggctatgt actattgtac gagagatggc	300
acgtattact ctaatgggtg tgtttatcag acatatcgaa ggttcttcga tttctggggc	360
cgtggcaccc tggtcaccgt ctctcagcg tcgaccaagg gcccatcgggt cttccccctg	420
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac	480
tacttccccg aacctgtgac ggtctcgtgg aactcaggcg ccctgaccag cggcgtgcac	540
accttccccg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg	600
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcacia gccagcaac	660
accaaggtgg acaagagagt tgagcccaaa tcttgtgaca aaactcacac atgcccaccg	720
tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaaccaag	780
gacaccctca tgatctcccc gaccctgag gtcacatgcg tgggtggtgga cgtgagccac	840
gaggatcctg aagtcaagtt caactggtac gtggatggcg tcgaggtgca taatgccaa	900
acaaaacccc gggaggaaca gtacaactca acttatagag tcgtgagcgt cctgaccgtg	960
ctgcatcagg actggctgaa cggcaaagaa tacaagtgca aagtgtctaa taaggccctg	1020
cctgctccaa tcgagaaaac aattagcaag gcaaaagggc agcccaggga acctcaggtg	1080
tacactctgc ctccaagccg cgaggaaatg accaagaacc aggtctccct gacatgtctg	1140
gtgaaaggat tctatcctag tgacattgcc gtggagtggg aatcaaatgg ccagccagag	1200
aacaattaca agaccacacc ccctgtgctg gactctgatg ggagtttctt tctgtattcc	1260
aagctgaccg tggataaatc tagatggcag cagggaatg tcttttagctg ttccgtgatg	1320
catgaggcac tgcacaacca ttacaccag aaatcactgt cactgtcccc aggaaaaggc	1380
gggggaggct ctggagtgca gctggtccag agcggaggag gactggtgca gccaggaggg	1440

HB01P012WO Sequence Listing\_ST25

tcactgaggc tgagctgcgc agcttccggc ttcaccgtgt caacaaacta catgagctgg	1500
gtccgccagg cacctgggaa gggactggag tgggtgtcca tcctgtacgc cggaggcgtg	1560
actcgatatg ctgactctgt caagactcgg ttcaccatct ctagagataa cagtaagaac	1620
accctgtttc tgcagatgaa tgcactgagt gccgaagaca cagctatcta ctattgtgca	1680
aaacactacg attctgggta tagtacaatt gaccattttg attcttgggg ccaggggaca	1740
ctggtgactg tcagctccgg cgggggaggc tctgggggag gcgggagtgg aggcggggga	1800
tcagacatcc agatgactca gtctcccgat agtgtggccg tctccctggg ggagagggct	1860
acaattaact gcaagagctc ccagtccgtg ttctacactt ctaagaacaa aaactatctg	1920
gcatggtttc agcagaagcc tggacagccc cctaaactgc tgatctactg ggcctcaacc	1980
cgagagagcg gagtcccaga cagattctca ggcagcgggt ccggaacaga ttttaccctg	2040
acaatttcta gtctgcggcc tgaagacgtg gctgtctact attgtcagca gtactatagc	2100
actccattca cctttggccc cgggacaaag gtggatatca aaggcggggg aggctctgag	2160
gtgcagctgg tcgaatctgg cggggacctg gtgaaggcag gaggcagtct gaggctgtca	2220
tgcgccgtct cagggtctgag cttcagctcc tctggaatga actgggtgcg ccaggcacca	2280
ggcaaaggac tggagtggat cagttcaatt tctggcagtc agaattacaa gtactatgct	2340
gacagtgtga aaggcgatt cgtggtctcc cgggataacg caagaaattt tctgtatctg	2400
cagatggaca gcctgagagc cgaagatact gctgtgtact tctgtgtcgg gggatttccc	2460
tattggctgc ccccttccga tttctctggc tttcacgtgt ggggacaggg caccacagtg	2520
accgtcagct ccggcggggg aggctctggg ggaggcggga gtggaggcgg gggatcatcc	2580
tacgtgctga ctcagccacc tagcgtgtcc gtcgcacctg gacagactgc cagcctgacc	2640
tgcggaggaa caaacatcgg gtctaagagt gtgactggt accagcagaa agccggacag	2700
gctcccgtcc tgggtgtcta tgccgacaat gatcggccat ctggcgtgcc cgaaagattc	2760
tcaggaagca actccggcaa taccgctaca ctgactattt ctagggtgga ggcagaagac	2820
gagagtgatt atttctgtca ggtctgggac gggaacacag atcatgtggt ctttggaggc	2880
gggaccaagc tgacagtgt g	2901



# HB01P012WO Sequence Listing\_ST25

<211> 962

<212> PRT

<213> Artificial Sequence

<220>

<223> Ts1GC2a heavy chain aa

<400> 153

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

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr Val Phe Thr Ser Tyr  
20 25 30

Tyr Leu Val Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Ala Thr Ile Ser Pro Gly Asp Val Asn Thr Ser Tyr Glu Gln Arg Phe  
50 55 60

Gln Gly Arg Val Thr Val Thr Thr Asp Ala Ser Thr Asn Thr Val Asp  
65 70 75 80

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

Ala Arg Gly Pro Arg Ser Lys Pro Pro Tyr Leu Tyr Phe Ala Leu Asp  
100 105 110

Val Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser Ala Ser Thr Lys  
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
130 135 140

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

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

# HB01P012W0 Sequence Listing\_ST25

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190

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

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

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

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

# HB01P012W0 Sequence Listing\_ST25

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Val Gln Leu Val  
450 455 460

Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser  
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Val Ser Thr Asn Tyr Met Ser Trp Val  
485 490 495

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ile Leu Tyr Ala  
500 505 510

Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys Thr Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asn Ala Leu  
530 535 540

Ser Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Asp Ser  
545 550 555 560

Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp Gly Gln Gly Thr Leu  
565 570 575

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
580 585 590

# HB01P012WO Sequence Listing\_ST25

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Val Ala  
595 600 605

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser  
610 615 620

Val Phe Tyr Thr Ser Lys Asn Lys Asn Tyr Leu Ala Trp Phe Gln Gln  
625 630 635 640

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
645 650 655

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
660 665 670

Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro Glu Asp Val Ala Val Tyr  
675 680 685

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr  
690 695 700

Lys Val Asp Ile Lys Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu  
705 710 715 720

Ser Gly Gly Asp Leu Val Lys Ala Gly Gly Ser Leu Arg Leu Ser Cys  
725 730 735

Ala Val Ser Gly Leu Ser Phe Ser Ser Ser Gly Met Asn Trp Val Arg  
740 745 750

Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Ser Ser Ile Ser Gly Ser  
755 760 765

Gln Asn Tyr Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Val Val  
770 775 780

Ser Arg Asp Asn Ala Arg Asn Phe Leu Tyr Leu Gln Met Asp Ser Leu  
785 790 795 800

# HB01P012WO Sequence Listing\_ST25

Arg Ala Glu Asp Thr Ala Val Tyr Phe Cys Val Gly Gly Phe Pro Tyr  
805 810 815

Trp Leu Pro Pro Ser Asp Phe Ser Gly Phe His Val Trp Gly Gln Gly  
820 825 830

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
835 840 845

Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu Thr Gln Pro Pro Ser Val  
850 855 860

Ser Val Ala Pro Gly Gln Thr Ala Ser Leu Thr Cys Gly Gly Thr Asn  
865 870 875 880

Ile Gly Ser Lys Ser Val His Trp Tyr Gln Gln Lys Ala Gly Gln Ala  
885 890 895

Pro Val Leu Val Val Tyr Ala Asp Asn Asp Arg Pro Ser Gly Val Pro  
900 905 910

Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile  
915 920 925

Ser Arg Val Glu Ala Glu Asp Glu Ser Asp Tyr Phe Cys Gln Val Trp  
930 935 940

Asp Gly Asn Thr Asp His Val Val Phe Gly Gly Gly Thr Lys Leu Thr  
945 950 955 960

Val Leu

<210> 154  
<211> 2886  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ts1GC2a heavy chain nucl

# HB01P012W0 Sequence Listing\_ST25

```

<400> 154
cagctgcagc tgggtccagtc aggcacagag gtcaaaaagc caggagcatc agtgaagggtg      60

tcttgtaagt catcaggata cgtgttcacc tcttactatc tgggtgtgggt ccggcaggca      120

ccaggacagg gactggagtg gatggccaca atctctcccg gagacgtgaa cactagttac      180

gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat      240

atggagctgc ggagcctgag atccgaagat acagccgtct actattgcgc tagggggccc      300

cgcagcaagc ctccttatct gtattttgct ctggatgtgt gggggcaggg gaccgctgtc      360

accgtgtcaa gcgcgtcgac caagggccca tcggctcttc ccctggcacc ctctccaag      420

agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaacct      480

gtgacggtct cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc      540

ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg      600

ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag      660

agagttgagc ccaaactctt tgacaaaact cacacatgcc caccgtgcc agcacctgaa      720

ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgac      780

tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgagga tcctgaagtc      840

aagttcaact ggtacgtgga tggcgtcgag gtgcataatg ccaagacaaa accccgggag      900

gaacagtaca actcaactta tagagtcgtg agcgtcctga ccgtgctgca tcaggactgg      960

ctgaacggca aagaatacaa gtgcaaagtg tctaataagg ccctgcctgc tccaatcgag     1020

aaaacaatta gcaaggcaaa agggcagccc agggaaacct aggtgtacac tctgcctcca     1080

agccgcgagg aaatgaccaa gaaccaggtc tccctgacat gtctggtgaa aggattctat     1140

cctagtgaca ttgccgtgga gtgggaatca aatggccagc cagagaacaa ttacaagacc     1200

acaccccctg tgctggactc tgatgggagt ttctttctgt attccaagct gaccgtggat     1260

aaatctagat ggcagcaggg aaatgtcttt agctgttccg tgatgcatga ggactgcac      1320

aaccattaca cccagaaatc actgtcactg tcccaggaa aaggcggggg aggctctgga      1380

gtgcagctgg tccagagcgg aggaggactg gtgcagccag gagggtcact gaggtgagc      1440

tgcgcagctt ccggcttcac cgtgtcaaca aactacatga gctgggtccg ccaggcacct      1500

```

## HB01P012WO Sequence Listing\_ST25

```

gggaagggac tggagtgggt gtccatcctg tacgccggag gcgtgactcg atatgctgac      1560
tctgtcaaga ctcggttcac catctctaga gataacagta agaacaccct gtttctgcag      1620
atgaatgcac tgagtgccga agacacagct atctactatt gtgcaaaaca ctacgattct      1680
gggtatagta caattgacca ttttgattct tggggccagg ggacactggt gactgtcagc      1740
tccggcgggg gagggctctgg gggaggcggg agtggaggcg ggggatcaga catccagatg      1800
actcagtctc ccgatatgtg ggccgtctcc ctgggggaga gggctacaat taactgcaag      1860
agctcccagt cctgtttcta cacttctaag aacaaaaact atctggcatg gtttcagcag      1920
aagcctggac agccccctaa actgctgata tactgggcct caaccgaga gagcggagtc      1980
ccagacagat tctcaggcag cgggtccgga acagatttta ccctgacaat ttctagtctg      2040
cggcctgaag acgtggctgt ctactattgt cagcagtact atagcactcc attcaccttt      2100
ggccccggga caaaggtgga tatcaaaggc gggggaggct ctgaggtgca gctggtcgaa      2160
tctggcgggg acctggtgaa ggcaggaggc agtctgaggc tgtcatgcgc cgtctcaggg      2220
ctgagcttca gtcctctgga aatgaactgg gtgcgccagg caccaggcaa aggactggag      2280
tggatcagtt caatttctgg cagtcagaat tacaagtact atgctgacag tgtgaaaggg      2340
cgattcgtgg tctcccggga taacgcaaga aattttctgt atctgcagat ggacagcctg      2400
agagccgaag atactgctgt gtacttctgt gtcgggggat ttccctattg gctgccccct      2460
tccgatttct ctggctttca cgtgtgggga cagggcacca cagtaccgt cagctccggc      2520
gggggaggct ctgggggagg cgggagtgga ggcgggggat catcctacgt gctgactcag      2580
ccacctagcg tgtccgtcgc acctggacag actgccagcc tgacctgcgg aggaacaaac      2640
atcgggtcta agagtgtgca ctggtaccag cagaaagccg gacaggctcc cgtcctggtg      2700
gtctatgccg acaatgatcg gccatctggc gtgcccgaag gattctcagg aagcaactcc      2760
ggcaataaccg ctacactgac tatttctagg gtggaggcag aagacgagag tgattatttc      2820
tgtcaggtct gggacgggaa cacagatcat gtggtctttg gaggcgggac caagctgaca      2880
gtgctg      2886

```

&lt;210&gt; 155

&lt;211&gt; 707

&lt;212&gt; PRT

HB01P012W0 Sequence Listing\_ST25

<213> Artificial Sequence

<220>

<223> Ts2GC2b/Bs1GC2a heavy chain aa

<400> 155

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Ala Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Leu Ser Phe Ser Ser Ser  
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Ser Ser Ile Ser Gly Ser Gln Asn Tyr Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Val Val Ser Arg Asp Asn Ala Arg Asn Phe Leu Tyr  
65 70 75 80

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

Val Gly Gly Phe Pro Tyr Trp Leu Pro Pro Ser Asp Phe Ser Gly Phe  
100 105 110

His Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly  
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu  
130 135 140

Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala Ser Leu  
145 150 155 160

Thr Cys Gly Gly Thr Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln  
165 170 175

Gln Lys Ala Gly Gln Ala Pro Val Leu Val Val Tyr Ala Asp Asn Asp



HB01P012W0 Sequence Listing\_ST25

180

185

190

Arg Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn  
195 200 205

Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Glu Ser Asp  
210 215 220

Tyr Phe Cys Gln Val Trp Asp Gly Asn Thr Asp His Val Val Phe Gly  
225 230 235 240

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gln Leu Gln  
245 250 255

Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro Gly Ala Ser Val Lys  
260 265 270

Val Ser Cys Lys Ser Ser Gly Tyr Val Phe Thr Ser Tyr Tyr Leu Val  
275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Ala Thr Ile  
290 295 300

Ser Pro Gly Asp Val Asn Thr Ser Tyr Glu Gln Arg Phe Gln Gly Arg  
305 310 315 320

Val Thr Val Thr Thr Asp Ala Ser Thr Asn Thr Val Asp Met Glu Leu  
325 330 335

Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
340 345 350

Pro Arg Ser Lys Pro Pro Tyr Leu Tyr Phe Ala Leu Asp Val Trp Gly  
355 360 365

Gln Gly Thr Ala Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
370 375 380

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala

HB01P012WO Sequence Listing\_ST25

385 390 395 400

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
405 410 415

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
420 425 430

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
435 440 445

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
450 455 460

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys  
465 470 475 480

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
485 490 495

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
500 505 510

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
515 520 525

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
530 535 540

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
545 550 555 560

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
565 570 575

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
580 585 590

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val

# HB01P012WO Sequence Listing\_ST25

595

600

605

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
610 615 620

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
625 630 635 640

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
645 650 655

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
660 665 670

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
675 680 685

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
690 695 700

Pro Gly Lys  
705

<210> 156  
<211> 2121  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ts2GC2b/Bs1GC2a heavy chain nucl

<400> 156  
gaggtgcagc tgggtggaaag cggaggggat ctggtgaaag caggagggag cctgagactg 60  
tcatgcgccg tgagcgggct gtcattcagc tcctctggca tgaactgggt gcgacaggct 120  
cctggaaagg gactggagtg gatcagttca attagcgggt ccagaatta caagtactat 180  
gcagactctg tcaaaggaag gttcgtggtc agccgggata acgccagaaa ttttctgtat 240  
ctgcagatgg acagcctgcg cgccgaagat accgccgtgt acttctgcgt cggcgggttt 300  
ccctattggc tgcctccaag cgatttcagc ggatttcatg tctgggggca gggaactaca 360

HB01P012W0 Sequence Listing\_ST25

gtgaccgtct catcaggcgg gggaggctct gggggaggcg ggagtggagg cgggggatca	420
tcttacgtcc tgaccagcc acctagcgtg agcgtcgac cagggcagac agcttactg	480
acttgcggag gcacaaacat tggcagcaag agcgtgcact ggtaccagca gaaagccgga	540
caggctcccc tcctgggtgt ctatgctgac aacgatcggc cctctggcgt gcctgaaaga	600
ttcagcggct ccaactctgg gaataccgca aactgacca tcagtagggg cgaggccgaa	660
gacgagtcag attacttttg ccagggtgtg gacggcaata ctgaccatgt cgtgttcggc	720
ggcgggacca aactgactgt gctgggcggg ggaggctctc agctgcagct ggtccagtca	780
ggcacagaag tcaaaaaacc cggcgcaagc gtgaaggctc catgtaaatc atcaggatac	840
gtctttacct cttactatct ggtgtgggtc cggcaggcac caggacaggg actggagtgg	900
atggccacaa tctctcccg agacgtgaac actagttacg aacagcgatt ccagggcaga	960
gtgaccgtca ccacagacgc ttcaactaat accgtggata tggagctgcg gagcctgaga	1020
tccgaagata cagccgtcta ctattgcgt agggggcccc gcagcaagcc tccttatctg	1080
tacttcgctc tggatgtctg ggggcagggg accgccgtca ccgtctcaag cgcgtcgacc	1140
aaggggccat cggctttccc cctggcacc tcctccaaga gcacctctgg gggcacagcg	1200
gccctgggct gcctgggtcaa ggactacttc cccgaacctg tgacggtctc gtggaactca	1260
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	1320
tccctcagca gcgtgggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	1380
aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt	1440
gacaaaactc acacatgccc accgtgcca gcacctgaac tcctgggggg accgtcagtc	1500
ttctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	1560
tgcgtgggtg tggacgtgag ccacaggat cctgaggtca agttcaactg gtacgtggac	1620
ggcgtggagg tgcataatgc caagacaaag ccgcgggagg agcagtacaa cagcacgtac	1680
cgtgtgggtca gcgtcctcac cgtcctgcac caggactggc tgaatggcaa ggagtacaag	1740
tgcaaggctc ccaacaaagc cctcccagcc cccatcgaga aaaccatctc caaagccaaa	1800
gggcagcccc gagaaccaca ggtgtacacc ctgccccat cccgggagga gatgaccaag	1860
aaccagggtca gcctgacctg cctgggtcaaa ggcttctatc ccagcgacat cgccgtggag	1920

# HB01P012WO Sequence Listing\_ST25

```

tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctcccgt gctggactcc      1980
gacggctcct tcttcctcta tagcaagctc accgtggaca agagcaggtg gcagcagggg      2040
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc      2100
ctctccctgt ccccgggtaa a                                              2121
    
```

```

<210> 157
<211> 469
<212> PRT
<213> Artificial Sequence
    
```

```

<220>
<223> Ts2GC2b/Bs2GC1c light chain aa
    
```

```

<400> 157
    
```

```

Gly Val Gln Leu Val Gln 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 Val Ser Thr Asn
          20           25           30
    
```

```

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
          35           40           45
    
```

```

Ser Ile Leu Tyr Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys
          50           55           60
    
```

```

Thr Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu
65           70           75           80
    
```

```

Gln Met Asn Ala Leu Ser Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
          85           90           95
    
```

```

Lys His Tyr Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp
          100          105          110
    
```

```

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
          115          120          125
    
```

```

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
    
```

# HB01P012WO Sequence Listing\_ST25

130

135

140

Pro Asp Ser Val Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys  
145 150 155 160

Lys Ser Ser Gln Ser Val Phe Tyr Thr Ser Lys Asn Lys Asn Tyr Leu  
165 170 175

Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr  
180 185 190

Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
195 200 205

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro Glu  
210 215 220

Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr  
225 230 235 240

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Gly Gly Gly Gly Ser Glu  
245 250 255

Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu  
260 265 270

Thr Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Leu  
275 280 285

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile  
290 295 300

Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Arg Gly Arg Phe Ser Gly  
305 310 315 320

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro  
325 330 335

Glu Asp Phe Val Leu Tyr Tyr Cys Gln His Tyr Gly Ser Arg Val Thr

# HB01P012WO Sequence Listing\_ST25

340

345

350

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala Pro  
355 360 365

Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr  
370 375 380

Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys  
385 390 395 400

Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu  
405 410 415

Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser  
420 425 430

Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala  
435 440 445

Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe  
450 455 460

Asn Arg Gly Glu Cys  
465

<210> 158  
<211> 1407  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ts2GC2b/Bs2GC1c light chain nucl

<400> 158  
ggcgtccagc tgggtgcagag cggaggggggc ctggtgcagc ctggcgggtc cctgagactg 60  
agttgtgccg caagtggcctt tactgtctct acaaactaca tgtcttgggt gaggcaggca 120  
cctggaaagg gactggagtg ggtctcaatc ctgtacgctg gcgggggtgac ccggtatgca 180  
gacagcgtca agacccggtt cacaattagc agagataact ccaaaaatac tctgtttctg 240

HB01P012WO Sequence Listing\_ST25

cagatgaatg ccctgtccgc tgaagacacc gcaatctact attgcgccaa acactatgat	300
agtgggtata gcacaatcga ccattttgac agctggggac agggaaactct ggtgacagtc	360
tcatcaggcg ggggaggctc tgggggaggc gggagtggag gcgggggatc agacattcag	420
atgaccacaga gtcctgattc cgtggctgtc tctactggggg agcgagcaac tattaactgc	480
aagtcttcac agagcgtgtt ctacaccagt aagaacaaaa actatctggc ctggtttcag	540
cagaagccag gccagcccc taaactgctg atctactggg ctagcactag agagtctgga	600
gtgccagaca gattctctgg cagtgggtca ggaaccgact tcaccctgac aattagctcc	660
ctgaggccccg aagacgtggc cgtctactat tgtcagcagt attacagcac cccattcaca	720
ttcggccctg gaaccaaagt ggatattaag ggcgggggag gctctgaaat cgtgctgacc	780
cagtctcctg gaactctgtc tctgtcacct ggcgaaaccg caatcctgtc ctgtagggca	840
agtcagtctg tgagctctc tctgtggca tgggtaccagc agaagcccgg acaggcccct	900
aggctgctga tctatggcgc ctccaaccgc gctactggca ttcgggggag attcagtggc	960
tcagggagcg gaaccgactt taccctgaca atcagccggc tggagcccga agatttcgtg	1020
ctgtattact gtcagcacta tggcagcagg gtcacttttg ggcaggggac taaactggag	1080
attaaacgta cgggtggctgc accatctgtc ttcattctcc cgccatctga tgagcagttg	1140
aaatctggaa ctgcctctgt tgtgtgcctg ctgaataact tctatcccag agaggccaaa	1200
gtacagtgga aggtggataa cgccctccaa tcgggtaact cccaggagag tgtcacagag	1260
caggacagca aggacagcac ctacagcctc agcagcacc tgacgctgag caaagcagac	1320
tacgagaaac acaaagtcta cgcctgcgaa gtcacccatc agggcctgag ctcgcccgtc	1380
acaaagagct tcaacagggg agagtgt	1407

<210> 159

<211> 705

<212> PRT

<213> Artificial Sequence

<220>

<223> Ts2GC2c/Bs1GC3a heavy chain aa

<400> 159

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Ala Gly Gly



## HB01P012W0 Sequence Listing\_ST25

```

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

```

HB01P012W0 Sequence Listing\_ST25

210

215

220

Tyr Phe Cys Gln Val Trp Asp Gly Asn Thr Asp His Val Val Phe Gly  
225 230 235 240

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Ser Gly Val Gln  
245 250 255

Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg  
260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Thr Asn Tyr Met Ser  
275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ile Leu  
290 295 300

Tyr Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys Thr Arg Phe  
305 310 315 320

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asn  
325 330 335

Ala Leu Ser Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr  
340 345 350

Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp Gly Gln Gly  
355 360 365

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
370 375 380

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
385 390 395 400

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
405 410 415

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu

## HB01P012W0 Sequence Listing\_ST25

420

425

430

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
 435 440 445

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
 450 455 460

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys  
 465 470 475 480

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
 485 490 495

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
 500 505 510

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
 515 520 525

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
 530 535 540

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
 545 550 555 560

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
 565 570 575

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
 580 585 590

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
 595 600 605

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr  
 610 615 620

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu

# HB01P012W0 Sequence Listing\_ST25

625 630 635 640

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
645 650 655

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
660 665 670

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
675 680 685

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
690 695 700

Lys  
705

<210> 160  
<211> 2115  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ts2GC2c/Bs1GC3a heavy chain nucl

<400> 160  
gaggtgcagc tgggtggaaaag tgggggcat ctggtcaaag ccggagggtc tctgcgactg 60  
tcttgtgctg tgagcggcct gtccttcagc tcctctggca tgaactgggt gcgacaggct 120  
cctggaaaagg gactggagtg gatcagttca attagcgggt ccagaatta caagtactat 180  
gcagactctg tcaaaggaag gttcgtggtc agccgggata acgcagaaa ttttctgtat 240  
ctgcagatgg acagcctgcg cgccgaagat accgccgtgt acttctgcgt cggcgggttt 300  
ccctattggc tgcctccaag cgacttttca gggtttcatg tctgggggca gggaactacc 360  
gtgaccgtct catctggcgg gggaggctct gggggaggcg ggagtggagg cgggggatca 420  
tcctacgtcc tgactcagcc acctagctg tccgtcgac ctgggcagac agcatcactg 480  
acttgcgggg gaaccaacat cggcagcaag agcgtgcact ggtaccagca gaaagccgga 540  
caggctcccc tcctggtggt ctatgctgac aacgatcggc cctctggcgt gcctgaaaga 600

## HB01P012WO Sequence Listing\_ST25

ttcagcggct ccaactctgg gaataccgca acactgacca tcagtagggg cgaggccgaa	660
gacgagtcag attacttttg ccaggtctgg gatgggaata ctgaccacgt cgtcttcgga	720
ggcggaaacca aactgactgt cctgggcggg ggaggctctg gcgtgcagct ggtgcagagc	780
ggcggcggcc tgggtgcagcc tggagggtca ctgagactgt catgcgcagc aagcgggttt	840
actgtgtcta caaactacat gtcttgggtg aggcaggcac ctggaaaggg actggagtgg	900
gtctcaatcc tgtacgttg cggggtgacc cggtatgcag acagcgtcaa gacccggttc	960
acaattagca gagataactc caaaaatact ctgtttctgc agatgaatgc cctgtccgct	1020
gaagacaccg caatctacta ttgcgcaaaa cactatgata gtgggtactc cactattgac	1080
cattttgact cttgggggca ggggactctg gtgactgtct cttcagcgtc gaccaagggc	1140
ccatcgggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg	1200
ggctgcctgg tcaaggacta cttccccgaa cctgtgacgg tctcgtggaa ctcaggcgcc	1260
ctgaccagcg gcgtgcacac cttcccggt gtcttacagt cctcaggact ctactccctc	1320
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	1380
aatcacaagc ccagcaacac caaggtggac aagagagttg agcccaaatc ttgtgacaaa	1440
actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc	1500
ttccccccaa aaccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	1560
gtggtggacg tgagccacga ggatcctgag gtcaagttca actggtacgt ggacggcgtg	1620
gaggtgcata atgccaagac aaagccgcgg gaggagcagt acaacagcac gtaccgtgtg	1680
gtcagcgtcc tcaccgtcct gcaccaggac tggctgaatg gcaaggagta caagtgaag	1740
gtctccaaca aagccctccc agccccatc gagaaaacca tctcaaagc caaagggcag	1800
ccccgagaac cacaggtgta caccctgccc ccatcccggg aggagatgac caagaaccag	1860
gtcagcctga cctgcctggt caaaggcttc tatcccagcg acatcgccgt ggagtgggag	1920
agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc	1980
tccttcttcc tctatagcaa gtcaccgtg gacaagagca ggtggcagca ggggaacgtc	2040
ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacgcagaa gagcctctcc	2100
ctgtccccgg gtaaa	2115

# HB01P012W0 Sequence Listing\_ST25

<210> 161

<211> 471

<212> PRT

<213> Artificial Sequence

<220>

<223> Ts2GC2c/Bs2GC1d light chain aa

<400> 161

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

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr Val Phe Thr Ser Tyr  
20 25 30

Tyr Leu Val Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Ala Thr Ile Ser Pro Gly Asp Val Asn Thr Ser Tyr Glu Gln Arg Phe  
50 55 60

Gln Gly Arg Val Thr Val Thr Thr Asp Ala Ser Thr Asn Thr Val Asp  
65 70 75 80

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

Ala Arg Gly Pro Arg Ser Lys Pro Pro Tyr Leu Tyr Phe Ala Leu Asp  
100 105 110

Val Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser Gly Gly Gly Gly  
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr  
130 135 140

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Thr Ala Ile Leu  
145 150 155 160

Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Leu Leu Ala Trp Tyr

HB01P012W0 Sequence Listing\_ST25

165

170

175

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser  
180 185 190

Asn Arg Ala Thr Gly Ile Arg Gly Arg Phe Ser Gly Ser Gly Ser Gly  
195 200 205

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Val  
210 215 220

Leu Tyr Tyr Cys Gln His Tyr Gly Ser Arg Val Thr Phe Gly Gln Gly  
225 230 235 240

Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Asp Ile Gln Met Thr  
245 250 255

Gln Ser Pro Asp Ser Val Ala Val Ser Leu Gly Glu Arg Ala Thr Ile  
260 265 270

Asn Cys Lys Ser Ser Gln Ser Val Phe Tyr Thr Ser Lys Asn Lys Asn  
275 280 285

Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu  
290 295 300

Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser  
305 310 315 320

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg  
325 330 335

Pro Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro  
340 345 350

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg Thr Val Ala  
355 360 365

Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser

HB01P012WO Sequence Listing\_ST25

370

375

380

Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu  
385 390 395 400

Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser  
405 410 415

Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu  
420 425 430

Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val  
435 440 445

Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
450 455 460

Ser Phe Asn Arg Gly Glu Cys  
465 470

<210> 162  
<211> 1413  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ts2GC2c/Bs2GC1d light chain nucl

<400> 162  
cagctgcagc tgggtccagag cggcacagag gtgaaaaagc caggagcatc agtcaaagtg 60  
tcttgtaagt catcaggata cgtcttcacc tcttactatc tgggtgtgggt ccggcaggca 120  
ccaggacagg gactggagtg gatggccaca atctctcccg gagacgtgaa cactagttac 180  
gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat 240  
atggagctgc ggagcctgag atccgaagat acagccgtct actattgctc tagggggccc 300  
cgcagcaagc ctccttatct gtatttcgct ctggatgtct gggggcaggg aacagcagtc 360  
accgtctctt ctggcggggg aggctctggg ggaggcgga gtggaggcgg gggatcagaa 420  
atcgtcctga cccagtcacc tggcaccctg agtctgagtc ctggcgaaac agcaatcctg 480



# HB01P012W0 Sequence Listing\_ST25

tcttgtcggg cttcacagtc cgtgagctcc tctctgctgg catggtacca gcagaagccc	540
ggacaggccc ctaggctgct gatctatggc gcctccaacc gcgctactgg cattcggggg	600
agattcagtg gctcaggag cggaaccgac ttaccctga caatcagccg gctggagccc	660
gaagatttcg tgctgtacta ctgtcagcat tatgggtcac gggtcacttt tgggcagggg	720
actaaactgg aaatcaaggg cgggggaggc tctgacattc agatgacca gagtccctgac	780
agcgtggccg tctcactggg ggaaagggt actatcaatt gtaaaagttc acagtccgtc	840
ttctacacca gtaagaacaa aaactatctg gcctggtttc agcagaagcc aggccagccc	900
cctaaactgc tgatctactg ggctagcact agagagtctg gagtgccaga cagattctct	960
ggcagtgggt caggaaccga cttcacctg acaattagct ccctgaggcc cgaagacgtg	1020
gccgtctatt attgtcagca gtattattct acccccttca cattcggacc tgggactaaa	1080
gtggatatca aacgtacggg ggctgcacca tctgtcttca tcttcccgcc atctgatgag	1140
cagttgaaat ctggaactgc ctctgttgtg tgctgtctga ataacttcta tcccagagag	1200
gccaaagtac agtggaagggt ggataacgcc ctccaatcgg gtaactcca ggagagtgtc	1260
acagagcagg acagcaagga cagcacctac agcctcagca gcaccctgac gctgagcaaa	1320
gcagactacg agaaacacaa agtctacgcc tgcgaagtca cccatcaggg cctgagctcg	1380
cccgtcacia agagcttcaa caggggagag tgt	1413

<210> 163

<211> 962

<212> PRT

<213> Artificial Sequence

<220>

<223> Ts3GC2d heavy chain aa

<400> 163

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Asp	Leu	Val	Lys	Ala	Gly	Gly
1			5						10					15	

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Val	Ser	Gly	Leu	Ser	Phe	Ser	Ser	Ser
			20						25				30		

Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## HB01P012WO Sequence Listing\_ST25

35

40

45

Ser Ser Ile Ser Gly Ser Gln Asn Tyr Lys Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Val Val Ser Arg Asp Asn Ala Arg Asn Phe Leu Tyr  
 65 70 75 80

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

Val Gly Gly Phe Pro Tyr Trp Leu Pro Pro Ser Asp Phe Ser Gly Phe  
 100 105 110

His Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly  
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu  
 130 135 140

Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala Ser Leu  
 145 150 155 160

Thr Cys Gly Gly Thr Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln  
 165 170 175

Gln Lys Ala Gly Gln Ala Pro Val Leu Val Val Tyr Ala Asp Asn Asp  
 180 185 190

Arg Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn  
 195 200 205

Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Glu Ser Asp  
 210 215 220

Tyr Phe Cys Gln Val Trp Asp Gly Asn Thr Asp His Val Val Phe Gly  
 225 230 235 240

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gln Leu Gln

# HB01P012W0 Sequence Listing\_ST25

245

250

255

Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro Gly Ala Ser Val Lys  
260 265 270

Val Ser Cys Lys Ser Ser Gly Tyr Val Phe Thr Ser Tyr Tyr Leu Val  
275 280 285

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Ala Thr Ile  
290 295 300

Ser Pro Gly Asp Val Asn Thr Ser Tyr Glu Gln Arg Phe Gln Gly Arg  
305 310 315 320

Val Thr Val Thr Thr Asp Ala Ser Thr Asn Thr Val Asp Met Glu Leu  
325 330 335

Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly  
340 345 350

Pro Arg Ser Lys Pro Pro Tyr Leu Tyr Phe Ala Leu Asp Val Trp Gly  
355 360 365

Gln Gly Thr Ala Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser  
370 375 380

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala  
385 390 395 400

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
405 410 415

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
420 425 430

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
435 440 445

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His

HB01P012WO Sequence Listing\_ST25

450

455

460

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys  
465 470 475 480

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
485 490 495

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
500 505 510

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
515 520 525

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
530 535 540

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
545 550 555 560

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
565 570 575

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
580 585 590

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
595 600 605

Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser  
610 615 620

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
625 630 635 640

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
645 650 655

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val

## HB01P012W0 Sequence Listing\_ST25

660

665

670

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 675 680 685

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 690 695 700

Pro Gly Lys Gly Gly Gly Gly Ser Gly Val Gln Leu Val Gln Ser Gly  
 705 710 715 720

Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala  
 725 730 735

Ser Gly Phe Thr Val Ser Thr Asn Tyr Met Ser Trp Val Arg Gln Ala  
 740 745 750

Pro Gly Lys Gly Leu Glu Trp Val Ser Ile Leu Tyr Ala Gly Gly Val  
 755 760 765

Thr Arg Tyr Ala Asp Ser Val Lys Thr Arg Phe Thr Ile Ser Arg Asp  
 770 775 780

Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asn Ala Leu Ser Ala Glu  
 785 790 795 800

Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Asp Ser Gly Tyr Ser  
 805 810 815

Thr Ile Asp His Phe Asp Ser Trp Gly Gln Gly Thr Leu Val Thr Val  
 820 825 830

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 835 840 845

Ser Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Val Ala Val Ser Leu  
 850 855 860

Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Phe Tyr

# HB01P012W0 Sequence Listing\_ST25

865 870 875 880

Thr Ser Lys Asn Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly  
885 890 895

Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly  
900 905 910

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
915 920 925

Thr Ile Ser Ser Leu Arg Pro Glu Asp Val Ala Val Tyr Tyr Cys Gln  
930 935 940

Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp  
945 950 955 960

Ile Lys

<210> 164  
<211> 2886  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ts3GC2d heavy chain nucl

<400> 164  
gaggtgcagc tgggtggaaag cggaggggat ctggtgaaag caggagggag cctgagactg 60  
tcatgcgccg tgagcgggct gtcattcagc tcctctggca tgaactgggt gcgacaggct 120  
cctggaaagg gactggagt gatcagttca attagcgggt cccagaatta caagtactat 180  
gcagactctg tcaaaggaag gttcgtggtc agccgggata acgccagaaa ttttctgtat 240  
ctgcagatgg acagcctgcg cgccgaagat accgccgtgt acttctgcgt cggcggggtt 300  
ccctattggc tgcctccaag cgatttcagc ggatttcatt tctgggggca gggaactaca 360  
gtgaccgtct catcaggcgg gggaggctct gggggaggcg ggagtggagg cgggggatca 420  
tcttacgtcc tgaccagcc acctagcgtg agcgtcgcac cagggcagac agcttcactg 480

## HB01P012W0 Sequence Listing\_ST25

acttgcggag gcacaaacat tggcagcaag agcgtgcact ggtaccagca gaaagccgga	540
caggctccccg tcctggtggt ctatgctgac aacgatcggc cctctggcgt gcctgaaaga	600
ttcagcggct ccaactctgg gaataccgca acactgacca tcagtagggg cgaggccgaa	660
gacgagtcag attacttttg ccagggtgtg gacggcaata ctgaccatgt cgtgttcggc	720
ggcgggacca aactgactgt gctgggcggg ggaggctctc agctgcagct ggtccagtca	780
ggcacagaag tcaaaaaacc cggcgcaagc gtgaaggtct catgtaaatc atcaggatac	840
gtctttacct cttactatct ggtgtgggtc cggcaggcac caggacaggg actggagtgg	900
atggccacaa tctctcccgg agacgtgaac actagttacg aacagcgatt ccagggcaga	960
gtgaccgtca ccacagacgc ttcaactaat accgtggata tggagctgcg gagcctgaga	1020
tccgaagata cagccgtcta ctattgcgct agggggcccc gcagcaagcc tccttatctg	1080
tacttcgctc tggatgtctg ggggcagggg accgccgtca ccgtctcaag cgcgtcgacc	1140
aagggcccat cggctctccc cctggcacc cctccaaga gcacctctgg gggcacagcg	1200
gccctgggct gcctggtcaa ggactacttc cccgaacctg tgacgggtctc gtggaactca	1260
ggcgccctga ccagcggcgt gcacaccttc ccggctgtcc tacagtcctc aggactctac	1320
tccctcagca gcgtggtgac cgtgccctcc agcagcttgg gcaccagac ctacatctgc	1380
aacgtgaatc acaagcccag caacaccaag gtggacaaga gagttgagcc caaatcttgt	1440
gacaaaactc acacatgccc accgtgcca gcacctgaac tcctgggggg accgtcagtc	1500
ttcctcttcc ccccaaaacc caaggacacc ctcatgatct cccggacccc tgaggtcaca	1560
tgcgtggtgg tggacgtgag ccacaggat cctgaagtca agttcaactg gtacgtggat	1620
ggcgtcgagg tgcataatgc caagacaaaa cccgggagg aacagtacaa ctcaacttat	1680
agagtcgtga gcgtcctgac cgtgctgcat caggactggc tgaacggcaa agaatacaag	1740
tgcaaagtgt ctaataaggc cctgcctgct ccaatcgaga aaacaattag caaggcaaaa	1800
gggcagccca gggaacctca ggtgtacact ctgcctcaa gccgcgagga aatgaccaag	1860
aaccaggtct ccctgacatg tctggtgaaa ggattctatc ctagtgacat tgccgtggag	1920
tgggaatcaa atggccagcc agagaacaat tacaagacca cccccctgt gctggactct	1980
gatgggagtt tctttctgta ttccaagctg accgtggata aatctagatg gcagcagga	2040

# HB01P012W0 Sequence Listing\_ST25

```

aatgtcttta gctgttccgt gatgcatgag gcactgcaca accattacac ccagaaatca      2100
ctgtcactgt ccccaggaaa aggcggggga ggctctggcg tgcagctggg ccagagcgga      2160
ggcggactgg tccagcccgg cggatcactg agactgtcat gtgccgcaag cgggtttacc      2220
gtctctacaa actacatgtc ttgggtgagg caggcacctg gaaagggact ggagtgggtc      2280
tcaatcctgt acgctggcgg ggtgacccgg tatgcagaca gcgtcaagac ccggttcaca      2340
attagcagag ataactccaa aaatactctg tttctgcaga tgaatgccct gtccgctgaa      2400
gacaccgcaa tctactattg cgccaaacac tatgatagtg ggtacagtac cattgaccat      2460
ttcgatagct gggggcaggg gactctgggt accgtctcat caggcggggg aggctctggg      2520
ggaggcggga gtggaggcgg gggatcagat attcagatga cccagagtcc tgattccgtc      2580
gctgtctcac tgggagaaaag ggcaaccatt aactgtaaaa gtcacagag tgtcttctac      2640
accagtaaga acaaaaaacta tctggcctgg tttcagcaga agccaggcca gccccctaaa      2700
ctgctgatct actgggctag cactagagag tctggagtgc cagacagatt ctctggcagt      2760
gggtcaggaa ccgacttcac cctgacaatt agctccctga ggcccgaaga cgtggccgtc      2820
tactattgtc agcagtatta ttcaacaccc ttcacattcg gaccaggaac aaaagtggat      2880
attaag                                          2886
  
```

<210> 165  
 <211> 956  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Ts3GC2e heavy chain aa

<400> 165

```

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Ala Gly Gly
1           5           10          15
  
```

```

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Leu Ser Phe Ser Ser Ser
          20          25          30
  
```

```

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
          35          40          45
  
```



# HB01P012W0 Sequence Listing\_ST25

Ser Ser Ile Ser Gly Ser Gln Asn Tyr Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Val Val Ser Arg Asp Asn Ala Arg Asn Phe Leu Tyr  
65 70 75 80

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

Val Gly Gly Phe Pro Tyr Trp Leu Pro Pro Ser Asp Phe Ser Gly Phe  
100 105 110

His Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly  
115 120 125

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Tyr Val Leu  
130 135 140

Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln Thr Ala Ser Leu  
145 150 155 160

Thr Cys Gly Gly Thr Asn Ile Gly Ser Lys Ser Val His Trp Tyr Gln  
165 170 175

Gln Lys Ala Gly Gln Ala Pro Val Leu Val Val Tyr Ala Asp Asn Asp  
180 185 190

Arg Pro Ser Gly Val Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn  
195 200 205

Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Glu Asp Glu Ser Asp  
210 215 220

Tyr Phe Cys Gln Val Trp Asp Gly Asn Thr Asp His Val Val Phe Gly  
225 230 235 240

Gly Gly Thr Lys Leu Thr Val Leu Gly Gly Gly Gly Ser Gly Val Gln  
245 250 255

# HB01P012WO Sequence Listing\_ST25

Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg  
260 265 270

Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Thr Asn Tyr Met Ser  
275 280 285

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ile Leu  
290 295 300

Tyr Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys Thr Arg Phe  
305 310 315 320

Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asn  
325 330 335

Ala Leu Ser Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr  
340 345 350

Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp Gly Gln Gly  
355 360 365

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe  
370 375 380

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu  
385 390 395 400

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp  
405 410 415

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu  
420 425 430

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser  
435 440 445

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro  
450 455 460

# HB01P012W0 Sequence Listing\_ST25

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys  
465 470 475 480

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro  
485 490 495

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser  
500 505 510

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp  
515 520 525

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn  
530 535 540

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val  
545 550 555 560

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
565 570 575

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
580 585 590

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr  
595 600 605

Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr  
610 615 620

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu  
625 630 635 640

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu  
645 650 655

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys  
660 665 670

# HB01P012WO Sequence Listing\_ST25

Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
675 680 685

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly  
690 695 700

Lys Gly Gly Gly Gly Ser Gln Leu Gln Leu Val Gln Ser Gly Thr Glu  
705 710 715 720

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ser Ser Gly  
725 730 735

Tyr Val Phe Thr Ser Tyr Tyr Leu Val Trp Val Arg Gln Ala Pro Gly  
740 745 750

Gln Gly Leu Glu Trp Met Ala Thr Ile Ser Pro Gly Asp Val Asn Thr  
755 760 765

Ser Tyr Glu Gln Arg Phe Gln Gly Arg Val Thr Val Thr Thr Asp Ala  
770 775 780

Ser Thr Asn Thr Val Asp Met Glu Leu Arg Ser Leu Arg Ser Glu Asp  
785 790 795 800

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Pro Arg Ser Lys Pro Pro Tyr  
805 810 815

Leu Tyr Phe Ala Leu Asp Val Trp Gly Gln Gly Thr Ala Val Thr Val  
820 825 830

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
835 840 845

Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro  
850 855 860

Gly Glu Thr Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser  
865 870 875 880

# HB01P012WO Sequence Listing\_ST25

Ser Leu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu  
885 890 895

Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Arg Gly Arg Phe  
900 905 910

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu  
915 920 925

Glu Pro Glu Asp Phe Val Leu Tyr Tyr Cys Gln His Tyr Gly Ser Arg  
930 935 940

Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
945 950 955

<210> 166  
<211> 2868  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Ts3GC2e heavy chain nucl

<400> 166  
gaggtgcagc tgggtggaaaag tggggggcgat ctggtcaaag ccggagggtc tctgcgactg 60  
tcttgtgctg tgagcggcct gtccttcagc tcctctggca tgaactgggt gcgacaggct 120  
cctggaaaagg gactggagtg gatcagttca attagcgggt ccagaatta caagtactat 180  
gcagactctg tcaaaggaag gttcgtggtc agccgggata acgccagaaa ttttctgtat 240  
ctgcagatgg acagcctgcg cgccgaagat accgccgtgt acttctgcgt cggcggggtt 300  
ccctattggc tgcctccaag cgacttttca gggtttcatg tctgggggca gggaactacc 360  
gtgaccgtct catctggcgg gggaggctct gggggaggcg ggagtggagg cgggggatca 420  
tcctacgtcc tgactcagcc acctagcgtg tccgtcgcac ctgggcagac agcatcactg 480  
acttgcgggg gaaccaacat cggcagcaag agcgtgcact ggtaccagca gaaagccgga 540  
caggctcccg tcctggtggt ctatgctgac aacgatcggc cctctggcgt gcctgaaaga 600  
ttcagcggct ccaactctgg gaataccgca aactgacca tcagtagggt cgaggccgaa 660

HB01P012W0 Sequence Listing\_ST25

gacgagtcag attacttttg ccagggtctgg gatgggaata ctgaccacgt cgtcttcgga	720
ggcggaaacca aactgactgt cctgggscggg ggaggctctg gcgtgcagct ggtgcagagc	780
ggcggscggcc tgggtgcagcc tggaggggtca ctgagactgt catgcgcagc aagcgggttt	840
actgtgtcta caaactacat gtcttgggtg aggcaggcac ctggaaaggg actggagtgg	900
gtctcaatcc tgtacgttg cggggtgacc cggatatgcag acagcgtcaa gacccggttc	960
acaattagca gagataactc caaaaatact ctgtttctgc agatgaatgc cctgtccgct	1020
gaagacaccg caatctacta ttgcgcaaaa cactatgata gtgggtactc cactattgac	1080
cattttgact cttgggggca ggggactctg gtgactgtct cttcagcgtc gaccaagggc	1140
ccatcgggtct tccccctggc accctcctcc aagagcacct ctgggggcac agcggccctg	1200
ggctgcctgg tcaaggacta cttccccgaa cctgtgacgg tctcgtggaa ctcaggcgcc	1260
ctgaccagcg gcgtgcacac cttcccggt gtcttacagt cctcaggact ctactccctc	1320
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcaccc agacctacat ctgcaacgtg	1380
aatcacaagc ccagcaacac caagggtggac aagagagttg agcccaaadc ttgtgacaaa	1440
actcacacat gcccaccgtg cccagcacct gaactcctgg ggggaccgtc agtcttcctc	1500
ttcccccaa aacccaagga caccctcatg atctcccgga cccctgaggt cacatgcgtg	1560
gtgggtggacg tgagccacga ggatcctgaa gtcaagttca actggtacgt ggatggcgtc	1620
gaggtgcata atgccaagac aaaaccccg gaggaacagt acaactcaac ttatagagtc	1680
gtgagcgtcc tgaccgtgct gcatcaggac tggctgaacg gcaaagaata caagtgcaaa	1740
gtgtctaata aggccctgcc tgctccaatc gagaaaacaa ttagcaaggc aaaagggcag	1800
cccagggaac ctcagggtgta cactctgcct ccaagccgcg aggaaatgac caagaaccag	1860
gtctccctga catgtctggt gaaaggattc tatcctagt acattgccgt ggagtgggaa	1920
tcaaatggcc agccagagaa caattacaag accacacccc ctgtgctgga ctctgatggg	1980
agtttctttc tgtattccaa gctgaccgtg gataaatcta gatggcagca gggaaatgtc	2040
tttagctgtt ccgtgatgca tgaggcactg cacaaccatt acaccagaa atcactgtca	2100
ctgtccccag gaaaaggcgg gggaggctct cagctgcagc tgggtccagag cggaaccgaa	2160
gtgaagaaac ccggcgcaag cgtcaaagtc tcatgcaaat caagcgata cgtcttcacc	2220

# HB01P012W0 Sequence Listing\_ST25

tcttactatc tgggtgtgggt ccggcaggca ccaggacagg gactggagtg gatggccaca	2280
atctctcccg gagacgtgaa cactagttac gaacagcgat tccagggcag agtgaccgtc	2340
accacagacg cttcaactaa taccgtggat atggagctgc ggagcctgag atccgaagat	2400
acagccgtct actattgcgc tagggggccc cgagcaagc ctccttatct gtatttcgct	2460
ctggatgtct gggggcaggg aacagcagtc accgtctcaa gcggcggggg aggctctggg	2520
ggaggcggga gtggaggcgg gggatcagag attgtcctga cccagtcacc tggcaccctg	2580
agcctgagtc ctggagagac cgctattctg tcttgtcggg catcacagtc cgtgagctcc	2640
tctctgctgg catggtacca gcagaagccc ggacaggccc ctaggctgct gatctatggc	2700
gcctccaacc gcgctactgg cattcggggg agattcagtg gctcaggag cggaaccgac	2760
tttaccctga caatcagccg gctggagccc gaagatttcg tgctgtacta ttgtcagcat	2820
tatggaagca gggtcacctt cggacaggga actaaactgg aaatcaag	2868

<210> 167  
 <211> 709  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Bs3GC1a heavy chain aa

<400> 167

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

Ser	Val	Lys	Val	Ser	Cys	Lys	Ser	Ser	Gly	Tyr	Val	Phe	Thr	Ser	Tyr
		20					25					30			

Tyr	Leu	Val	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
	35					40					45				

Ala	Thr	Ile	Ser	Pro	Gly	Asp	Val	Asn	Thr	Ser	Tyr	Glu	Gln	Arg	Phe
	50					55				60					

Gln	Gly	Arg	Val	Thr	Val	Thr	Thr	Asp	Ala	Ser	Thr	Asn	Thr	Val	Asp
65				70					75					80	

# HB01P012WO Sequence Listing\_ST25

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

Ala Arg Gly Pro Arg Ser Lys Pro Pro Tyr Leu Tyr Phe Ala Leu Asp  
100 105 110

Val Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser Ala Ser Thr Lys  
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
130 135 140

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

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190

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

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285



# HB01P012W0 Sequence Listing\_ST25

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

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Val Gln Leu Val  
450 455 460

Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser  
465 470 475 480

Cys Ala Ala Ser Gly Phe Thr Val Ser Thr Asn Tyr Met Ser Trp Val  
485 490 495

# HB01P012W0 Sequence Listing\_ST25

Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ile Leu Tyr Ala  
500 505 510

Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys Thr Arg Phe Thr Ile  
515 520 525

Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asn Ala Leu  
530 535 540

Ser Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Asp Ser  
545 550 555 560

Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp Gly Gln Gly Thr Leu  
565 570 575

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
580 585 590

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Val Ala  
595 600 605

Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser  
610 615 620

Val Phe Tyr Thr Ser Lys Asn Lys Asn Tyr Leu Ala Trp Phe Gln Gln  
625 630 635 640

Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg  
645 650 655

Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
660 665 670

Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro Glu Asp Val Ala Val Tyr  
675 680 685

Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr  
690 695 700

# HB01P012WO Sequence Listing\_ST25

Lys Val Asp Ile Lys  
705

<210> 168  
<211> 2127  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Bs3GC1a heavy chain nucl

```

<400> 168
cagctgcagc tgggtccagtc aggcacagag gtcaaaaagc caggagcatc agtgaagggtg      60
tcttgtaagt catcaggata cgtgttcacc tcttactatc tgggtgtgggt ccggcaggca      120
ccaggacagg gactggagtg gatggccaca atctctcccg gagacgtgaa cactagttac      180
gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat      240
atggagctgc ggagcctgag atccgaagat acagccgtct actattgcgc taggggggccc      300
cgcagcaagc ctccttatct gtattttgct ctggatgtgt ggggggcaggg gaccgctgtc      360
accgtgtcaa gcgcgtcgac caagggccca tcggtcttcc ccctggcacc ctctccaag      420
agcacctctg ggggcacagc ggccctgggc tgcctggtca aggactactt ccccgaaact      480
gtgacggtct cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc      540
ctacagtcct caggactcta ctccctcagc agcgtggtga ccgtgccctc cagcagcttg      600
ggcacccaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag      660
agagttgagc ccaaattctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa      720
ctcctggggg gaccgtcagt cttcctcttc ccccaaaac ccaaggacac cctcatgac      780
tcccggaccc ctgaggtcac atgcgtggtg gtggacgtga gccacgagga tcctgaagtc      840
aagttcaact ggtacgtgga tggcgtcgag gtgcataatg ccaagacaaa accccgggag      900
gaacagtaca actcaactta tagagtcgtg agcgtcctga ccgtgctgca tcaggactgg      960
ctgaacggca aagaatacaa gtgcaaagtg tctaataagg ccctgcctgc tccaatcgag     1020
aaaacaatta gcaaggcaaa agggcagccc agggaaacctc aggtgtacac tctgcctcca     1080
agccgcgagg aaatgaccaa gaaccaggtc tccctgacat gtctggtgaa aggattctat     1140

```

# HB01P012WO Sequence Listing\_ST25

```

cctagtgcaca ttgccgtgga gtgggaatca aatggccagc cagagaacaa ttacaagacc      1200
acacccccctg tgctggactc tgatgggagt ttctttctgt attccaagct gaccgtggat      1260
aaatctagat ggcagcaggg aaatgtcttt agctgttccg tgatgcatga ggcactgcac      1320
aaccattaca cccagaaatc actgtcactg tccccaggaa aaggcggggg aggctctggc      1380
gtgcagctgg tccagagcgg aggcggactg gtccagcccg gcggatcact gagactgtca      1440
tgtgccgcaa gcggggtttac cgtctctaca aactacatgt cttgggtgag gcaggcacct      1500
ggaaagggac tggagtgggt ctcaatcctg tacgctggcg gggtgacccg gtatgcagac      1560
agcgtcaaga cccggttcac aattagcaga gataactcca aaaatactct gtttctgcag      1620
atgaatgccc tgtccgctga agacaccgca atctactatt gcgccaaaca ctatgatagt      1680
gggtacagta ccattgacca tttcgatagc tgggggcagg ggactctggt gaccgtctca      1740
tcaggcgggg gaggtctctg gggaggcggg agtggaggcg ggggatcaga tattcagatg      1800
acccagagtc ctgattccgt cgctgtctca ctgggagaaa gggcaaccat taactgtaaa      1860
agctcacaga gtgtcttcta caccagtaag aacaaaaact atctggcctg gtttcagcag      1920
aagccaggcc agccccctaa actgctgata tactgggcta gcactagaga gtctggagtg      1980
ccagacagat tctctggcag tgggtcagga accgacttca ccctgacaat tagctccctg      2040
aggcccgaag acgtggccgt ctactattgt cagcagtatt attcaacacc cttcacattc      2100
ggaccaggaa caaaagtgga tattaag                                           2127

```

<210> 169  
 <211> 703  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Bs3GC1b heavy chain aa

<400> 169

Gly	Val	Gln	Leu	Val	Gln	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	Val	Ser	Thr	Asn
			20					25					30		

# HB01P012W0 Sequence Listing\_ST25

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

Ser Ile Leu Tyr Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys  
50 55 60

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

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

Lys His Tyr Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp  
100 105 110

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr  
130 135 140

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

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

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
180 185 190

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser  
210 215 220

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
225 230 235 240

# HB01P012W0 Sequence Listing\_ST25

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
260 265 270

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
385 390 395 400

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
435 440 445

# HB01P012W0 Sequence Listing\_ST25

Ser Pro Gly Lys Gly Gly Gly Gly Ser Gln Leu Gln Leu Val Gln Ser  
450 455 460

Gly Thr Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys  
465 470 475 480

Ser Ser Gly Tyr Val Phe Thr Ser Tyr Tyr Leu Val Trp Val Arg Gln  
485 490 495

Ala Pro Gly Gln Gly Leu Glu Trp Met Ala Thr Ile Ser Pro Gly Asp  
500 505 510

Val Asn Thr Ser Tyr Glu Gln Arg Phe Gln Gly Arg Val Thr Val Thr  
515 520 525

Thr Asp Ala Ser Thr Asn Thr Val Asp Met Glu Leu Arg Ser Leu Arg  
530 535 540

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Pro Arg Ser Lys  
545 550 555 560

Pro Pro Tyr Leu Tyr Phe Ala Leu Asp Val Trp Gly Gln Gly Thr Ala  
565 570 575

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
580 585 590

Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
595 600 605

Leu Ser Pro Gly Glu Thr Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser  
610 615 620

Val Ser Ser Ser Leu Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala  
625 630 635 640

Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Arg  
645 650 655

# HB01P012W0 Sequence Listing\_ST25

Gly Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
660 665 670

Ser Arg Leu Glu Pro Glu Asp Phe Val Leu Tyr Tyr Cys Gln His Tyr  
675 680 685

Gly Ser Arg Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys  
690 695 700

<210> 170

<211> 2109

<212> DNA

<213> Artificial Sequence

<220>

<223> Bs3GC1b heavy chain nucl

<400> 170

ggggtgcaac tgggtgcagtc tgggggaggc ttggtccagc cggggggggtc cctgagactc	60
tcctgtgcag cctctggatt caccgtcagt accaactaca tgagctgggt ccgccaggct	120
ccagggaagg ggctggagtg ggtctcaatt ctttatgccg gaggtgtcac aaggtacgca	180
gactccgtga agaccagatt caccatctcc agagacaatt ccaagaacac tctctttctt	240
caaatgaacg ccctgagcgc cgaggacacg gctatatatt actgtgcgaa acactatgat	300
tcgggatatt ctaccataga tcactttgac tcctggggcc agggaaccct ggtcaccgtc	360
tcctcagcgt cgaccaaggg cccatcggtc ttccccctgg caccctcttc caagagcacc	420
tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga acctgtgacg	480
gtctcgtgga actcaggcgc cctgaccagc ggcgtgcaca ccttcccggc tgtcctacag	540
tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc	600
cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt	660
gagcccaaat cttgtgacaa aactcacaca tgcccaccgt gcccagcacc tgaactcctg	720
gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg	780
accctgagg tcacatgcgt ggtggtggac gtgagccacg aggatcctga agtcaagttc	840
aactggtacg tggatggcgt cgagggtgcat aatgccaaga caaaaccccg ggaggaacag	900



HB01P012WO Sequence Listing\_ST25

tacaactcaa cttatagagt cgtgagcgtc ctgaccgtgc tgcacagga ctggctgaac	960
ggcaaagaat acaagtgcaa agtgtctaata aaggccctgc ctgctccaat cgagaaaaca	1020
attagcaagg caaaagggca gcccagggaa cctcaggtgt acactctgcc tccaagccgc	1080
gaggaaatga ccaagaacca ggtctccctg acatgtctgg tgaaaggatt ctatcctagt	1140
gacattgccg tggagtggga atcaaatggc cagccagaga acaattacaa gaccacaccc	1200
cctgtgctgg actctgatgg gagtttcttt ctgtattcca agctgaccgt ggataaatct	1260
agatggcagc agggaaatgt ctttagctgt tccgtgatgc atgaggcact gcacaaccat	1320
tacaccaga aatcactgtc actgtcccca ggaaaaggcg ggggaggctc tcagctgcag	1380
ctgggtccaga gcggaaccga agtgaagaaa cccggcgcaa gcgtcaaagt ctcatgcaaa	1440
tcaagcggat acgtcttcac ctcttactat ctgggtgtggg tccggcaggc accaggacag	1500
ggactggagt ggatggccac aatctctccc ggagacgtga acactagtta cgaacagcga	1560
ttccagggca gaggaccgt caccacagac gcttcaacta ataccgtgga tatggagctg	1620
cggagcctga gatccgaaga tacagccgtc tactattgcg ctagggggcc ccgcagcaag	1680
cctccttacc tgtatttcgc tctggatgtc tgggggcagg gaacagcagt caccgtctca	1740
agcggcgggg gaggtctctg gggaggcggg agtggaggcg ggggatcaga gattgtcctg	1800
accagtcac ctggcaccct gagcctgagt cctggagaga ccgctattct gtcttgtcgg	1860
gcatcacagt ccgtgagctc ctctctgctg gcatggtacc agcagaagcc cggacaggcc	1920
cctaggctgc tgatctatgg cgcctccaac cgcgtactg gcattcgggg gagattcagt	1980
ggctcaggga gcggaaccga ctttaccctg acaatcagcc ggctggagcc cgaagatttc	2040
gtgctgtact attgtcagca ttatggaagc agggtcacct tcggacaggg aactaaactg	2100
gaaatcaag	2109

<210> 171  
 <211> 706  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Bs3GC2b heavy chain aa

<400> 171

# HB01P012WO Sequence Listing\_ST25

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

# HB01P012WO Sequence Listing\_ST25

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
405 410 415

# HB01P012W0 Sequence Listing\_ST25

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
435 440 445

Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gln Leu Gln Leu  
450 455 460

Val Gln Ser Gly Thr Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val  
465 470 475 480

Ser Cys Lys Ser Ser Gly Tyr Val Phe Thr Ser Tyr Tyr Leu Val Trp  
485 490 495

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Ala Thr Ile Ser  
500 505 510

Pro Gly Asp Val Asn Thr Ser Tyr Glu Gln Arg Phe Gln Gly Arg Val  
515 520 525

Thr Val Thr Thr Asp Ala Ser Thr Asn Thr Val Asp Met Glu Leu Arg  
530 535 540

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Pro  
545 550 555 560

Arg Ser Lys Pro Pro Tyr Leu Tyr Phe Ala Leu Asp Val Trp Gly Gln  
565 570 575

Gly Thr Ala Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly  
580 585 590

Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr Gln Ser Pro Gly  
595 600 605

Thr Leu Ser Leu Ser Pro Gly Glu Thr Ala Ile Leu Ser Cys Arg Ala  
610 615 620

# HB01P012WO Sequence Listing\_ST25

Ser Gln Ser Val Ser Ser Ser Leu Leu Ala Trp Tyr Gln Gln Lys Pro  
625 630 635 640

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Asn Arg Ala Thr  
645 650 655

Gly Ile Arg Gly Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
660 665 670

Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Val Leu Tyr Tyr Cys  
675 680 685

Gln His Tyr Gly Ser Arg Val Thr Phe Gly Gln Gly Thr Lys Leu Glu  
690 695 700

Ile Lys  
705

<210> 172  
<211> 2118  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Bs3GC2b heavy chain nucl

<400> 172  
gaggtacaat tggtggagtc tgggggagac ctggtcaagg cggggggggtc cctgagactc 60  
tcctgtgccg tctctggatt gtccttcagt agttcaggca tgaattgggt ccgccaggct 120  
ccagggaagg ggctggagtg gatctcatcg attagtggta gtcagaacta caaatactat 180  
gcagactcag tgaagggccg attcgtcgtc tccagagaca acgcccgcaa ctttctatat 240  
ctgcaaattg acagcctgag ggccgaggat acggctgtgt atttttgtgt gggagggttc 300  
ccctattggt taccctcgag cgacttctcc ggtttccatg tctggggcca agggaccacg 360  
gtcaccgtct cctcagcgtc gaccaagggc ccatcggtct tccccctggc accctcctcc 420  
aagagcacct ctggggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa 480  
cctgtgacgg tctcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct 540

# HB01P012W0 Sequence Listing\_ST25

gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc	600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	660
aagagagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtgggtggacg tgagccacga ggatcctgaa	840
gtcaagttca actggtacgt ggatggcgtc gaggtgcata atgccaagac aaaaccccg	900
gaggaacagt acaactcaac ttatagagtc gtgagcgtcc tgaccgtgct gcatcaggac	960
tggctgaacg gcaaagaata caagtcaaaa gtgtctaata aggccctgcc tgctccaatc	1020
gagaaaacaa ttagcaaggc aaaagggcag cccagggaac ctcaggtgta cactctgcct	1080
ccaagccgcg aggaaatgac caagaaccag gtctccctga catgtctggt gaaaggattc	1140
tatcctagt acattgccgt ggagtgggaa tcaaatggcc agccagagaa caattacaag	1200
accacacccc ctgtgctgga ctctgatggg agtttctttc tgtattccaa gctgaccgtg	1260
gataaatcta gatggcagca gggaaatgtc tttagctgtt ccgtgatgca tgaggcactg	1320
cacaaccatt acaccagaa atcactgtca ctgtccccag gaaaaggcgg gggaggctct	1380
cagctgcagc tgggtccagag cggaaccgaa gtgaagaaac ccggcgcaag cgtcaaagtc	1440
tcatgcaaat caagcggata cgtcttcacc tcttactatc tgggtgtgggt ccggcaggca	1500
ccaggacagg gactggagt gatggccaca atctctcccg gagacgtgaa cactagttac	1560
gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat	1620
atggagctgc ggagcctgag atccgaagat acagccgtct actattgcgc tagggggccc	1680
cgcagcaagc ctcttatct gtatttcgct ctggatgtct gggggcaggg aacagcagtc	1740
accgtctcaa gcggcggggg aggctctggg ggaggcggga gtggaggcgg gggatcagag	1800
attgtcctga cccagtcacc tggcacctg agcctgagtc ctggagagac cgctattctg	1860
tcttgctggg catcacagtc cgtgagctcc tctctgctgg catggtacca gcagaagccc	1920
ggacaggccc ctaggctgct gatctatggc gcctccaacc gcgctactgg cattcggggg	1980
agattcagtg gctcaggag cggaaccgac ttaccctga caatcagccg gctggagccc	2040
gaagatttcg tgctgtacta ttgtcagcat tatggaagca gggtcacctt cggacaggga	2100

HB01P012WO Sequence Listing\_ST25

actaaactgg aaatcaag

2118

<210> 173  
<211> 710  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Bs3GC3b heavy chain aa

<400> 173

Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Lys Ala Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Leu Ser Phe Ser Ser Ser  
20 25 30

Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile  
35 40 45

Ser Ser Ile Ser Gly Ser Gln Asn Tyr Lys Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Val Val Ser Arg Asp Asn Ala Arg Asn Phe Leu Tyr  
65 70 75 80

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

Val Gly Gly Phe Pro Tyr Trp Leu Pro Pro Ser Asp Phe Ser Gly Phe  
100 105 110

His Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr  
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser  
130 135 140

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

# HB01P012WO Sequence Listing\_ST25

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His  
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser  
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys  
195 200 205

Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu  
210 215 220

Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
225 230 235 240

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
245 250 255

Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
260 265 270

Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
275 280 285

Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
290 295 300

Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
305 310 315 320

Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
325 330 335

Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
340 345 350

Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys  
355 360 365



# HB01P012WO Sequence Listing\_ST25

Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 370 375 380

Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 385 390 395 400

Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 405 410 415

Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 420 425 430

Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 435 440 445

Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser Gly Val Gln Leu  
 450 455 460

Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu  
 465 470 475 480

Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Thr Asn Tyr Met Ser Trp  
 485 490 495

Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ile Leu Tyr  
 500 505 510

Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys Thr Arg Phe Thr  
 515 520 525

Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu Gln Met Asn Ala  
 530 535 540

Leu Ser Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys His Tyr Asp  
 545 550 555 560

Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp Gly Gln Gly Thr  
 565 570 575

# HB01P012WO Sequence Listing\_ST25

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
580 585 590

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Val  
595 600 605

Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln  
610 615 620

Ser Val Phe Tyr Thr Ser Lys Asn Lys Asn Tyr Leu Ala Trp Phe Gln  
625 630 635 640

Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr  
645 650 655

Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr  
660 665 670

Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro Glu Asp Val Ala Val  
675 680 685

Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly  
690 695 700

Thr Lys Val Asp Ile Lys  
705 710

<210> 174  
<211> 2130  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Bs3GC3b heavy chain nucl

<400> 174  
gaggtacaat tgggtggagtc tggggggagac ctgggtcaagg cggggggggtc cctgagactc 60  
tcctgtgccg tctctggatt gtccttcagt agttcaggca tgaattgggt ccgccaggct 120  
ccaggggaagg ggctggagtg gatctcatcg attagtggta gtcagaacta caaatactat 180

HB01P012W0 Sequence Listing\_ST25

gcagactcag tgaagggccg attcgtcgtc tccagagaca acgcccgcga ctttctatat	240
ctgcaaatgg acagcctgag ggccgaggat acggctgtgt atttttgtgt gggagggttc	300
ccctattggt tacccccagag cgacttctcc ggtttccatg tctggggcca agggaccacg	360
gtcaccgtct cctcagcgtc gaccaagggc ccatcgggtc tccccctggc accctcctcc	420
aagagcacct ctgggggcac agcggccctg ggctgcctgg tcaaggacta cttccccgaa	480
cctgtgacgg tctcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac cttcccggct	540
gtcctacagt cctcaggact ctactccctc agcagcgtgg tgaccgtgcc ctccagcagc	600
ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac caaggtggac	660
aagagagttg agcccaaadc ttgtgacaaa actcacacat gccaccgtg cccagcacct	720
gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aaccaagga caccctcatg	780
atctcccga cccctgaggt cacatgcgtg gtggtggacg tgagccacga ggatcctgaa	840
gtcaagttca actggtacgt ggatggcgtc gaggtgcata atgccaagac aaaaccccgg	900
gaggaacagt acaactcaac ttatagagtc gtgagcgtcc tgaccgtgct gcatcaggac	960
tggctgaacg gcaaagaata caagtgcaaa gtgtctaata aggccctgcc tgctccaatc	1020
gagaaaacaa ttagcaaggc aaaagggcag cccagggaac ctcaggtgta cactctgcct	1080
ccaagccgcg aggaaatgac caagaaccag gtctccctga catgtctggt gaaaggattc	1140
tatcctagt acattgccgt ggagtgggaa tcaaatggcc agccagagaa caattacaag	1200
accacacccc ctgtgctgga ctctgatggg agtttctttc tgtattccaa gctgaccgtg	1260
gataaatcta gatggcagca gggaaatgtc tttagctgtt ccgtgatgca tgaggcactg	1320
cacaaccatt acaccagaa atcactgtca ctgtccccag gaaaaggcgg gggaggctct	1380
ggcgtgcagc tgggtccagag cggaggcgga ctggtccagc ccggcggatc actgagactg	1440
tcatgtgccg caagcgggtt taccgtctct acaaactaca tgtcttgggt gaggcaggca	1500
cctggaaaagg gactggagt ggtctcaatc ctgtacgctg gcgggggtgac ccggtatgca	1560
gacagcgtca agacccggtt cacaattagc agagataact ccaaaaatac tctgtttctg	1620
cagatgaatg ccctgtccgc tgaagacacc gcaatctact attgcgcaa acactatgat	1680
agtgggtaca gtaccattga ccatttcgat agctgggggc aggggactct ggtgaccgtc	1740

HB01P012WO Sequence Listing\_ST25

tcatcaggcg ggggaggctc tgggggaggc gggagtggag gcgggggatc agatattcag	1800
atgacccaga gtcctgattc cgtcgctgtc tctctgggag aaagggcaac cattaactgt	1860
aaaagctcac agagtgtctt ctacaccagt aagaacaaaa actatctggc ctggtttcag	1920
cagaagccag gccagcccc taaactgctg atctactggg ctagcactag agagtctgga	1980
gtgccagaca gattctctgg cagtgggtca ggaaccgact tcaccctgac aattagctcc	2040
ctgaggcccc aagacgtggc cgtctactat tgtcagcagt attattcaac acccttcaca	2100
ttcggaccag gaacaaaagt ggatattaag	2130

<210> 175  
 <211> 710  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Bs3GC4 heavy chain aa

<400> 175

Gln Val Gln Leu Met Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg	
1                    5                                    10                                    15	

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

Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35                                    40                                    45	

Ala Ile Ile Leu Pro Asp Gly Asn Arg Lys Asn Tyr Gly Arg Ser Val	
50                                    55                                    60	

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

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

Thr Arg Asp Gly Thr Tyr Tyr Ser Asn Gly Gly Val Tyr Gln Thr Tyr	
100                                    105                                    110	

# HB01P012W0 Sequence Listing\_ST25

Arg Arg Phe Phe Asp Phe Trp Gly Arg Gly Thr Leu Val Thr Val Ser  
115 120 125

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
145 150 155 160

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
165 170 175

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
180 185 190

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
210 215 220

Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro  
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
260 265 270

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
290 295 300

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
305 310 315 320

# HB01P012WO Sequence Listing\_ST25

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
355 360 365

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
405 410 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser  
450 455 460

Gln Leu Gln Leu Val Gln Ser Gly Thr Glu Val Lys Lys Pro Gly Ala  
465 470 475 480

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr Val Phe Thr Ser Tyr  
485 490 495

Tyr Leu Val Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
500 505 510

Ala Thr Ile Ser Pro Gly Asp Val Asn Thr Ser Tyr Glu Gln Arg Phe  
515 520 525

# HB01P012W0 Sequence Listing\_ST25

Gln Gly Arg Val Thr Val Thr Thr Asp Ala Ser Thr Asn Thr Val Asp  
530 535 540

Met Glu Leu Arg Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys  
545 550 555 560

Ala Arg Gly Pro Arg Ser Lys Pro Pro Tyr Leu Tyr Phe Ala Leu Asp  
565 570 575

Val Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser Gly Gly Gly Gly  
580 585 590

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Leu Thr  
595 600 605

Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu Thr Ala Ile Leu  
610 615 620

Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser Leu Leu Ala Trp Tyr  
625 630 635 640

Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser  
645 650 655

Asn Arg Ala Thr Gly Ile Arg Gly Arg Phe Ser Gly Ser Gly Ser Gly  
660 665 670

Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu Pro Glu Asp Phe Val  
675 680 685

Leu Tyr Tyr Cys Gln His Tyr Gly Ser Arg Val Thr Phe Gly Gln Gly  
690 695 700

Thr Lys Leu Glu Ile Lys  
705 710

<210> 176  
<211> 2130  
<212> DNA

HB01P012WO Sequence Listing\_ST25

<213> Artificial Sequence

<220>

<223> Bs3GC4 heavy chain nucl

<400> 176

caggtgcaat tgatggagtc tgggggaggc gtggtccagc ctgggaggtc cctgcgactc	60
tcatgcagtg cctttggatt caccttttcg aactatccta tgcactgggt ccgccaggct	120
ccaggcaagg gacttgagtg ggtggctatc attttacctg atgggaacag aaaaaactat	180
ggaagggtccg tgacgggccg attcaccatc tccagagaca attccaaca cagcctttat	240
ttgcaaatga acaacctgac gactgaggac acggctatgt actattgtac gagagatggc	300
acgtattact ctaatgggtg tgtttatcag acatatcgaa ggttcttcga tttctggggc	360
cgtggcaccc tggtcaccgt ctctcagcg tcgaccaagg gcccatcggc cttccccctg	420
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac	480
tacttccccg aacctgtgac ggtctcgtgg aactcaggcg ccctgaccag cggcgtgcac	540
accttccccg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg	600
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcaca gccagcaac	660
accaagggtg acaagagagt tgagcccaa tcttgtgaca aaactcacac atgcccaccg	720
tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaaccaag	780
gacaccctca tgatctcccc gaccctgag gtcacatgcg tgggtggtgga cgtgagccac	840
gaggatcctg aagtcaagtt caactggtac gtggatggcg tcgaggtgca taatgccaa	900
acaaaacccc gggaggaaca gtacaactca acttatagag tcgtgagcgt cctgaccgtg	960
ctgcatcagg actggctgaa cggcaaagaa tacaagtga aagtgtctaa taaggccctg	1020
cctgctcaa tcgagaaaac aattagcaag gcaaaagggc agcccaggga acctcaggtg	1080
tacactctgc ctccaagccg cgaggaaatg accaagaacc aggtctccct gacatgtctg	1140
gtgaaaggat tctatcctag tgacattgcc gtggagtggg aatcaaatgg ccagccagag	1200
aacaattaca agaccacacc ccctgtgctg gactctgatg ggagtttctt tctgtattcc	1260
aagctgaccg tggataaatc tagatggcag cagggaatg tctttagctg ttccgtgatg	1320
catgaggcac tgcacaacca ttacaccag aaatcactgt cactgtcccc aggaaaaggc	1380



# HB01P012WO Sequence Listing\_ST25

```

gggggaggct ctcagctgca gctgggtccag agcgggaaccg aagtgaagaa acccgggcgca      1440
agcgtcaaag tctcatgcaa atcaagcgga tacgtcttca cctcttacta tctgggtgtgg      1500
gtccggcagg caccaggaca gggactggag tggatggcca caatctctcc cggagacgtg      1560
aacactagtt acgaacagcg attccagggc agagtgaccg tcaccacaga cgcttcaact      1620
aataccgtgg atatggagct gcggagcctg agatccgaag atacagccgt ctactattgc      1680
gctagggggc cccgcagcaa gcctccttat ctgtatttcg ctctggatgt ctggggggcag      1740
ggaacagcag tcaccgtctc aagcggcggg ggaggctctg ggggaggcgg gagtggaggc      1800
gggggatcag agattgtcct gaccagtc cctggcacc tgagcctgag tcctggagag      1860
accgctattc tgtcttgtcg ggcatcacag tccgtgagct cctctctgct ggcatggtac      1920
cagcagaagc ccggacaggc ccctaggctg ctgatctatg ggcctccaa ccgcgctact      1980
ggcattcggg ggagattcag tggctcaggg agcgggaaccg actttaccct gacaatcagc      2040
cggctggagc ccgaagattt cgtgctgtac tattgtcagc attatggaag cagggtcacc      2100
ttcggacagg gaactaaact ggaaatcaag      2130

```

```

<210> 177
<211> 714
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Bs3GC5 heavy chain aa

```

```

<400> 177

```

```

Gln Val Gln Leu Met Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1           5           10           15

```

```

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

```

```

Pro Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35           40           45

```

```

Ala Ile Ile Leu Pro Asp Gly Asn Arg Lys Asn Tyr Gly Arg Ser Val
50           55           60

```

# HB01P012WO Sequence Listing\_ST25

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

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

Thr Arg Asp Gly Thr Tyr Tyr Ser Asn Gly Gly Val Tyr Gln Thr Tyr  
100 105 110

Arg Arg Phe Phe Asp Phe Trp Gly Arg Gly Thr Leu Val Thr Val Ser  
115 120 125

Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser  
130 135 140

Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
145 150 155 160

Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr  
165 170 175

Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr  
180 185 190

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln  
195 200 205

Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp  
210 215 220

Lys Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro  
225 230 235 240

Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro  
245 250 255

Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr  
260 265 270

# HB01P012WO Sequence Listing\_ST25

Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn  
275 280 285

Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg  
290 295 300

Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val  
305 310 315 320

Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser  
325 330 335

Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
340 345 350

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu  
355 360 365

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe  
370 375 380

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu  
385 390 395 400

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe  
405 410 415

Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
420 425 430

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr  
435 440 445

Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Gly Gly Gly Gly Ser  
450 455 460

Gly Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
465 470 475 480

# HB01P012WO Sequence Listing\_ST25

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Thr Asn  
485 490 495

Tyr Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
500 505 510

Ser Ile Leu Tyr Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys  
515 520 525

Thr Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe Leu  
530 535 540

Gln Met Asn Ala Leu Ser Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala  
545 550 555 560

Lys His Tyr Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp  
565 570 575

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
580 585 590

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser  
595 600 605

Pro Asp Ser Val Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys  
610 615 620

Lys Ser Ser Gln Ser Val Phe Tyr Thr Ser Lys Asn Lys Asn Tyr Leu  
625 630 635 640

Ala Trp Phe Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr  
645 650 655

Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser  
660 665 670

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Arg Pro Glu  
675 680 685

# HB01P012WO Sequence Listing\_ST25

Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Thr Pro Phe Thr  
690 695 700

Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
705 710

<210> 178  
<211> 2142  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Bs3GC5 heavy chain nucl

<400> 178  
caggtgcaat tgatggagtc tgggggaggc gtggtccagc ctgggaggtc cctgcgactc 60  
tcatgcagtg cctttggatt caccttttcg aactatccta tgcactgggt ccgccaggct 120  
ccaggcaagg gacttgagtg ggtggctatc attttacctg atgggaacag aaaaaactat 180  
ggaagggtccg tgacgggccg attcaccatc tccagagaca attccaacaa cagcctttat 240  
ttgcaaatga acaacctgac gactgaggac acggctatgt actattgtac gagagatggc 300  
acgtattact ctaatgggtg tgtttatcag acatatcgaa ggttcttcga tttctggggc 360  
cgtggcaccc tggtcaccgt ctctcagcg tcgaccaagg gcccatcggg cttccccctg 420  
gcaccctcct ccaagagcac ctctgggggc acagcggccc tgggctgcct ggtcaaggac 480  
tacttccccg aacctgtgac ggtctcgtgg aactcaggcg ccctgaccag cggcgtgcac 540  
accttccccg ctgtcctaca gtcctcagga ctctactccc tcagcagcgt ggtgaccgtg 600  
ccctccagca gcttgggcac ccagacctac atctgcaacg tgaatcaca gccagcaac 660  
accaaggtgg acaagagagt tgagcccaa tcttgtgaca aaactcacac atgcccaccg 720  
tgcccagcac ctgaactcct ggggggaccg tcagtcttcc tcttcccccc aaaaccaag 780  
gacaccctca tgatctcccg gaccctgag gtcacatgcg tgggtggtgga cgtgagccac 840  
gaggatcctg aagtcaagtt caactggtac gtggatggcg tcgaggtgca taatgccaag 900  
acaaaacccc gggaggaaca gtacaactca acttatagag tcgtgagcgt cctgaccgtg 960  
ctgcatcagg actggctgaa cggcaaagaa tacaagtga aagtgcttaa taaggccctg 1020

# HB01P012WO Sequence Listing\_ST25

```

cctgctccaa tcgagaaaac aattagcaag gcaaaagggc agcccagggg acctcaggtg      1080
tacactctgc ctccaagccg cgaggaaatg accaagaacc aggtctccct gacatgtctg      1140
gtgaaaggat tctatcctag tgacattgcc gtggagtggg aatcaaattg ccagccagag      1200
aacaattaca agaccacacc ccctgtgctg gactctgatg ggagtttctt tctgtattcc      1260
aagctgaccg tggataaatc tagatggcag cagggaaatg tcttttagctg ttccgtgatg      1320
catgaggcac tgcacaacca ttacaccag aaatcactgt cactgtcccc aggaaaaggc      1380
gggggaggct ctggcgtgca gctgggtccag agcggaggcg gactgggtcca gcccggcgga      1440
tcactgagac tgtcatgtgc cgcaagcggg tttaccgtct ctacaaacta catgtcttgg      1500
gtgaggcagg cacctggaaa gggactggag tgggtctcaa tcctgtacgc tggcgggggtg      1560
acccggtatg cagacagcgt caagaccggtg ttcacaatta gcagagataa ctcaaaaat      1620
actctgtttc tgcagatgaa tgccctgtcc gctgaagaca ccgcaatcta ctattgcgcc      1680
aaacactatg atagtgggta cagtaccatt gaccatttcg atagctgggg gcagggggact      1740
ctggtgaccg tctcatcagg cgggggaggc tctgggggag gcgggagtgg aggcggggga      1800
tcagatattc agatgacca gagtcctgat tccgtcgctg tctcactggg agaaagggca      1860
accattaact gtaaaagctc acagagtgtc ttctacacca gtaagaacaa aaactatctg      1920
gcctggtttc agcagaagcc aggccagccc ctaaactgc tgatctactg ggctagcact      1980
agagagtctg gagggtccaga cagattctct ggcagtgggt caggaaccga cttcacctg      2040
acaattagct ccctgaggcc cgaagacgtg gccgtctact attgtcagca gtattattca      2100
acacccttca cattcggacc aggaacaaaa gtggatatta ag                        2142

```

<210> 179  
 <211> 452  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCA7 heavy chain aa

<400> 179

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

# HB01P012WO Sequence Listing\_ST25

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Val Ser Thr Asn  
20 25 30

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

Ser Ile Leu Tyr Ala Gly Gly Val Thr Arg Tyr Ala Asp Ser Val Lys  
50 55 60

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

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

Lys His Tyr Asp Ser Gly Tyr Ser Thr Ile Asp His Phe Asp Ser Trp  
100 105 110

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

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr  
130 135 140

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

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

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr  
180 185 190

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

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser  
210 215 220

# HB01P012WO Sequence Listing\_ST25

Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu  
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu  
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  
260 265 270

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

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

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro  
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln  
340 345 350

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val  
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val  
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro  
385 390 395 400

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

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val  
420 425 430



# HB01P012WO Sequence Listing\_ST25

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu  
 435 440 445

Ser Pro Gly Lys  
 450

<210> 180  
 <211> 1356  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCA7 heavy chain nucl

<400> 180  
 ggggtgcaac tgggtgcagtc tgggggaggc ttggtccagc cggggggggtc cctgagactc 60  
 tcctgtgcag cctctggatt caccgtcagt accaactaca tgagctgggt ccgccaggct 120  
 ccagggaagg ggctggagtg ggtctcaatt ctttatgccg gaggtgtcac aaggtagcga 180  
 gactccgtga agaccagatt caccatctcc agagacaatt ccaagaacac tctctttctt 240  
 caaatgaacg ccctgagcgc cgaggacacg gctatatatt actgtgcgaa acactatgat 300  
 tcgggatatt ctacataga tcactttgac tcctggggcc agggaaccct ggtcaccgtc 360  
 tcctcagcgt cgaccaaggg cccatcggtc ttccccctgg caccctcctc caagagcacc 420  
 tctgggggca cagcggccct gggctgcctg gtcaaggact acttccccga acctgtgacg 480  
 gtctcgtgga actcaggcgc cctgaccagc ggcgtgcaca ctttcccggc tgtcctacag 540  
 tcctcaggac tctactccct cagcagcgtg gtgaccgtgc cctccagcag cttgggcacc 600  
 cagacctaca tctgcaacgt gaatcacaag cccagcaaca ccaaggtgga caagagagtt 660  
 gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg 720  
 gggggaccgt cagtcttcct cttcccccca aaaccaagg acaccctcat gatctcccgg 780  
 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aggatcctga ggtcaagttc 840  
 aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag 900  
 tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 960  
 ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc 1020

# HB01P012WO Sequence Listing\_ST25

```

atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      1080
gaggagatga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc      1140
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      1200
cccgtgctgg actccgacgg ctcttcttc ctctatagca agctcaccgt ggacaagagc      1260
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      1320
tacacgcaga agagcctctc cctgtccccg ggtaaa                                1356

```

<210> 181  
 <211> 220  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCA7 light chain aa

<400> 181

```

Asp Ile Gln Met Thr Gln Ser Pro Asp Ser Val Ala Val Ser Leu Gly
1           5           10           15

```

```

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Phe Tyr Thr
          20           25           30

```

```

Ser Lys Asn Lys Asn Tyr Leu Ala Trp Phe Gln Gln Lys Pro Gly Gln
          35           40           45

```

```

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
          50           55           60

```

```

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65           70           75           80

```

```

Ile Ser Ser Leu Arg Pro Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
          85           90           95

```

```

Tyr Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
          100          105          110

```

```

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp

```

# HB01P012WO Sequence Listing\_ST25

115

120

125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
210 215 220

<210> 182  
<211> 660  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA7 light chain nucl

<400> 182  
gacatccaga tgaccagtc tccagactcc gtggctgtgt ctctgggcga gagggccacc 60  
atcaactgca agtccagcca gagtgttttc tacacctcca aaaataaaaa ctacttagct 120  
tggttccagc agaaaccagg acagcctcct aaactgctca tttactgggc atctaccgg 180  
gagtccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240  
atcagcagcc tgcggcctga agatgtggca gtttattact gtcagcaata ttatagtacc 300  
cctttcactt tcggccctgg gaccaaagtg gatatcaaac gtacggtggc tgcaccatct 360  
gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 420  
ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaaggtgga taacgccctc 480

# HB01P012W0 Sequence Listing\_ST25

caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 540

ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 600

gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 660

<210> 183

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> GCA21 light chain aa

<400> 183

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Thr Ser Val Gly  
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Leu Asn Trp  
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Asn Ala Pro Asn Leu Leu Ile  
35 40 45

Tyr Lys Ala Ser Asp Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

Asp Asp Phe Ala Thr Tyr Tyr Cys Gln His Tyr Asn Ser Tyr Pro Leu  
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

# HB01P012WO Sequence Listing\_ST25

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 184  
<211> 642  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCA21 light chain nucl

<400> 184  
gacatccaga tgacccagtc tccttcacc ctgtctacat ctgtgggaga cagagtcacc 60  
atcacttgcc gggccagtca gaatatcctt aattggttgg cctggtatca acagaaacca 120  
gggaacgccc ctaacctcct gatataaag gcgtctgatt tacaaagtgg ggtcccctca 180  
agattcagcg gcagtgggtc tgggacagaa ttcactctca ccatcagcag cctgcagcct 240  
gatgattttg caacttatta ctgccagcat tataatagtt atcctctcac tttcggcgga 300  
gggaccaagg tggaaatcaa acgtacggtg gctgcacat ctgtcttcat cttcccgcca 360  
tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420  
cccagagagg ccaaagtaca gtggaagggtg gataacgccc tccaatcggg taactcccag 480  
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540  
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600  
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt 642

# HB01P012WO Sequence Listing\_ST25

<210> 185  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCB59 light chain aa

<400> 185

Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Gln  
 1 5 10 15

Thr Ala Ser Leu Thr Cys Gly Gly Thr Asn Ile Gly Ser Lys Ser Val  
 20 25 30

His Trp Tyr Gln Gln Lys Ala Gly Gln Ala Pro Val Leu Val Val Tyr  
 35 40 45

Ala Asp Asn Asp Arg Pro Ser Gly Val 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 Glu  
 65 70 75 80

Asp Glu Ser Asp Tyr Phe Cys Gln Val Trp Asp Gly Asn Thr Asp His  
 85 90 95

Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys  
 100 105 110

Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln  
 115 120 125

Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly  
 130 135 140

Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly  
 145 150 155 160

Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala

## HB01P012W0 Sequence Listing\_ST25

165

170

175

Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg Ser  
 180 185 190

Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val  
 195 200 205

Ala Pro Thr Glu Cys Ser  
 210

<210> 186  
 <211> 642  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> GCB59 light chain nucl

<400> 186  
 tcatatgtgc tgactcaacc accctcgggtg tcagtggccc caggacagac ggccagtcta 60  
 acctgtggggg gaactaacat tggaagtaaa agtgttcatt ggtaccagca aaaggcaggc 120  
 caggccccctg tgttgggtcgt ctatgctgat aacgacaggc cctcaggggt ccctgagcga 180  
 ttctctgggt ccaactctgg gaacacggcc accctgacca tcagcaggggt cgaggccgag 240  
 gatgagtccg actatttctg tcagggtgtgg gatggtaata ctgatcatgt ggtcttcggc 300  
 ggagggacca agctgaccgt cctgggtcag cccaaggctg cccctcgggt cactctgttc 360  
 ccgcccctct ctgaggagct tcaagccaac aaggccacac tgggtgtgtct cataagtgc 420  
 ttctacccgg gagccgtgac agtggcttgg aaagcagata gcagccccgt caaggcggga 480  
 gtggagacca ccacaccctc caaacaagc aacaacaagt acgcggccag cagctatctg 540  
 agcctgacgc ctgagcagtg gaagtccac agaagctaca gctgccagggt cacgcatgaa 600  
 gggagaccg tggagaagac agtggccccct acagaatgtt ca 642

<210> 187  
 <211> 454  
 <212> PRT  
 <213> Artificial Sequence

# HB01P012W0 Sequence Listing\_ST25

<220>

<223> GCE536 heavy chain aa

<400> 187

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

Ser Val Lys Val Ser Cys Lys Ser Ser Gly Tyr Val Phe Thr Ser Tyr  
20 25 30

Tyr Leu Val Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met  
35 40 45

Ala Thr Ile Ser Pro Gly Asp Val Asn Thr Ser Tyr Glu Gln Arg Phe  
50 55 60

Gln Gly Arg Val Thr Val Thr Thr Asp Ala Ser Thr Asn Thr Val Asp  
65 70 75 80

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

Ala Arg Gly Pro Arg Ser Lys Pro Pro Tyr Leu Tyr Phe Ala Leu Asp  
100 105 110

Val Trp Gly Gln Gly Thr Ala Val Thr Val Ser Ser Ala Ser Thr Lys  
115 120 125

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
130 135 140

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

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
165 170 175

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
180 185 190



# HB01P012WO Sequence Listing\_ST25

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

Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro  
210 215 220

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
225 230 235 240

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
245 250 255

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
260 265 270

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
275 280 285

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

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
325 330 335

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395 400

# HB01P012WO Sequence Listing\_ST25

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

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
435 440 445

Ser Leu Ser Pro Gly Lys  
450

<210> 188  
<211> 1362  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> GCE536 heavy chain nucl

<400> 188  
cagctgcagc tgggtccagtc aggcacagag gtcaaaaagc caggagcatc agtgaagggt 60  
tcttgtaagt catcaggata cgtgttcacc tcttactatc tgggtgtgggt ccggcaggca 120  
ccaggacagg gactggagtg gatggccaca atctctcccg gagacgtgaa cactagttac 180  
gaacagcgat tccagggcag agtgaccgtc accacagacg cttcaactaa taccgtggat 240  
atggagctgc ggagcctgag atccgaagat acagccgtct actattgcgc tagggggccc 300  
cgcagcaagc ctccttatct gtattttgct ctggatgtgt gggggcaggg gaccgctgtc 360  
accgtgtcaa gcgcgtcgac caagggccca tcggtcttcc ccctggcacc ctcctccaag 420  
agcacctctg ggggcacagc ggccctgggc tgcctgggtca aggactactt ccccgaacct 480  
gtgacggtct cgtggaactc aggcgccctg accagcggcg tgcacacctt cccggctgtc 540  
ctacagtcct caggactcta ctccctcagc agcgtgggtga ccgtgccctc cagcagcttg 600  
ggcaccacaga cctacatctg caacgtgaat cacaagccca gcaacaccaa ggtggacaag 660  
agagttgagc ccaaactctg tgacaaaact cacacatgcc caccgtgccc agcacctgaa 720  
ctcctggggg gaccgtcagt cttcctcttc ccccaaaaac ccaaggacac cctcatgatc 780

# HB01P012W0 Sequence Listing\_ST25

tcccggaccc ctgaggtcac atgcgtgggtg gtggacgtga gccacgagga tcctgaggtc	840
aagttcaact ggtacgtgga cggcgtggag gtgcataatg ccaagacaaa gccgcgggag	900
gagcagtaca acagcacgta ccgtgtgggtc agcgtcctca ccgtcctgca ccaggactgg	960
ctgaatggca aggagtacaa gtgcaagggtc tccaacaaag ccctcccagc ccccatcgag	1020
aaaaccatct ccaaagccaa agggcagccc cgagaaccac aggtgtacac cctgccccca	1080
tcccggggagg agatgaccaa gaaccagggtc agcctgacct gcctgggtcaa aggcttctat	1140
cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc	1200
acgcctcccg tgctggactc cgacggctcc ttcttctct atagcaagct caccgtggac	1260
aagagcaggt ggcagcaggg gaacgtcttc tcatgtccg tgatgcatga ggctctgcac	1320
aaccactaca cgcagaagag cctctccctg tccccgggta aa	1362

<210> 189  
 <211> 214  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> GCE536 light chain aa

<400> 189

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly	
1                    5                    10                    15	

Glu Thr Ala Ile Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser	
20                    25                    30	

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

Ile Tyr Gly Ala Ser Asn Arg Ala Thr Gly Ile Arg Gly Arg Phe Ser	
50                    55                    60	

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu	
65                    70                    75                    80	

Pro Glu Asp Phe Val Leu Tyr Tyr Cys Gln His Tyr Gly Ser Arg Val	
---	--

HB01P012W0 Sequence Listing\_ST25

85

90

95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala  
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser  
195 200 205

Phe Asn Arg Gly Glu Cys  
210

<210> 190

<211> 642

<212> DNA

<213> Artificial Sequence

<220>

<223> GCE536 light chain nucl

<400> 190

gaaattgtgt tgacgcagtc tcctggcacc ctgtctttgt ctccagggga aacagccatc 60

ctctcctgca gggccagtca gagggtcagc agcagcctct tagcctggta ccagcaaaaa 120

cctggccagg ctcccaggct cctcatctac ggtgcatcca atagggccac tggcatcaga 180

ggcagggttta gtggcagtgg gtctgggaca gacttcactc tcaccatcag tagattggag 240

HB01P012W0 Sequence Listing\_ST25

cctgaagatt ttgtacttta ttactgtcag cactatggct cacgggtcac ttttggccag	300
gggaccaagc tggagatcaa acgtacgggtg gctgcaccat ctgtcttcat cttcccgccca	360
tctgatgagc agttgaaatc tggaactgcc tctgtttgtgt gcctgctgaa taacttctat	420
cccagagagg ccaaagtaca gtggaagggtg gataacgcc tccaatcggg taactcccag	480
gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg	540
ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc	600
ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gt	642