

SEQUENCE LISTING

<110> Nanjingjinsirui Science & Technology Biology Corp.

<120> SINGLE-DOMAIN ANTIBODIES AND VARIANTS
THEREOF AGAINST CTLA-4

<130> 761422000341

<140> Not Yet Assigned

<141> Concurrently Herewith

<150> PCT/CN2016/101777

<151> 2016-10-11

<150> PCT/CN2017/093644

<151> 2017-07-20

<160> 379

<170> FastSEQ for Windows Version 4.0

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Ser Leu Arg Leu Ser Cys Ala Thr Ser
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Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Val Ala Ser
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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Val Gly Asp
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser
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Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
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Ala Val Gln Leu Val Asp Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
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Ser Leu Arg Leu Ser Cys Ala Ala Ser
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Gln Val His Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser
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Ser Leu Arg Leu Ser Cys Ala Ala Ser
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Gln Met Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
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Gly Phe Thr Phe Asp Asp Tyr Ala Ile Gly
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Gly Arg Thr Ile Thr Thr Ile Thr Met Gly
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Gly Ser Ile Asp Ser Thr Tyr Thr Met Gly
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Gly Arg Ser Phe Glu Asn Tyr Ala Ile Gly
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<400> 22
Gly Arg Leu Ser Arg Thr Phe Thr Met Gly
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Gly Ser Ile Ser Ser Leu Asn Ala Met Ala
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Gly Tyr Thr Tyr Ser Arg His Cys Leu Gly
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Gly Asp Asp Leu Ser Asn Tyr Cys Met Gly
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Gly Asp Ser Pro Ser Val Asn Tyr Met Gly
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Gly Asp Ser Tyr Ser Val Lys Tyr Met Gly
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<400> 28

Gly Tyr Thr Tyr Ser Arg Tyr Cys Leu Gly
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Gly Asp Ser Tyr Ser Val Asn Tyr Met Gly
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<223> AS07745 CDR1

<400> 31

Gly Phe Thr Phe Ser Ser Tyr Tyr Met Ser
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<400> 32

Gly Tyr Tyr Asn Arg Tyr Cys Leu Gly
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<400> 33

Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val Ser
1 5 10

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<223> A34311 FR2

<400> 34

Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Gln Phe Val Ala
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Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg	Glu	Leu	Val	Ala
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Trp	Tyr	Arg	Gln	Ala	Pro	Gly	Lys	Gln	Arg	Asp	Leu	Val	Ala
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Trp Phe Arg Arg Ala Pro Gly Lys Gln Arg Asp Gln Arg Glu Glu Val
1 5 10 15
Ala

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<400> 44
Trp Phe Arg Gln Thr Pro Gly Lys Glu Arg Glu Ala Val Ala
1 5 10

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Trp Phe Arg Arg Ala Pro Gly Gln Gln Arg Glu Gln Arg Glu Glu Val
1 5 10 15
Ala

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Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Glu	Gly	Val	Ala
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Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ser
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Trp	Phe	Arg	Gln	Thr	Pro	Gly	Lys	Glu	Arg	Glu	Ala	Val	Ala
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Cys	Ile	Ser	Ser	Gly	Gly	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
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<400> 50
Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val Lys
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Gly

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<400> 51
Ala Ile Ser Arg Ser Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 52
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<400> 52
Ser Ile Thr Ser Ser Gly Ser Thr Asn His Ala Asp Ser Val Lys Gly
1 5 10 15

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<400> 53

Thr Ile Ser Trp Ile Pro Arg Thr Ala Tyr Ser Thr Thr Tyr Tyr Ala
1 5 10 15
Asp Ser Val Lys Gly
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Ser Ile Thr Thr Ser Gly Ser Thr Asn Tyr Ala Asp Ser Val Lys Gly
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Ser Ile Thr Arg Gly Gly Ser Thr Ala Tyr Thr Asp Ser Val Lys Gly
1 5 10 15

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<400> 56
Thr Ile Asp Ser Asp Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

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Thr	Ile	Asp	Tyr	Ala	Phe	Lys	Thr	Asn	Tyr	Ala	Asp	Ser	Val	Lys	Gly
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Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly
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Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly
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Thr	Ile	Asp	Ile	Asp	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	Gly
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<400> 61

Ser	Ile	Tyr	Ala	Thr	Gly	Gly	Thr	Phe	Tyr	Arg	Asp	Ser	Val	Lys	Gly
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Thr	Met	Asp	Thr	Asp	Gly	Ser	Thr	Arg	Tyr	Ala	Asp	Ser	Val	Lys	Gly
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Ser	Ile	Tyr	Ser	Asp	Gly	Ser	Asn	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
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Gly

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Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Val Phe Leu Gln
1 5 10 15
Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Gly Ala
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<400> 66
Arg Phe Ile Ile Ser Arg Asp Asn Ala Gly Asn Arg Val Tyr Leu Gln
1 5 10 15
Met His Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
20 25 30

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<223> A34313 FR3

<400> 67
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Glu
1 5 10 15
Met Asn Ser Leu Lys Gly Glu Asp Thr Val Val Tyr Tyr Cys Ala Ala
20 25 30

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<400> 68

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr	Leu	Gln
1				5					10					15	
Met	Asn	Thr	Leu	Lys	Pro	Glu	Asp	Ala	Ala	Val	Tyr	Tyr	Cys	Arg	Tyr
			20					25					30		

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<400> 69

Arg	Phe	Thr	Ile	Ser	Gly	Asp	Asn	Ser	Lys	Asn	Thr	Val	Tyr	Leu	Gln
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Met	Thr	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala
			20					25					30		

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Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Ile	Leu	Gln
1				5					10					15	
Met	Asn	Ser	Leu	Val	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Arg	Phe
			20					25					30		

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<400> 71

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Val	Tyr	Leu	Gln
1				5					10					15	
Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Arg	Ala
			20					25					30		

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Arg	Phe	Thr	Ile	Ser	Ser	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	
Met	Asn	Ser	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Ile
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Arg	Phe	Thr	Ile	Ser	Lys	Asp	Asn	Ala	Glu	Asn	Ser	Leu	Arg	Val	Asn
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Leu	Glu	Met	Asn	Asp	Leu	Lys	Pro	Asp	Asp	Thr	Ala	Met	Tyr	Tyr	Cys
			20					25					30		
Ala	Ala														

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Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
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Met	Thr	Ala	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Ala

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Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr Leu Tyr Leu Gln
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Met Thr Ala Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala Ala
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<400> 76
Arg Phe Thr Ile Ser Asn Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ile Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala Ala
20 25 30

<210> 77
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<400> 77
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Thr Ala Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala Ala
20 25 30

<210> 78
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Arg Phe Thr Ile Ser Thr Asp Ser Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Glu Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala Val
20 25 30

<210> 79
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<400> 79
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Lys Ser Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Thr
20 25 30

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<400> 80
Arg Phe Thr Ile Ser Phe Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala Ala
20 25 30

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<400> 81

Val Ser Ser Leu Leu Ser Val Glu Arg Phe Pro Gly Gly His Cys Gly
1 5 10 15
Pro Arg Tyr Gly Tyr Tyr Arg His Gly Tyr
20 25

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<400> 82

Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu Ala Arg
1 5 10 15
Gln Tyr Asp Tyr
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<210> 83

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<400> 83

Lys Ile Ala Gly Met Asn Asn Ile Val Phe Ile Gly Ala Pro Gln Tyr
1 5 10 15
Asn Tyr

<210> 84

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<223> A34625 CDR3

<400> 84

Leu Ser Val Leu Ser Ala Tyr
1 5

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<400> 85
Gly Gly Ala Thr Gly Pro Leu Ala Leu Asp Ser His Tyr Gly Tyr
1 5 10 15

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Leu Ser Ala Ser Thr Ala Ala
1 5

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<400> 87
Val Trp Gly Phe Gly Asp Tyr Gly Ser
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<220>
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<400> 88
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Asn Thr Arg Gly Ala

1	5	10	15
Glu	His	Tyr	Phe
	Gly	Tyr	
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Asp	Trp	Ser	Ser	Gly	Gly	Val	Cys	Phe	Gly	Leu	Ala	Asp	Phe	Gly	Thr
1				5				10						15	

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<400> 90							
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1			5				

<210> 91
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<400> 91							
Gly	Lys	Trp	Gly	Thr	Asp	Tyr	
1			5				

<210> 92
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<212> PRT
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<220>

<223> AS07678 CDR3

<400> 92

Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Val Tyr Thr Arg Gly Ala
1 5 10 15

Glu His Tyr Phe Gly Tyr
20

<210> 93

<211> 7

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> AS07688 CDR3

<400> 93

Gly Lys Trp Gly Thr Asp Tyr
1 5

<210> 94

<211> 22

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> AS07712 CDR3

<400> 94

Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Ile Asn Thr Arg Gly Ala
1 5 10 15

Glu His Tyr Phe Gly Tyr
20

<210> 95

<211> 17

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> AS07745 CDR3

<400> 95

Pro Arg Gly Ala His Gly Pro Thr Tyr Cys Ser Gly Gly Tyr Cys Tyr
1 5 10 15

Tyr

<210> 96
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07832 CDR3

<400> 96
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Val Asn Thr Arg Gly Ala
1 5 10 15
Glu His Tyr Phe Gly Tyr
20

<210> 97
<211> 399
<212> DNA
<213> Artificial Sequence

<220>
<223> A34310 sdAb

<400> 97
cagggtacagc tgggtggagtc tggggggaggc ttggtgcagg ctgggggggtc tctgagactc 60
tcctgtgcag cctctggatt cactttcgat gattatgccca taggctgggtt ccgccaggcc 120
ccagggaagg agcgtgaggg ggtctcatgt attagtagtg gtggcacata ctatgcagac 180
tccgtgaagg gccgattcac catctccagt gacaacgccca agaacacggg gtttctgcaa 240
atgaacagcc tgaaacctga ggacacggct gtttattact gtggagcagt ttcgtcgctc 300
ttaagtgtgg agagggtccc tggagggtcat tgcggccccc gttatgggta ctaccgtcac 360
ggctactggg gccagggggac ccagggtcacc gtctcctca 399

<210> 98
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> A34311 sdAb

<400> 98
caggtaaaagc tggaggagtc tggggggaggc ttggtgctgc ctgggggagtc tctgagactc 60
tcctgtgaag cctctgggtcg caccatcaca acgattacta tgggctgggtt ccgccaggct 120
ccagggaagg agcgtcagtt tgtagcgtct catagttaga ctgataataa cccatactat 180
gcagactccg ttaaggggccg attcatcatc tccagagaca acgccgggaa cagggtatat 240
ctgcagatgc atagcctgga acctgaggac acggccgttt attactgcgc agcaaccgct 300
agaagatcat tcgtgggtag acagtggtag actgaagcac gccagtatga ctactggggc 360
caggggaccc aggtcaccgt ctccctca 387

<210> 99
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> A34313 sdAb

<400> 99
cagggtacagc tgggtggagtc tggggggagga ttggtgcagg ctggggggctc tctgagactc 60
tcctgtgcaa cctctgtacg cccccccctc agtaactttg ccatgggctg gttccgccag 120
actccaggga aagagcgtga gttttagtagca gcaattagca ggagtgggtg aagcacatcg 180
tatgcagact ccgtgaaggg ccgattcacc atctccaggg acaacgcaa gaacacgggtg 240
tatctcgaaa tgaacagcct gaaaggcgag gacacggtcg tttattactg tgcagccaaa 300
atagcgggga tgaataatat tgtctttatc ggcgcgcccc agtataacta ctggggccag 360
gggacccagg tcaccgtctc ctca 384

<210> 100
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> A34625 sdAb

<400> 100
caggtaaagc tggaggagtc tggggggaggc ttggtgcagc ctgggggggtc tctgagactc 60
tcctgtgtag cgtctggaag catcgacagc acctatacca tgggctggta ccgccaggct 120
ccagggaaac agcgcgagtt ggtcgcttct attactagtt ctggtagcac aaaccatgca 180
gactccgtga agggccgatt cacaatctcc agagacaacg ccaagaacac ggtgtatctt 240
caaataaaca ccctgaaacc cgaggacgcg gccgtctatt actgtagata cctaagtgtg 300
cttagtgcct actggggcca ggggacccag gtcaccgtct cctca 345

<210> 101
<211> 384
<212> DNA
<213> Artificial Sequence

<220>
<223> A36566 sdAb

<400> 101
gaggtgcagc tgggtggagtc tggggggagga ttggtgcagg ttgggggactc tctgagactc 60
tcctgtgcag cctctggacg ctcgttcgag aactatgcc a taggctgggt ccgccaggct 120
ccaggcaagg agcgtgagtt tgtagcaaca atttcgtgga ttcctcgtag cgcatatctt 180
accacatact atgcagactc cgtgaagggc agattcacca tctctggaga caacagcaag 240
aacacggtgt atctgcaa at gacgagcctg aaacctgagg acacggccgt ttattactgt 300
gcagcaggcg gggcgacagg accgttggcg ttggactccc actatgggta ctggggccag 360
gggacccagg tcaccgtctc ctca 384

<210> 102
<211> 345
<212> DNA
<213> Artificial Sequence

<220>
<223> A36922 sdAb

<400> 102
caggtacagc tgggtggagtc tgggggaggc ttggtgcagg ctgggggggtc gctgagactc 60
tcctgtgcag cctctggtcg cctcagtagg acgtttacca tgggctggta ccgccaggct 120
ccagggaagc agcgcgactt ggtcgcgtct attactacaa gtggtagcac gaactatgca 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaaaaacac ggtgattctg 240
caaatgaaca gcctggtacc tgaggacaca gccgtctatt actgccgttt tcttagcgca 300
agtactgcag cctggggcca ggggacccag gtcaccatct ccacg 345

<210> 103
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> A37067 sdAb

<400> 103
gccgtgcagc tgggtggattc tgggggaggc ttggtgcagg ctgggggggtc gctgagactc 60
tcctgtgcag cctctggaag catcagcagt ctcaacgcca tggcatggta ccgccagggt 120
ccagggaagg agcgcgagct ggtcgcaagt attactaggg gtggtagtac agcctataca 180
gactccgtga agggccgatt caccatctcc agagacaacg ccaagaacac ggtgtatctg 240
caaatgaaca gcctgaaacc tgaggacaca gccgtctatt actgtagagc ggtttgggg 300
tttgggggatt atggttcctg gggccagggg acccagggtca ccgtctcttc g 351

<210> 104
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07014 sdAb

<400> 104
caggtgcacc tgggtggagtc tgggggaggc tcggtgcagg ctggagggtc tctgagactc 60
tcctgtgcag cctctggata cacctacagt agacactgcc tgggctgggtt ccgccagact 120
ccagggaagg agcgcgaggc ggtcgcgact attgatagtg atggtagcac aagctacgca 180
gactccgtga agggccgatt caccatctcc agtgacaacg ccaagaacac tctatatctg 240
caaatgaaca gcctgaaacc tgaggacact gccatgtact actgtgcat agggccgaac 300
ccgcgatatt gtagtggcgc gcccaacact cggggcgccg aacactactt tggttactgg 360
ggccaggggga cccagggtcac cgtctcctca 390

<210> 105
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07172 sdAb

<400> 105
caggtgaagt tagtggagtc tgggggaggc tcggtgcagg ctggagggtc tctaagactt 60
tcctgtgcag tgtctggaga cgatttgagt aactactgca tgggctgggt ccgccaggct 120
ccagggaagg agcgcgaaga ggtcgcaact attgattatg cctttaagac aaattacgca 180
gactccgtga agggccggtt caccatctcc aaagacaacg ccgagaatag tctacgcgta 240
aatttggaat tgaacgacct gaaacctgac gacactgcca tgtactattg tgcggcagat 300
tggagtagtg gtggtgtgtg ttttggatta gcggactttg gtacccgggg ccaggggacc 360
caggtcaccg tctcctca 378

<210> 106
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07189 sdAb

<400> 106
caggtgcagc tgggtggagtc tgggggaggc tcggtgcagg ctggagggtc tctgagactc 60
tcctgtgcag cctctggaga cagtcctagt gtgaactaca tgggctgggt ccgccgggct 120
ccagaaaaac agcgcgagca gcgcgaggag gtcgcaagta tttatccac aggtggcacg 180
ttttacacag actccgtgaa gggccgattc accatctccc gagacaacgc caagaacact 240
ctgtatctcc aaatgaccgc cctgaaacct gaggatactg ccatgtacta ctgtgcggca 300
ggaaaaatggg ggactgacta ctggggccag gggacccagg tcatcgtctc ctca 354

<210> 107
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07392 sdAb

<400> 107
caggtgaagt tgggtggagtc tgggggaggc tcggtgcagg ctggagggtc tctgagactc 60
tcctgtgcag cctctggaga cagttatagt gtgaagtaca tgggctgggt ccgccgggct 120
ccagggaaac agcgcgacca gcgcgaggag gtcgcaagta tttatccac aggtggcacg 180
ttttacacag actccgtgaa gggccgattc accatctccc gagacaacgc caagagcact 240
ctgtatctcc aaatgaccgc cctgaaacct gaggatactg ccatgtacta ctgtgcggca 300
ggcaaatggg ggactgacta ctggggccag gggacccagg tcaccgtctc ctca 354

<210> 108

<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07678 sdAb

<400> 108
caggtgcacc tgatggagtc tgggggaggc tcggtgcagg ctggagggtc tctgagactc 60
tcctgtgcag cctctggata cacctacagt aggtactgcc tgggctgggt ccgccagact 120
ccagggaagg agcgcgaggc ggtcgcaact attgatattg atggtagcac aagctacgca 180
gactccgtga agggccgatt caccatctcc aatgacaacg ccaagaacac tctatatctg 240
caaatgaaca tcctgaaacc tgaggacact gccatgtact actgtgcggc agggccgaac 300
ccgcgatatt gtagtggcgc agtctacact cggggcgccg aacactactt tggttactgg 360
ggccagggga cccaggtcac cgtctcctca 390

<210> 109
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07688 sdAb

<400> 109
cagattcagc tgggtggagtc tgggggaggc tcggtgcagg ctggagggtc tctgagactc 60
tcctgtgcag cctctggaga cagttatagt gtgaactaca tgggctgggt ccgccgggct 120
ccagggaac agcgcgagca gcgcgaggag gtcgcaagta tttatgccac ggggtggcacg 180
ttttacagag actccgtgaa gggccgattc accatctccc gagacaacgc caagaacact 240
ctgtatctcc aaatgaccgc cctgaaacct gaggatactg ccatgtacta ctgtgcggca 300
ggcaaatggg ggactgacta ctggggccag gggaccagg tcatcgtctc ctca 354

<210> 110
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07712 sdAb

<400> 110
cagattcagc tgggtggagtc tgggggaggc tcggtgcagg ctggagggtc tctgagactc 60
tcctgtgcag cctctgcata caccgacaga cgctactgca tggcctgggt ccgccaggct 120
ccagggaagg agcgcgaggg ggtcgcaact atggatactg atggtagtac aaggtagca 180
gactccgtga agggccgatt caccatctcc acagacagcg ccaagaacac tctgtatctg 240
caaatgaaca gcctggaacc tgaggacact gccatgtact actgtgcggg ggggcccgaac 300
ccgcgatatt gtagtggcgc aatcaacact cggggcgccg aacactactt tggttactgg 360
ggccagggga cccaggtcac cgtctcctca 390

<210> 111

<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07745 sdAb

<400> 111
cagatgcagc tgggtggagtc tggggggaggc ttggtgcagc ctgggggggtc tctgagactc 60
tcctgtgcag cctctggatt caccttcagt agctactaca tgagctgggt ccgccaggct 120
ccagggaagg ggctggagtg ggtgtccagt atttatagtg atggtagtaa cacatactat 180
gcagactccg tgaagggccg attcaccatc tccagagaca acgccaagaa cacggtgtat 240
ctgcaaatga acagcctgaa atctgaggac acggccctgt attactgtgc caccccaagg 300
gggtgctcacg gacctacata ttgtagtggt ggttactgct actacggggg ccagggggacc 360
caggtcaccg tctcctca 378

<210> 112
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07832 sdAb

<400> 112
caggttcagc tgggtggagtc tggggggaggc tcggtgcagg ctggagggtc tctgagactc 60
tcctgtgcag cctctggata ctacaatagg tactgcctgg gctggttccg ccagactcca 120
gggaaggagc gcgaggcggc cgcaactatt gatacggatg gtagcacaag ctacgcagac 180
tccgtgaagg gccgattcac catctccttt gacaacgcca agaacactct atatctgcaa 240
atgaacagcc tgaaacctga ggacactgcc atgtactact gtgcggcagg gccgaacccg 300
cgatatgtga gtggcgcggt caacactcgg ggcgccgaac actacttttg ttactgggcc 360
caggggaccc aggtcaccgt ctcctca 387

<210> 113
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> A34310 sdAb

<400> 113
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr
20 25 30
Ala Ile Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Glu Gly Val
35 40 45
Ser Cys Ile Ser Ser Gly Gly Thr Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

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

<210> 116
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A34625 sdAb

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

<210> 117
 <211> 128
 <212> PRT
 <213> Artificial Sequence

<220>

<223> A36566 sdAb

<400> 117

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

<210> 118

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> A36922 sdAb

<400> 118

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

<210> 119

<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> A37067 sdAb

<400> 119
Ala Val Gln Leu Val Asp Ser Gly Gly Gly Leu Val Gln Ala Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Ser Ile Ser Ser Leu Asn
20 25 30
Ala Met Ala Trp Tyr Arg Gln Gly Pro Gly Lys Glu Arg Glu Leu Val
35 40 45
Ala Ser Ile Thr Arg Gly Gly Ser Thr Ala Tyr Thr Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Val Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Val Tyr Tyr Cys Arg
85 90 95
Ala Val Trp Gly Phe Gly Asp Tyr Gly Ser Trp Gly Gln Gly Thr Gln
100 105 110
Val Thr Val Ser Ser
115

<210> 120
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014 sdAb

<400> 120
Gln Val His Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His
20 25 30
Cys Leu Gly Trp Phe Arg Gln Thr Pro Gly Lys Glu Arg Glu Ala Val
35 40 45
Ala Thr Ile Asp Ser Asp Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Ser Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95
Ile Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Asn Thr Arg Gly
100 105 110
Ala Glu His Tyr Phe Gly Tyr Trp Ala Gln Gly Thr Gln Val Thr Val

115 120 125
 Ser Ser
 130

<210> 121
 <211> 126
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AS07172 sdAb

<400> 121
 Gln Val Lys Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Val Ser Gly Asp Asp Leu Ser Asn Tyr
 20 25 30
 Cys Met Gly Trp Val Arg Gln Ala Pro Gly Lys Glu Arg Glu Glu Val
 35 40 45
 Ala Thr Ile Asp Tyr Ala Phe Lys Thr Asn Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Lys Asp Asn Ala Glu Asn Ser Leu Arg Val
 65 70 75 80
 Asn Leu Glu Met Asn Asp Leu Lys Pro Asp Asp Thr Ala Met Tyr Tyr
 85 90 95
 Cys Ala Ala Asp Trp Ser Ser Gly Gly Val Cys Phe Gly Leu Ala Asp
 100 105 110
 Phe Gly Thr Arg Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 115 120 125

<210> 122
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AS07189 sdAb

<400> 122
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asp Ser Pro Ser Val Asn
 20 25 30
 Tyr Met Gly Trp Phe Arg Arg Ala Pro Glu Lys Gln Arg Glu Gln Arg
 35 40 45
 Glu Glu Val Ala Ser Ile Tyr Pro Thr Gly Gly Thr Phe Tyr Thr Asp
 50 55 60
 Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr

65					70					75					80
Leu	Tyr	Leu	Gln	Met	Thr	Ala	Leu	Lys	Pro	Glu	Asp	Thr	Ala	Met	Tyr
				85					90					95	
Tyr	Cys	Ala	Ala	Gly	Lys	Trp	Gly	Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Gln	Val	Ile	Val	Ser	Ser										
			115												

<210> 123
 <211> 118
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AS07392 sdAb

<400> 123
Gln Val Lys Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Asp Ser Tyr Ser Val Lys
20 25 30
Tyr Met Gly Trp Phe Arg Arg Ala Pro Gly Lys Gln Arg Asp Gln Arg
35 40 45
Glu Glu Val Ala Ser Ile Tyr Pro Thr Gly Gly Thr Phe Tyr Thr Asp
50 55 60
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Ser Thr
65 70 75 80
Leu Tyr Leu Gln Met Thr Ala Leu Lys Pro Glu Asp Thr Ala Met Tyr
85 90 95
Tyr Cys Ala Ala Gly Lys Trp Gly Thr Asp Tyr Trp Gly Gln Gly Thr
100 105 110
Gln Val Thr Val Ser Ser
115

<210> 124
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AS07678 sdAb

<400> 124
Gln Val His Leu Met Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg Tyr
20 25 30
Cys Leu Gly Trp Phe Arg Gln Thr Pro Gly Lys Glu Arg Glu Ala Val

<400> 126

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

<210> 127

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07745 sdAb

<400> 127

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

<210> 128

<211> 129

<212> PRT
<213> Artificial Sequence

<220>
<223> AS07832 sdAb

<400> 128
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Ser Val Gln Ala Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Tyr Asn Arg Tyr Cys
20 25 30
Leu Gly Trp Phe Arg Gln Thr Pro Gly Lys Glu Arg Glu Ala Val Ala
35 40 45
Thr Ile Asp Thr Asp Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys Gly
50 55 60
Arg Phe Thr Ile Ser Phe Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80
Met Asn Ser Leu Lys Pro Glu Asp Thr Ala Met Tyr Tyr Cys Ala Ala
85 90 95
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Val Asn Thr Arg Gly Ala
100 105 110
Glu His Tyr Phe Gly Tyr Trp Ala Gln Gly Thr Gln Val Thr Val Ser
115 120 125
Ser

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

<220>
<223> AS02640 humanized sdAb

<400> 129
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Ile Thr Thr Ile
20 25 30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Phe Val
35 40 45
Ala Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu
100 105 110

Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125
Ser

<210> 130
<211> 361
<212> PRT
<213> Artificial Sequence

<220>
<223> A34311 HCAb monomeric form

<400> 130
Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Leu Pro Gly Glu
1 5 10 15
Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Arg Thr Ile Thr Thr Ile
20 25 30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Gln Phe Val
35 40 45
Ala Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ala Gly Asn Arg Val Tyr
65 70 75 80
Leu Gln Met His Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu
100 105 110
Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
115 120 125
Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro
130 135 140
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
145 150 155 160
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
165 170 175
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
180 185 190
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
195 200 205
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
210 215 220
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
225 230 235 240
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
245 250 255
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
260 265 270
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro

		275					280				285						
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn		
	290						295				300						
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu		
305					310					315					320		
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val		
			325						330					335			
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln		
		340						345					350				
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys									
		355					360										

<210> 131

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311 HCAb dimeric form

<400> 131

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

Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
225					230					235					240
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
				245					250					255	
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu
			260					265					270		
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
	275						280					285			
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
290					295					300					
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu
305					310					315					320
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val
				325					330					335	
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln
			340					345					350		
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
		355					360								

<210> 132

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640 HCAb monomeric form

<400> 132

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

				165					170				175			
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	
			180					185					190			
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
		195					200					205				
Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	
	210					215					220					
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	
	225				230					235					240	
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	
			245						250					255		
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	
		260						265					270			
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
	275						280					285				
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
	290					295					300					
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
	305				310					315					320	
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	
			325						330					335		
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
		340						345					350			
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
		355					360									

<210> 133

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640 HCAb dimeric form

<400> 133

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

50		55		60											
Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr
65					70					75					80
Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			115					120				125			
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
			165					170						175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195				200						205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			245					250						255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
	275						280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
			325						330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345					350		
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
	355					360					365				
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405					410						415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
		420						425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gly
	435					440						445			
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly

450		455		460
Gly Gly Leu Val Leu Pro Gly Glu Ser Leu Arg Leu Ser Cys Glu Ala				
465		470		480
Ser Gly Arg Thr Ile Thr Thr Ile Thr Met Gly Trp Phe Arg Gln Ala				
	485		490	495
Pro Gly Lys Glu Arg Gln Phe Val Ala Ser His Ser Trp Thr Asp Asn				
	500		505	510
Asn Pro Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Ile Ile Ser Arg				
	515		520	525
Asp Asn Ala Gly Asn Arg Val Tyr Leu Gln Met His Ser Leu Glu Pro				
	530		535	540
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala Thr Ala Arg Arg Ser Phe				
545		550		560
Val Gly Arg Gln Trp Tyr Thr Glu Ala Arg Gln Tyr Asp Tyr Trp Gly				
	565		570	575
Gln Gly Thr Gln Val Thr Val Ser Ser				
	580		585	

<210> 135

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-311K heavy chain fusion polypeptide

<400> 135

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

Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Gly	Ile	Asn	Pro	Ser	
			180					185					190			
Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe	Lys	Asn	Arg	Val	Thr	Leu	
		195					200					205				
Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr	Met	Glu	Leu	Lys	Ser	Leu	
		210				215					220					
Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Arg	Asp	Tyr	Arg	
225					230					235					240	
Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	
			245					250						255		
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	
			260					265					270			
Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
		275					280					285				
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
	290					295					300					
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
305					310					315					320	
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
				325					330					335		
Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
			340				345						350			
Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	
		355					360					365				
Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
					375						380					
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
385					390					395					400	
Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	
				405					410					415		
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
			420					425					430			
Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	
		435					440					445				
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	
	450				455						460					
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	
465					470					475					480	
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	
				485					490					495		
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
			500					505					510			
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
		515					520					525				
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
		530				535					540					
Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	
545					550					555					560	
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
				565					570						575	

Lys Ser Leu Ser Leu Ser Leu Gly Lys
580 585

<210> 136

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> Keytruda-hIgG1 hinge-A34311 heavy chain fusion sequence

<400> 136

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

290		295		300											
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330						335
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345						350	
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405						410						415
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu
	435						440					445			
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	Val
	450					455					460				
Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu
465					470					475					480
Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met
			485						490						495
Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser
			500					505					510		
His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
	515						520					525			
Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln
	530					535					540				
Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala
545					550					555					560
Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg
			565						570						575
Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	
		580						585					590		

<210> 137

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-hIgG1 hinge-Keytruda heavy chain fusion sequence

<400> 137

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

Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
			20					25				30			
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val
		35					40					45			
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
		50				55					60				
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr
65				70					75					80	
Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
			100					105					110		
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser
		115					120					125			
Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
		130				135					140				
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys	Lys	Pro	Gly	Ala
145				150					155					160	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			165					170						175	
Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
			180					185					190		
Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe
		195				200					205				
Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr
		210				215					220				
Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
225				230					235					240	
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln
			245					250						255	
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			260					265					270		
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
		275				280						285			
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
	290				295					300					
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
305				310					315					320	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			325					330					335		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
			340				345						350		
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
		355				360						365			
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
		370				375					380				
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
385				390						395					400
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			405					410						415	

Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
			420					425					430		
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
		435					440					445			
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
	450					455					460				
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
465					470					475					480
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			485					490						495	
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		500						505					510		
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	515						520					525			
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
	530					535					540				
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
545					550					555					560
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			565					570						575	
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
			580					585					590		

<210> 138

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> Keytruda-A34311 heavy chain fusion sequence

<400> 138

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

130		135		140											
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170						175
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185						190	
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
	195					200						205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
	210					215						220			
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
			245					250							255
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265						270	
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
	275						280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325				330						335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345					350		
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
	355						360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405					410							415
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425						430	
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gln
	435					440						445			
Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser
	450					455					460				
Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr
465					470					475					480
Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala
			485					490						495	
Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
			500					505					510		
Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu
	515						520					525			
Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala

530		535		540
Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu Ala				
545		550		555
Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser				
	565		570	575

<210> 139

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-Keytruda heavy chain fusion sequence

<400> 139

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

Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	275						280					285			
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
	290					295					300				
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
305					310					315					320
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
				325					330					335	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
			340					345					350		
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
		355					360					365			
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
	370					375					380				
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
385					390					395					400
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
				405					410					415	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
			420					425					430		
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
	435						440					445			
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
	450					455					460				
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
465					470					475					480
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
			485						490					495	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
			500					505					510		
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
		515					520					525			
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
	530					535					540				
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
545					550					555					560
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
				565					570					575	

<210> 140

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Keytruda-9GS-AS02640 heavy chain fusion sequence

<400> 140

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

1				5				10					15			
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	
			20					25					30			
Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35					40					45				
Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe	
		50				55					60					
Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr	
65					70				75						80	
Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85				90						95		
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	
			100					105					110			
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
		115					120					125				
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	
	130					135					140					
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
145					150					155					160	
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
			165					170						175		
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
		180						185					190			
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	
	195					200						205				
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	
	210					215					220					
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	
225					230					235					240	
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	
			245					250						255		
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	
			260					265					270			
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	
	275						280					285				
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	
	290					295					300					
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	
305					310					315					320	
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	
				325				330						335		
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	
		340						345					350			
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	
		355					360					365				
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	
	370					375					380					
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	
385					390					395					400	
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	

				405					410					415		
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	
			420					425					430			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gly	
		435					440					445				
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	
	450					455					460					
Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	
465				470						475					480	
Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	
			485					490					495			
Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	
		500						505					510			
Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	
	515					520						525				
Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	
	530					535				540						
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	
545				550						555					560	
Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	
			565					570					575			
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		580					585									

<210> 141

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-9GS-Keytruda heavy chain fusion sequence

<400> 141

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

Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Gln
130						135					140				
Ser	Gly	Val	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys
145					150					155					160
Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Tyr	Met	Tyr	Trp	Val	Arg
			165						170					175	
Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Gly	Ile	Asn	Pro	Ser
			180					185					190		
Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe	Lys	Asn	Arg	Val	Thr	Leu
	195						200					205			
Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr	Met	Glu	Leu	Lys	Ser	Leu
	210					215					220				
Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Arg	Asp	Tyr	Arg
225					230					235					240
Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val
			245					250						255	
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys
			260					265					270		
Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys
	275						280					285			
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu
	290					295					300				
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
305					310					315					320
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr
			325						330					335	
Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
			340					345					350		
Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro
	355						360					365			
Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
	370				375						380				
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
385					390					395					400
Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr
			405						410					415	
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
			420					425					430		
Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His
		435					440					445			
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
	450					455					460				
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
465					470					475					480
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met
			485						490					495	
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
			500					505					510		
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
		515					520					525			

Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu
530						535					540				
Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val
545					550					555					560
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln
				565					570					575	
Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys							
		580						585							

<210> 142

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> Keytruda-hIgG1 hinge-AS02640 heavy chain fusion sequence

<400> 142

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

				245					250				255				
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu		
			260					265					270				
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys		
		275					280					285					
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser		
	290					295					300						
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys		
305				310						315					320		
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile		
			325					330					335				
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro		
		340						345					350				
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu		
	355						360					365					
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn		
	370				375						380						
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser		
385				390						395				400			
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg		
			405					410					415				
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu		
		420					425					430					
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu		
	435					440					445						
Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	Val		
	450				455					460							
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu		
465				470				475					480				
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met		
			485					490					495				
Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala	Ser		
		500					505					510					
His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly		
	515					520					525						
Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln		
	530				535					540							
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala		
545				550				555					560				
Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg		
			565				570					575					
Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
		580					585					590					

<210> 143

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-hIgG1 hinge-Keytruda heavy chain fusion sequence

<400> 143

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
			20					25					30		
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val
		35					40					45			
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
		50				55					60				
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
			100					105					110		
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			
Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
		130				135					140				
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys	Lys	Pro	Gly	Ala
145					150				155					160	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			165						170					175	
Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
			180					185					190		
Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe
		195					200					205			
Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr
		210				215					220				
Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
225					230					235				240	
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln
			245						250					255	
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			260					265					270		
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
		275					280					285			
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
		290				295					300				
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
305					310					315				320	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			325						330					335	
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
			340					345					350		
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
		355					360					365			

Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
370						375					380				
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
385					390					395					400
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
				405					410					415	
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
			420					425					430		
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
		435					440					445			
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
450						455					460				
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
465					470					475					480
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
				485				490						495	
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
			500					505					510		
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
		515					520					525			
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
530						535					540				
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
545					550					555					560
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
				565				570						575	
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	
			580					585					590		

<210> 144

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> Keytruda-AS02640 heavy chain fusion sequence

<400> 144

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

				85				90				95			
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			115					120				125			
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
			130					135				140			
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145						150					155				160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165						170				175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
			195					200				205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
						215						220			
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225						230					235				240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
					245					250					255
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
			275					280					285		
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
						295						300			
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305						310					315				320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325						330				335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
			355					360					365		
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
			370				375					380			
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385						390					395				400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
				405						410				415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gln
			435					440					445		
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser
			450				455					460			
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr
465					470						475				480
Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala

				485					490					495			
Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys		
			500					505					510				
Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu		
		515					520					525					
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala		
	530					535					540						
Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala		
545					550				555						560		
Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
				565					570					575			

<210> 145

<211> 576

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-Keytruda heavy chain fusion sequence

<400> 145

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

Cys	Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly
225					230					235					240
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
				245					250					255	
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
			260					265					270		
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
		275					280					285			
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
	290				295						300				
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
305					310					315					320
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
				325				330						335	
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
			340					345					350		
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
		355					360					365			
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
	370					375					380				
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
385					390					395					400
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
				405					410					415	
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
			420					425					430		
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
		435					440					445			
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
	450					455					460				
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
465					470					475					480
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
			485						490					495	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
			500					505					510		
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
		515					520					525			
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
	530					535					540				
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
545					550					555					560
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
				565					570					575	

<210> 146

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> Opdivo-9GS-A34311 heavy chain fusion sequence

<400> 146

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	Ser
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe
65					70					75				80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
			100					105						110	
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser
	115					120						125			
Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
	130					135					140				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
145					150					155				160	
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
			165						170					175	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys
			180					185					190		
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
	195					200					205				
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
	210					215					220				
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
225				230						235				240	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
			245						250					255	
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
			260					265					270		
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	275					280						285			
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	290					295					300				
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
305				310						315				320	
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
			325						330					335	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
			340					345					350		
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser

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

Ser Ser

<210> 147

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-9GS-Opdivo heavy chain fusion sequence

<400> 147

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

Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90					95		
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	
			100					105					110			
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	
		115					120					125				
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Glu	
	130					135					140					
Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Asp	Cys	
145				150						155					160	
Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	Ser	Gly	Met	His	Trp	Val	Arg	
			165						170					175		
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Trp	Tyr	Asp	
			180					185					190			
Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	
	195						200					205				
Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	Leu	Gln	Met	Asn	Ser	Leu	
	210					215					220					
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Asn	Asp	Asp	Tyr	
225					230					235					240	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	
			245						250					255		
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	
			260					265					270			
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	
		275					280					285				
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	
	290					295					300					
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	
305					310					315					320	
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	
			325						330					335		
Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	
		340						345					350			
Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	
	355						360					365				
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
	370					375					380					
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	
385					390					395					400	
Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
			405						410					415		
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	
		420						425					430			
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
		435					440					445				
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	
	450					455					460					
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
465					470					475					480	

Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu
				485					490					495	
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
			500					505					510		
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
		515					520					525			
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp
	530					535					540				
Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
545					550					555					560
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu
				565					570						575

Gly Lys

<210> 148

<211> 584

<212> PRT

<213> Artificial Sequence

<220>

<223> Opdivo-hIgG1 hinge-A34311 heavy chain fusion sequence

<400> 148

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

Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp

		195					200				205				
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
	210					215					220				
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
225				230						235					240
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
				245					250					255	
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
			260					265					270		
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
		275					280					285			
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	290					295					300				
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
305				310						315					320
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
				325					330					335	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
			340					345					350		
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
		355					360					365			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
	370					375					380				
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
385					390					395					400
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe
				405					410					415	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
			420					425					430		
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
		435					440					445			
His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly
	450					455					460				
Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser
465					470					475					480
Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro
				485					490					495	
Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn
			500					505					510		
Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp
		515					520					525			
Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu
		530				535					540				
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val
545					550										

<210> 149
 <211> 584
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A34311-hIgG1 hinge-Opdivo heavy chain fusion sequence

<400> 149
 Gln Val Lys Leu Glu Glu Ser Gly Gly Gly Leu Val Leu Pro Gly Glu
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Glu Ala Ser Gly Arg Thr Ile Thr Thr Ile
 20 25 30
 Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Glu Arg Gln Phe Val
 35 40 45
 Ala Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ala Gly Asn Arg Val Tyr
 65 70 75 80
 Leu Gln Met His Ser Leu Glu Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu
 100 105 110
 Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser
 115 120 125
 Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 130 135 140
 Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 145 150 155 160
 Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
 165 170 175
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 180 185 190
 Ala Val Ile Trp Tyr Asp Gly Ser Lys Arg Tyr Tyr Ala Asp Ser Val
 195 200 205
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Phe
 210 215 220
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 225 230 235 240
 Ala Thr Asn Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 245 250 255
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser
 260 265 270
 Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
 275 280 285
 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
 290 295 300
 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
 305 310 315 320

Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys
 325 330 335
 Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp
 340 345 350
 Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala
 355 360 365
 Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
 370 375 380
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 385 390 395 400
 Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val
 405 410 415
 Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
 420 425 430
 Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
 435 440 445
 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly
 450 455 460
 Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
 465 470 475 480
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr
 485 490 495
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 500 505 510
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 515 520 525
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 530 535 540
 Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe
 545 550 555 560
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 565 570 575
 Ser Leu Ser Leu Ser Leu Gly Lys
 580

<210> 150

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> Opdivo-A34311 heavy chain fusion sequence

<400> 150

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Asp Cys Lys Ala Ser Gly Ile Thr Phe Ser Asn Ser
 20 25 30
 Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

		35				40				45					
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
			100				105					110			
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser
		115				120					125				
Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
	130					135					140				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
145					150					155					160
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
				165					170					175	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys
			180					185					190		
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
		195				200						205			
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
	210					215					220				
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
225				230						235					240
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
				245					250					255	
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
			260					265					270		
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	275					280						285			
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	290					295					300				
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
305				310						315					320
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
				325					330					335	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
			340					345					350		
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
		355				360						365			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
	370					375					380				
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
385					390					395					400
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe
				405					410					415	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
			420					425					430		
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly

		435					440				445				
Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala
	450					455					460				
Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala
465					470					475					480
Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn
				485					490					495	
Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg
		500						505				510			
Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu	Pro
		515					520					525			
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe
	530					535					540				
Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly
545					550					555					560
Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser							
				565											

<210> 151

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-Opdivo heavy chain fusion sequence

<400> 151

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

Val	Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	180	185	190
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	195	200	205
Phe	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	210	215	220
Cys	Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	225	230	235
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	245	250	255
Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	260	265	270
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	275	280	285
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	290	295	300
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	305	310	315
Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	325	330	335
Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	340	345	350
Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	355	360	365
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	370	375	380
Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	385	390	395
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	405	410	415
Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	420	425	430
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	435	440	445
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	450	455	460
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	465	470	475
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	485	490	495
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	500	505	510
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	515	520	525
Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	530	535	540
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	545	550	555
Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys								565		

<210> 152

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> Opdivo-9GS-AS02640 heavy chain fusion sequence

<400> 152

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	
1				5				10						15		
Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	Ser	
			20					25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	
65					70					75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
			100					105						110		
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	
		115					120					125				
Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	
	130					135					140					
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	
145					150					155					160	
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	
			165						170					175		
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	
			180					185					190			
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	
	195						200					205				
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	
	210					215					220					
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	
225					230					235					240	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	
			245						250					255		
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	
			260					265						270		
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	
	275						280					285				
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	
	290					295					300					
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	

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

<210> 153

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-9GS-Opdivo heavy chain fusion sequence

<400> 153

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
			20					25					30		

Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val
		35					40					45			
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr
65				70						75				80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
			100					105					110		
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Glu
	130					135					140				
Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Asp	Cys
145				150						155				160	
Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	Ser	Gly	Met	His	Trp	Val	Arg
				165					170					175	
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	Trp	Tyr	Asp
			180					185					190		
Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
		195					200					205			
Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	Leu	Gln	Met	Asn	Ser	Leu
	210					215					220				
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Thr	Asn	Asp	Asp	Tyr
225					230					235				240	
Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
				245					250					255	
Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser
			260					265					270		
Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
		275						280				285			
Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
						295					300				
Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
305				310						315				320	
Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val
				325					330					335	
Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys
			340					345					350		
Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly
		355					360					365			
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
						375					380				
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val</							

Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
		435					440					445			
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu
	450					455					460				
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
465					470					475					480
Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu
				485					490					495	
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
			500					505					510		
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
		515					520					525			
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp
	530					535					540				
Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
545					550					555					560
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu
				565					570					575	

Gly Lys

<210> 154

<211> 584

<212> PRT

<213> Artificial Sequence

<220>

<223> Opdivo-hIgG1 hinge-AS02640 heavy chain fusion sequence

<400> 154

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

145					150					155					160		
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr		
					165						170						
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys		
					180						185						
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp		
					195						200						
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala		
					210						220						
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro		
225						230						235					
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val		
					245						250						
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val		
					260						265						
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
					275						280						
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
					290						300						
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly		
305						310						315					
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		
					325						330						
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr		
					340						345						
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser		
					355						360						
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr		
					370						375						
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr		
385						390						395					
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe		
					405						410						
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys		
					420						425						
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr		
					435						440						
His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly		
					450						455						
Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser		
465						470						475					
Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro		
					485						490						
Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn		
					500						505						
Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp		
					515						520						
Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu		
					530						535						
Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val		

545		550		555		560									
Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln
		565				570								575	
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
		580													

<210> 155

<211> 584

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-hIgG1 hinge-Opdivo heavy chain fusion sequence

<400> 155

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

Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
		275					280					285			
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
		290					295				300				
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
305					310					315					320
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys
				325					330					335	
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
			340					345					350		
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
		355					360					365			
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
		370				375					380				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
385					390					395					400
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
				405					410					415	
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
			420					425					430		
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
		435					440					445			
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
		450				455					460				
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
465					470					475					480
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
				485					490					495	
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
		500						505					510		
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
		515					520					525			
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
		530				535					540				
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe
545					550					555					560
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
				565					570					575	
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys								
			580												

<210> 156

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> Opdivo-AS02640 heavy chain fusion sequence

<400> 156

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5				10						15	
Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	Ser
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe
65					70				75						80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
			100					105						110	
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser
		115					120					125			
Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
	130					135					140				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
145					150					155					160
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
			165						170					175	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys
			180					185					190		
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
		195					200					205			
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
	210					215				220					
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
225				230						235					240
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
			245						250					255	
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
			260					265						270	
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	275						280					285			
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	290					295					300				
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
305				310						315					320
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
			325						330					335	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
			340					345						350	
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
		355					360					365			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
	370					375					380				
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr

385					390					395					400
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe
				405					410					415	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
			420					425					430		
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly
		435					440					445			
Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala
	450					455					460				
Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala
465				470					475					480	
Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn
			485					490					495		
Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg
		500						505					510		
Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala
		515					520					525			
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe
	530					535					540				
Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly
545				550					555					560	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
			565												

<210> 157

<211> 569

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-Opdivo heavy chain fusion sequence

<400> 157

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

Ser	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	
130						135					140					
Arg	Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	
145					150					155					160	
Ser	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
				165					170					175		
Val	Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	
			180					185					190			
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	
	195						200				205					
Phe	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	
	210					215					220					
Cys	Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
225					230					235					240	
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	
				245					250					255		
Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
			260					265					270			
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
	275						280					285				
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
	290					295					300					
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
305					310					315					320	
Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
				325					330					335		
Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	
			340					345					350			
Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
		355					360					365				
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
	370					375					380					
Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	
385					390					395					400	
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
				405					410					415		
Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	
			420					425					430			
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	
		435					440					445				
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	
	450					455					460					
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	
465					470					475					480	
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
				485					490					495		
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
			500					505					510			
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
		515					520					525				

Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val
530						535					540				
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln
545					550					555					560
Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys							
				565											

<210> 158

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Keytruda heavy chain

<400> 158

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

				260					265					270			
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys		
		275					280					285					
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser		
		290				295					300						
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys		
305					310					315					320		
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile		
			325						330					335			
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro		
		340						345				350					
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu		
		355					360					365					
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn		
	370					375					380						
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser		
385				390						395					400		
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg		
			405					410						415			
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu		
		420						425				430					
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys			
		435					440					445					

<210> 159

<211> 218

<212> PRT

<213> Artificial Sequence

<220>

<223> Keytruda light chain amino acid sequence

<400> 159

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

Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr
130						135				140					
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser
145					150					155					160
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
			165						170					175	
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys
		180						185					190		
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro
	195					200						205			
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys						
	210					215									

<210> 160

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Opdivo heavy chain

<400> 160

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

210		215		220
Pro Glu Phe Leu Gly Gly	Pro Ser Val Phe Leu Phe	Pro Pro Lys Pro		
225	230	235	240	
Lys Asp Thr Leu Met Ile	Ser Arg Thr Pro Glu Val Thr	Cys Val Val		
245	250	255		
Val Asp Val Ser Gln Glu	Asp Pro Glu Val Gln Phe	Asn Trp Tyr Val		
260	265	270		
Asp Gly Val Glu Val His	Asn Ala Lys Thr Lys	Pro Arg Glu Glu Gln		
275	280	285		
Phe Asn Ser Thr Tyr Arg	Val Val Ser Val Leu Thr	Val Leu His Gln		
290	295	300		
Asp Trp Leu Asn Gly Lys	Glu Tyr Lys Cys Lys	Val Ser Asn Lys Gly		
305	310	315	320	
Leu Pro Ser Ser Ile Glu	Lys Thr Ile Ser Lys	Ala Lys Gly Gln Pro		
325	330	335		
Arg Glu Pro Gln Val Tyr	Thr Leu Pro Pro Ser	Gln Glu Glu Met Thr		
340	345	350		
Lys Asn Gln Val Ser Leu	Thr Cys Leu Val Lys	Gly Phe Tyr Pro Ser		
355	360	365		
Asp Ile Ala Val Glu Trp	Glu Ser Asn Gly Gln	Pro Glu Asn Asn Tyr		
370	375	380		
Lys Thr Thr Pro Pro Val	Leu Asp Ser Asp Gly	Ser Phe Phe Leu Tyr		
385	390	395	400	
Ser Arg Leu Thr Val Asp	Lys Ser Arg Trp Gln	Glu Gly Asn Val Phe		
405	410	415		
Ser Cys Ser Val Met His	Glu Ala Leu His Asn	His Tyr Thr Gln Lys		
420	425	430		
Ser Leu Ser Leu Ser Leu	Gly Lys			
435	440			

<210> 161

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Opdivo light chain amino acid sequence

<400> 161

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

Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Ser	Ser	Asn	Trp	Pro	Arg	
				85					90					95		
Thr	Phe	Gly	Gln	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					
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> 162
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Linker peptide

<400> 162
 Gly Gly Gly Gly Ser Gly Gly Gly Ser
 1 5

<210> 163
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> IgG1 hinge

<400> 163
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1 5 10 15

<210> 164
 <211> 125
 <212> PRT
 <213> Homo sapiens

<400> 164

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

<210> 165

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> A34310/A34311/A34313/A34625/A36566/A37067/
AS07392/AS07678/AS07712 FR4

<400> 165

Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 166

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> A36922 FR4

<400> 166

Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Ile	Ser	Thr
1				5					10	

<210> 167

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014/AS07832 FR4

<400> 167

Trp	Ala	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 168

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07172 FR4

<400> 168

Arg	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 169

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189/AS07688 FR4

<400> 169

Trp	Gly	Gln	Gly	Thr	Gln	Val	Ile	Val	Ser	Ser
1				5					10	

<210> 170

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07745 FR4

<400> 170

Gly	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser
1				5					10	

<210> 171

<211> 586
<212> PRT
<213> Artificial Sequence

<220>
<223> Tecentriq-9GS-A34311 heavy chain fusion sequence

<400> 171

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Ser
			20					25					30		
Trp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Trp	Ile	Ser	Pro	Tyr	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr
65					70				75						80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
		115					120					125			
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
	130					135					140				
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
145					150				155						160
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
			165						170					175	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
		180					185						190		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
	195					200						205			
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
	210				215						220				
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
225					230				235						240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
			245						250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
		260						265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
	275						280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
			325						330					335	

Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	
			340					345					350			
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	
		355					360					365				
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	
	370					375					380					
Asn	Gly	Gln	Pro	Glu	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp		
385				390				395						400		
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	
			405					410					415			
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	
		420					425					430				
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	
	435					440					445					
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Lys	Leu	Glu	Glu	Ser	
	450				455				460							
Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu	
465				470				475							480	
Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	
			485					490						495		
Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	
		500					505					510				
Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	
	515					520					525					
Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu	
	530				535					540						
Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	
545				550				555							560	
Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	
			565					570						575		
Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser							
		580					585									

<210> 172

<211> 586

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-9GS-Tecentriq heavy chain fusion sequence

<400> 172

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

50	55	60													
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr
65					70					75					80
Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
			100					105					110		
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser
	115						120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu
	130					135				140					
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
145					150					155					160
Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Ser	Trp	Ile	His	Trp	Val	Arg
			165					170						175	
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Trp	Ile	Ser	Pro	Tyr
			180					185					190		
Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
	195						200					205			
Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu
	210					215					220				
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Arg	His	Trp	Pro
225					230					235					240
Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
			245					250						255	
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
			260					265					270		
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
	275					280						285			
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
	290					295					300				
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
305					310				315						320
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
			325						330					335	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			340					345					350		
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
	355						360					365			
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
	370					375					380				
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
385					390					395					400
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
			405					410						415	
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
			420					425					430		
Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
	435						440					445			
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn

Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	
			180					185					190			
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	
		195					200					205				
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	
	210					215					220					
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	
225					230					235					240	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	
				245					250						255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	
			260					265					270			
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	
		275					280					285				
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val	
	290					295					300					
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	
305					310					315					320	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	
				325					330						335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	
			340					345					350			
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	
		355					360					365				
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	
	370					375					380					
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	
385					390					395					400	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	
				405					410					415		
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	
			420					425					430			
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	
		435					440					445				
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	
	450					455					460					
Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	
465					470					475					480	
Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	
				485					490					495		
Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	
			500					505					510			
Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	
		515					520					525				
Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	
	530					535					540					
Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
545					550					555					560	
Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	
				565					570					575		

Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
580 585 590

<210> 174

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-hIgG1 hinge-Tecentriq heavy chain fusion sequence

<400> 174

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

290		295		300											
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
305					310					315					320
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
				325					330						335
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
			340					345					350		
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
		355					360					365			
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
		370				375					380				
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
385					390					395					400
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
				405					410					415	
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
			420					425					430		
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
		435					440					445			
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
		450				455					460				
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
465					470					475					480
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			485						490					495	
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
			500					505					510		
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
		515					520					525			
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
		530				535					540				
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
545					550					555					560
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
				565					570					575	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
			580				585						590		

<210> 175

<211> 577

<212> PRT

<213> Artificial Sequence

<220>

<223> Tecentriq-A34311 heavy chain fusion sequence

<400> 175

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Ser
			20					25					30		
Trp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Trp	Ile	Ser	Pro	Tyr	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr
65					70					75				80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90				95		
Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
		115					120					125			
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
	130					135					140				
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
145					150					155					160
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
				165					170					175	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
		180						185					190		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
	195					200					205				
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
	210					215					220				
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
			260					265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
				325					330				335		
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370					375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	

Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
		420						425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
		435					440					445			
Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu
	450					455					460				
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
465					470					475					480
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val
			485						490					495	
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
			500					505					510		
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr
	515						520					525			
Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
	530					535					540				
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
545					550					555					560
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser
			565						570					575	

Ser

<210> 176

<211> 577

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-Tecentriq heavy chain fusion sequence

<400> 176

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

Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly

130		135		140											
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp
145					150					155					160
Ser	Trp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp
				165					170						175
Val	Ala	Trp	Ile	Ser	Pro	Tyr	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser
			180					185					190		
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala
	195						200					205			
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr
	210					215				220					
Cys	Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly
225					230					235					240
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
				245					250					255	
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu
		260					265						270		
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp
	275						280					285			
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
	290					295				300					
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
305					310					315					320
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro
				325					330					335	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys
			340					345					350		
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro
		355					360						365		
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
	370					375					380				
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp
385					390					395					400
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn
			405						410					415	
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val
		420						425					430		
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
	435					440					445				
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys
	450					455				460					
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
465					470					475					480
Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
			485						490					495	
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
		500						505					510		
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
	515						520					525			
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys

530		535		540											
Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
545				550		555									560
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly
			565						570						575
Lys															

<210> 177

<211> 586

<212> PRT

<213> Artificial Sequence

<220>

<223> Tecentriq-9GS-AS02640 heavy chain fusion sequence

<400> 177

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

Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
			260					265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
	290				295						300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
			325						330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370					375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
			420					425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
		435					440					445			
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Glu	Ser
	450					455					460				
Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala
465					470					475					480
Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln
				485					490					495	
Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp
			500					505					510		
Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser
		515					520					525			
Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg
	530					535					540				
Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser
545					550					555					560
Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp
				565					570					575	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser						
			580					585							

<210> 178

<211> 586

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-9GS-Tecentriq heavy chain fusion sequence

<400> 178

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
			20					25					30		
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val
		35					40					45			
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr
65					70					75				80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
			100					105					110		
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Val	Gln	Leu	Val	Glu
	130					135					140				
Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys
145					150					155				160	
Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Ser	Trp	Ile	His	Trp	Val	Arg
			165					170						175	
Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Trp	Ile	Ser	Pro	Tyr
			180					185					190		
Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
	195						200					205			
Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu
	210					215					220				
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Arg	His	Trp	Pro
225					230					235					240
Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
			245						250					255	
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys
		260						265					270		
Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
	275					280						285			
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
	290					295					300				
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
305					310					315				320	
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
			325						330					335	
Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
		340						345					350		
Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
	355						360					365			
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro

370		375		380
Lys Pro Lys Asp Thr	Leu Met Ile Ser Arg Thr	Pro Glu Val Thr Cys		
385	390	395	400	
Val Val Val Asp Val	Ser His Glu Asp Pro	Glu Val Lys Phe Asn Trp		
	405	410	415	
Tyr Val Asp Gly Val	Glu Val His Asn Ala	Lys Thr Lys Pro Arg Glu		
	420	425	430	
Glu Gln Tyr Ala Ser	Thr Tyr Arg Val Val	Ser Val Leu Thr Val Leu		
	435	440	445	
His Gln Asp Trp Leu	Asn Gly Lys Glu Tyr	Lys Cys Lys Val Ser Asn		
	450	455	460	
Lys Ala Leu Pro Ala	Pro Ile Glu Lys Thr	Ile Ser Lys Ala Lys Gly		
465	470	475	480	
Gln Pro Arg Glu Pro	Gln Val Tyr Thr Leu	Pro Pro Ser Arg Glu Glu		
	485	490	495	
Met Thr Lys Asn Gln	Val Ser Leu Thr Cys	Leu Val Lys Gly Phe Tyr		
	500	505	510	
Pro Ser Asp Ile Ala	Val Glu Trp Glu Ser	Asn Gly Gln Pro Glu Asn		
	515	520	525	
Asn Tyr Lys Thr Thr	Pro Pro Val Leu Asp	Ser Asp Gly Ser Phe Phe		
	530	535	540	
Leu Tyr Ser Lys Leu	Thr Val Asp Lys Ser	Arg Trp Gln Gln Gly Asn		
545	550	555	560	
Val Phe Ser Cys Ser	Val Met His Glu Ala	Leu His Asn His Tyr Thr		
	565	570	575	
Gln Lys Ser Leu Ser	Leu Ser Pro Gly Lys			
	580	585		

<210> 179

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> Tecentriq-hIgG1 hinge-AS02640 heavy chain fusion sequence

<400> 179

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

Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	
			100					105					110			
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	
		115						120					125			
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	
	130					135					140					
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	
145					150					155					160	
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	
			165						170						175	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	
			180					185					190			
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	
		195					200					205				
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	
	210					215					220					
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	
225					230						235				240	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	
				245					250						255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	
			260					265					270			
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	
		275					280					285				
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val	
	290					295					300					
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	
305					310					315					320	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	
				325					330					335		
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	
			340					345					350			
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	
		355					360					365				
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	
	370					375					380					
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	
385					390					395					400	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	
				405					410					415		
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	
			420					425					430			
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	
		435					440					445				
Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	
	450					455					460					
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	
465					470					475					480	
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	
				485					490					495		

Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala
			500					505					510		
Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
		515					520					525			
Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu
	530					535					540				
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
545					550					555					560
Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala
			565					570						575	
Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
			580					585					590		

<210> 180

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-hIgG1 hinge-Tecentriq heavy chain fusion sequence

<400> 180

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

210		215		220
Leu Gln Met Asn Ser	Leu Arg Ala Glu Asp Thr	Ala Val Tyr Tyr Cys		
225	230	235	240	
Ala Arg Arg His Trp	Pro Gly Gly Phe Asp Tyr	Trp Gly Gln Gly Thr		
245	250	255		
Leu Val Thr Val Ser	Ser Ala Ser Thr Lys Gly	Pro Ser Val Phe Pro		
260	265	270		
Leu Ala Pro Ser Ser	Lys Ser Thr Ser Gly Gly	Thr Ala Ala Leu Gly		
275	280	285		
Cys Leu Val Lys Asp Tyr	Phe Pro Glu Pro Val Thr	Val Ser Trp Asn		
290	295	300		
Ser Gly Ala Leu Thr Ser	Gly Val His Thr Phe Pro	Ala Val Leu Gln		
305	310	315	320	
Ser Ser Gly Leu Tyr Ser	Leu Ser Ser Val Val Thr	Val Pro Ser Ser		
325	330	335		
Ser Leu Gly Thr Gln Thr	Tyr Ile Cys Asn Val Asn	His Lys Pro Ser		
340	345	350		
Asn Thr Lys Val Asp Lys	Lys Val Glu Pro Lys Ser	Cys Asp Lys Thr		
355	360	365		
His Thr Cys Pro Pro Cys	Pro Ala Pro Glu Leu Leu	Gly Gly Pro Ser		
370	375	380		
Val Phe Leu Phe Pro Pro	Lys Pro Lys Asp Thr Leu	Met Ile Ser Arg		
385	390	395	400	
Thr Pro Glu Val Thr Cys	Val Val Val Asp Val Ser	His Glu Asp Pro		
405	410	415		
Glu Val Lys Phe Asn Trp	Tyr Val Asp Gly Val Glu	Val His Asn Ala		
420	425	430		
Lys Thr Lys Pro Arg Glu	Glu Gln Tyr Ala Ser Thr	Tyr Arg Val Val		
435	440	445		
Ser Val Leu Thr Val Leu	His Gln Asp Trp Leu Asn	Gly Lys Glu Tyr		
450	455	460		
Lys Cys Lys Val Ser Asn	Lys Ala Leu Pro Ala Pro	Ile Glu Lys Thr		
465	470	475	480	
Ile Ser Lys Ala Lys Gly	Gln Pro Arg Glu Pro Gln	Val Tyr Thr Leu		
485	490	495		
Pro Pro Ser Arg Glu Glu	Met Thr Lys Asn Gln Val	Ser Leu Thr Cys		
500	505	510		
Leu Val Lys Gly Phe Tyr	Pro Ser Asp Ile Ala Val	Glu Trp Glu Ser		
515	520	525		
Asn Gly Gln Pro Glu Asn	Asn Tyr Lys Thr Thr Pro	Pro Val Leu Asp		
530	535	540		
Ser Asp Gly Ser Phe Phe	Leu Tyr Ser Lys Leu Thr	Val Asp Lys Ser		
545	550	555	560	
Arg Trp Gln Gln Gly Asn	Val Phe Ser Cys Ser Val	Met His Glu Ala		
565	570	575		
Leu His Asn His Tyr Thr	Gln Lys Ser Leu Ser Leu	Ser Pro Gly Lys		
580	585	590		

<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> Tecentriq-AS02640 heavy chain fusion sequence

<400> 181

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly		
1				5					10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Ser		
			20					25					30				
Trp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val		
		35					40					45					
Ala	Trp	Ile	Ser	Pro	Tyr	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val		
	50					55					60						
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr		
65					70				75						80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys		
			85						90					95			
Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr		
			100					105					110				
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro		
		115					120					125					
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly		
	130					135					140						
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn		
145					150				155						160		
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln		
				165					170					175			
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser		
			180					185					190				
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser		
		195				200						205					
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr		
	210					215					220						
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser		
225					230					235					240		
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg		
				245					250					255			
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro		
			260					265					270				
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala		
		275					280					285					
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val		
	290					295					300						
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr		
305					310					315					320		
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr		
				325					330					335			

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

Ser

<210> 182

<211> 577

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-Tecentriq heavy chain fusion sequence

<400> 182

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

50	55	60
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr		
65	70	75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
	85	90
Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu		
	100	105
Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser		
	115	120
Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly		
	130	135
Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp		
	145	150
Ser Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp		
	165	170
Val Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser		
	180	185
Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala		
	195	200
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr		
	210	215
Cys Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly		
	225	230
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe		
	245	250
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu		
	260	265
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp		
	275	280
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu		
	290	295
Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser		
	305	310
Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro		
	325	330
Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys		
	340	345
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro		
	355	360
Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser		
	370	375
Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp		
	385	390
Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn		
	405	410
Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val		
	420	425
Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu		
	435	440
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys		
	445	

450		455		460	
Thr	Ile	Ser	Lys	Ala	Lys
465		470		475	480
Leu	Pro	Pro	Ser	Arg	Glu
		485		490	495
Cys	Leu	Val	Lys	Gly	Phe
		500		505	510
Ser	Asn	Gly	Gln	Pro	Glu
		515		520	525
Asp	Ser	Asp	Gly	Ser	Phe
		530		535	540
Ser	Arg	Trp	Gln	Gln	Gly
545				550	555
Ala	Leu	His	Asn	His	Tyr
		565		570	575

Lys

<210> 183

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> Durvalumab-9GS-A34311 heavy chain fusion sequence

<400> 183

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

Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
			180					185					190			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
		195					200					205				
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	
	210					215					220					
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	
225					230					235					240	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
			245						250					255		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	
			260					265					270			
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
		275					280					285				
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
	290					295					300					
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
305					310					315					320	
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Ser	Ile	
				325					330					335		
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
			340					345					350			
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	
		355					360					365				
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
	370					375					380					
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
385					390					395					400	
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
				405					410					415		
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
			420					425					430			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
		435					440					445				
Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Lys	Leu	
	450					455					460					
Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	
465					470					475					480	
Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	
				485					490					495		
Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	
			500					505					510			
Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	
		515					520					525				
Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	
	530					535					540					
Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	
545					550					555					560	
Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	
				565					570					575		

Asp Tyr Trp Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 580 585

<210> 184

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-9GS-Durvalumab heavy chain fusion sequence

<400> 184

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Tyr
Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
Ala	Asn	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Glu	Gly	Gly	Trp	Phe	Gly	Glu	Leu	Ala	Phe	Asp	Tyr	Trp	Gly
			100					105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
			115				120					125			
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
						135					140				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
145					150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				165					170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
			180					185				190			
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
			195				200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys
						215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
				245					250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
			275				280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
						295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Ser	Ile
				325					330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser
			355				360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
						375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385															

Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
		435					440					445			
Pro	Gly	Lys	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
	450					455					460				
Cys	Pro	Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro
465					470				475						480
Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr
			485						490					495	
Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln
			500					505					510		
Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp
		515					520					525			
Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg
	530					535					540				
Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr
545					550					555					560
Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr
				565					570					575	
Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr
			580					585					590		
Val	Ser	Ser													
		595													

<210> 186

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-hIgG1 hinge-Durvalumab heavy chain fusion sequence

<400> 186

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

		115					120					125			
Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro
	130					135					140				
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
145					150					155					160
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Tyr
					165				170					175	
Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
			180					185					190		
Ala	Asn	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val
		195					200					205			
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
	210					215					220				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
225					230					235					240
Ala	Arg	Glu	Gly	Gly	Trp	Phe	Gly	Glu	Leu	Ala	Phe	Asp	Tyr	Trp	Gly
				245					250					255	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
			260					265					270		
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
		275					280					285			
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	290					295					300				
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
305					310					315					320
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
				325					330					335	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
			340					345					350		
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys
		355					360					365			
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly
	370					375					380				
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
385					390					395					400
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
				405					410					415	
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
			420					425					430		
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
		435					440					445			
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
	450					455					460				
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Ser	Ile
465					470		</								

		515					520					525					
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro		
	530						535				540						
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val		
545					550					555					560		
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met		
			565						570					575			
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser		
			580					585					590				
Pro	Gly	Lys															
		595															

<210> 187

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Durvalumab-A34311 heavy chain fusion sequence

<400> 187

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

Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
				245					250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		275					280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Ser	Ile
				325					330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
		370				375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				405					410					415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
		435					440					445			
Pro	Gly	Lys	Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu
	450					455					460				
Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile
465					470					475					480
Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg
				485					490					495	
Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala
			500					505					510		
Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn
		515					520				525				
Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val
		530				535					540				
Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp
545					550					555					560
Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val
				565					570					575	
Thr	Val	Ser	Ser												
			580												

<210> 188

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311-Durvalumab heavy chain fusion sequence

<400> 188

Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	
1				5				10						15		
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	
			20					25					30			
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	
		35					40					45				
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	
65				70					75					80		
Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	
			100					105					110			
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	
	115						120					125				
Ser	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
	130					135					140					
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	
145				150					155					160		
Tyr	Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
			165					170						175		
Val	Ala	Asn	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	
		180					185						190			
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	
	195					200						205				
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	
	210				215						220					
Cys	Ala	Arg	Glu	Gly	Gly	Trp	Phe	Gly	Glu	Leu	Ala	Phe	Asp	Tyr	Trp	
225				230					235					240		
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	
			245					250					255			
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	
		260					265						270			
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	
	275					280						285				
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	
	290				295						300					
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	
305				310					315					320		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	
			325					330					335			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	

Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Glu	Gly	Gly	Trp	Phe	Gly	Glu	Leu	Ala	Phe	Asp	Tyr	Trp	Gly
			100					105					110		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
		115					120					125			
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala
	130					135					140				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
145					150					155					160
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
				165					170					175	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
		180						185					190		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His
		195					200					205			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys
	210					215					220				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly
225					230					235					240
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
				245					250					255	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His
			260					265					270		
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
		275					280					285			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr
	290					295					300				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
305					310					315					320
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Ser	Ile
				325					330					335	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
			340					345					350		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser
		355					360					365			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
	370					375					380				
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
385					390					395					400
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				405					410					415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
		435					440					445			
Pro	Gly	Lys	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu
	450					455					460				

Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu
465					470					475					480
Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp
				485					490						495
Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala	Ser	His	Ser
			500					505					510		
Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe
		515					520					525			
Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln	Met	Asn
	530					535					540				
Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala
545					550					555					560
Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr
			565						570					575	
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
			580					585							

<210> 190

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-9GS-Durvalumab heavy chain fusion sequence

<400> 190

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

			180				185				190				
Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
		195					200					205			
Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu
	210					215					220				
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Glu	Gly	Gly	Trp
225					230					235					240
Phe	Gly	Glu	Leu	Ala	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
				245					250					255	
Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro
			260					265					270		
Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val
		275					280						285		
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala
	290					295					300				
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly
305					310					315					320
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly
				325					330					335	
Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys
			340					345					350		
Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys
	355						360					365			
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	Gly	Pro	Ser	Val	Phe	Leu
	370					375					380				
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
385					390					395					400
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys
				405					410					415	
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
			420					425					430		
Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
		435					440					445			
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
	450					455					460				
Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys
465					470					475					480
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
				485					490					495	
Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
			500					505					510		
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
		515					520					525			
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
	530					535					540				
Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
545					550					555					560
Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
				565					570					575	
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys			

<210> 191

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> Durvalumab-hIgG1 hinge-AS02640 heavy chain fusion sequence

<400> 191

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Arg Tyr
 20           25           30
Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ala Asn Ile Lys Gln Asp Gly Ser Glu Lys Tyr Tyr Val Asp Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Arg Glu Gly Gly Trp Phe Gly Glu Leu Ala Phe Asp Tyr Trp Gly
100          105          110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115          120          125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130          135          140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145          150          155          160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165          170          175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180          185          190
Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
195          200          205
Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys
210          215          220
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly
225          230          235          240
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245          250          255
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260          265          270
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275          280          285
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290          295          300

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Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
 450 455 460
 Cys Pro Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro
 465 470 475 480
 Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Ile Thr
 485 490 495
 Thr Ile Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu
 500 505 510
 Phe Val Ala Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp
 515 520 525
 Ser Val Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Arg
 530 535 540
 Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 545 550 555 560
 Tyr Cys Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr
 565 570 575
 Thr Glu Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 580 585 590
 Val Ser Ser
 595

<210> 192

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-hIgG1 hinge-Durvalumab heavy chain fusion sequence

<400> 192

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1				5				10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	
			20					25					30			
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	
		35					40					45				
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	
65				70					75					80		
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	
			100					105					110			
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
	115						120					125				
Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	
	130					135					140					
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
145				150						155				160		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Arg	Tyr	
			165					170						175		
Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		180						185					190			
Ala	Asn	Ile	Lys	Gln	Asp	Gly	Ser	Glu	Lys	Tyr	Tyr	Val	Asp	Ser	Val	
	195					200						205				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Ser	Leu	Tyr	
	210					215					220					
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
225				230					235					240		
Ala	Arg	Glu	Gly	Gly	Trp	Phe	Gly	Glu	Leu	Ala	Phe	Asp	Tyr	Trp	Gly	
			245					250						255		
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	
		260						265					270			
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	
	275					280						285				
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	
	290					295					300					
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	
305				310					315					320		
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	
			325					330						335		
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	
	340							345					350			
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	
	355					360						365				
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	
	370					375					380					
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	
385				390						395				400		
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	

				405					410				415			
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	
			420					425					430			
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	
		435					440					445				
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	
	450					455					460					
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Ser	Ile	
465				470						475					480	
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	
			485					490						495		
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	
			500					505					510			
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	
	515					520					525					
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	
	530				535					540						
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	
545					550				555						560	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	
			565					570						575		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	
			580					585					590			
Pro	Gly	Lys														
		595														

<210> 193

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> Durvalumab-AS02640 heavy chain fusion sequence

<400> 193

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

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	115	120	125
Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	130	135	140
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	145	150	155
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	165	170	175
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	180	185	190
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	195	200	205
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	210	215	220
Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Glu	Gly	225	230	235
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	245	250	255
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	260	265	270
Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	275	280	285
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	290	295	300
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	305	310	315
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Ser	Ile	325	330	335
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	340	345	350
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	355	360	365
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	370	375	380
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	385	390	395
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	405	410	415
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	420	425	430
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	435	440	445
Pro	Gly	Lys	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	450	455	460
Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	465	470	475
Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	485	490	495
Glu	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	500	505	510

Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn
		515					520					525			
Arg	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val
		530				535					540				
Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp
545					550					555					560
Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val
				565					570					575	
Thr	Val	Ser	Ser												
			580												

<210> 194

<211> 580

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640-Durvalumab heavy chain fusion sequence

<400> 194

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

225					230					235				240
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly
				245					250				255	
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly
			260					265					270	
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val
		275					280					285		
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe
	290				295					300				
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val
305				310					315					320
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val
			325					330					335	
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys
		340						345				350		
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe
	355					360					365			
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
	370					375				380				
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
385				390					395					400
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
			405					410					415	
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
		420					425					430		
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
	435					440					445			
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala
	450					455				460				
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
465				470					475					480
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln
			485					490					495	
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala
		500					505					510		
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr
	515					520					525			
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu
	530				535				540					
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser
545				550					555					560
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
			565				570						575	
Ser	Pro	Gly	Lys											
			580											

<210> 195

<211> 448

<212> PRT

<213> Artificial Sequence

<220>

<223> Tecentriq heavy chain

<400> 195

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Ser
			20					25					30		
Trp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Trp	Ile	Ser	Pro	Tyr	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
			100					105					110		
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
	115						120					125			
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
	130				135						140				
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
145					150					155					160
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
				165					170					175	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
		180						185					190		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
	195					200						205			
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
	210					215					220				
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
			260					265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
	275						280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		

<210> 197

<211> 451

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Durvalumab heavy chain

<400> 197

Glu 1	Val	Gln	Leu	Val 5	Glu	Ser	Gly	Gly	Gly 10	Leu	Val	Gln	Pro	Gly 15	Gly
Ser	Leu	Arg	Leu 20	Ser	Cys	Ala	Ala	Ser 25	Gly	Phe	Thr	Phe	Ser 30	Arg	Tyr
Trp	Met	Ser 35	Trp	Val	Arg	Gln	Ala 40	Pro	Gly	Lys	Gly 45	Leu	Glu	Trp	Val
Ala	Asn 50	Ile	Lys	Gln	Asp 55	Gly	Ser	Glu	Lys	Tyr 60	Tyr	Val	Asp	Ser	Val
Lys 65	Gly	Arg	Phe	Thr 70	Ile	Ser	Arg	Asp	Asn 75	Ala	Lys	Asn	Ser	Leu	Tyr 80
Leu	Gln	Met	Asn 85	Ser	Leu	Arg	Ala	Glu	Asp 90	Thr	Ala	Val	Tyr	Tyr	Cys 95
Ala	Arg	Glu	Gly 100	Gly	Trp	Phe	Gly	Glu 105	Leu	Ala	Phe	Asp	Tyr 110	Trp	Gly
Gln	Gly 115	Thr	Leu	Val	Thr	Val	Ser 120	Ser	Ala	Ser	Thr 125	Lys	Gly	Pro	Ser
Val	Phe 130	Pro	Leu	Ala	Pro	Ser 135	Ser	Lys	Ser	Thr 140	Ser	Gly	Gly	Thr	Ala
Ala 145	Leu	Gly	Cys	Leu 150	Val	Lys	Asp	Tyr	Phe 155	Pro	Glu	Pro	Val	Thr	Val 160
Ser	Trp	Asn	Ser 165	Gly	Ala	Leu	Thr	Ser	Gly 170	Val	His	Thr	Phe	Pro	Ala 175
Val	Leu	Gln 180	Ser	Gly	Leu	Tyr	Ser 185	Leu	Ser	Ser	Val 190	Val	Val	Thr	Val
Pro	Ser 195	Ser	Ser	Leu	Gly	Thr	Gln 200	Thr	Tyr	Ile	Cys 205	Asn	Val	Asn	His
Lys	Pro 210	Ser	Asn	Thr	Lys	Val 215	Asp	Lys	Arg	Val 220	Glu	Pro	Lys	Ser	Cys
Asp 225	Lys	Thr	His	Thr 230	Cys	Pro	Pro	Cys	Pro 235	Ala	Pro	Glu	Phe	Glu	Gly 240
Gly	Pro	Ser	Val 245	Phe	Leu	Phe	Pro	Pro	Lys 250	Pro	Lys	Asp	Thr	Leu	Met 255
Ile	Ser	Arg	Thr 260	Pro	Glu	Val	Thr	Cys 265	Val	Val	Val	Asp	Val	Ser	His
Glu	Asp 275	Pro	Glu	Val	Lys	Phe	Asn 280	Trp	Tyr	Val	Asp 285	Gly	Val	Glu	Val
His	Asn 290	Ala	Lys	Thr	Lys	Pro	Arg 295	Glu	Glu	Gln	Tyr 300	Asn	Ser	Thr	Tyr

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 305 310 315 320
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
 325 330 335
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 340 345 350
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 355 360 365
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 370 375 380
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 385 390 395 400
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 405 410 415
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 420 425 430
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 435 440 445
 Pro Gly Lys
 450

<210> 198

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Durvalumab light chain amino acid sequence

<400> 198

Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Ser Ser
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp 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 Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Leu Pro
 85 90 95
 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala
 100 105 110
 Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser
 115 120 125
 Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
 130 135 140
 Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser

145		150		155		160									
Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu
		165				170								175	
Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val
		180					185						190		
Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys
		195					200					205			
Ser	Phe	Asn	Arg	Gly	Glu	Cys									
	210					215									

<210> 199
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 199
Ala Met His Val Ala Gln Pro Ala Val Val Leu Ala Ser Ser Arg Gly
1 5 10 15
Ile Ala Ser Phe Val Cys Glu Tyr Ala Ser Pro Gly Lys Ala Thr Glu
20 25 30
Val Arg Val Thr Val Leu Arg Gln Ala Asp Ser Gln Val Thr Glu Val
35 40 45
Cys Ala Ala Thr Tyr Met Met Gly Asn Glu Leu Thr Phe Leu Asp Asp
50 55 60
Ser Ile Cys Thr Gly Thr Ser Ser Gly Asn Gln Val Asn Leu Thr Ile
65 70 75 80
Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile Cys Lys Val Glu
85 90 95
Leu Met Tyr Pro Pro Pro Tyr Tyr Leu Gly Ile Gly Asn Gly Thr Gln
100 105 110
Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser Asp Phe Leu Leu
115 120 125
Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe Tyr Ser Phe Leu
130 135 140
Leu Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys Arg Ser Pro Leu
145 150 155 160
Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu Pro Glu Cys Glu
165 170 175
Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn
180 185

<210> 200
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A34311-direct grafted amino acid

<400> 200

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

Ser

<210> 201

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02636 humanized sdAb

<400> 201

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

Ser

<210> 202
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> AS02626 humanized sdAb

<400> 202
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Ile Thr Thr Ile
20 25 30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Phe Val
35 40 45
Ala Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Ile Ile Ser Arg Asp Asn Ser Lys Asn Arg Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu
100 105 110
Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125
Ser

<210> 203
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> AS02640 FR1

<400> 203
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 204
<211> 25
<212> PRT
<213> Artificial Sequence

<220>

<223> A34311VH11, A34311VH2, A34311VH2F53, A34311VH11F53 FR1

<400> 204

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser							
			20					25							

<210> 205

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11, AS07014 direct grafted FR1

<400> 205

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser							
			20					25							

<210> 206

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11G54 FR1

<400> 206

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser							
			20					25							

<210> 207

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGA FR1

<400> 207

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 208

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGQ FR1

<400> 208

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 209

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGS FR1

<400> 209

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 210

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11, AS07189 direct grafted FR1

<400> 210

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 211

<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11F27 FR1

<400> 211
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 212
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11FY, AS07189TKDVH21FY FR1

<400> 212
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser
20 25

<210> 213
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> AS02640 CDR1

<400> 213
Gly Arg Thr Ile Thr Thr Ile Thr Met Gly
1 5 10

<210> 214
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> A34311VH11, A34311VH2, A34311VH2F53, A34311VH11F53 CDR1

<400> 214
Gly Arg Thr Ile Thr Thr Ile Thr Met Gly
1 5 10

<210> 215
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11 CDR1

<400> 215
Gly Tyr Thr Tyr Ser Arg His Cys Leu Gly
1 5 10

<210> 216
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11G54 CDR1

<400> 216
Gly Tyr Thr Tyr Ser Arg His Cys Leu Gly
1 5 10

<210> 217
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGA CDR1

<400> 217
Gly Tyr Thr Tyr Ser Arg His Cys Leu Gly
1 5 10

<210> 218
<211> 10
<212> PRT
<213> Artificial Sequence

<220>

<223> AS07014VH11SGQ CDR1

<400> 218

Gly	Tyr	Thr	Tyr	Ser	Arg	His	Cys	Leu	Gly
1				5					10

<210> 219

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGS CDR1

<400> 219

Gly	Tyr	Thr	Tyr	Ser	Arg	His	Cys	Leu	Gly
1				5					10

<210> 220

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11 CDR1

<400> 220

Gly	Asp	Ser	Pro	Ser	Val	Asn	Tyr	Met	Gly
1				5					10

<210> 221

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11F27 CDR1

<400> 221

Gly	Phe	Ser	Pro	Ser	Val	Asn	Tyr	Met	Gly
1				5					10

<210> 222

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11FY, AS07189TKDVH21FY CDR1

<400> 222

Gly Phe Ser Pro Ser Val Asn Tyr Met Gly
1 5 10

<210> 223

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640, A34311VH2, A34311VH2F53 FR2

<400> 223

Trp Phe Arg Gln Ala Pro Gly Lys Gly Leu Glu Phe Val Ala
1 5 10

<210> 224

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311VH11, A34311VH11F53 FR2

<400> 224

Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Phe Val Ala
1 5 10

<210> 225

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11 FR2

<400> 225

Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val Ser
1 5 10

<210> 226

<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11G54 FR2

<400> 226
Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val Ser
1 5 10

<210> 227
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGA FR2

<400> 227
Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val Ser
1 5 10

<210> 228
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGQ FR2

<400> 228
Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val Ser
1 5 10

<210> 229
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGS FR2

<400> 229
Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val Ser
1 5 10

<210> 230
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11 FR2

<400> 230
Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Glu Val Ser
1 5 10

<210> 231
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11F27 FR2

<400> 231
Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Glu Val Ser
1 5 10

<210> 232
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11FY FR2

<400> 232
Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Glu Val Ser
1 5 10

<210> 233
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> AS02640 CDR2

<400> 233
Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 234
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> A34311VH11, A34311VH2 CDR2

<400> 234
Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15
Gly

<210> 235
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11 CDR2

<400> 235
Thr Ile Asp Ser Asp Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 236
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11G54 CDR2

<400> 236
Thr Ile Asp Ser Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 237
<211> 16
<212> PRT
<213> Artificial Sequence

<220>

<223> AS07014VH11SGA CDR2

<400> 237

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

<210> 238

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGQ CDR2

<400> 238

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

<210> 239

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGS CDR2

<400> 239

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

<210> 240

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11 CDR2

<400> 240

Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly
1				5					10					15	

<210> 241

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11F27 CDR2

<400> 241

Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly
1				5				10						15	

<210> 242

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11FY, AS07189TKDVH21FY CDR2

<400> 242

Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly
1				5				10						15	

<210> 243

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640 FR3

<400> 243

Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Arg	Leu	Tyr	Leu	Gln
1				5				10						15	
Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala
			20					25					30		

<210> 244

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311VH11 FR3

<400> 244

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5				10						15	
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala

20

25

30

<210> 245

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11 FR3

<400> 245

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5				10						15	
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile
			20					25					30		

<210> 246

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11G54 FR3

<400> 246

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5				10						15	
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile
			20					25					30		

<210> 247

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGA FR3

<400> 247

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5				10						15	
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile
			20					25					30		

<210> 248

<211> 32

<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGQ FR3

<400> 248
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ile
20 25 30

<210> 249
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGS FR3

<400> 249
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ile
20 25 30

<210> 250
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11 FR3

<400> 250
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
20 25 30

<210> 251
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11F27 FR3

<400> 251

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala
			20					25					30		

$\langle 210 \rangle$ 252

<211> 32

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> AS07189TKDVH11FY, A34311VH11F53 FR3

<400> 252

Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
1				5					10					15	
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala
			20					25					30		

<210> 253

$\langle 211 \rangle$ 20

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> AS02640 CDR3

<400> 253

Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu Ala Arg
1 5 10 15
Gln Tyr Asp Tyr
20

<210> 254

$\langle 211 \rangle$ 20

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> A34311VH11, A34311VH2, A34311VH2F53, A34311VH11F53 CDR3

<400> 254

Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu Ala Arg
1 5 10 15
Gln Tyr Asp Tyr

20

<210> 255
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11 CDR3

<400> 255
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Asn Thr Arg Gly Ala
1 5 10 15
Glu His Tyr Phe Gly Tyr
20

<210> 256
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11G54 CDR3

<400> 256
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Asn Thr Arg Gly Ala
1 5 10 15
Glu His Tyr Phe Gly Tyr
20

<210> 257
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGA CDR3

<400> 257
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Ala Thr Arg Gly Ala
1 5 10 15
Glu His Tyr Phe Gly Tyr
20

<210> 258
<211> 22

<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGQ CDR3

<400> 258
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Gln Thr Arg Gly Ala
1 5 10 15
Glu His Tyr Phe Gly Tyr
20

<210> 259
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGS CDR3

<400> 259
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Ser Thr Arg Gly Ala
1 5 10 15
Glu His Tyr Phe Gly Tyr
20

<210> 260
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11 CDR3

<400> 260
Gly Lys Trp Gly Thr Asp Tyr
1 5

<210> 261
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11F27 CDR3

<400> 261

Gly Lys Trp Gly Thr Asp Tyr
1 5

<210> 262

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11FY, AS07189TKDVH21FY CDR3

<400> 262

Gly Lys Tyr Gly Thr Asp Tyr
1 5

<210> 263

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> AS02640, A34311VH11, AS07014VH11, AS07014VH11G54, AS07014VH11SGA,
AS07014VH11SGQ, AS07014VH11SGS, AS07189TKDVH11, AS07189TKDVH11F27,
AS07189TKDVH11FY, AS07189TKDVH21FY, A34311VH2, A34311VH2F53,
A34311VH11F53, AS07014 direct grafted, AS07189 direct grafted FR4

<400> 263

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
1 5 10

<210> 264

<211> 387

<212> DNA

<213> Artificial Sequence

<220>

<223> AS02640 sdAb

<400> 264

caagttcaac tgggtgaaag cggcggcggc gtggtgcaac cgggtcgtag cctgcgtctg 60
agctgcgcgg cgagcggtcg taccatcacc accatcacca tgggttggtt ccgtcaggcg 120
ccgggcaagg gtcttgaatt tgtggcgagc cacagctgga ccgacaacaa cccgtactat 180
gcggatagcg ttaagggccg tttcatcatt agccgtgaca acagcaaaaa caggctgtac 240
ctgcagatga acagcctgcg tgcggaggat accgcggtgt actattgcgc ggcgaccgcg 300
cgtcgtagct ttgttggtcg tcaatggtac accgaggcgc gtcaatacga ttactggggc 360
caaggcacc c tggttaccgt gagcagc 387

<210> 265
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> A34311VH11 sdAb

<400> 265
gaagtgcagc tgggtggaaag tggagggggc gtggtgcagc ctggaagaag cctgagactg 60
tcctgtgccg catctgggag aactattacc acaatcacca tgggatgggt cgcacaggct 120
ccaggcaagg gaagagagtt tgtggcaagc cactcctgga cagacaacaa tccttactat 180
gccgattctg tcaagggcag gttcacaatt tctcgcgaca acgcaaaaaa tactctgtac 240
ctgcagatga actcactgcg acccgaagat actgccgtgt actattgcgc agctaccgct 300
cgacggagct tcgtcgggag acagtgggtac accgaagcaa gacagtatga ttattgggga 360
cagggcactc tggtcaccgt cagcagt 387

<210> 266
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07014VH11 sdAb

<400> 266
gaggtgcagc tgggtggaatc tgggggagga ctggtgcagc ctgggggaag cctgagactg 60
agttgtgccg caagcggata cacttacagc aggcactgcc tgggatgggt cgcacaggca 120
ccaggcaagg gacgagaggc cgtgtctacc atcgacagtg atgggagcac atcctacgct 180
gactcagtca agggacgggt tactatcagc agagataacg caaagaacac cctgtatctg 240
cagatgaact ccctgagacc agaagacaca gccgtgtact attgcgctat cggacccaac 300
cctcgggtact gttctggcgc cccaataacc cggggagccg aacattactt tgggtattgg 360
ggacagggca cactggtgac cgtgagcagc 390

<210> 267
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07014VH11G54 sdAb

<400> 267
gaagtccaac tggtcgaatc ggggtggtggt ctggtccaac cgggcggctc cctgcgtctg 60
tcgtgtgcgg cgtcgggcta tacctattcc cgtcattgcc tgggttggtt tcgtcaggca 120
ccgggcaaaag gtcgtgaagc tgtgagtacc attgattccg gcggtagcac gtcttatgcg 180
gactcagtta aaggctcgtt caccatctcg cgcgataacg ccaaaaaatac gctgtacctg 240
caaatgaaca gcctgcgccc ggaagacacc gcggtctatt actgcgccat tggcccgaac 300
ccgcgttatt gttctgggtgc gccgaatacg cgtggtgcgg aacattactt tggctactgg 360
ggtcagggta cgctgggttac ggtgtcctcg 390

<210> 268
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07014VH11SGA sdAb

<400> 268
gaagtccaac tggtcgaaag tgggtgggtggc ctgggtccaac cgggcgggctc gctgcgtctg 60
tcgtgtgctg cgtctggcta tacctacagc cgtcattgcc tgggttgggtt tcgtcaggca 120
ccgggcaaag gtcgtgaagc cgtgtctacc attagctctg gcggtagtagt gtcctatgca 180
gattcagtta aaggctcgttt caccatctcg cgcgacaacg ccaaaaatac gctgtacctg 240
caaatgaact ccctgcgccc ggaagatacc gcagtctatt actgcgctat tggcccgaat 300
ccgcgttatt gtagcgggtgc gccggccacg cgcggcgag aacactattt cggctactgg 360
ggtcagggca cgctgggttac cgtttcgtcg 390

<210> 269
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07014VH11SGQ sdAb

<400> 269
gaagtccaac tggtcgaaag cggcggcggc ctgggtccaac cgggcgggctc actgcgtctg 60
tcctgtgcgg catcgggcta cacctatagc cgtcattgcc tgggttgggtt tcgtcaggca 120
ccgggcaaag gtcgtgaagc tgtgtctacc attagctctg gcggtagtagt gtcctatgca 180
gattcagtta aaggctcgttt caccatctcg cgcgacaacg ccaaaaatac gctgtacctg 240
cagatgaact ccctgcgccc ggaagatacc gcgggtctatt actgcgccat tggcccgaat 300
ccgcgttatt gtagcgggtgc gccgcaaacg cgtgggtgcgg aacattactt tggttattgg 360
ggtcagggta cgctgggttac ggtttcgtcg 390

<210> 270
<211> 390
<212> DNA
<213> Artificial Sequence

<220>
<223> AS07014VH11SGS sdAb

<400> 270
gaagtccaac tggtcgaatc gggcggcggc ctgggtccaac cgggtgggctc actgcgtctg 60
tcctgtgcgg caagcggcta cacgtattcc cgtcattgcc tgggttgggtt tcgtcaggca 120
ccgggcaaag gtcgtgaagc tgtgagcacc attagctctg gcggtagtagt gtcctatgca 180
gatagcggtta aaggctcgttt caccatctct cgcgacaacg ccaaaaatac gctgtacctg 240
caaatgaaca gtctgcgccc ggaagatacc gcgggtctatt actgcgccat tggcccgaat 300
ccgcgttatt gttcagggtgc gccgtcgacg cgcgggtgccg aacattattt tggttactgg 360

ggtcagggta cgctggtcac ggtttcatca

390

<210> 271

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11 sdAb

<400> 271

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gaggtgcagc tgggtggaaag cgggggggggc ctgggtgcagc ctggaggaag cctgagactg 60
agttgtgccg caagtggcga tagcccaagc gtgaactaca tggggtgggt caggcaggca 120
ccaggaaagg gacgagagga agtgagctcc atctacccta ccggcgggac attctatact 180
gactctgtca agggccggtt taccattagt agagataacg ccaaaaatac actgtatctg 240
cagatgaaca gcctgcgacc cgaggacacc gctgtctact attgcgctgc tgggaaatgg 300
gggaccgact attggggaca ggggacactg gtgaccgtct catca 345
```

<210> 272

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11F27 sdAb

<400> 272

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gaagtgaac tgggtggaatc ggggtggtggt ctggttcagc cgggtggtag cctgcgtctg 60
tcctgtgcgg caagcggttt ttcgccgagc gtcaactata tgggctgggt tcgtcaggcg 120
ccgggcaaag gtcgcgaaga agtgagctct atctatccga ccggcggcac gttttacacc 180
gatatgttta aaggtcgttt cacgatctcc cgcgacaacg cgaaaaatac cctgtacctg 240
caaatgaata gcctgcgtcc ggaagatacg gccgtttatt actgcgcggc aggcaaattg 300
ggcacggatt actgggggtca gggcacgctg gtcacgggtgt cgtcc 345
```

<210> 273

<211> 345

<212> DNA

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11FY sdAb

<400> 273

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gaagtgcagc tgggtggaaag cggaggagga ctgggtgcagc ctggcggaag cctgagactg 60
agttgtgccg catctggggt tagccccagc gtgaactaca tggggtgggt caggcaggca 120
ccaggaaagg gacgagagga agtgagctcc atctacccta ccggcgggac attctatact 180
gactctgtca agggccggtt taccattagt agagataacg ccaaaaatac actgtatctg 240
cagatgaaca gcctgcgacc cgaggacacc gctgtctact attgcgcagc agggaaatac 300
ggaaccgatt actggggggca gggaactctg gtcactgtca gcagc 345
```

<210> 274
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> A34311VH11 humanized sdAb

<400> 274
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Ile Thr Thr Ile
20 25 30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Phe Val
35 40 45
Ala Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu
100 105 110
Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120 125
Ser

<210> 275
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11 humanized sdAb

<400> 275
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His
20 25 30
Cys Leu Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val
35 40 45
Ser Thr Ile Asp Ser Asp Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Ile Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Asn Thr Arg Gly
100 105 110
Ala Glu His Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
115 120 125
Ser Ser
130

<210> 276
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11G54 humanized sdAb

<400> 276
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His
20 25 30
Cys Leu Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val
35 40 45
Ser Thr Ile Asp Ser Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Ile Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Asn Thr Arg Gly
100 105 110
Ala Glu His Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
115 120 125
Ser Ser
130

<210> 277
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014VH11SGA humanized sdAb

<400> 277
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His
20 25 30

Cys Leu Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val
 35 40 45
 Ser Thr Ile Ser Ser Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Ile Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Ala Thr Arg Gly
 100 105 110
 Ala Glu His Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 115 120 125
 Ser Ser
 130

<210> 278
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AS07014VH11SGQ humanized sdAb

<400> 278
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His
 20 25 30
 Cys Leu Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val
 35 40 45
 Ser Thr Ile Ser Ser Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Ile Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Gln Thr Arg Gly
 100 105 110
 Ala Glu His Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 115 120 125
 Ser Ser
 130

<210> 279
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>

<223> AS07014VH11SGS humanized sdAb

<400> 279

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

<210> 280

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11 humanized sdAb

<400> 280

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

<210> 281
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11F27 humanized sdAb

<400> 281
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Pro Ser Val Asn
20 25 30
Tyr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Glu Val
35 40 45
Ser Ser Ile Tyr Pro Thr Gly Gly Thr Phe Tyr Thr Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Ala Gly Lys Trp Gly Thr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115

<210> 282
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11FY humanized sdAb

<400> 282
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Pro Ser Val Asn
20 25 30
Tyr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Glu Val
35 40 45
Ser Ser Ile Tyr Pro Thr Gly Gly Thr Phe Tyr Thr Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Ala Gly Lys Tyr Gly Thr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr

	100	105	110
Val Ser Ser			
115			

<210> 283
 <211> 361
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A34311VH11 HCAB dimeric form

<400> 283
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Ile Thr Thr Ile
 20 25 30
 Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Phe Val
 35 40 45
 Ala Ser His Ser Trp Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu
 100 105 110
 Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120 125
 Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 130 135 140
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 145 150 155 160
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 165 170 175
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 180 185 190
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 195 200 205
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 210 215 220
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 225 230 235 240
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 245 250 255
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 260 265 270
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 275 280 285

Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
290						295					300				
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu
305					310					315					320
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val
			325						330					335	
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln
		340						345					350		
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
		355					360								

<210> 284

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11 HCAb dimeric form

<400> 284

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

225					230					235				240	
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
				245					250					255	
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
			260					265					270		
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
		275					280					285			
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
	290					295				300					
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
305					310				315					320	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
			325					330						335	
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
			340					345				350			
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
	355						360								

<210> 285

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11G54 HCAB dimeric form

<400> 285

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

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

<210> 286

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGA HCAb dimeric form

<400> 286

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

		115					120					125					
Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys		
	130					135					140						
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro		
145					150					155					160		
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys		
			165						170					175			
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp		
			180					185					190				
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu		
	195						200					205					
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu		
	210					215					220						
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn		
225				230						235					240		
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly		
			245						250					255			
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu		
		260						265					270				
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr		
	275						280					285					
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn		
	290					295					300						
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe		
305					310					315					320		
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn		
			325						330					335			
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr		
		340						345				350					
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
	355						360										

<210> 287

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGQ HCAB dimeric form

<400> 287

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

Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu
65					70					75					80
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Gln	Thr	Arg	Gly
			100					105					110		
Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
		115					120					125			
Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys
	130					135					140				
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
145					150					155					160
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
			165						170					175	
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp
			180					185					190		
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
		195					200					205			
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
	210					215					220				
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
225					230					235					240
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
			245						250					255	
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu
		260						265					270		
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
		275					280					285			
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
	290					295					300				
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
305					310					315					320
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn
			325						330					335	
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
		340						345				350			
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys						
		355					360								

<210> 288

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07014VH11SGS HCAb dimeric form

<400> 288

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1				5				10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His	
			20					25					30			
Cys	Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val	
		35					40					45				
Ser	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	
		50				55					60					
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	
65					70					75					80	
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
				85					90					95		
Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Ser	Thr	Arg	Gly	
			100					105					110			
Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
		115					120					125				
Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	
		130				135					140					
Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	
145					150					155					160	
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	
				165					170					175		
Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	
			180					185					190			
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	
		195					200					205				
Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	
		210				215					220					
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
225					230					235					240	
Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
				245					250					255		
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	
			260					265					270			
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	
		275					280					285				
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	
		290				295					300					
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	
305					310					315					320	
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	
				325					330					335		
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	
			340					345					350			
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
		355					360									

<210> 289

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11 HCAb dimeric form

<400> 289

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Asp	Ser	Pro	Ser	Val	Asn
			20					25					30		
Tyr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Glu	Val
		35					40					45			
Ser	Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys
	50					55					60				
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu
65				70					75					80	
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85				90						95	
Ala	Gly	Lys	Trp	Gly	Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
			100					105					110		
Val	Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro
	115					120					125				
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro
	130					135					140				
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
145				150					155					160	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn
				165					170					175	
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg
			180					185					190		
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val
		195					200					205			
Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
	210					215					220				
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
225				230						235				240	
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
			245					250						255	
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
			260					265					270		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
		275					280					285			
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	290					295				300					
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
305				310					315					320	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				325					330					335	
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
			340					345							

<210> 290
<211> 347
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH11F27 HCAB dimeric form

<400> 290
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Pro Ser Val Asn
20 25 30
Tyr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Glu Val
35 40 45
Ser Ser Ile Tyr Pro Thr Gly Gly Thr Phe Tyr Thr Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Ala Gly Lys Trp Gly Thr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
115 120 125
Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
130 135 140
Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
145 150 155 160
Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
165 170 175
Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
180 185 190
Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
195 200 205
Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
210 215 220
Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
225 230 235 240
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
245 250 255
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
260 265 270
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
275 280 285
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
290 295 300
Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly

305		310		315		320									
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				325					330					335	
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
			340					345							

<210> 291

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH11FY HCAb dimeric form

<400> 291

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

Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
			275				280					285			
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
			290				295					300			
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
305					310					315					320
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				325					330					335	
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
			340					345							

<210> 292

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-73 heavy chain fusion polypeptide

<400> 292

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

225					230					235				240
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly
				245					250					255
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
			260					265					270	
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
		275					280					285		Ala
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	290					295					300			Ser
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
305					310					315				320
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
				325					330					335
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
			340					345					350	Lys
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
		355					360					365		Pro
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
	370					375					380			Val
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
385					390					395				400
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
				405					410					415
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
			420					425					430	Lys
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
		435					440					445		Ser
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
	450					455					460			Lys
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
465					470				475					480
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
				485					490					495
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		500						505					510	Leu
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	515						520					525		Asn
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
	530					535				540				Ser
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
545					550					555				560
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
				565					570					575
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
			580					585					590	

<210> 293

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-74 heavy chain fusion polypeptide

<400> 293

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5				10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His
			20					25					30		
Cys	Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val
		35					40					45			
Ser	Thr	Ile	Asp	Ser	Asp	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys
	50					55					60				
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu
65				70					75					80	
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85				90						95	
Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Asn	Thr	Arg	Gly
			100					105					110		
Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
		115					120					125			
Ser	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser
	130					135					140				
Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys	Lys	Pro	Gly
145				150					155					160	
Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn
				165				170					175		
Tyr	Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp
		180					185					190			
Met	Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys
	195						200					205			
Phe	Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala
	210					215					220				
Tyr	Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr
225				230					235					240	
Cys	Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly
			245					250					255		
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
		260					265					270			
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
	275					280						285			
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	290					295					300				
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
305				310					315					320	
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
			325						330					335	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
			340				345						350		

Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
		355					360					365			
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
		370					375					380			
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
385						390					395				400
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
				405					410					415	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
			420					425					430		
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
		435					440					445			
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
		450				455					460				
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
465					470					475					480
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			485						490					495	
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
			500					505					510		
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
		515					520					525			
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
		530				535					540				
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser
545					550					555					560
Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
				565					570					575	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys
			580					585					590		

<210> 294

<211> 577

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-75 heavy chain fusion polypeptide

<400> 294

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

65					70					75					80
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Ala	Gly	Lys	Trp	Gly	Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
			100					105					110		
Val	Ser	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro
		115					120					125			
Ser	Pro	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys	Lys	Pro
	130					135				140					
Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
145				150					155					160	
Asn	Tyr	Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu
			165					170						175	
Trp	Met	Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu
		180						185					190		
Lys	Phe	Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr
	195					200					205				
Ala	Tyr	Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr
	210					215				220					
Tyr	Cys	Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp
225				230					235					240	
Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
			245					250					255		
Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr
		260					265					270			
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
	275					280					285				
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
	290					295				300					
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
305				310					315					320	
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp
			325					330					335		
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr
		340					345					350			
Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro
	355					360				365					
Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser
	370				375				380						
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp
385				390					395					400	
Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn
			405					410					415		
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val
		420					425					430			
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
	435				440						445				
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys
450					455				460						
Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr

465					470					475				480	
Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
				485					490					495	
Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
			500					505					510		
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
		515					520					525			
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys
	530					535					540				
Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
545					550					555					560
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly
			565						570					575	

Lys

<210> 295
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCP-90 heavy chain fusion polypeptide

<400> 295

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

Met	Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys
		195					200					205			
Phe	Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala
	210					215					220				
Tyr	Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr
225					230					235					240
Cys	Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly
				245					250					255	
Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser
			260					265					270		
Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala
		275					280					285			
Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val
	290					295					300				
Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala
305					310					315					320
Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val
				325					330					335	
Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His
			340					345					350		
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly
		355					360					365			
Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser
	370					375					380				
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
385					390					395					400
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro
				405					410					415	
Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
			420					425					430		
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val
		435					440					445			
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
	450					455					460				
Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr
465					470					475					480
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
				485					490				495		
Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
			500					505					510		
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
		515					520					525			
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
	530					535					540				
Ser	Asp	Gly	Ser	Phe	Phe	Leu									

<210> 296
<211> 577
<212> PRT
<213> Artificial Sequence

<220>
<223> BCP-91 heavy chain fusion polypeptide

<400> 296
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Pro Ser Val Asn
20 25 30
Tyr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Glu Val
35 40 45
Ser Ser Ile Tyr Pro Thr Gly Gly Thr Phe Tyr Thr Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Ala Gly Lys Tyr Gly Thr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
115 120 125
Ser Pro Gln Val Gln Leu Val Gln Ser Gly Val Glu Val Lys Lys Pro
130 135 140
Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
145 150 155 160
Asn Tyr Tyr Met Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
165 170 175
Trp Met Gly Gly Ile Asn Pro Ser Asn Gly Gly Thr Asn Phe Asn Glu
180 185 190
Lys Phe Lys Asn Arg Val Thr Leu Thr Thr Asp Ser Ser Thr Thr Thr
195 200 205
Ala Tyr Met Glu Leu Lys Ser Leu Gln Phe Asp Asp Thr Ala Val Tyr
210 215 220
Tyr Cys Ala Arg Arg Asp Tyr Arg Phe Asp Met Gly Phe Asp Tyr Trp
225 230 235 240
Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
245 250 255
Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
260 265 270
Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
275 280 285
Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
290 295 300
Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr

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

<210> 297

<211> 583

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-78 heavy chain fusion polypeptide

<400> 297

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5				10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
			20					25					30		

Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Phe	Val
		35					40					45			
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr
65					70					75				80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Gln
			100					105					110		
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			
Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro
	130					135					140				
Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
145					150					155				160	
Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	Ser
				165					170					175	
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
			180					185					190		
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val
		195				200						205			
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe
	210					215					220				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
225					230					235				240	
Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
				245					250					255	
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser
			260					265					270		
Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
		275					280					285			
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
		290				295					300				
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
305					310					315				320	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys
				325					330					335	
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
			340					345					350		
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
		355					360					365			
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
						375					380				
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg								

Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	435						440					445			
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
	450					455					460				
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
465					470					475					480
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
			485						490					495	
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
	500						505					510			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
	515					520					525				
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
	530					535				540					
Ser	Arg	Leu	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser
545					550					555					560
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
			565						570					575	
Leu	Ser	Leu	Ser	Leu	Gly	Lys									
			580												

<210> 298

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-79 heavy chain fusion polypeptide

<400> 298

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

145					150					155					160
Arg	Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn
				165					170						175
Ser	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp
			180					185							190
Val	Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser
			195				200					205			
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu
	210					215				220					
Phe	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr
225					230					235					240
Cys	Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
				245					250						255
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys
			260					265						270	
Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys
		275					280					285			
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu
	290					295					300				
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
305					310					315					320
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr
				325					330					335	
Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
			340					345					350		
Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro
		355					360					365			
Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
	370					375					380				
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
385					390					395					400
Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr
				405					410					415	
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
			420					425					430		
Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His
		435					440					445			
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
	450					455					460				
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
465					470					475					480
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met
				485					490					495	
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
		500						505					510		
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
		515					520					525			
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu
	530					535					540				
Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val

545		550		555		560									
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln
				565					570						575
Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys							
			580					585							

<210> 299

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-80 heavy chain fusion polypeptide

<400> 299

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

Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala
	275						280					285			
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly
	290					295					300				
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly
305					310					315					320
Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys
				325					330					335	
Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys
		340						345				350			
Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
	355						360					365			
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
	370					375					380				
Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp
385					390					395					400
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
			405						410					415	
Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
			420					425						430	
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
	435					440						445			
Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
	450					455					460				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu
465					470					475					480
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
			485						490					495	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
		500						505					510		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
	515						520					525			
Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn
	530					535					540				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
545					550					555					560
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys						
			565					570							

<210> 300

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-94 heavy chain fusion polypeptide

<400> 300

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

1				5				10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His	
			20					25					30			
Cys	Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val	
		35					40					45				
Ser	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	
	50				55						60					
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	
65					70					75					80	
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
				85				90						95		
Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Gln	Thr	Arg	Gly	
			100					105					110			
Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
		115					120					125				
Ser	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	
	130				135						140					
Pro	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	
145				150						155					160	
Arg	Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	
				165				170						175		
Ser	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
		180					185						190			
Val	Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	
		195				200						205				
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	
	210					215				220						
Phe	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	
225				230						235					240	
Cys	Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
			245					250						255		
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	
		260					265						270			
Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
	275						280					285				
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
	290				295						300					
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
305				310						315					320	
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
			325					330						335		
Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
		340					345					350				
Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	
	355					360					365					
Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
	370				375						380					
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
385				390						395					400	
Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	

				405					410					415		
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
			420					425					430			
Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	
		435					440						445			
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	
	450					455					460					
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	
465					470					475					480	
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	
				485					490					495		
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
		500						505					510			
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
	515						520					525				
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
	530					535					540					
Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	
545					550					555					560	
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
				565					570					575		
Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys								
		580						585								

<210> 301

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-95 heavy chain fusion polypeptide

<400> 301

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

Ser	Pro	Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro
130						135					140				
Gly	Arg	Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser
145					150					155					160
Asn	Ser	Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
				165					170					175	
Trp	Val	Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp
			180					185					190		
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr
		195				200					205				
Leu	Phe	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
		210				215					220				
Tyr	Cys	Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
225					230					235					240
Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro
					245				250					255	
Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val
			260					265					270		
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala
		275					280					285			
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly
	290					295					300				
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly
305					310					315					320
Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys
				325					330					335	
Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys
			340					345					350		
Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro
		355					360					365			
Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys
					375						380				
Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp
385					390					395					400
Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu
			405						410					415	
Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu
			420					425					430		
His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn
		435				440					445				
Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly
		450				455					460				
Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu
465					470					475					480
Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr
			485						490					495	
Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn
			500					505					510		
Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe
		515					520					525			

Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn
530						535					540				
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr
545					550					555					560
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys						
				565					570						

<210> 302

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-83 heavy chain fusion polypeptide

<400> 302

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

<400> 303

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	
1				5				10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His	
			20					25					30			
Cys	Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val	
		35				40						45				
Ser	Thr	Ile	Asp	Ser	Asp	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	
	50				55					60						
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	
65				70				75							80	
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
			85					90						95		
Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Asn	Thr	Arg	Gly	
			100					105						110		
Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
		115					120					125				
Ser	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	
	130					135					140					
Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
145				150						155					160	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	
			165					170						175		
Ser	Trp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	
		180					185						190			
Val	Ala	Trp	Ile	Ser	Pro	Tyr	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	
		195					200					205				
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	
	210					215					220					
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	
225				230						235					240	
Cys	Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	
			245					250						255		
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
		260					265						270			
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
	275					280						285				
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
	290					295					300					
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
305				310						315					320	
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
			325					330						335		
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
		340					345						350			
Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
	355					360						365				
Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
	370					375					380					

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 385 390 395 400
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 405 410 415
 Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 420 425 430
 Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val
 435 440 445
 Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 450 455 460
 Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 465 470 475 480
 Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 485 490 495
 Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 500 505 510
 Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 515 520 525
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 530 535 540
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys
 545 550 555 560
 Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 565 570 575
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
 580 585 590
 Lys

<210> 304

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-85 heavy chain fusion polypeptide

<400> 304

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

				85				90					95			
Ala	Gly	Lys	Trp	Gly	Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	
			100					105					110			
Val	Ser	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	
		115					120					125				
Ser	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	
	130					135					140					
Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	
145				150						155					160	
Asp	Ser	Trp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	
			165					170						175		
Trp	Val	Ala	Trp	Ile	Ser	Pro	Tyr	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	
		180						185					190			
Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	
	195						200					205				
Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	
	210					215					220					
Tyr	Cys	Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	
225					230					235					240	
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	
			245					250						255		
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	
		260					265						270			
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	
	275					280						285				
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	
	290					295					300					
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
305					310					315					320	
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
			325					330					335			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	
		340						345					350			
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	
	355						360					365				
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	
	370					375					380					
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	
385					390					395					400	
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	
			405					410					415			
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	
		420						425					430			
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	
		435					440					445				
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	
	450					455					460					
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	
465					470					475					480	
Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	

				485					490					495			
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp		
			500					505					510				
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val		
		515					520					525					
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp		
	530					535					540						
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His		
545				550						555					560		
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro		
			565					570						575			

Gly Lys

<210> 305

<211> 593

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-92 heavy chain fusion polypeptide

<400> 305

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

[illegible]

<210> 306
 <211> 578
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCP-93 heavy chain fusion polypeptide

<400> 306
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Pro Ser Val Asn
 20 25 30
 Tyr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Glu Val
 35 40 45
 Ser Ser Ile Tyr Pro Thr Gly Gly Thr Phe Tyr Thr Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Ala Gly Lys Tyr Gly Thr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110
 Val Ser Ser Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro
 115 120 125
 Ser Pro Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro
 130 135 140
 Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
 145 150 155 160
 Asp Ser Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 165 170 175
 Trp Val Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp
 180 185 190
 Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr
 195 200 205
 Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
 210 215 220
 Tyr Cys Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln
 225 230 235 240
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 245 250 255
 Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
 260 265 270
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 275 280 285
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 290 295 300
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro

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

<210> 307

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> mutated human IgG1 (hIgG1) hinge

<400> 307

Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro
1				5					10					15

<210> 308
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PD1BMmin heavy chain

<400> 308
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Val Phe Ser Arg Tyr
 20 25 30
 Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Phe Ile Ser Gly Gly Gly Ser Asn Thr Tyr Tyr Pro Asp Thr Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ile Ser Pro Tyr Tyr Tyr Ala Met Glu Tyr Trp Gly Gln Gly Thr Thr
 100 105 110
 Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
 115 120 125
 Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
 130 135 140
 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 145 150 155 160
 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 165 170 175
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
 180 185 190
 Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
 195 200 205
 Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
 210 215 220
 Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
 225 230 235 240
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 245 250 255
 Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
 260 265 270
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 275 280 285
 Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 290 295 300
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 305 310 315 320
 Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala

				325					330					335			
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln		
			340					345					350				
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly		
		355					360					365					
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro		
	370					375					380						
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser		
385					390					395					400		
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu		
			405					410						415			
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His		
		420						425					430				
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys						
		435					440										

<210> 309

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> PD1BMmin light chain

<400> 309

Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Val	Ser	Ala	Ser	Val	Gly		
1				5				10						15			
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Asp	Thr	Ala		
		20						25				30					
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile		
		35				40						45					
Tyr	Trp	Ala	Ser	Thr	Arg	His	Thr	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly		
	50				55					60							
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro		
65				70						75				80			
Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Ser	Thr	Phe	Pro	Trp		
			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						
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> 310
 <211> 574
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCP-100 heavy chain fusion polypeptide

<400> 310

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

	275		280		285										
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
	290					295					300				
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
305					310					315					320
Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro
			325						330					335	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro
		340						345					350		
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe
	355						360					365			
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
	370					375					380				
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val
385					390					395					400
Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
			405						410					415	
Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
			420					425					430		
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
	435					440						445			
Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser
	450					455					460				
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
465					470					475					480
Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
			485						490					495	
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
		500						505					510		
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
	515						520					525			
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
	530					535					540				
Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
545					550					555					560
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys		
			565						570						

<210> 311

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-101 heavy chain fusion polypeptide

<400> 311

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

Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His
			20					25					30		
Cys	Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val
		35					40					45			
Ser	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys
	50				55						60				
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu
65				70						75				80	
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
			85					90					95		
Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Gln	Thr	Arg	Gly
			100					105					110		
Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
		115					120					125			
Ser	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser
	130				135						140				
Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
145				150						155				160	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser	Arg
			165					170					175		
Tyr	Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp
		180					185						190		
Val	Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp	Thr
		195					200					205			
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu
	210					215					220				
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr
225				230						235				240	
Cys	Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr
			245					250					255		
Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
		260					265						270		
Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly
		275					280					285			
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
	290					295					300				
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
305				310						315				320	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
			325					330					335		
Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser
		340						345					350		
Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys
	355					360						365			
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
	370					375					380				
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
385				390						395				400	
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln
			405						410					415	

Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
			420					425					430		
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
		435					440					445			
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
	450					455					460				
Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys
465				470						475					480
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
			485						490					495	
Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
			500					505					510		
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
		515					520					525			
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
	530					535					540				
Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
545					550					555					560
Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
				565					570					575	
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys			
			580					585							

<210> 312

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-103 heavy chain fusion polypeptide

<400> 312

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

130		135		140											
Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser
145					150					155					160
Arg	Tyr	Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
				165					170						175
Trp	Val	Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp
			180					185					190		
Thr	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr
		195					200				205				
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
	210					215				220					
Tyr	Cys	Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly
225					230					235					240
Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
				245					250						255
Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu
			260					265					270		
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp
		275					280					285			
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
	290					295					300				
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
305					310					315					320
Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro
				325					330					335	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro
			340					345					350		
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe
		355					360					365			
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
	370					375					380				
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val
385					390					395					400
Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
				405					410					415	
Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
			420					425					430		
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
		435				440						445			
Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser
	450					455					460				
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro
465					470					475					480
Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
				485					490					495	
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
			500					505					510		
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
		515					520					525			
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp

530		535		540	
Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His					
545		550		555	560
Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys					
	565		570		

<210> 313
 <211> 588
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCP-104 heavy chain fusion polypeptide

<400> 313

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

Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
		275					280					285			
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
		290				295					300				
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
305					310					315					320
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
				325					330					335	
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
			340					345					350		
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
		355					360					365			
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
		370				375					380				
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
385					390					395					400
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
				405					410					415	
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
			420					425					430		
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
		435					440					445			
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
		450				455				460					
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
465					470					475					480
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
				485					490					495	
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		500						505					510		
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
		515					520					525			
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
		530				535					540				
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
545					550					555					560
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
				565					570					575	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys				
			580					585							

<210> 314

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-105 heavy chain fusion polypeptide

<400> 314

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5				10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
			20					25						30	
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val
		35					40					45			
Ala	Ser	His	Ser	Phe	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
			100					105						110	
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
		115					120					125			
Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro
	130					135					140				
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
145					150					155					160
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser	Arg	Tyr
			165						170					175	
Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
			180					185					190		
Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
		195					200					205			
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
	210					215					220				
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
225					230					235					240
Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			245						250					255	
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
			260					265					270		
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
		275					280					285			
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
	290					295					300				
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
305					310					315					320
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
			325						330					335	
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
		340						345					350		
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
		355					360					365			
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
	370					375					380				
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val

385					390					395				400	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
				405					410					415	
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
			420					425					430		
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
		435					440					445			
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
	450					455				460					
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
465					470				475					480	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
				485					490					495	
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
			500					505					510		
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
		515					520					525			
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
	530					535					540				
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
545					550				555					560	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
				565				570						575	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys				
			580					585							

<210> 315

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-106 heavy chain fusion polypeptide

<400> 315

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

Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	115	120	125
Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	130	135	140
Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	145	150	155
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser	Arg	Tyr	165	170	175
Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	180	185	190
Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp	Thr	Val	195	200	205
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	210	215	220
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	225	230	235
Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	245	250	255
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	260	265	270
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	275	280	285
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	290	295	300
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	305	310	315
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	325	330	335
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	340	345	350
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	355	360	365
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	370	375	380
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	385	390	395
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	405	410	415
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	420	425	430
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	435	440	445
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	450	455	460
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	465	470	475
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	485	490	495
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	500	505	510

Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
		515					520					525			
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
		530				535					540				
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
545					550					555					560
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
				565					570					575	
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys				
			580					585							

<210> 316

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-107 heavy chain fusion polypeptide

<400> 316

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

225					230					235				240
Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr
				245					250					255
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
			260					265					270	Leu
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly
		275					280				285		Cys	
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
	290					295				300			Ser	
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
305					310				315				320	Ser
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
				325				330					335	
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser
		340					345					350	Asn	
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys
	355					360					365		Pro	
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
	370				375					380			Phe	
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
385				390					395				400	Val
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln
			405					410					415	Phe
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
		420					425				430		Pro	
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
	435						440				445		Thr	
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
	450					455			460				Val	
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys
465				470					475				480	Ala
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
			485					490					495	Gln
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
		500						505				510	Gly	
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
	515					520					525		Pro	
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
	530				535				540				Ser	
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
545				550					555				560	Glu
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
			565					570					575	His
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys			
		580					585							

<210> 317
 <211> 589
 <212> PRT

<213> Artificial Sequence

<220>

<223> BCP-108 heavy chain fusion polypeptide

<400> 317

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5				10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His
			20					25					30		
Cys	Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val
		35					40					45			
Ser	Thr	Ile	Asp	Ser	Asp	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys
	50					55					60				
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu
65					70					75					80
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Asn	Thr	Arg	Gly
			100					105						110	
Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
		115					120					125			
Ser	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser
	130					135					140				
Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
145					150					155					160
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser	Arg
			165						170					175	
Tyr	Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp
		180						185					190		
Val	Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp	Thr
		195					200					205			
Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu
	210					215					220				
Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr
225					230					235					240
Cys	Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr
			245						250					255	
Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
			260					265					270		
Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly
		275					280					285			
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
	290					295					300				
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
305					310					315					320
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
				325					330					335	
Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser
			340					345					350		

Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys
		355					360					365			
Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu
		370				375					380				
Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
385					390					395					400
Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln
			405						410					415	
Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
		420						425					430		
Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
		435					440					445			
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
		450			455						460				
Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys
465					470					475					480
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
			485						490					495	
Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
			500					505					510		
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
		515					520					525			
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
		530				535					540				
Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
545					550					555					560
Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
			565						570					575	
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys			
			580					585							

<210> 318

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-109 heavy chain fusion polypeptide

<400> 318

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

65				70				75					80		
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85				90						95	
Ala	Gly	Lys	Trp	Gly	Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
			100					105					110		
Val	Ser	Ser	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro
		115					120					125			
Ser	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro
	130					135					140				
Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser
145				150						155				160	
Arg	Tyr	Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu
			165					170						175	
Trp	Val	Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp
			180					185					190		
Thr	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr
		195					200					205			
Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr
	210					215					220				
Tyr	Cys	Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly
225				230						235				240	
Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
			245						250					255	
Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu
			260					265					270		
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp
		275					280					285			
Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu
	290					295					300				
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
305				310						315				320	
Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro
			325						330					335	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro
		340					345						350		
Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe
	355						360					365			
Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro
	370					375					380				
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val
385				390						395				400	
Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr
			405						410					415	
Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val
			420					425					430		
Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys
	435					440						445			
Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser
	450					455					460				
Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro

465					470					475					480
Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val
				485					490					495	
Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly
			500					505					510		
Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp
		515					520					525			
Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp
	530					535				540					
Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His
545					550				555					560	
Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys		
				565					570						

<210> 319

<211> 591

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-73C heavy chain fusion polypeptide

<400> 319

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

Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
210						215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245					250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
	290					295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
			340					345					350		
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
	370					375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
			405						410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu
	435						440					445			
Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val
	450					455					460				
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu
465					470					475					480
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met
			485						490					495	
Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Phe	Val	Ala	Ser
			500					505					510		
His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly
		515					520					525			
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
	530					535					540				
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala
545					550					555					560
Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg
			565						570					575	
Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	
			580					585					590		

<210> 320
 <211> 592
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCP-74C heavy chain fusion polypeptide

<400> 320

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys	Lys	Pro	Gly	Ala	1	5	10	15
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	20	25	30	
Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	35	40	45	
Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe	50	55	60	
Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr	65	70	75	80
Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	100	105	110	
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	115	120	125	
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	130	135	140	
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	145	150	155	160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	165	170	175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	180	185	190	
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	195	200	205	
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	210	215	220	
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	225	230	235	240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	245	250	255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	260	265	270	
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	275	280	285	
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	290	295	300	
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	305	310	315	320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile				

				325					330					335			
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro		
			340					345					350				
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu		
		355					360					365					
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn		
	370					375					380						
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser		
385				390						395					400		
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg		
			405					410					415				
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu		
			420					425					430				
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu		
	435					440						445					
Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val		
	450				455					460							
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu		
465				470					475						480		
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His	Cys	Leu		
			485					490						495			
Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val	Ser	Thr		
		500					505					510					
Ile	Asp	Ser	Asp	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg		
	515					520					525						
Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met		
	530				535						540						
Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile	Gly		
545				550					555					560			
Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Asn	Thr	Arg	Gly	Ala	Glu		
			565				570						575				
His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
		580					585						590				

<210> 321

<211> 577

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-75C heavy chain fusion polypeptide

<400> 321

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

Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe
50						55				60					
Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr
65					70				75						80
Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			115					120				125			
Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala
						135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys
		195				200						205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro
		210				215					220				
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val
225					230					235					240
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr
				245					250					255	
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu
			260					265					270		
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys
		275					280					285			
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser
		290				295					300				
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys
305					310					315					320
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile
				325					330					335	
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro
		340						345					350		
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu
		355					360					365			
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn
		370				375					380				
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser
385					390					395					400
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg
				405					410					415	
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu
			420					425					430		
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu
		435					440					445			

Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val
450						455					460				
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu
465					470					475					480
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Asp	Ser	Pro	Ser	Val	Asn	Tyr	Met
				485					490					495	
Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Glu	Val	Ser	Ser
			500					505					510		
Ile	Tyr	Pro	Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly	Arg
		515					520					525			
Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met
	530					535					540				
Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Gly
545					550					555					560
Lys	Trp	Gly	Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
				565					570					575	

Ser

<210> 322

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-90C heavy chain fusion polypeptide

<400> 322

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

				165				170					175			
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	
			180					185					190			
Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	
		195					200					205				
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	
	210					215					220					
Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	
225				230						235					240	
Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	
			245					250						255		
Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	
			260					265					270			
Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	
		275					280					285				
Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	
	290					295					300					
Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	
305				310						315					320	
Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	
			325					330						335		
Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	
		340						345					350			
Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	
		355					360					365				
Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	
	370					375					380					
Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	
385				390						395					400	
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	
			405					410						415		
Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	
			420					425					430			
His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	
		435					440					445				
Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	
	450					455					460					
Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	
465				470						475					480	
Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His	Cys	Leu	
			485					490						495		
Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val	Ser	Thr	
		500					505						510			
Ile	Ser	Ser	Gly	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	
		515					520					525				
Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	
	530					535					540					
Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile	Gly	
545				550						555					560	
Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Gln	Thr	Arg	Gly	Ala	Glu	

				565					570					575			
His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
			580					585					590				

<210> 323
 <211> 577
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BCP-91C heavy chain fusion polypeptide

<400> 323

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

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

Ser

<210> 324

<211> 583

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-78C heavy chain fusion polypeptide

<400> 324

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1				5				10					15			
Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	Ser	
			20					25					30			
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	
		35					40					45				
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe	
65					70				75						80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
			100					105					110			
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	
	115						120					125				
Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	
	130					135					140					
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	
145					150					155					160	
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	
			165						170					175		
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	
		180						185					190			
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	
	195						200					205				
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	
	210					215					220					
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	
225				230					235						240	
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	
			245						250					255		
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	
		260						265					270			
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	
	275						280					285				
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	
	290					295					300					
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	
305				310					315						320	
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	
			325						330					335		
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	
		340						345					350			
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	
	355						360					365				
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	
	370					375					380					
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	
385					390					395					400	
Ser	Arg	Leu	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	

				405					410					415		
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	
			420					425					430			
Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	
		435					440					445				
Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	
	450					455					460					
Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	
465				470						475					480	
Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	
			485					490						495		
Lys	Gly	Arg	Glu	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	
		500						505					510			
Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	
		515					520					525				
Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	
	530					535					540					
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	
545					550					555					560	
Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	
			565					570						575		
Thr	Leu	Val	Thr	Val	Ser	Ser										
			580													

<210> 325

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-79C heavy chain fusion polypeptide

<400> 325

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

Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
130						135					140				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
145					150					155					160
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
				165					170					175	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys
			180					185					190		
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
		195				200					205				
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
	210					215				220					
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
225				230					235						240
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
				245					250					255	
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
			260					265					270		
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
		275					280					285			
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	290					295				300					
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
305				310					315						320
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
				325					330					335	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
			340					345					350		
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
	355						360					365			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
	370					375					380				
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
385					390					395					400
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe
				405					410					415	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
			420					425					430		
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr
		435				440						445			
His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly
	450					455					460				
Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser
465					470					475					480
Gly	Tyr	Thr	Tyr	Ser	Arg	His	Cys	Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro
				485					490					495	
Gly	Lys	Gly	Arg	Glu	Ala	Val	Ser	Thr	Ile	Asp	Ser	Asp	Gly	Ser	Thr
			500					505					510		
Ser	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn
	515						520					525			

Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp
530						535					540				
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser
545					550					555					560
Gly	Ala	Pro	Asn	Thr	Arg	Gly	Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly
			565						570					575	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
			580					585							

<210> 326

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-80C heavy chain fusion polypeptide

<400> 326

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

				245				250					255				
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val		
			260					265					270				
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln		
		275					280					285					
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln		
	290					295					300						
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly		
305				310					315						320		
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro		
			325					330						335			
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr		
		340					345						350				
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser		
	355					360					365						
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr		
	370					375				380							
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr		
385				390						395					400		
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe		
			405					410						415			
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys		
		420					425					430					
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr		
	435					440					445						
His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly		
	450				455					460							
Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser		
465				470					475						480		
Gly	Asp	Ser	Pro	Ser	Val	Asn	Tyr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro		
			485					490						495			
Gly	Lys	Gly	Arg	Glu	Glu	Val	Ser	Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr		
		500					505						510				
Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn		
	515					520						525					
Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp		
	530					535					540						
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Gly	Lys	Trp	Gly	Thr	Asp	Tyr	Trp		
545				550						555					560		
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser								
			565					570									

<210> 327

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-94C heavy chain fusion polypeptide

<400> 327

Gln	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg
1				5				10						15	
Ser	Leu	Arg	Leu	Asp	Cys	Lys	Ala	Ser	Gly	Ile	Thr	Phe	Ser	Asn	Ser
			20					25					30		
Gly	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ala	Val	Ile	Trp	Tyr	Asp	Gly	Ser	Lys	Arg	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Phe
65					70				75						80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Thr	Asn	Asp	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
			100					105						110	
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser
		115					120					125			
Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
	130					135					140				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
145					150					155					160
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
			165						170					175	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys
			180					185					190		
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
			195				200					205			
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
	210					215				220					
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
225				230						235					240
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
				245					250					255	
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
			260					265					270		
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	275					280						285			
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	290					295					300				
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
305				310						315					320
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
			325						330					335	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
			340					345					350		
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
		355					360					365			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
	370					375					380				

Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
385					390					395					400
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe
				405					410					415	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
			420					425						430	
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr
		435					440						445		
His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly
	450					455					460				
Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser
465					470					475					480
Gly	Tyr	Thr	Tyr	Ser	Arg	His	Cys	Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro
				485					490					495	
Gly	Lys	Gly	Arg	Glu	Ala	Val	Ser	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Thr
			500					505					510		
Ser	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn
		515					520						525		
Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp
	530					535					540				
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser
545					550					555					560
Gly	Ala	Pro	Gln	Thr	Arg	Gly	Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly
				565					570					575	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
			580					585							

<210> 328

<211> 570

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-95C heavy chain fusion polypeptide

<400> 328

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

			100				105				110				
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser
		115					120					125			
Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp
	130					135					140				
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr
145					150					155					160
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr
			165						170					175	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys
		180						185					190		
Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
		195					200					205			
Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala
	210					215					220				
Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro
225				230						235					240
Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val
			245						250					255	
Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val
		260						265					270		
Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln
	275					280						285			
Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln
	290					295					300				
Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly
305				310						315					320
Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro
			325						330					335	
Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr
		340						345					350		
Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser
	355						360					365			
Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr
	370					375					380				
Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr
385					390					395					400
Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe
		405							410					415	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys
		420						425					430		
Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr
		435					440					445			
His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly
	450					455					460				
Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser
465					470					475					480
Gly	Phe	Ser	Pro	Ser	Val	Asn	Tyr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro
			485						490					495	
Gly	Lys	Gly	Arg	Glu	Glu	Val	Ser	Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr

			500					505					510			
Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	
			515					520					525			
Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	
			530					535					540			
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Gly	Lys	Tyr	Gly	Thr	Asp	Tyr	Trp	
545					550					555					560	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser							
				565					570							

<210> 329

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-100C heavy chain fusion polypeptide

<400> 329

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

Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				245					250					255	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
			260					265					270		
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
		275					280					285			
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
	290					295					300				
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305				310						315					320
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
			325						330					335	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
			340					345					350		
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
	355						360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
	370					375					380				
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385					390					395					400
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
			405						410					415	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
		420						425					430		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser
		435					440					445			
Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val
	450					455					460				
Glu	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	Ser	Pro	Ser	Val	Asn	Tyr	Met	Gly	Trp	Phe
				485					490					495	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Glu	Val	Ser	Ser	Ile	Tyr	Pro
			500					505					510		
Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
	515						520					525			
Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu
	530					535					540				
Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Gly	Lys	Tyr	Gly
545					550					555					560
Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
				565					570						

<210> 330

<211> 589

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-101C heavy chain fusion polypeptide

<400> 330

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser	Arg	Tyr
			20					25					30		
Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
		115					120					125			
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
	130					135					140				
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
145					150					155				160	
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
				165					170					175	
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
			180					185					190		
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
		195					200					205			
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
	210					215					220				
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
225					230					235				240	
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				245					250					255	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
			260					265					270		
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
		275					280					285			
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
	290					295					300				
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305					310					315				320	
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
				325					330					335	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
			340					345					350		
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		355					360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro

370		375		380
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser				
385		390		400
Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu				
	405		410	415
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His				
	420		425	430
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys Glu Pro Lys Ser				
	435		440	445
Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Glu Val Gln Leu Val				
	450		455	460
Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser				
465		470		480
Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His Cys Leu Gly Trp Phe				
	485		490	495
Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val Ser Thr Ile Ser Ser				
	500		505	510
Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile				
	515		520	525
Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu				
	530		535	540
Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ile Gly Pro Asn Pro				
545		550		560
Arg Tyr Cys Ser Gly Ala Pro Gln Thr Arg Gly Ala Glu His Tyr Phe				
	565		570	575
Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser				
	580		585	

<210> 331

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-103C heavy chain fusion polypeptide

<400> 331

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

Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
		115					120					125			
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
		130				135					140				
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
145					150					155					160
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
				165					170					175	
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
			180					185					190		
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
		195					200					205			
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
		210				215					220				
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
225					230					235					240
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				245					250					255	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
			260					265					270		
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
		275					280				285				
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
		290				295					300				
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305					310					315					320
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
				325					330					335	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
			340					345					350		
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		355					360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
		370				375					380				
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385					390					395					400
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
				405					410					415	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
			420					425					430		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser
		435					440					445			
Ser	Asp	Lys	Thr	His	Thr	Ser	Pro</								

Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Glu	Val	Ser	Ser	Ile	Tyr	Pro
			500					505					510		
Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
		515					520					525			
Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu
		530				535					540				
Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Gly	Lys	Tyr	Gly
545					550					555					560
Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
				565					570						

<210> 332

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-104C heavy chain fusion polypeptide

<400> 332

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

225					230					235				240
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu
				245					250					255
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln
			260					265						270
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys
		275					280					285		Pro
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
	290					295					300			Thr
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
305					310					315				320
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys
				325					330					335
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
			340					345					350	Gln
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
		355					360					365		Gly
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
	370					375					380			Pro
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
385					390					395				400
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
				405					410					415
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
		420					425					430		His
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys
		435				440						445		Ser
Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu
	450					455					460			Val
Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu
465					470					475				480
Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp
				485					490					495
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala	Ser	His	Ser
			500					505					510	Trp
Thr	Asp	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr
	515					520					525			
Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn
	530					535					540			Ser
Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala
545					550					555				560
Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr
				565					570					575
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
			580					585						

<210> 333

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-105C heavy chain fusion polypeptide

<400> 333

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser	Arg	Tyr
			20					25					30		
Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70				75					80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
	115						120					125			
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
	130					135					140				
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
145					150				155					160	
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
				165					170					175	
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
			180					185					190		
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
	195						200					205			
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
	210					215					220				
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
225					230					235				240	
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				245					250					255	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
			260					265					270		
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
		275					280					285			
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
	290					295					300				
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305					310					315				320	
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
				325					330					335	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
			340					345					350		

Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		355					360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
		370				375					380				
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385					390					395					400
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
				405					410					415	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
			420					425					430		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser
		435					440					445			
Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val
		450				455					460				
Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser
465					470					475					480
Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe
				485					490					495	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Phe	Val	Ala	Ser	His	Ser	Phe
			500					505					510		
Thr	Asp	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	
		515				520					525				
Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser
		530				535					540				
Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg
545					550					555					560
Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp
				565					570					575	
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
			580					585							

<210> 334

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-106C heavy chain fusion polypeptide

<400> 334

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

65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
		115					120					125			
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
	130					135					140				
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
145					150					155				160	
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
			165					170					175		
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
		180						185				190			
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
	195					200					205				
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
	210				215						220				
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
225				230						235				240	
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
			245					250					255		
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
		260			265							270			
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
	275				280						285				
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
	290				295					300					
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305				310					315					320	
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
			325					330					335		
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
		340					345					350			
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
	355				360						365				
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
	370				375					380					
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385				390					395					400	
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
			405					410					415		
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
		420					425					430			
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser
	435					440					445				
Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val
	450				455					460					
Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser

465					470					475				480	
Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe
				485					490					495	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Phe	Val	Ala	Ser	His	Ser	Trp
			500					505					510		
Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr
	515						520					525			
Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser
	530					535					540				
Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg
545					550					555					560
Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp
				565					570					575	
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
			580					585							

<210> 335

<211> 588

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-107C heavy chain fusion polypeptide

<400> 335

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

Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
	195						200					205			
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
	210					215					220				
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
225					230					235					240
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				245					250					255	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
			260					265					270		
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
		275					280					285			
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
	290					295					300				
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305				310						315					320
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
				325					330					335	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
			340					345						350	
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		355					360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
	370					375					380				
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385					390					395					400
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
				405					410					415	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
			420					425					430		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser
		435					440					445			
Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val
	450					455					460				
Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro	Gly	Arg	Ser	Leu	Arg	Leu	Ser
465					470					475					480
Cys	Ala	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe
				485					490					495	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Phe	Val	Ala	Ser	His	Ser	Phe
			500					505					510		
Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr
		515					520					525			
Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser
	530					535					540				
Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg
545					550					555					560
Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp
				565					570					575	
Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser				
			580					585							

<210> 336
<211> 589
<212> PRT
<213> Artificial Sequence

<220>
<223> BCP-108C heavy chain fusion polypeptide

<400> 336
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Val Phe Ser Arg Tyr
20 25 30
Asp Met Ala Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Phe Ile Ser Gly Gly Gly Ser Asn Thr Tyr Tyr Pro Asp Thr Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ile Ser Pro Tyr Tyr Tyr Ala Met Glu Tyr Trp Gly Gln Gly Thr Thr
100 105 110
Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125
Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140
Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160
Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190
Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205
Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
210 215 220
Pro Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255
Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285
Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val

305					310					315					320
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
				325					330						335
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
			340					345						350	
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		355					360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
	370					375				380					
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser
385					390					395					400
Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu
				405					410					415	
Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His
		420						425					430		
Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser
		435					440					445			
Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val
	450					455					460				
Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser
465					470					475					480
Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His	Cys	Leu	Gly	Trp	Phe
				485					490					495	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val	Ser	Thr	Ile	Asp	Ser
			500					505					510		
Asp	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
		515					520					525			
Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu
	530					535					540				
Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile	Gly	Pro	Asn	Pro
545					550					555					560
Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Asn	Thr	Arg	Gly	Ala	Glu	His	Tyr	Phe
				565					570					575	
Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser			
			580					585							

<210> 337

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-109C heavy chain fusion polypeptide

<400> 337

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1				5				10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Val	Phe	Ser	Arg	Tyr
			20					25					30		

Asp	Met	Ala	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Phe	Ile	Ser	Gly	Gly	Gly	Ser	Asn	Thr	Tyr	Tyr	Pro	Asp	Thr	Val
	50					55					60				
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
65					70					75					80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ile	Ser	Pro	Tyr	Tyr	Tyr	Ala	Met	Glu	Tyr	Trp	Gly	Gln	Gly	Thr	Thr
			100					105					110		
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu
		115					120					125			
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys
	130					135					140				
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser
145					150					155					160
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser
				165					170					175	
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser
			180					185					190		
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn
		195					200					205			
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro
	210					215					220				
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe
225					230					235					240
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val
				245					250					255	
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe
			260					265						270	
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro
		275					280					285			
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr
	290					295					300				
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val
305					310					315					320
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala
				325					330					335	
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln
			340					345					350		
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly
		355					360					365			
Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro
	370					375					380				
Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro							

Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys	Glu	Pro	Lys	Ser
		435					440					445			
Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu	Val	Gln	Leu	Val
	450					455					460				
Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser
465					470					475					480
Cys	Ala	Ala	Ser	Gly	Asp	Ser	Pro	Ser	Val	Asn	Tyr	Met	Gly	Trp	Phe
				485					490					495	
Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Glu	Val	Ser	Ser	Ile	Tyr	Pro
		500						505					510		
Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile
	515						520					525			
Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu
	530					535					540				
Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Gly	Lys	Trp	Gly
545					550					555					560
Thr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser		
			565						570						

<210> 338
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AS07189TKDVH21FY FR2

<400> 338
 Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Glu Val Ser
 1 5 10

<210> 339
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A34311VH2F53, A34311VH11F53 CDR2

<400> 339
 Ser His Ser Phe Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15
 Gly

<210> 340
 <211> 32

<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH21FY, A34311VH2, A34311VH2F53 FR3

<400> 340
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ala
20 25 30

<210> 341
<211> 115
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07189TKDVH21FY humanized sdAb

<400> 341
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Pro Ser Val Asn
20 25 30
Tyr Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Glu Val
35 40 45
Ser Ser Ile Tyr Pro Thr Gly Gly Thr Phe Tyr Thr Asp Ser Val Lys
50 55 60
Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
65 70 75 80
Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95
Ala Gly Lys Tyr Gly Thr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
100 105 110
Val Ser Ser
115

<210> 342
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> A34311VH2 humanized sdAb

<400> 342
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

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

Ser

<210> 343

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311VH2F53 humanized sdAb

<400> 343

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

Ser

<210> 344

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311VH11F53 humanized sdAb

<400> 344

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Arg Thr Ile Thr Thr Ile
 20          25          30
Thr Met Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Phe Val
 35          40          45
Ala Ser His Ser Phe Thr Asp Asn Asn Pro Tyr Tyr Ala Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65          70          75          80
Leu Gln Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys
 85          90          95
Ala Ala Thr Ala Arg Arg Ser Phe Val Gly Arg Gln Trp Tyr Thr Glu
100          105          110
Ala Arg Gln Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115          120          125
Ser
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<210> 345

<211> 592

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-83C heavy chain fusion polypeptide

<400> 345

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Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser
 20          25          30
Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35          40          45
Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50          55          60
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85          90          95
Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr
100          105          110
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Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
		115					120					125			
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
		130					135					140			
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
145						150					155				160
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
					165					170				175	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
					180								190		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
							200					205			
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
						215						220			
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
225						230						235			240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
					245						250				255
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
					260				265				270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
							280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
						295						300			
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305						310					315				320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
					325						330				335
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
					340				345				350		
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
					355			360				365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
						375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385						390					395				400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
					405					410				415	
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
					420				425				430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
							440					445			
Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu
						455					460				
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Val	Val	Gln	Pro			

Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys
		515					520					525			
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu
		530				535					540				
Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
545					550					555					560
Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala
			565					570						575	
Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
			580					585					590		

<210> 346

<211> 593

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-84C heavy chain fusion polypeptide

<400> 346

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

225					230				235				240		
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
			260					265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280				285				
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
	290				295					300					
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305				310					315					320	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
			325					330					335		
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
		340					345					350			
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
	355					360					365				
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370				375				380						
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385				390					395					400	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
			405					410					415		
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
		420			425						430				
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
	435				440				445						
Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu
	450				455				460						
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser
465				470					475					480	
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Thr	Tyr	Ser	Arg	His	Cys
			485					490					495		
Leu	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Ala	Val	Ser
		500						505				510			
Thr	Ile	Asp	Ser	Asp	Gly	Ser	Thr	Ser	Tyr	Ala	Asp	Ser	Val	Lys	Gly
	515				520						525				
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
	530				535				540						
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ile
545				550					555					560	
Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Asn	Thr	Arg	Gly	Ala
			565					570					575		
Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser
			580				585					590			
Ser															

<211> 578
<212> PRT
<213> Artificial Sequence

<220>
<223> BCP-85C heavy chain fusion polypeptide

<400> 347

Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
1			5					10					15		
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Asp	Ser
		20					25					30			
Trp	Ile	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35					40					45				
Ala	Trp	Ile	Ser	Pro	Tyr	Gly	Gly	Ser	Thr	Tyr	Tyr	Ala	Asp	Ser	Val
	50				55					60					
Lys	Gly	Arg	Phe	Thr	Ile	Ser	Ala	Asp	Thr	Ser	Lys	Asn	Thr	Ala	Tyr
65				70				75						80	
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Arg	Arg	His	Trp	Pro	Gly	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
	100					105						110			
Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
	115					120					125				
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
	130				135						140				
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
145				150				155						160	
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
			165					170					175		
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
		180					185						190		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
	195					200						205			
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
	210				215						220				
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
225				230					235					240	
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
			245						250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
		260						265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
	275					280						285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
	290				295						300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305				310						315				320	
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
			325					330					335		

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

Ser Ser

<210> 348

<211> 593

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-92C heavy chain fusion polypeptide

<400> 348

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

50		55		60	
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr					
65		70		75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys					
	85		90		95
Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr					
	100		105		110
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro					
	115		120		125
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly					
	130		135		140
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn					
145		150		155	160
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln					
	165		170		175
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser					
	180		185		190
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser					
	195		200		205
Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr					
	210		215		220
His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser					
225		230		235	240
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg					
	245		250		255
Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro					
	260		265		270
Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala					
	275		280		285
Lys Thr Lys Pro Arg Glu Glu Gln Tyr Ala Ser Thr Tyr Arg Val Val					
	290		295		300
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr					
305		310		315	320
Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr					
	325		330		335
Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu					
	340		345		350
Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys					
	355		360		365
Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser					
	370		375		380
Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp					
385		390		395	400
Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser					
	405		410		415
Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala					
	420		425		430
Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys					
	435		440		445
Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Glu					

450		455		460
Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser				
465		470		480
Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His Cys				
	485		490	495
Leu Gly Trp Phe Arg Gln Ala Pro Gly Lys Gly Arg Glu Ala Val Ser				
	500		505	510
Thr Ile Ser Ser Gly Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys Gly				
	515		520	525
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln				
	530		535	540
Met Asn Ser Leu Arg Pro Glu Asp Thr Ala Val Tyr Tyr Cys Ala Ile				
	545		550	560
Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Gln Thr Arg Gly Ala				
	565		570	575
Glu His Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser				
	580		585	590
Ser				

<210> 349

<211> 578

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-93C heavy chain fusion polypeptide

<400> 349

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
1	5	10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Ser		
	20	25
Trp Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
	35	40
Ala Trp Ile Ser Pro Tyr Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val		
	50	55
Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr		
	65	70
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
	85	90
Ala Arg Arg His Trp Pro Gly Gly Phe Asp Tyr Trp Gly Gln Gly Thr		
	100	105
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro		
	115	120
Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly		
	130	135
Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn		
	145	150
		155
		160

Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
				165					170					175	
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
			180					185					190		
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
		195					200					205			
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
	210					215					220				
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
225					230					235					240
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
				245					250					255	
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
			260					265					270		
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
		275					280					285			
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Ala	Ser	Thr	Tyr	Arg	Val	Val
	290					295					300				
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
305					310					315					320
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
				325					330					335	
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
			340					345					350		
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
		355					360					365			
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
	370					375					380				
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
385					390					395					400
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
				405					410					415	
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
			420					425					430		
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
		435					440					445			
Glu	Pro	Lys	Ser	Ser	Asp	Lys	Thr	His	Thr	Ser	Pro	Pro	Ser	Pro	Glu
	450					455					460				
Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser
465					470					475					480
Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Pro	Ser	Val	Asn	Tyr
				485					490					495	
Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Arg	Glu	Glu	Val	Ser
			500					505					510		
Ser	Ile	Tyr	Pro	Thr	Gly	Gly	Thr	Phe	Tyr	Thr	Asp	Ser	Val	Lys	Gly
		515					520					525			
Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln
	530					535					540				
Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala
545					550					555					560

Gly Lys Tyr Gly Thr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
565 570 575
Ser Ser

<210> 350
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014 direct grafted, AS07189 direct grafted FR2

<400> 350
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
1 5 10

<210> 351
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014 direct grafted, AS07189 direct grafted FR3

<400> 351
Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
1 5 10 15
Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 352
<211> 130
<212> PRT
<213> Artificial Sequence

<220>
<223> AS07014 direct grafted humanized sdAb

<400> 352
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His
20 25 30
Cys Leu Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45
Ser Thr Ile Asp Ser Asp Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys

50		55		60											
Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu
65					70					75					80
Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala
				85					90					95	
Arg	Gly	Pro	Asn	Pro	Arg	Tyr	Cys	Ser	Gly	Ala	Pro	Asn	Thr	Arg	Gly
			100					105					110		
Ala	Glu	His	Tyr	Phe	Gly	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val
		115					120					125			
Ser	Ser														
	130														

<210> 353

<211> 115

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189 direct grafted humanized sdAb

<400> 353

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

<210> 354

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-16 light chain fusion polypeptide

<400> 354

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

1				5				10					15			
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	
			20					25					30			
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	
		35					40					45				
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	
	50					55					60					
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	
65				70					75					80		
Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85					90					95			
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	
			100					105					110			
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	
	115						120					125				
Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	
	130					135					140					
Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	
145				150					155					160		
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Lys	Gly	Val	Ser	Thr	Ser	
			165					170					175			
Gly	Tyr	Ser	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	
		180					185					190				
Arg	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Tyr	Leu	Glu	Ser	Gly	Val	Pro	Ala	
	195					200					205					
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	
	210				215				220							
Ser	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	His	Ser	Arg	
225				230					235					240		
Asp	Leu	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	
			245					250					255			
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	
		260					265						270			
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
	275					280					285					
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	
	290				295					300						
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
305				310				315						320		
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	
			325				330						335			
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	
		340					345					350				
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys							
	355					360										

<210> 355

<211> 362

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-17 light chain fusion polypeptide

<400> 355

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
1				5					10					15	
Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Lys	Gly	Val	Ser	Thr	Ser
			20					25					30		
Gly	Tyr	Ser	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro
		35					40					45			
Arg	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Tyr	Leu	Glu	Ser	Gly	Val	Pro	Ala
	50					55					60				
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser
65					70					75				80	
Ser	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	His	Ser	Arg
				85					90					95	
Asp	Leu	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg
			100					105						110	
Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln
		115					120						125		
Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr
	130					135					140				
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser
145					150					155				160	
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
			165						170					175	
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys
		180						185					190		
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro
	195						200					205			
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	Glu	Pro	Lys	Ser	Cys	Asp
	210					215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	Val	Lys	Leu	Glu	Glu	Ser
225					230					235				240	
Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu
			245						250					255	
Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln
			260					265					270		
Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp
		275					280					285			
Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser
	290					295					300				
Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu
305					310					315				320	
Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser
			325						330					335	
Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp
			340					345					350		

Gly Gln Gly Thr Gln Val Thr Val Ser Ser
 355 360

<210> 356

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-31 heavy chain fusion polypeptide

<400> 356

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

290	295	300													
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu
305					310					315					320
Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr
				325					330					335	
Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val
			340					345					350		
Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro
	355						360				365				
Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys
370					375					380					
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val
385					390					395					400
Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr
			405					410						415	
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu
		420					425						430		
Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His
	435					440					445				
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys
450					455					460					
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln
465				470					475						480
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met
			485					490						495	
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro
	500						505					510			
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn
	515					520					525				
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu
530					535				540						
Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val
545				550				555							560
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln
			565					570						575	
Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys							
	580						585								

<210> 357

<211> 356

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-31 light chain fusion polypeptide

<400> 357

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

Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
			20					25					30		
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val
		35					40					45			
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
		50				55					60				
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr
65				70					75					80	
Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
			100					105					110		
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser
		115					120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Glu	Ile	Val	Leu	Thr	Gln
	130					135					140				
Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser
145				150						155				160	
Cys	Arg	Ala	Ser	Lys	Gly	Val	Ser	Thr	Ser	Gly	Tyr	Ser	Tyr	Leu	His
			165					170					175		
Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Leu
		180					185						190		
Ala	Ser	Tyr	Leu	Glu	Ser	Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly
		195				200					205				
Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	Asp
	210					215					220				
Phe	Ala	Val	Tyr	Tyr	Cys	Gln	His	Ser	Arg	Asp	Leu	Pro	Leu	Thr	Phe
225					230					235					240
Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser
			245					250						255	
Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala
		260						265					270		
Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val
		275				280						285			
Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser
	290					295					300				
Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr
305					310					315					320
Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys
			325					330					335		
Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn
		340						345					350		
Arg	Gly	Glu	Cys												
		355													

<210> 358

<211> 723

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-32 heavy chain fusion polypeptide

<400> 358

Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu
1				5				10						15	
Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile
			20					25					30		
Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val
		35					40					45			
Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val
	50					55					60				
Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr
65				70					75					80	
Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85					90					95		
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu
			100					105					110		
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser
	115						120					125			
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gln	Val	Lys	Leu	Glu	Glu
	130					135					140				
Ser	Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys
145				150					155					160	
Glu	Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg
			165					170						175	
Gln	Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr
			180					185					190		
Asp	Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile
	195					200						205			
Ser	Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu
	210				215						220				
Glu	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg
225				230					235					240	
Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr
			245						250					255	
Trp	Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser
		260						265					270		
Gly	Gly	Gly	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys
	275					280						285			
Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr
	290					295					300				
Phe	Thr	Asn	Tyr	Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly
305				310					315					320	
Leu	Glu	Trp	Met	Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe
			325					330						335	
Asn	Glu	Lys	Phe	Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr
	340							345					350		
Thr	Thr	Ala	Tyr	Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala

		355				360				365					
Val	Tyr	Tyr	Cys	Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp
	370					375					380				
Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys
385					390					395					400
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu
			405						410						415
Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro
		420					425						430		
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr
	435					440					445				
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
	450					455					460				
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn
465					470					475					480
Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser
			485					490						495	
Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly
		500					505					510			
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
	515						520					525			
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln
	530				535					540					
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
545					550					555					560
His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr
			565					570						575	
Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly
		580					585					590			
Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile
	595					600					605				
Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val
	610					615				620					
Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser
625					630					635					640
Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu
			645					650						655	
Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro
		660					665					670			
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val
	675					680					685				
Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
	690				695					700					
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
705					710					715					720
Leu	Gly	Lys													

<211> 594
<212> PRT
<213> Artificial Sequence

<220>
<223> BCP-33 heavy chain fusion polypeptide

<400> 359

Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys	Lys	Pro	Gly	Ala
1				5					10					15	
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr
			20					25					30		
Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
			35				40					45			
Gly	Gly	Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe
	50					55				60					
Lys	Asn	Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr
65					70				75						80
Met	Glu	Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Arg	Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln
			100					105					110		
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
			115				120					125			
Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
	130					135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
			165						170					175	
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185					190		
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp
	210					215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	Val	Lys	Leu	Glu	Glu	Ser
225					230					235					240
Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu
			245						250					255	
Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln
			260					265					270		
Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp
		275					280					285			
Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser
	290					295					300				
Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu
305					310					315					320
Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser
				325					330					335	

Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp
			340					345					350		
Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp
		355					360					365			
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
	370					375					380				
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
385					390					395					400
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
			405						410					415	
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
		420						425					430		
Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg
	435						440					445			
Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys
	450					455					460				
Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu
465				470						475					480
Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr
			485					490						495	
Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu
		500					505						510		
Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp
	515					520					525				
Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
	530					535				540					
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp
545				550						555					560
Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His
			565					570						575	
Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro
		580						585					590		

Gly Lys

<210> 360

<211> 622

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-34

<400> 360

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

		35					40					45			
Arg 50	Leu	Ile	Tyr	Leu	Ala 55	Ser	Tyr	Leu	Glu 60	Ser	Gly	Val	Pro	Ala	
Arg 65	Phe	Ser	Gly	Ser	Gly 70	Ser	Gly	Thr	Asp 75	Phe	Thr	Leu	Thr	Ile	Ser 80
Ser	Leu	Glu	Pro	Glu 85	Asp	Phe	Ala	Val	Tyr 90	Tyr	Cys	Gln	His	Ser 95	Arg
Asp	Leu	Pro	Leu 100	Thr	Phe	Gly	Gly 105	Gly	Thr	Lys	Val	Glu	Ile 110	Lys	Gly
Gly	Gly	Gly 115	Ser	Gly	Gly	Gly 120	Gly	Ser	Gly	Gly	Gly 125	Gly	Ser	Gln	Val
Gln	Leu 130	Val	Gln	Ser	Gly 135	Val	Glu	Val	Lys	Lys 140	Pro	Gly	Ala	Ser	Val
Lys 145	Val	Ser	Cys	Lys	Ala 150	Ser	Gly	Tyr	Thr	Phe 155	Thr	Asn	Tyr	Tyr	Met 160
Tyr	Trp	Val	Arg	Gln 165	Ala	Pro	Gly	Gln	Gly 170	Leu	Glu	Trp	Met	Gly 175	Gly
Ile	Asn	Pro	Ser 180	Asn	Gly	Gly	Thr	Asn	Phe 185	Asn	Glu	Lys	Phe	Lys	Asn
Arg	Val 195	Thr	Leu	Thr	Thr	Asp 200	Ser	Thr	Thr	Thr 205	Ala	Tyr	Met	Glu	
Leu	Lys 210	Ser	Leu	Gln	Phe	Asp 215	Asp	Thr	Ala	Val 220	Tyr	Tyr	Cys	Ala	Arg
Arg 225	Asp	Tyr	Arg	Phe	Asp 230	Met	Gly	Phe	Asp 235	Tyr	Trp	Gly	Gln	Gly	Thr 240
Thr	Val	Thr	Val	Ser 245	Ser	Glu	Pro	Lys	Ser 250	Cys	Asp	Lys	Thr	His 255	Thr
Cys	Pro	Pro	Cys 260	Pro	Gln	Val	Lys	Leu	Glu 265	Glu	Ser	Gly	Gly	Gly 270	Leu
Val	Leu 275	Pro	Gly	Glu	Ser	Leu	Arg 280	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg
Thr	Ile 290	Thr	Thr	Ile	Thr	Met 295	Gly	Trp	Phe	Arg 300	Gln	Ala	Pro	Gly	Lys
Glu 305	Arg	Gln	Phe	Val	Ala 310	Ser	His	Ser	Trp	Thr 315	Asp	Asn	Asn	Pro	Tyr 320
Tyr	Ala	Asp	Ser	Val 325	Lys	Gly	Arg	Phe	Ile 330	Ile	Ser	Arg	Asp	Asn 335	Ala
Gly	Asn	Arg	Val 340	Tyr	Leu	Gln	Met	His 345	Ser	Leu	Glu	Pro	Glu	Asp	Thr
Ala	Val 355	Tyr	Tyr	Cys	Ala	Ala	Thr 360	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg
Gln	Trp 370	Tyr	Thr	Glu	Ala	Arg 375	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
Gln 385	Val	Thr	Val	Ser	Ser 390	Glu	Pro	Lys	Ser	Cys 395	Asp	Lys	Thr	His	Thr 400
Cys	Pro	Pro	Cys 405	Pro	Ala	Pro	Glu	Leu	Leu 410	Gly	Gly	Pro	Ser	Val	Phe
Leu	Phe	Pro	Pro 420	Lys	Pro	Lys	Asp	Thr 425	Leu	Met	Ile	Ser	Arg	Thr	Pro
Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val

Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala
130						135					140				
Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser
145					150					155					160
Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
				165					170						175
Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro
			180					185						190	
Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys
		195					200					205			
Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp
		210				215					220				
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	Val	Lys	Leu	Glu	Glu	Ser
225					230					235					240
Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu
				245					250						255
Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln
			260					265						270	
Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp
		275					280						285		
Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser
		290				295					300				
Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu
305					310					315					320
Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser
				325					330						335
Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp
			340					345					350		
Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro
		355					360						365		
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr
		370				375					380				
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr
385					390					395					400
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro
				405					410						415
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr
			420					425					430		
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn
		435					440					445			
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser
		450				455					460				
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
465					470					475					480
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
				485					490						495
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
			500					505					510		
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
		515					520					525			

Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
530						535					540				
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
545					550					555					560
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
				565					570						575
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
			580					585					590		
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val
		595					600					605			
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val
610						615					620				
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro
625					630					635					640
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr
				645					650						655
Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
			660					665					670		
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu
		675					680						685		
Ser	Pro	Gly	Lys												
		690													

<210> 362

<211> 469

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-35 light chain fusion polypeptide

<400> 362

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

130	135	140													
Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser
145					150					155					160
Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr
				165					170						175
Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys
			180					185					190		
His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro
	195					200						205			
Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	Glu	Pro	Lys	Ser	Cys	Asp
	210				215					220					
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Gln	Val	Lys	Leu	Glu	Glu	Ser
225				230					235						240
Gly	Gly	Gly	Leu	Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu
			245					250						255	
Ala	Ser	Gly	Arg	Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln
			260					265					270		
Ala	Pro	Gly	Lys	Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp
	275					280						285			
Asn	Asn	Pro	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser
	290					295					300				
Arg	Asp	Asn	Ala	Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu
305				310						315					320
Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser
			325					330						335	
Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp
			340					345					350		
Gly	Gln	Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	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> 363

<211> 720

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-36 heavy chain fusion polypeptide

<400> 363

Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Thr	Leu	Ser	Leu	Ser	Pro	Gly
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Glu	Arg	Ala	Thr	Leu	Ser	Cys	Arg	Ala	Ser	Lys	Gly	Val	Ser	Thr	Ser
			20					25					30		
Gly	Tyr	Ser	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro
		35					40					45			
Arg	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Tyr	Leu	Glu	Ser	Gly	Val	Pro	Ala
	50					55					60				
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser
65					70					75				80	
Ser	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	His	Ser	Arg
				85					90					95	
Asp	Leu	Pro	Leu	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Val	Glu	Ile	Lys	Gly
			100					105					110		
Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gln	Val
		115					120					125			
Gln	Leu	Val	Gln	Ser	Gly	Val	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val
	130					135					140				
Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Asn	Tyr	Tyr	Met
145					150					155					160
Tyr	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Gly
			165					170						175	
Ile	Asn	Pro	Ser	Asn	Gly	Gly	Thr	Asn	Phe	Asn	Glu	Lys	Phe	Lys	Asn
			180					185					190		
Arg	Val	Thr	Leu	Thr	Thr	Asp	Ser	Ser	Thr	Thr	Thr	Ala	Tyr	Met	Glu
	195						200					205			
Leu	Lys	Ser	Leu	Gln	Phe	Asp	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg
	210					215					220				
Arg	Asp	Tyr	Arg	Phe	Asp	Met	Gly	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
225					230					235					240
Thr	Val	Thr	Val	Ser	Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr
			245						250					255	
Cys	Pro	Pro	Cys	Pro	Gln	Val	Lys	Leu	Glu	Glu	Ser	Gly	Gly	Gly	Leu
			260					265					270		
Val	Leu	Pro	Gly	Glu	Ser	Leu	Arg	Leu	Ser	Cys	Glu	Ala	Ser	Gly	Arg
	275						280					285			
Thr	Ile	Thr	Thr	Ile	Thr	Met	Gly	Trp	Phe	Arg	Gln	Ala	Pro	Gly	Lys
	290					295					300				
Glu	Arg	Gln	Phe	Val	Ala	Ser	His	Ser	Trp	Thr	Asp	Asn	Asn	Pro	Tyr
305					310					315					320
Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala
			325						330					335	
Gly	Asn	Arg	Val	Tyr	Leu	Gln	Met	His	Ser	Leu	Glu	Pro	Glu	Asp	Thr
			340					345					350		
Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg
		355					360					365			

Gln	Trp	Tyr	Thr	Glu	Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr
370						375					380				
Gln	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro
385					390					395					400
Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly
				405					410					415	
Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn
			420					425					430		
Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln
		435				440					445				
Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser
		450				455					460				
Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser
465				470					475						480
Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr
			485					490						495	
His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser
			500					505					510		
Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg
		515					520					525			
Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro
	530					535					540				
Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala
545				550					555						560
Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val
			565					570						575	
Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr
			580					585				590			
Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr
	595					600						605			
Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu
	610					615					620				
Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys
625				630					635						640
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser
			645					650						655	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp
			660					665					670		
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser
		675				680						685			
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala
	690				695						700				
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys
705					710				715						720

<210> 364

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> BCP-36 light chain fusion polypeptide

<400> 364

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

<210> 365

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> linker peptide

<400> 365

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

<210> 366
 <211> 362
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AS07014 direct grafted HCAb dimeric form

<400> 366
 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Thr Tyr Ser Arg His
 20 25 30
 Cys Leu Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Thr Ile Asp Ser Asp Gly Ser Thr Ser Tyr Ala Asp Ser Val Lys
 50 55 60
 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu
 65 70 75 80
 Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Gly Pro Asn Pro Arg Tyr Cys Ser Gly Ala Pro Asn Thr Arg Gly
 100 105 110
 Ala Glu His Tyr Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
 115 120 125
 Ser Ser Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 130 135 140
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 145 150 155 160
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 165 170 175
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 180 185 190
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 195 200 205
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 210 215 220
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 225 230 235 240
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 245 250 255
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 260 265 270
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 275 280 285
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 290 295 300
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 305 310 315 320
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn

				325					330					335		
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	
			340						345				350			
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys							
		355					360									

<210> 367

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189 direct grafted HCAb dimeric form

<400> 367

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

Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
		275					280					285			
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	290					295					300				
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
305					310					315					320
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				325					330					335	
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
			340					345							

<210> 368

<211> 347

<212> PRT

<213> Artificial Sequence

<220>

<223> AS07189TKDVH21FY HCAb dimeric form

<400> 368

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

225		230		235		240									
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
		245		250		255									
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
		260		265		270									
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
		275		280		285									
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	290			295		300									
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
305				310		315									320
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
			325			330								335	
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
		340				345									

<210> 369

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311VH2 HCAb dimeric form

<400> 369

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

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

<210> 370

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311VH2F53 HCAb dimeric form

<400> 370

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

130		135		140
Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys				
145		150		155
Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val				160
	165		170	
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr				175
	180		185	
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu				190
	195		200	
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His				205
	210		215	
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys				220
	225		230	
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln				235
	245		250	
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu				240
	260		265	
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro				255
	275		280	
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn				285
	290		295	
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu				300
	305		310	
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val				315
	325		330	
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln				320
	340		345	
Lys Ser Leu Ser Leu Ser Pro Gly Lys				335
	355		360	

<210> 371

<211> 361

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311VH11F53 HCAb dimeric form

<400> 371

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

Leu	Gln	Met	Asn	Ser	Leu	Arg	Pro	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
			85						90					95		
Ala	Ala	Thr	Ala	Arg	Arg	Ser	Phe	Val	Gly	Arg	Gln	Trp	Tyr	Thr	Glu	
			100					105					110			
Ala	Arg	Gln	Tyr	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	
		115					120					125				
Ser	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	
		130				135					140					
Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	
145					150					155					160	
Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	
				165					170					175		
Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	
			180					185					190			
Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	
		195					200					205				
Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	
		210				215					220					
Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	
225					230					235					240	
Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	
				245					250					255		
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	
			260					265					270			
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
		275					280					285				
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
		290				295				300						
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
305					310					315					320	
Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	
				325					330					335		
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
			340					345					350			
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys								
		355					360									

<210> 372

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> A34311 consensus

<400> 372

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

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

Ser

<210> 373
 <211> 130
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> AS07014 consensus

<400> 373

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

Ser Ser
 130

<210> 374
 <211> 115
 <212> PRT
 <213> Artificial Sequence

<220>

<223> AS07189 consensus

<400> 374

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

<210> 375

<211> 1

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence

<220>

<221> VARIANT

<222> (1)...(1)

<223> Can be present in repeats of at least one time

<400> 375

Gly

1

<210> 376

<211> 2

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence

<220>

<221> VARIANT
<222> (1)...(2)
<223> Can be present in repeats of at least one time

<400> 376

Gly Ser

1

<210> 377

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence

<220>

<221> VARIANT

<222> (1)...(5)

<223> Can be present in repeats of at least one time

<400> 377

Gly Ser Gly Gly Ser

1

5

<210> 378

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence

<220>

<221> VARIANT

<222> (1)...(4)

<223> Can be present in repeats of at least one time

<400> 378

Gly Gly Gly Ser

1

<210> 379

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Linker amino acid sequence

<220>

<221> VARIANT

<222> (1)...(5)

<223> Can be present in repeats of at least one time

<400> 379

Gly Gly Gly Gly Ser

1

5