

SEQUENCE LISTING

<110> JIANGSU HENGRUI PHARMACEUTICALS CO., LTD.
SHANGHAI HENGRUI PHARMACEUTICAL CO., LTD.

<120> ANTIGEN BINDING MOLECULE SPECIFICALLY BINDING TO RANKL AND NGF, AND
MEDICAL USE THEREOF

<130> 722048

<140> PCT/CN2022/092333

<141> 2022-05-12

<150> 202110515444.9

<151> 2021-05-12

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<170> PatentIn 3.5

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<223> 1-22H HCDR1

<400> 1

Asp Tyr Ala Met Ser

1 5

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<223> 1-22H HCDR2

<400> 2

Gly Ile Ser Ala Ser Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 3

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<400> 3

Asp Pro Gly Thr Thr Val Ile Met Ser Trp Phe Asp Pro
1 5 10

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<223> 1-22H LCDR1

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Arg Ala Ser Gln Ser Val Arg Gly Arg Tyr Leu Ala
1 5 10

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<223> 1-22H LCDR2

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Gly Ala Ser Ser Arg Ala Thr
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<223> 1-22H LCDR3

<400> 6

Gln Gln Tyr Gly Ser Ser Pro Arg Thr
1 5

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<223> 5-16H HCDR1

<400> 7

Ser Tyr Ala Met Ser
1 5

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<223> 5-16H HCDR2

<400> 8

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

<210> 9

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<223> 5-16H HCDR3

<400> 9

Asp Pro Ala Ser Ile Val Ile Met Ser Trp Phe Asp Pro
1 5 10

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<223> 5-51H HCDR3

<400> 10

Asp Pro Cys Phe Ser Tyr Ile Met Ser Trp Phe Asp Pro
1 5 10

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<223> 5-53H HCDR3

<400> 11

Asp Pro Cys Phe Thr Tyr Ile Met Ser Trp Phe Asp Pro
1 5 10

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<223> 5-58H HCDR3

<400> 12

Asp Pro Gly Phe Thr Tyr Ile Met Ser Trp Phe Asp Pro
1 5 10

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<223> D35H HCDR1

<400> 13

Ala Tyr Pro Met Ser
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<223> D75H HCDR3

<400> 14

Asp Pro Gly Thr Thr Ser Ile Met Ser Trp Phe Asp Pro
1 5 10

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<223> D80H HCDR3

<400> 15

Asp Pro Gly Ser Thr Ile Ile Met Ser Trp Phe Asp Pro
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<223> 2-52L LCDR2

<400> 16

Gln Gly Ser Ser Arg Ala Thr
1 5

<210> 17

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<223> 2-72L LCDR1

<400> 17

Arg Ala Ser Gln Ser Leu Gly Ala Arg Gly Leu Ala
1 5 10

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<223> 2-72L LCDR2

<400> 18

Gly Thr Ser Ser Arg Ala Thr
1 5

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<223> 2-76L LCDR1

<400> 19
Arg Ala Ser Gln Ala Ile Pro Tyr Asn Gln Leu Ala
1 5 10

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<400> 20
Gly Val Ser Ser Arg Ala Thr
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<400> 21
Gly Ser Ser Ser Arg Ala Thr
1 5

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<223> 2-87L LCDR1

<400> 22
Arg Ala Ser Gln Tyr Leu Pro Phe His Arg Leu Ala
1 5 10

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<400> 23
Asp Thr Ser Ser Arg Ala Thr
1 5

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<223> 3-20L LCDR1

<400> 24
Arg Ala Ser Gln Ala Ile Arg Gly Pro Asn Leu Ala
1 5 10

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<400> 25
Asp Thr Ser Ser Arg Ala Thr
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<223> 3-37L LCDR1

<400> 26
Arg Ala Ser Gln Ala Ile Arg Gly Arg Lys Leu Ala
1 5 10

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<223> 3-37L LCDR2

<400> 27
Asp Thr Ser Ser Arg Ala Thr
1 5

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<223> 3-83L LCDR1

<400> 28
Arg Ala Ser Gln Ala Leu Gly Val Arg Gly Leu Ala
1 5 10

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<220>
<223> 3-85L LCDR1

<400> 29
Arg Ala Ser Gln Ser Ile Pro Gly Pro Arg Leu Ala
1 5 10

<210> 30
<211> 9
<212> PRT
<213> Artificial sequence

<220>
<223> 4-64L LCDR3

<400> 30
Gln Gln Tyr Gly Ser Ser Pro Arg Ile
1 5

<210> 31
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<212> PRT
<213> Artificial sequence

<220>
<223> 1-22H heavy chain variable region

<400> 31

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

<210> 32
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 <212> PRT
 <213> Artificial sequence

<220>
 <223> 5-16H heavy chain variable region

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

<210> 33
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 <213> Artificial sequence

<220>
 <223> 5-51H heavy chain variable region

<400> 33
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Pro Cys Phe Ser Tyr Ile Met Ser Trp Phe Asp Pro Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 34
 <211> 122
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 5-53H heavy chain variable region

<400> 34
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Gln Asp Pro Cys Phe Thr Tyr Ile Met Ser Trp Phe Asp Pro Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 35
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 <212> PRT
 <213> Artificial sequence

<220>
 <223> 5-58H heavy chain variable region

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

<210> 36
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<220>
 <223> D35H heavy chain variable region

<400> 36
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ala Tyr
 20 25 30
 Pro Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Asp Pro Gly Thr Thr Val Ile Met Ser Trp Phe Asp Pro Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37
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 <212> PRT
 <213> Artificial sequence

<220>
 <223> D75H heavy chain variable region

<400> 37
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Lys Asp Pro Gly Thr Thr Ser Ile Met Ser Trp Phe Asp Pro Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 38
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 <212> PRT
 <213> Artificial sequence

<220>
 <223> D80H heavy chain variable region

<400> 38
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45
 Ser Gly Ile Thr Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Lys Asp Pro Gly Ser Thr Ile Ile Met Ser Trp Phe Asp Pro Trp
 100 105 110
 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 39
 <211> 122
 <212> PRT
 <213> Artificial sequence

<220>

<223> 2-52L heavy chain variable region

<400> 39

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

<211> 108

<212> PRT

<213> Artificial sequence

<220>

<223> Light chain variable region

<400> 40

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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 Ser Val Arg Gly Arg
20      25      30
Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
35      40      45
Ile Tyr Gly 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 Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
85      90      95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100     105
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<210> 41

<211> 108

<212> PRT

<213> Artificial sequence

<220>

<223> 2-52L light chain variable region

<400> 41
 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 Ser Val Arg Gly Arg
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gln Gly 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 Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95
 Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 42
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 2-72L light chain variable region

<400> 42
 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 Ser Leu Gly Ala Arg
 20 25 30
 Gly Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly Thr 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 Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95
 Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 43
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 2-76L light chain variable region

<400> 43

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	Ala	Ile	Pro	Tyr	Asn
			20					25					30		
Gln	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Val	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	Phe	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
				85					90					95	
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys				
			100					105							

<210> 44
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 <213> Artificial sequence

<220>
 <223> 2-79L light chain variable region

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	Ser	Val	Arg	Gly	Arg
			20					25					30		
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35					40					45			
Ile	Tyr	Gly	Ser	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	Phe	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
				85					90					95	
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys				
			100					105							

<210> 45
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 2-87L light chain variable region

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	Tyr	Leu	Pro	Phe	His

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          20          25          30
Arg Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
      35          40          45
Ile Tyr Asp Thr 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 Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
      85          90          95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
      100          105

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<210> 46
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 3-20L light chain variable region

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<400> 46
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 Ala Ile Arg Gly Pro
      20          25          30
Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
      35          40          45
Ile Tyr Asp Thr 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 Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
      85          90          95
Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
      100          105

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<210> 47
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 3-37L light chain variable region

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<400> 47
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 Ala Ile Arg Gly Arg
      20          25          30
Lys Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
      35          40          45

```

Ile	Tyr	Asp	Thr	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	Phe	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
			85					90					95		
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys				
			100					105							

<210> 48
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<220>
 <223> 3-83L light chain variable region

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	Ala	Leu	Gly	Val	Arg
			20					25					30		
Gly	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35				40						45			
Ile	Tyr	Gly	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	Phe	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
			85					90					95		
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys				
			100					105							

<210> 49
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 3-85L light chain variable region

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	Ser	Ile	Pro	Gly	Pro
			20					25					30		
Arg	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35				40						45			
Ile	Tyr	Gly	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	Phe	Tyr	Cys	Gln	Tyr	Gly	Ser
				85				90				95
Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	
			100				105					

<210> 50
 <211> 108
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 4-64L light chain variable region

<400>	50														
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	Ser	Val	Arg	Gly	Arg
		20					25					30			
Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	Leu	Leu
		35				40					45				
Ile	Tyr	Gly	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	Phe	Tyr	Cys	Gln	Gln	Tyr	Gly	Ser	Ser	Pro
			85					90					95		
Arg	Ile	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys				
			100				105								

<210> 51
 <211> 327
 <212> PRT
 <213> homo sapiens

<400>	51														
Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg
1			5					10					15		
Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr
		20					25					30			
Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser
		35				40					45				
Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser
	50				55					60					
Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr
65				70				75						80	
Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys
			85					90					95		
Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro
			100				105					110			

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

<210> 52
 <211> 107
 <212> PRT
 <213> homo sapiens

<400> 52
 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
 1 5 10 15
 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
 20 25 30
 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
 35 40 45
 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
 50 55 60
 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
 65 70 75 80
 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 85 90 95
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 100 105

<210> 53
 <211> 449
 <212> PRT

<213> Artificial sequence

<220>

<223> D35H heavy chain

<400> 53

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

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380
 Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
 405 410 415
 Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430
 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 435 440 445
 Lys

<210> 54
 <211> 215
 <212> PRT
 <213> Artificial sequence

<220>
 <223> D35H light chain

<400> 54
 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 Ser Val Arg Gly Arg
 20 25 30
 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
 35 40 45
 Ile Tyr Gly 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 Phe Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
 85 90 95
 Arg 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> 55

<211> 509
 <212> PRT
 <213> Artificial sequence

<220>
 <223> D75H heavy chain

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

Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu
		355				360					365				
Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys
	370					375				380					
Val	Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys
385					390					395					400
Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser
				405					410					415	
Gln	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys
			420					425					430		
Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln
	435						440					445			
Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly
	450					455					460				
Ser	Phe	Phe	Leu	Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln
465					470					475					480
Glu	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn
				485					490					495	
His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys			
			500					505							

<210> 56

<211> 449

<212> PRT

<213> Artificial sequence

<220>

<223> D80H heavy chain

<400> 56

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

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

<210> 57
 <211> 448
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Denosumab heavy chain

<400> 57
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30
 Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

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

<210> 58

<211> 5

<212> PRT
<213> Artificial sequence

<220>
<223> Tanezumab HCDR1

<400> 58
Gly Tyr Asp Leu Asn
1 5

<210> 59
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Tanezumab HCDR2

<400> 59
Ile Ile Trp Gly Asp Gly Thr Thr Asp Tyr Asn Ser Ala Val Lys Ser
1 5 10 15

<210> 60
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Tanezumab HCDR3

<400> 60
Gly Gly Tyr Trp Tyr Ala Thr Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 61
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> Tanezumab LCDR1

<400> 61
Arg Ala Ser Gln Ser Ile Ser Asn Asn Leu Asn
1 5 10

<210> 62
<211> 7
<212> PRT

<213> Artificial sequence

<220>

<223> Tanezumab LCDR2

<400> 62

Tyr Thr Ser Arg Phe His Ser
1 5

<210> 63

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<223> Tanezumab LCDR3

<400> 63

Gly Gly Tyr Trp Tyr Ala Thr Ser Tyr Tyr Phe Asp Tyr
1 5 10

<210> 64

<211> 121

<212> PRT

<213> Artificial sequence

<220>

<223> Tanezumab heavy chain variable region

<400> 64

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

<210> 65

<211> 107

<212> PRT

<213> Artificial sequence

<220>

<223> Tanezumab light chain variable region

<400> 65

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

<210> 66

<211> 326

<212> PRT

<213> Artificial sequence

<220>

<223> Heavy chain constant region

<400> 66

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


				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	Asn	Phe	Gly	Thr	Gln	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His		
		195					200					205					
Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Thr	Val	Glu	Arg	Lys	Cys	Cys		
	210					215					220						
Val	Glu	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Pro	Val	Ala	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	His	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	Phe	Arg	Val	Val	Ser		
	290					295					300						
Val	Leu	Thr	Val	Val	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	Thr	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro		
			340					345						350			
Pro	Ser	Arg	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	Met	Leu	Asp	Ser		
385					390					395					400		
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg		
			405						410					415			
Trp	Gln	Gln	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	Pro	Gly	Lys			
		435					440					445					

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<220>
 <223> Linker

<400> 70
 Ala Ser Thr Lys Gly Pro
 1 5

<210> 71
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
<223> Linker

<400> 71
Thr Val Ala Ala Pro Ser
1 5

<210> 72
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 72
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
1 5 10

<210> 73
<211> 12
<212> PRT
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<220>
<223> Linker

<400> 73
Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
1 5 10

<210> 74
<211> 16
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 74
Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala Arg
1 5 10 15

<210> 75
<211> 17
<212> PRT
<213> Artificial sequence

<220>

<223> Linker

<400> 75

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

Val

<210> 76

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 76

Ala Lys Thr Thr Pro Lys Leu Gly Gly
1 5

<210> 77

<211> 10

<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 77

Ser Ala Lys Thr Thr Pro Lys Leu Gly Gly
1 5 10

<210> 78

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 78

Ser Ala Lys Thr Thr Pro
1 5

<210> 79

<211> 6

<212> PRT

<213> Artificial sequence

<220>
<223> Linker

<400> 79
Arg Ala Asp Ala Ala Pro
1 5

<210> 80
<211> 9
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<220>
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<400> 80
Arg Ala Asp Ala Ala Pro Thr Val Ser
1 5

<210> 81
<211> 12
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 81
Arg Ala Asp Ala Ala Ala Ala Gly Gly Pro Gly Ser
1 5 10

<210> 82
<211> 18
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 82
Ser Ala Lys Thr Thr Pro Lys Leu Glu Glu Gly Glu Phe Ser Glu Ala
1 5 10 15
Arg Val

<210> 83
<211> 5
<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 83

Ala Asp Ala Ala Pro
1 5

<210> 84

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 84

Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
1 5 10

<210> 85

<211> 5

<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 85

Thr Val Ala Ala Pro
1 5

<210> 86

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 86

Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
1 5 10

<210> 87

<211> 6

<212> PRT

<213> Artificial sequence

<220>
<223> Linker

<400> 87
Gln Pro Lys Ala Ala Pro
1 5

<210> 88
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 88
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro
1 5 10

<210> 89
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 89
Ala Lys Thr Thr Pro Pro
1 5

<210> 90
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<220>
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<400> 90
Ala Lys Thr Thr Pro Pro Ser Val Thr Pro Leu Ala Pro
1 5 10

<210> 91
<211> 6
<212> PRT
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<220>
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<400> 91
Ala Lys Thr Thr Ala Pro
1 5

<210> 92
<211> 13
<212> PRT
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<400> 92
Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro Leu Ala Pro
1 5 10

<210> 93
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<212> PRT
<213> Artificial sequence

<220>
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<400> 93
Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
1 5 10

<210> 94
<211> 15
<212> PRT
<213> Artificial sequence

<220>
<223> Linker

<400> 94
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 95
<211> 15
<212> PRT
<213> Artificial sequence

<220>

<223> Linker

<400> 95

Gly Glu Asn Lys Val Glu Tyr Ala Pro Ala Leu Met Ala Leu Ser
1 5 10 15

<210> 96

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 96

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

<210> 97

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<223> Linker

<400> 97

Gly His Glu Ala Ala Ala Val Met Gln Val Gln Tyr Pro Ala Ser
1 5 10 15

<210> 98

<211> 576

<212> PRT

<213> Artificial sequence

<220>

<223> First chain of bispecific antibody 1

<400> 98

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

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85					90						95	
Val	Lys	Asp	Pro	Gly	Thr	Thr	Ser	Ile	Met	Ser	Trp	Phe	Asp	Pro	Trp	
			100					105					110			
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	
		115					120					125				
Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Lys	Pro	Ser	Glu	
	130				135						140					
Thr	Leu	Ser	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ile	Gly	Tyr	
145					150					155					160	
Asp	Leu	Asn	Trp	Ile	Arg	Gln	Pro	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile	
				165					170						175	
Gly	Ile	Ile	Trp	Gly	Asp	Gly	Thr	Thr	Asp	Tyr	Asn	Ser	Ala	Val	Lys	
			180					185					190			
Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	Asn	Gln	Phe	Ser	Leu	
		195					200					205				
Lys	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
	210					215					220					
Arg	Gly	Gly	Tyr	Trp	Tyr	Ala	Thr	Ser	Tyr	Tyr	Phe	Asp	Tyr	Trp	Gly	
225					230					235					240	
Gln	Gly	Thr	Leu	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> 99

<211> 327

<212> PRT

<213> Artificial sequence

<220>

<223> Second chain of bispecific antibody 1

<400> 99

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

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> 102
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> AMR2 HCDR1

<400> 102
 Asp Tyr Asp Met Ser
 1 5

<210> 103
 <211> 17
 <212> PRT
 <213> Artificial sequence

<220>
 <223> AMR2 HCDR2

<400> 103
 Trp Ile Tyr Pro Ser Gly Gly Ser Ile Tyr Tyr Ala Asp Ser Val Lys
 1 5 10 15
 Gly

<210> 104
 <211> 18
 <212> PRT
 <213> Artificial sequence

<220>
 <223> AMR2 HCDR3

<400> 104
Ser Gly Leu Thr Arg Thr Arg Trp Pro Ile Tyr Tyr Ala Asp Gly Met
1 5 10 15
Asp Val

<210> 105
<211> 13
<212> PRT
<213> Artificial sequence

<220>
<223> AMR2 LCDR1

<400> 105
Thr Gly Ser Ser Ser Asn Ile Gly Asn Asn Ala Val Ser
1 5 10

<210> 106
<211> 7
<212> PRT
<213> Artificial sequence

<220>
<223> AMR2 LCDR2

<400> 106
Ser Asp Arg His Arg Pro Ser
1 5

<210> 107
<211> 11
<212> PRT
<213> Artificial sequence

<220>
<223> AMR2 LCDR3

<400> 107
Gly Ser Trp Asp Ala Ser Leu Ser Gly Tyr Val
1 5 10

<210> 108
<211> 126
<212> PRT
<213> Artificial sequence

<220>
<223> AMR2 heavy chain variable region

<400> 108
Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser
1 5 10 15
Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asp Tyr Asp
20 25 30
Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
35 40 45
Trp Ile Tyr Pro Ser Gly Gly Ser Ile Tyr 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 Ser Gly Leu Thr Arg Thr Arg Trp Pro Ile Tyr Tyr Ala Asp Gly
100 105 110
Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 109
<211> 110
<212> PRT
<213> Artificial sequence

<220>
<223> AMR2 light chain variable region

<400> 109
Gln Ser Val Leu Thr Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln
1 5 10 15
Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30
Ala Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45
Ile Tyr Ser Asp Arg His Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60
Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg
65 70 75 80
Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gly Ser Trp Asp Ala Ser Leu
85 90 95
Ser Gly Tyr Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 110
<211> 454
<212> PRT
<213> Artificial sequence

<220>
<223> AMR2 heavy chain

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

				405					410					415			
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys		
			420					425					430				
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu		
		435					440					445					
Ser	Leu	Ser	Leu	Gly	Lys												
	450																

<210> 111
 <211> 216
 <212> PRT
 <213> Artificial sequence

<220>
 <223> AMR2 light chain

<400> 111

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