

2009-203.txt  
SEQUENCE LISTING

<110> Sanofi-Aventis  
 <120> Polypeptides for binding to the "receptor for advanced glycation endproducts" as well as compositions and methods involving the same  
 <130> DE2009/203  
 <160> 51  
 <170> PatentIn version 3.5  
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Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly
1           5           10
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Ile Asn
          20           25           30
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Ile
          35           40           45
Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly
          50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Ile Ile Ser Asn Val Gln Ser
65           70           75           80
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Asn Tyr Pro Arg
          85           90           95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
          100          105

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<210> 2  
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 <400> 2

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

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2009-203.txt

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly  
35 40 45

Leu Thr Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe  
50 55 60

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala  
65 70 75 80

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

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

<210> 3  
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<212> PRT  
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<220>  
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<400> 3

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met  
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Ser  
35 40 45

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu  
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Pro Thr  
85 90 95

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

<210> 4  
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<212> PRT  
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<400> 4

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

Glu Lys Val Thr Ile Ser Cys Ser Ala Ser Ser Ser Val Ser Tyr Met  
 20 25 30

Tyr Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr  
 35 40 45

Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu  
 65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Tyr His Ser Tyr Pro Pro Met  
 85 90 95

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

<210> 5

<211> 110

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<400> 5

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Gly Thr Ser  
 20 25 30

Asp Ser Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
 35 40 45

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

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

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg  
 85 90 95

Glu Leu Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
 100 105 110

<210> 6

<211> 113

<212> PRT

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<400> 6

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

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

Ser Asp Gly Phe Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln  
35 40 45

Ser Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser Gly Val  
50 55 60

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

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

Ser Asn Tyr Leu Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile  
100 105 110

Lys

<210> 7

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

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<400> 7

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly  
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Gly Thr Tyr  
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile  
35 40 45

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

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala  
65 70 75 80

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr Thr Tyr Pro Tyr  
                     85                    90                    95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
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<210> 8  
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<400> 8

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

Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser  
                     20                    25                    30

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

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

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

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

Tyr Leu Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
                     100                    105                    110

<210> 9  
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<220>  
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<400> 9

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly  
 1                    5                    10                    15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
                     20                    25                    30

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

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly  
   Seite 5

50

55

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser  
65 70 75 80

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
100 105

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

<220>  
<223> variable region for light chain

<400> 10

Asn Ile Val Met Thr Gln Ser Pro Lys Ser Met Ser Met Ser Val Gly  
1 5 10 15

Glu Arg Val Thr Leu Ser Cys Lys Ala Ser Glu Asn Val Gly Thr Tyr  
20 25 30

Val Ser Trp Tyr Gln Gln Lys Pro Glu Gln Ser Pro Lys Leu Leu Ile  
35 40 45

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

Ser Gly Ser Ala Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala  
65 70 75 80

Glu Asp Leu Ala Asp Tyr His Cys Gly Gln Ser Tyr Ser Tyr Pro Tyr  
85 90 95

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

<210> 11  
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<212> PRT  
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<220>  
<223> variable region for light chain

<400> 11

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser  
20 25 30

Gly Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro  
35 40 45

Lys Leu Leu Ile Tyr Leu Ala Ser His Leu Glu Ser Gly Val Pro Ala  
50 55 60

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

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg  
85 90 95

Glu Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105 110

<210> 12  
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<400> 12

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

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

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly  
35 40 45

Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe  
50 55 60

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala  
65 70 75 80

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

His Phe Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
100 105 110

<210> 13  
<211> 113  
<212> PRT  
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<220>  
<223> variable region for light chain

<400> 13

2009-203.txt

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

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

Ser Asp Gly Phe Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln  
35 40 45

Ser Pro Gln Leu Leu Ile Tyr Leu Val Ser Asn Arg Phe Ser Gly Val  
50 55 60

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

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

Ser Asn Tyr Phe Pro Leu Thr Phe Gly Gly Gly Thr Thr Leu Glu Ile  
100 105 110

Lys

<210> 14  
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<212> PRT  
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<223> variable region for light chain

<400> 14

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly  
1 5 10 15

Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
20 25 30

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

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp Arg Phe Thr Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Val Gln Ser  
65 70 75 80

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
100 105



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

Lys

<210> 16  
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 <400> 16

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

2009-203.txt

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala  
65 70 75 80

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

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

<210> 17  
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<400> 17

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

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

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly  
35 40 45

Leu Ile Arg Gly Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe  
50 55 60

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala  
65 70 75 80

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

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

<210> 18  
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<212> PRT  
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<220>  
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<400> 18

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

Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Ile Ser  
20 25 30

2009-203.txt

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

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

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg  
85 90 95

Glu Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
100 105 110

<210>	19
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<212>	PRT
<213>	Artificial Sequence

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<220>
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<400> 19

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly  
1 5 10 15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Ala  
20 25 30

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Asn Met Gln Ser  
65 70 75 80

Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser Tyr Pro Leu  
85 90 95

Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
100 105

<210>	20
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<212>	PRT
<213>	Artificial Sequence

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<220>  
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<400> 20

Asp Ile Gln Met Thr Gln Ser Ser Ser Tyr Leu Ser Val Ser Leu Gly  
Seite 11

1

5

10

15

Gly Arg Val Thr Ile Thr Cys Lys Ala Ser Asp Arg Ile Asn Tyr Trp  
                   20                  25                  30

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

Ser Gly Ala Thr Thr Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly  
       50                  55                  60

Ser Gly Ser Gly Lys Asp Tyr Thr Leu Ser Ile Thr Ser Leu Gln Thr  
  65                  70                  75                  80

Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Tyr Trp Ser Thr Pro Tyr  
                   85                  90                  95

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

<210> 21  
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 <212> PRT  
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<400> 21

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly  
  1                  5                  10                  15

Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser Thr Ala  
           20                  25                  30

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

Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly  
       50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Val Gln Ala  
  65                  70                  75                  80

Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln His Tyr Asn Thr Pro Arg  
           85                  90                  95

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

<210> 22  
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 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; variable region for light chain

&lt;400&gt; 22

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

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

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly  
 35 40 45

Leu Ile Gly Gly Thr Asn Asn Arg Ala Pro Asp Val Pro Ala Arg Phe  
 50 55 60

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala  
 65 70 75 80

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

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

&lt;210&gt; 23

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; variable region for light chain

&lt;400&gt; 23

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

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

Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly  
 35 40 45

Leu Ile Gly Gly Thr Asn Asn Arg Ser Pro Gly Val Pro Ala Arg Phe  
 50 55 60

Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala  
 65 70 75 80

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

His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu  
 Seite 13

100

2009-203.txt  
105

<210> 24  
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<223> variable region for heavy chain

<400> 24

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

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30

Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

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

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

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

Val Arg Gly Gln Leu Gly Asp Tyr Trp Gly Gln Gly Ile Thr Leu Thr  
100 105 110

Val Ser Ser  
115

<210> 25  
<211> 117  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> variable region for heavy chain

<400> 25

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

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

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

Gly Glu Ser Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

Lys Asn Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

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

Ala Arg Ala Pro Tyr Tyr Gly Phe Asp Tyr Trp Gly Gln Gly Thr Thr  
100 105 110

Leu Thr Val Ser Ser  
115

<210> 26  
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<400> 26

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
20 25 30

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

Ala Glu Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Thr Val  
50 55 60

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

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

Ala Arg Pro Pro Tyr Gly Lys Asp Ala Met Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Ser Val Thr Val Ser Ser  
115

<210> 27  
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<400> 27

2009-203.txt

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

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

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

Gly Glu Ile Asn Pro Ser Asn Gly Arg Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

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

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

Ala Arg Asp Gly Leu Gly Tyr Arg Pro Ile Ala Met Asp Tyr Trp Gly  
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser  
115 120

<210> 28  
<211> 115  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> variable region for heavy chain

<400> 28

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

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Gly  
20 25 30

Tyr Ser Trp His Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp  
35 40 45

Met Gly Tyr Ile His Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu  
50 55 60

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

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

Ala Arg Gly Gly Asp Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110



Val Ser Ala  
115

<210> 29  
<211> 119  
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<220>  
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<400> 29

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

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

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

Gly Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe  
50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr  
65 70 75 80

Leu Leu Ile Asn Asn Leu Lys Thr Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95

Ala Arg Asp Tyr Leu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Ser Val Thr Val Ser Ser  
115

<210> 30  
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<220>  
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<400> 30

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

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

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

2009-203.txt

Gly Asn Ile Tyr Pro Gly Ser Gly Ser Thr Asn Tyr Asp Glu Lys Phe  
50 55 60

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

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

Thr Arg Leu Arg Arg Gly Ile Ala Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Ala  
115

<210> 31  
<211> 115  
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<220>  
<223> variable region for heavy chain

<400> 31

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

Ser Val Arg Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr  
20 25 30

Tyr Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Val Ile Thr Asn Tyr His Glu Lys Phe  
50 55 60

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

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

Ala Arg Glu Asp Pro Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr  
100 105 110

Val Ser Ala  
115

<210> 32  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>

<223> variable region for heavy chain

<400> 32

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

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

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

Ala Glu Ile Arg Leu Lys Ser Asn Asn Tyr Ala Thr His Tyr Ala Glu  
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ser  
65 70 75 80

Val Tyr Leu Gln Met Asn Asp Leu Arg Ala Glu Asp Pro Gly Ile Tyr  
85 90 95

Tyr Cys Ile Arg Asp Tyr Gly Asn Tyr Ala Met Asp His Trp Gly Gln  
100 105 110

Gly Thr Ser Val Thr Val Ser Ser  
115 120

<210> 33

<211> 116

<212> PRT

<213> Artificial Sequence

<220>

<223> variable region for heavy chain

<400> 33

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

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

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

Gly Ala Ile Phe Pro Gly Asn Ser Asp Thr Thr Tyr Asn Gln Lys Phe  
50 55 60

Lys Gly Lys Ala Lys Leu Thr Ala Val Thr Ser Ala Ser Thr Ala Tyr  
65 70 75 80

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

Thr Gly Leu Arg Arg Gly Phe Pro Tyr Trp Gly Gln Gly Thr Leu Val  
100 105 110

Thr Val Ser Val  
115

<210> 34  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> variable region for heavy chain

<400> 34

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

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

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

Gly Met Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
50 55 60

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

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

Ala Arg Gly Arg Gly Gly His Tyr Arg Tyr Phe Asp Val Trp Gly Ala  
100 105 110

Gly Thr Thr Val Thr Val Ser Ser  
115 120

<210> 35  
<211> 119  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> variable region for heavy chain

<400> 35

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

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

Asp Tyr Ile Met Val Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu  
 35 40 45

Trp Ile Gly Thr Ile Asn Pro Tyr Tyr Gly Ser Thr Ser Tyr Asn Leu  
 50 55 60

Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr  
 65 70 75 80

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

Tyr Cys Ala Arg Leu Arg Leu Tyr Ala Met Asp Tyr Trp Gly Gln Gly  
 100 105 110

Thr Ser Val Thr Val Ser Ser  
 115

<210> 36  
 <211> 119  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variable region for heavy chain

<400> 36

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

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

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

Gly Trp Ile Asn Thr Glu Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe  
 50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr  
 65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys  
 85 90 95

Ala Arg Asp Tyr Leu Tyr Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly  
 100 105 110

Thr Ser Val Thr Val Ser Ser  
 115

<210> 37  
 <211> 120  
 <212> PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; variable region for heavy chain

&lt;400&gt; 37

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

&lt;210&gt; 38

&lt;211&gt; 118

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; variable region for heavy chain

&lt;400&gt; 38

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

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

Ala Arg Tyr Asp Tyr Asp Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
                     100                    105                    110

Ser Val Thr Val Ser Ser  
                     115

<210> 39  
 <211> 117  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variable region for heavy chain

<400> 39

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

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

Leu Ile Asp Trp Val Asn Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
                     35                    40                    45

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe  
                     50                    55                    60

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

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

Ala Arg Arg Arg Val Asp Thr Met Asp Tyr Trp Gly Gln Gly Thr Ser  
                     100                    105                    110

Val Thr Val Ser Ser  
                     115

<210> 40  
 <211> 118  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variable region for heavy chain

<400> 40

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

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

20

25

30

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

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

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

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

Ala Ser Tyr Arg Tyr Asp Gly Gly Met Asp Tyr Trp Gly Gln Gly Thr  
          100                 105                 110

Ser Val Thr Val Ser Ser  
      115

<210> 41  
 <211> 118  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variable region for heavy chain

<400> 41

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

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

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

Gly Met Ile Asp Pro Ser Asn Ser Glu Thr Arg Leu Asn Gln Lys Phe  
      50                 55                 60

Lys Asp Lys Ala Thr Leu Asn Val Asp Lys Ser Ser Asn Thr Ala Tyr  
   65                 70                 75                 80

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

Ala Arg Asn Phe Tyr Gly Ser Ser Leu Arg Val Trp Gly Ala Gly Thr  
          100                 105                 110

Thr Val Thr Val Ser Ser  
      115



<210> 42  
 <211> 119  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variable region for heavy chain

<400> 42

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

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr  
 20 25 30

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val  
 35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Ser Tyr Pro Asp Ser Val  
 50 55 60

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

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

Ala Ser Ser Gln Leu Pro Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly  
 100 105 110

Thr Ser Val Thr Val Ser Ser  
 115

<210> 43  
 <211> 118  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> variable region for heavy chain

<400> 43

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

Ser Val Lys Met Ser Cys Arg Ala Ser Gly Tyr Thr Phe Thr Asp Tyr  
 20 25 30

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

Gly Phe Ile Asn Pro Ser Thr Val Tyr Thr Glu Tyr Ile Pro Lys Phe  
 50 55 60

Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
 Seite 25

65                      70                      80  
Met Gln Leu Ser Ser<sub>85</sub> Leu Thr Ser Glu Asp<sub>90</sub> Ser Ala Val Tyr Tyr<sub>95</sub> Cys

Ala Arg Ser Asp<sub>100</sub> Gly Gly Trp Tyr Phe<sub>105</sub> Asp Val Trp Gly Ala<sub>110</sub> Gly Thr

Thr Val Thr<sub>115</sub> Val Ser Ser

<210> 44  
<211> 113  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> variable region for heavy chain

<400> 44

Glu Val Gln Leu Gln Gln Ser Gly Thr Val<sub>10</sub> Leu Ala Arg Pro Gly<sub>15</sub> Ala

Ser Val Lys Met<sub>20</sub> Ser Cys Lys Ala Ser<sub>25</sub> Gly Tyr Thr Phe Thr<sub>30</sub> Ser Tyr

Trp Met His<sub>35</sub> Trp Val Lys Gln Arg<sub>40</sub> Pro Gly Gln Gly Leu<sub>45</sub> Glu Trp Ile

Gly Ala Ile Tyr Pro Gly Asp<sub>55</sub> Ser Asp Thr Tyr Tyr<sub>60</sub> Asn Gln Lys Phe

Lys Gly Lys Ala Lys Leu<sub>70</sub> Thr Ala Val Thr Ser<sub>75</sub> Thr Ser Thr Ala Tyr<sub>80</sub>

Met Glu Leu Ser Ser<sub>85</sub> Leu Thr Asn Glu Asp<sub>90</sub> Ser Ala Val Tyr Tyr<sub>95</sub> Cys

Thr Arg Asn Trp<sub>100</sub> Asp Tyr Trp Gly Gln<sub>105</sub> Gly Thr Thr Leu Thr<sub>110</sub> Val Ser

Ser

<210> 45  
<211> 120  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> variable region for heavy chain

<400> 45

Glu Val Met Leu<sub>5</sub> Val Asp Ser Gly Gly<sub>10</sub> Gly Leu Val Lys Pro Gly<sub>15</sub> Gly

2009-203.txt

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

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

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val  
50 55 60

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

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

Ala Arg His Gly Gly Asn Tyr Ser Ala Trp Phe Thr Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ala  
115 120

<210> 46  
<211> 119  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> variable region for heavy chain  
<400> 46

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

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

Asp Tyr Ile Met Leu Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu  
35 40 45

Trp Ile Gly Asn Ile Asn Pro Tyr Tyr Gly Ser Thr Phe Tyr Asn Leu  
50 55 60

Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr  
65 70 75 80

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

Tyr Cys Ala Arg Ser Asp Tyr Trp Tyr Phe Asp Val Trp Gly Ala Gly  
100 105 110

Thr Thr Val Thr Val Ser Ser

115

<210> 47  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> motif after CDR-L3

<220>  
 <221> Variant  
 <222> (3)..(3)  
 <223> Xaa = any amino acid

<400> 47

Phe Gly Xaa Gly  
 1

<210> 48  
 <211> 4  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> motif before CDR-H1

<220>  
 <221> Variant  
 <222> (2)..(2)  
 <223> Xaa = any amino acid

<220>  
 <221> Variant  
 <222> (3)..(3)  
 <223> Xaa = any amino acid

<220>  
 <221> Variant  
 <222> (4)..(4)  
 <223> Xaa = any amino acid

<400> 48

Cys Xaa Xaa Xaa  
 1

<210> 49  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> motif before CDR-H2

<400> 49

Leu Glu Trp Ile Gly  
 1 5

<210> 50  
 <211> 4

<212> PRT  
<213> Artificial Sequence

<220>  
<223> motif after CDR-H3

<220>  
<221> Variant  
<222> (3)..(3)  
<223> Xaa = any amino acid

<400> 50

Trp Gly Xaa Gly  
1

<210> 51  
<211> 11  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> immunostimulatory substance

<400> 51

Lys Leu Lys Leu Leu Leu Leu Lys Leu Lys  
1 5 10