SEQUENCE LISTING

<110> TANOX, INC.
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HUANG, Danyang
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<120> Identification of Unique, High Affinity IgE Epitopes

<130> TNX-1030

<150> PCT/US04/02892
<151> 2004-02-02

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<151> 2004-02-02

<160> 77

<170> PatentIn version 3.2

<210> 1
<211> 107
<212> PRT
<213> Murine

<220>
<221> misc_feature
<223> TES-C21 LIGHT CHAIN

<400> 1

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

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

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

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

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

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

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

<210> 2
<211> 107
<212> PRT
<213> Human

<220>
<221> misc_feature

<223> L16/-JK4 human light chain consensus sequence template

<400> 2

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

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

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

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

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

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

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

<210> 3
<211> 123
<212> PRT
<213> MURINE

<220>
<221> misc_feature
<223> TES-C21 Heavy Chain

<400> 3

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

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

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

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

Lys Ala Lys Ala Thr Phe Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr

100 105 110

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

<210> 4
<211> 113
<212> PRT
<213> Human

<220>
<221> misc_feature
<223> DP88/JH4b human heavy chain consensus sequence template

<400> 4

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

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

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

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

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

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

Ser

<210> 5
<211> 11
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<220>
<223> TES-C21 CDRL1 SEQUENCE (TABLE 1)

<400> 5

Arg Ala Ser Gln Ser Ile Gly Thr Asn Ile His
1 5 10

<210> 6
<211> 11
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRL1 VARIANT SEQUENCE #1 (TABLE 1)

<400> 6

Arg Ala Ser Arg Ser Ile Gly Thr Asn Ile His
1 5 10

<210> 7
<211> 11
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRL1 VARIANT SEQUENCE #2 (TABLE 1)

<400> 7

Arg Ala Ser Gln Arg Ile Gly Thr Asn Ile His
1 5 10

<210> 8
<211> 7
<212> PRT
<213> ARTIFICIAL

<220>
<223> TES-C21 CDRL2 SEQUENCE (TABLE 1)

<400> 8

Tyr Ala Ser Glu Ser Ile Ser
1 5

<210> 9
<211> 7
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRL2 VARIANT #1 (TABLE 1)

<400> 9

Tyr Ala Tyr Glu Ser Ile Ser
1 5

<210> 10
<211> 7
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRL2 VARIANT #2 (TABLE 1)

<400> 10

Tyr Ala Ser Glu Ser Ile Tyr
1 5

<210> 11
<211> 7
<212> PRT

<213> ARTIFICIAL

<220>
<223> CDRL2 VARIANT #3 (TABLE 1)

<400> 11

Tyr Ala Ser Glu Ser Asp Ser
1 5

<210> 12
<211> 7
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRL2 VARIANT #4 (TABLE 1)

<400> 12

Tyr Ala Ser Glu Ser Glu Ser
1 5

<210> 13
<211> 9
<212> PRT
<213> ARTIFICIAL

<220>
<223> TES-C21 CDRL3 (TABLE 1)

<400> 13

Gln Gln Ser Asp Ser Trp Pro Thr Thr
1 5

<210> 14
<211> 9
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRL3 VARIANT (TABLE)

<400> 14

Ala Ala Ser Trp Ser Trp Pro Thr Thr
1 5

<210> 15
<211> 5
<212> PRT
<213> ARTIFICIAL

<220>
<223> TES-C21 CDRH1

<400> 15

Met Tyr Trp Leu Glu
1 5

<210> 16
<211> 5

<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH1 VARIANT #1 (TABLE 1)

<400> 16

Trp Tyr Trp Leu Glu
1 5

<210> 17
<211> 5
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH1 #2 (TABLE 1)

<400> 17

Tyr Tyr Trp Leu Glu
1 5

<210> 18
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> TES-C21 CDRH2 (TABLE 1)

<400> 18

Glu Ile Ser Pro Gly Thr Phe Thr Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 19
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH2 VARIANT #1 (TABLE 1)

<400> 19

Glu Ile Glu Pro Gly Thr Phe Thr Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 20
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH2 VARIANT #2 (TABLE 1)

<400> 20

Glu Ile Asp Pro Gly Thr Phe Thr Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 21
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH2 VARIANT #3 (TABLE 1)

<400> 21

Glu Ile Ser Pro Asp Thr Phe Thr Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 22
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH2 VARIANT #4 (TABLE 1)

<400> 22

Glu Ile Ser Pro Glu Thr Phe Thr Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 23
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH2 VARIANT #5 (TABLE 1)

<400> 23

Glu Ile Ser Pro Gly Thr Phe Glu Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 24
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH2 VARIANT #6 (TABLE 1)

<400> 24

Glu Ile Glu Pro Gly Thr Phe Glu Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 25
<211> 17
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH2 VARIANT #7 (TABLE 1)

<400> 25

Glu Ile Asp Pro Gly Thr Phe Glu Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Ala

<210> 26
<211> 14
<212> PRT
<213> ARTIFICIAL

<220>
<223> TES-C21 CDRH3 (TABLE 1)

<400> 26

Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
1 5 10

<210> 27
<211> 14
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH3 VARIANT #1 (TABLE 1)

<400> 27

Phe Ser His Phe Ser Gly Met Asn Tyr Asp Tyr Phe Asp Tyr
1 5 10

<210> 28
<211> 14
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH3 VARIANT #2 (TABLE 1)

<400> 28

Phe Ser His Phe Ser Gly Gln Asn Tyr Asp Tyr Phe Asp Tyr
1 5 10

<210> 29
<211> 14
<212> PRT
<213> ARTIFICIAL

<220>
<223> CDRH3 VARIANT #3 (TABLE 1)

<400> 29

Phe Ser His Phe Thr Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
1 5 10

<210> 30
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL1 VARIANT 136

<400> 30

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 31
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL1 VARIANT 1

<400> 31

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 32
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL1 VARIANT 2

<400> 32

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 33
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL1 VARIANT 4

<400> 33

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 34
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL1 VARIANT 13

<400> 34

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 35
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL1 VARIANT 18

<400> 35

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 36
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL1 VARIANT 25

<400> 36

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

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys
20

<210> 37
<211> 23
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL1 VARIANT 27

<400> 37

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

Glu Arg Ala Thr Leu Ser Cys
20

<210> 38
<211> 15
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL2 VARIANT 136

<400> 38

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 39
<211> 15
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL2 VARIANT 1

<400> 39

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Lys
1 5 10 15

<210> 40
<211> 32
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL3 VARIANT 136

<400> 40

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

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 41
<211> 32
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL3 VARIANT 1

<400> 41

Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
20 25 30

<210> 42
<211> 32
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL3 VARIANT 13

<400> 42

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

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Asp Tyr Tyr Cys
20 25 30

<210> 43
<211> 32
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL3 VARIANT 18

<400> 43

Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Asp Tyr Tyr Cys
20 25 30

<210> 44
<211> 10
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRL4 VARIANT

<400> 44

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 45
<211> 30
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH1 VARIANT 136

<400> 45

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

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

<210> 46
<211> 30
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH1 VARIANT 2

<400> 46

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

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

<210> 47
<211> 14
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH2 VARIANT 136

<400> 47

Trp Val Arg Gln Ala Pro Gly His Gly Leu Glu Trp Met Gly
1 5 10

<210> 48
<211> 14
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH2 VARIANT 2

<400> 48

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

<210> 49
<211> 14
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH2 VARIANT 8

<400> 49

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

<210> 50
<211> 14
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH2 VARIANT 21

<400> 50

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

<210> 51
<211> 32
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH3 VARIANT 136

<400> 51

Arg Val Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 52
<211> 32
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH3 VARIANT 1

<400> 52

Arg Ala Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 53
<211> 32
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH3 VARIANT 43

<400> 53

Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 54
<211> 32
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH3 VARIANT 103

<400> 54

Arg Ala Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 55
<211> 11
<212> PRT
<213> ARTIFICIAL

<220>
<223> FRH4 VARIANT 136

<400> 55

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

<210> 56
<211> 19
<212> PRT
<213> Bacteriophage M13mp18

<220>
<221> misc_feature
<223> Gene III signal Sequence

<400> 56

Met Glu Trp Ser Gly Val Phe Met Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

Val His Ser

<210> 57
<211> 107
<212> PRT
<213> ARTIFICIAL

<220>
<223> LIGHT CHAIN VARIABLE REGION OF CLONE 136

<400> 57

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

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

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

Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

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

<210> 58
<211> 106
<212> PRT
<213> ARTIFICIAL

<220>
<223> LIGHT CHAIN CONSTANT REGION OF CLONE 136

<400> 58

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

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

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

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

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

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

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

<210> 59

<211> 123
<212> PRT
<213> ARTIFICIAL

<220>
<223> HEAVY CHAIN VARIABLE REGION OF CLONE 136

<400> 59

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

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

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

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

Lys Ala Arg Val Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

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

<210> 60
<211> 330
<212> PRT
<213> ARTIFICIAL

<220>
<223> CONSTANT REGION OF HUMAN IgG1

<400> 60

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

<210> 61
<211> 107
<212> PRT

<213> ARTIFICIAL

<220>
<223> LIGHT CHAIN VARIABLE REGION OF CLONE CL-2C

<400> 61

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

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

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

Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

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

<210> 62
<211> 123
<212> PRT
<213> ARTIFICIAL

<220>
<223> HEAVY CHAIN VARIABLE REGION OF CLONE CL-2C

<400> 62

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

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

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

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

Lys Ala Arg Val Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

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

<210> 63
<211> 107
<212> PRT
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<223> LIGHT CHAIN VARIABLE REGION OF CLONE CL-5I

<400> 63

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

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

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

Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

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

<210> 64
<211> 123
<212> PRT
<213> ARTIFICIAL

<220>
<223> HEAVY CHAIN VARIABLE REGION OF CLONE CL-5I

<400> 64

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

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

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

Gly Glu Ile Asp Pro Gly Thr Phe Glu Thr Asn Tyr Asn Glu Lys Phe

50 55 60

Lys Ala Arg Val Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

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

<210> 65
<211> 107
<212> PRT
<213> ARTIFICIAL

<220>
<223> LIGHT CHAIN VARIABLE REGION OF CLONE CL-5A

<400> 65

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

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

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

Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

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

<210> 66
<211> 123
<212> PRT
<213> ARTIFICIAL

<220>
<223> HEAVY CHAIN VARIABLE REGION OF CLONE CL-5A

<400> 66

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

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

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

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

Lys Ala Arg Val Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

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

<210> 67
<211> 107
<212> PRT
<213> ARTIFICIAL

<220>
<223> LIGHT CHAIN VARIABLE REGION OF CLONE CL-2B

<400> 67

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

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

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

Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

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

<210> 68

<211> 123
<212> PRT
<213> ARTIFICIAL

<220>
<223> HEAVY CHAIN VARIABLE REGION OF CLONE CL-2B

<400> 68

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

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

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

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

Lys Ala Arg Val Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

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

<210> 69
<211> 107
<212> PRT
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<220>
<223> LIGHT CHAIN VARIABLE REGION OF CLONE CL-1136-2C

<400> 69

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

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

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

Tyr Tyr Ala Ser Glu Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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

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

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

<210> 70
<211> 123
<212> PRT
<213> ARTIFICIAL

<220>
<223> HEAVY CHAIN VARIABLE REGION OF CLONE CL-1136-2C

<400> 70

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

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

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

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

Lys Ala Arg Val Thr Phe Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Phe Ser His Phe Ser Gly Ser Asn Tyr Asp Tyr Phe Asp Tyr
100 105 110

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

<210> 71
<211> 108
<212> PRT
<213> Homo sapiens

<400> 71

Asp Ser Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro Ser Pro
1 5 10 15

Phe Asp Leu Phe Ile Arg Lys Ser Pro Thr Ile Thr Cys Leu Val Val
20 25 30

Asp Leu Ala Pro Ser Lys Gly Thr Val Asn Leu Thr Trp Ser Arg Ala
35 40 45

Ser Gly Lys Pro Val Asn His Ser Thr Arg Lys Glu Glu Lys Gln Arg
50 55 60

Asn Gly Thr Leu Thr Val Thr Ser Thr Leu Pro Val Gly Thr Arg Asp
65 70 75 80

Trp Ile Glu Gly Glu Thr Tyr Gln Cys Arg Val Thr His Pro His Leu
85 90 95

Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr Ser
100 105

<210> 72
<211> 12
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<400> 72

Asn Pro Arg Gly Val Ser Xaa Tyr Xaa Xaa Arg Xaa
1 5 10

<210> 73
<211> 12
<212> PRT
<213> ARTIFICIAL

<220>
<223> PEPTIDE DERIVED FROM CH3 DOMAIN OF IGE

<400> 73

Asn Pro Arg Gly Val Ser Ala Tyr Leu Ser Arg Pro
1 5 10

<210> 74
<211> 9
<212> PRT
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<223> Xaa can be any naturally occurring amino acid

<400> 74

Leu Pro Arg Ala Leu Xaa Arg Ser Xaa
1 5

<210> 75
<211> 9
<212> PRT
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<220>
<223> PEPTIDE DERIVED FROM CH3 DOMAIN OF IGE

<400> 75

Leu Pro Arg Ala Leu Met Arg Ser Thr
1 5

<210> 76
<211> 12
<212> PRT
<213> ARTIFICIAL

<220>
<223> PEPTIDE DERIVED FROM CH3 DOMAIN OF IGE

<400> 76

His Pro His Leu Pro Arg Ala Leu Met Arg Ser Thr
1 5 10

<210> 77
<211> 12
<212> PRT
<213> ARTIFICIAL

<220>
<223> PEPTIDE DERIVED FROM CH3 DOMAIN OF IGE

<400> 77

Leu Pro Arg Ala Leu Met Arg Ser Thr Thr Lys Thr
1 5 10