

SEQUENCE LISTING

<110> MEDIMMUNE LTD and THE JOHNS HOPKINS UNIVERSITY

<120> LOX1-BINDING PROTEINS AND METHODS OF USE BASED THEREON

<130> LOX1-100W01

<140> 62/058,254

<141> 1 October 2014

<160> 82

<170> PatentIn version 3.5

<210> 1

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Lox514 CDR-1 Heavy Chain sequence

<400> 1

Glu Leu Ser Met His

1 5

<210> 2

<211> 17

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<220>

<223> LX5140110 CDR-2 Heavy Chain sequence

<400> 2

Gly Phe Asp Pro Glu Asp Phe Lys Tyr His Thr His Gln Lys Phe Gln

1 5 10 15

Gly

<210> 3

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<400> 3

Val Trp Gly Thr Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 4

<211> 129

<212> PRT

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<220>

<223> LX5140110 Heavy Chain sequence

<400> 4

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

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

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

Gly Gly Phe Asp Pro Glu Asp Phe Lys Tyr His Thr His Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Leu Val Trp Gly Thr Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr

100

105

110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 5
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<400> 5

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

Gly

<210> 6
<211> 17
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<223> LX5140011 CDR-2 Heavy Chain sequence

<400> 6

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

Gly

<210> 7
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<223> LX5140014 CDR-2 Heavy Chain sequence

<400> 7

Gly	Phe	Asp	Pro	Glu	Asp	Tyr	Thr	Ile	Arg	Val	Gly	Gln	Lys	Phe	Gln
1				5				10						15	

Gly

<210> 8

<211> 17

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<400> 8

Gly	Phe	Asp	Pro	Glu	Asp	Trp	Gln	Thr	His	Thr	Ala	Gln	Lys	Phe	Gln
1				5				10						15	

Gly

<210> 9

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<400> 9

Gly	Phe	Asp	Pro	Glu	Asp	Trp	Thr	Ile	His	Val	Asp	Gln	Lys	Phe	Gln
1				5				10						15	

Gly

<210> 10
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<400> 10

Gly	Phe	Asp	Pro	Glu	Asp	Trp	Gln	Tyr	His	Val	Ser	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 11
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<400> 11

Gly	Phe	Asp	Pro	Glu	Asp	Trp	Ser	Asn	His	Val	Ser	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 12
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<400> 12

Gly	Phe	Asp	Pro	Glu	Asp	Trp	Lys	Tyr	His	Leu	Ser	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

<210> 13
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<400> 13

Gly	Phe	Asp	Pro	Glu	Asp	Trp	Ala	Tyr	His	Gln	Ala	Gln	Lys	Phe	Gln
1				5					10					15	

Gly

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<400> 14

Pro	Asn	Gly	Gln	Gln	Gly	Lys	Gly	Val	Arg	Gly	Trp	Asp	Tyr	Tyr	Tyr
1			5						10					15	

Gly	Met	Asp	Val
			20

<210> 15
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<400> 15

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

Gly Met Asp Val
20

<210> 16
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<400> 16

Pro Asp Gly Thr His Gln Gly Gly Val Arg Gly Trp Asp Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 17
<211> 20
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<220>
<223> LX5140092_N CDR-3 Heavy Chain sequence

<400> 17

Pro Asn Gly Thr His Gln Gly Gly Val Arg Gly Trp Asp Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 18
<211> 20
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<400> 18

Pro Asp Gly Gln Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr Tyr Tyr
1 5 10 15

Gly Met Asp Val
20

<210> 19

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<400> 19

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

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

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

Gly Gly Phe Asp Pro Glu Asp Trp Glu Tyr Ala Tyr Asp Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Thr Pro Asn Gly Gln Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 20
<211> 129
<212> PRT
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<400> 20

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

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

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

Gly Gly Phe Asp Pro Glu Asp Tyr Thr Ile Arg Val Gly Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Thr Pro Asn Gly Gln Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 21
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<400> 21

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

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

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

Gly Gly Phe Asp Pro Glu Asp Trp Gln Thr His Thr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Thr Pro Asn Gly Gln Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 22
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<400> 22

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

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

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

Gly Gly Phe Asp Pro Glu Asp Trp Thr Ile His Val Asp Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Thr Pro Asn Gly Gln Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 23
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<400> 23

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

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

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

Gly Gly Phe Asp Pro Glu Asp Trp Gln Tyr His Val Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Thr Pro Asn Gly Gln Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 24

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<400> 24

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

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

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

Gly Gly Phe Asp Pro Glu Asp Trp Ser Asn His Val Ser Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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

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

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 25

<211> 129

<212> PRT

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<400> 25

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

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

Ser

<210> 26
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<400> 26

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

20

25

30

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

Gly Gly Phe Asp Pro Glu Asp Trp Lys Tyr His Leu Ser Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Thr Pro Asn Gly Thr His Gln Gly Gly Val Arg Gly Trp Asp Tyr
 100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120 125

Ser

<210> 27

<211> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> LX5140093_D Heavy Chain sequence

<400> 27

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

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

Ser Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met

35

40

45

Gly Gly Phe Asp Pro Glu Asp Trp Ala Tyr His Gln Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Thr Pro Asp Gly Gln Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr
 100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
 115 120 125

Ser

<210> 28

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<400> 28

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

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

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

Gly Gly Phe Asp Pro Glu Asp Trp Ala Tyr His Gln Ala Gln Lys Phe

50

55

60

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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 Thr Pro Asn Gly Gln Gln Gly Lys Gly Val Arg Gly Trp Asp Tyr
100 105 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
115 120 125

Ser

<210> 29

<211> 129

<212> PRT

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<400> 29

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

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

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

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

Gln Gly Arg Val Thr Met Thr Glu Asp Thr Ser Thr Asp 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	Thr	Pro	Asn	Gly	Gln	Gln	Gly	Lys	Gly	Val	Arg	Gly	Trp	Asp	Tyr
			100					105					110		
Tyr	Tyr	Gly	Met	Asp	Val	Trp	Gly	Arg	Gly	Thr	Thr	Val	Thr	Val	Ser
		115					120					125			
Ser															

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 <400> 30

Thr	Gly	Ser	Ser	Ser	Asn	Ile	Gly	Ala	Gly	Tyr	Asp	Val	His
1				5					10				

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 <400> 31

Gly	Asn	Ser	Asn	Arg	Pro	Ser
1			5			

<210> 32
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<400> 32

Gln Ser Tyr Asp Ser Ser Leu Ser Gly Trp Val
1 5 10

<210> 33

<211> 111

<212> PRT

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<220>

<223> LX5140110 Light Chain sequence

<400> 33

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

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

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

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

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

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

<210> 34

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

<220>
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<400> 34

Gln Ser Tyr Asp Ser Met Tyr Arg Phe Gly
1 5 10

<210> 35
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LX5140093 CDR-3 Light Chain sequence

<400> 35

Gln Ser Tyr Asp Ser Ser His Arg Ala Trp Ala
1 5 10

<210> 36
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> LX5140094 Light Chain sequence

<400> 36

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

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

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

Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly Val Pro Asp Arg Phe

50

55

60

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Met
85 90 95

Tyr Arg Phe Gly Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 37

<211> 111

<212> PRT

<213> Artificial Sequence

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<223> LX5140093 Light Chain sequence

<400> 37

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

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

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

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

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

His Arg Ala Trp Ala Phe Gly Gly Gly Thr Lys Leu Thr Val Leu

100

105

110

<210> 38
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<400> 38

Asp Tyr Ala Met His
1 5

<210> 39
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox696 CDR-2 Heavy Chain sequence

<400> 39

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

Gly

<210> 40
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960073_G82bS_g1 CDR-3 Heavy Chain sequence

<400> 40

Glu Gly Ser Trp Asn Tyr Asp Ala Leu Asp Ile
1 5 10

<210> 41

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

<220>
<223> LX6960073_G82bS_g1 Heavy Chain sequence

<400> 41

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

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Gly Ser Trp Asn Tyr Asp Ala Leu Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 42
<211> 17
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<220>
<223> LX6960067_ng11 CDR-2 Heavy Chain sequence

<400> 42

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

Gly

<210> 43
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960086_ngl1 CDR-2 Heavy Chain sequence

<400> 43

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

Gly

<210> 44
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox696 CDR-3 Heavy Chain sequence

<400> 44

Glu Gly Asn Trp Asn Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 45
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960067_ngl1 CDR-3 Heavy Chain sequence

<400> 45

Glu Gly Ser Trp Asn Tyr Asp Ala Phe Asp Ile
1 5 10

<210> 46
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960073_ngl1 CDR-3 Heavy Chain sequence

<400> 46

Glu Gly Ser Trp Asn Tyr Asp Ala Leu Asp Ile
1 5 10

<210> 47
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960101_ngl1 CDR-3 Heavy Chain sequence

<400> 47

Glu Gly Asn Trp Asn Tyr Asp Ala Phe Asp Val
1 5 10

<210> 48
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960067_ngl1 Heavy Chain sequence

<400> 48

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

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

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

Ser Gly Val Ser Leu Gln Glu Leu Tyr Thr Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Gly Ser Trp Asn Tyr Asp Ala Phe Asp Ile Trp Gly Arg
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 49

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> LX6960071_ngl1 Heavy Chain sequence

<400> 49

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

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Gly Asn Trp Asn Tyr Asp Ala Phe Asp Ile Trp Gly Arg
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 50

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<223> LX6960073_ngl1 Heavy Chain sequence

<400> 50

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

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Gly Ser Trp Asn Tyr Asp Ala Leu Asp Ile Trp Gly Arg
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 51
<211> 120
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<220>
<223> LX6960086_ngl1 Heavy Chain sequence

<400> 51

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

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

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

Ser Gly Ile Ser Trp Asn Ser Pro Asp Arg Tyr Met Asp Asp Ser Val
50 55 60

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

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

Ala Arg Glu Gly Asn Trp Asn Tyr Asp Ala Phe Asp Ile Trp Gly Arg
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 52
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960101_ngl1 Heavy Chain sequence

<400> 52

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

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Gly Asn Trp Asn Tyr Asp Ala Phe Asp Val Trp Gly Arg
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 53
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960073_g1 Heavy Chain sequence

<400> 53

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

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

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
50 55 60

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

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

Ala Arg Glu Gly Ser Trp Asn Tyr Asp Ala Leu Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 54

<211> 120

<212> PRT

<213> Artificial Sequence

<220>

<223> Lox696 Heavy Chain sequence

<400> 54

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asp Asp Tyr

20

25

30

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

Ser Gly Ile Ser Trp Asn Ser Gly Ser Ile Gly Tyr Ala Asp Ser Val
 50 55 60

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

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

Ala Arg Glu Gly Asn Trp Asn Tyr Asp Ala Phe Asp Ile Trp Gly Arg
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 55
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LX6960073_G82bS_g1 CDR-1 Light Chain sequence

<400> 55

Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser
 1 5 10

<210> 56
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LX6960073_G82bS_g1 CDR-2 Light Chain sequence

<400> 56

Asp Val Ser Lys Arg Pro Ser
1 5

<210> 57
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960073_G82bS_g1 CDR-3 Light Chain sequence

<400> 57

Met Gly Gly Met Gly Arg Ser Thr Asn Trp Val
1 5 10

<210> 58
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960073_G82bS_g1 Light Chain sequence

<400> 58

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

Pro Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

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

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Met Gly Gly Met Gly Arg

85

90

95

Ser Thr Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 59

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> LX6960116_ngl1 CDR-1 Light Chain sequence

<400> 59

Thr Gly Thr Ser Asn Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 60

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Lox696 CDR-2 Light Chain sequence

<400> 60

Asp Val Ser Asn Arg Pro Ser
1 5

<210> 61

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Lox696 CDR-3 Light Chain sequence

<400> 61

Ser Ser Tyr Thr Ser Ser Ser Thr Asn Trp Val
1 5 10

<210> 62

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

<220>
<223> LX6960067_ngl1 CDR-3 Light Chain sequence

<400> 62

Leu Gly Arg Thr Trp Ser Ser Thr Asn Trp Val
1 5 10

<210> 63
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960071_ngl1 CDR-3 Light Chain sequence

<400> 63

Met Gly Ser Met Gly Arg Ser Thr Asn Trp Val
1 5 10

<210> 64
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960094_ngl1 CDR-3 Light Chain sequence

<400> 64

Ala Gln Arg Thr Val Ser Ser Thr Asn Trp Val
1 5 10

<210> 65
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960067_ngl1 Light Chain sequence

<400> 65

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

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

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

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

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

Ser Thr Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 66
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960071_ngl1 Light Chain sequence

<400> 66

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

Pro Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

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

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

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

Ser Thr Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 67

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> LX6960073_ngl1 Light Chain sequence

<400> 67

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

Pro Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
20 25 30

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

Met Ile Tyr Asp Val Ser Lys Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Met Gly Gly Met Gly Arg
85 90 95

Ser Thr Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 68
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960094_ngl1 Light Chain sequence

<400> 68

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

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

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

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

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

Ser Thr Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 69
<211> 111
<212> PRT
<213> Artificial Sequence

<220>
<223> LX6960116_ngl1 Light Chain sequence

<400> 69

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Asn Asp Val Gly Gly Tyr
20 25 30

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

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

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

Ser Thr Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 70

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> Lox696 Light Chain sequence

<400> 70

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

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

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu

35

40

45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
50 55 60

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Ser Ser Tyr Thr Ser Ser
85 90 95

Ser Thr Asn Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 71
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox514 VH CDR2

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa is Gly, Trp, Tyr, or Phe

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa is Glu, Thr, Gln, Ser, Lys, or Ala

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa is Thr, Tyr, Ile, or Asn

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa is Ile, Ala, Arg, or His

<220>
<221> misc_feature

<222> (11)..(11)
<223> Xaa is Tyr, Val, Thr, Leu, or Gln

<220>
<221> misc_feature
<222> (12)..(12)
<223> Xaa is Ala, Asp, Gly, Ser, or His

<400> 71

Gly	Phe	Asp	Pro	Glu	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Lys	Phe	Gln
1				5				10						15	

Gly

<210> 72
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox514 VH CDR3

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa is Pro, Ser, or Val

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa is Asn, Thr, Trp, or Asp

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa is Gln, Arg, or Thr

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is Gln or His

<220>
<221> misc_feature
<222> (6)..(6)

<223> Xaa is Gly or Gln

<220>

<221> misc_feature

<222> (7)..(7)

<223> Xaa is Lys or Gly

<400> 72

Xaa	Xaa	Gly	Xaa	Xaa	Xaa	Xaa	Gly	Val	Arg	Gly	Trp	Asp	Tyr	Tyr	Tyr
1				5					10					15	

Gly Met Asp Val
20

<210> 73

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Lox514 VL CDR3

<220>

<221> misc_feature

<222> (6)..(6)

<223> Xaa is Ser or Met

<220>

<221> misc_feature

<222> (7)..(7)

<223> Xaa is Leu, Tyr, or His

<220>

<221> misc_feature

<222> (8)..(8)

<223> Xaa is Ser or Arg

<220>

<221> misc_feature

<222> (9)..(9)

<223> Xaa is Gly, Ala, or no amino acid

<220>

<221> misc_feature

<222> (10)..(10)

<223> Xaa is Trp or Phe

<220>
<221> misc_feature
<222> (11)..(11)
<223> Xaa is Val, Gly, or Ala

<400> 73

Gln Ser Tyr Asp Ser Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

<210> 74
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox696 VH CDR2

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa is Ile or Val

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa is Trp or Leu

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is Asn or Gln

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa is Ser or Glu

<220>
<221> misc_feature
<222> (7)..(7)
<223> Xaa is Gly, Leu, or Pro

<220>
<221> misc_feature
<222> (8)..(8)
<223> Xaa is Ser, Tyr, or Asp

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa is Ile, Thr, or Arg

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa is Gly or Tyr

<220>
<221> misc_feature
<222> (11)..(11)
<223> Xaa is Tyr or Met

<220>
<221> misc_feature
<222> (12)..(12)
<223> Xaa is Ala or Asp

<400> 74

Gly	Xaa	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Ser	Val	Lys
1			5					10						15	

Gly

<210> 75
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox696 VH CDR3

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa is Asn or Ser

<220>
<221> misc_feature
<222> (9)..(9)
<223> Xaa is Phe or Leu

<220>
<221> misc_feature
<222> (11)..(11)
<223> Xaa is Ile or Val

<400> 75

Glu Gly Xaa Trp Asn Tyr Asp Ala Xaa Asp Xaa
1 5 10

<210> 76
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox696 VL CDR1

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is Ser or Asn

<400> 76

Thr Gly Thr Ser Xaa Asp Val Gly Gly Tyr Asn Tyr Val Ser
1 5 10

<210> 77
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox696 VL CDR2

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa is Asn or Lys

<400> 77

Asp Val Ser Xaa Arg Pro Ser
1 5

<210> 78
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Lox696 VL CDR3

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa is Ser, Leu, Met, or Ala

<220>
<221> misc_feature
<222> (2)..(2)
<223> Xaa is Ser, Gly, or Gln

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa is Tyr, Arg, Ser, or Gly

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa is Thr or Met

<220>
<221> misc_feature
<222> (5)..(5)
<223> Xaa is Ser, Trp, Gly, or Val

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa is Ser or Arg

<400> 78

Xaa Xaa Xaa Xaa Xaa Xaa Ser Thr Asn Trp Val
1 5 10

<210> 79
<211> 50
<212> DNA
<213> Artificial Sequence

<220>

<223> Top Ad-shNontargeted synthetic primer

<400> 79

caccgatgga ttgcacgcag gttctcgaaa gaacctgcgt gcaatccatc 50

<210> 80

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Bottom Ad-shNontargeted synthetic primer

<400> 80

aaaagatgga ttgcacgcag gttctttcga gaacctgcgt gcaatccatc 50

<210> 81

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Top LOX1sh synthetic primer

<400> 81

caccgcttca ctctctcatt cttagcgaac taagaatgag agagtgaagc 50

<210> 82

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Bottom LOX1sh synthetic primer

<400> 82

aaaagcttca ctctctcatt cttagttcgc taagaatgag agagtgaagc 50