

eolf-seql
SEQUENCE LISTING

<110> Singapore Health Services Pte. Ltd
National University of Singapore
Clegg, Richard I

<120> IL-11Ralpha Antibodies

<130> RIC/FP7324841

<150> GB1621439.7

<151> 2016-12-16

<160> 99

<170> PatentIn version 3.5

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<223> BSO-1E3_1

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

Phe Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser

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85

90

95

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

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

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

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

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

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Arg Leu Glu Ser
65 70 75 80

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

Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
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<400> 4

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

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Gln Ser Val Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Glu Tyr Ser
20 25 30

Gly Thr Thr Leu Met Gln Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Tyr Gly Ala Ser Asn Val 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 Asp Asp Ile Ala Met Tyr Phe Cys Gln Gln Ser Arg
85 90 95

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

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<400> 5

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

Glu Asn Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Gly
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

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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 Lys Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
85 90 95

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

Lys

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

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

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

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

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

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

Thr His Val Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
100 105 110

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

Asp Ser Val Ser Leu Ser Cys Arg Ala Ser Gln Ser Ile Ser Asn Asn
20 25 30

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

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

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

Glu Asp Phe Gly Val Tyr Phe Cys Gln Gln Arg Tyr Ser Trp Pro Leu
85 90 95

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

<210> 8

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<400> 8

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

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

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

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

Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65 70 75 80

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

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

<210> 9
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<400> 9

Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val Gly

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

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

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

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

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

Arg Ser Asp Gly Thr Tyr Glu Gly Tyr Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Pro Leu Thr Val Ser Ser
115

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<223> BSO-1E3_2

<400> 11

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

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

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

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

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Asn Thr Ala Tyr

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

Ala

<210> 13
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 <212> PRT
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 <223> BS0-4G3

<400> 13

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 Thr Tyr
 20 25 30

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

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

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

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

Ala His Gly Leu Leu Phe Ala His Trp Gly Gln Gly Thr Leu Val Thr
 100 105 110

Val Ser Ala

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115

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 <223> BSO-5E5

<400> 14

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

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

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

Met Gly Tyr Ile Ser Tyr Asp Ser Ser Asn Asn Tyr Asn Pro Ser Leu
 50 55 60

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

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

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

Gly Thr Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 15
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<223> BSO-7G9

<400> 15

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

Lys Ile Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala His
65 70 75 80

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

Ala Arg Gly Gly Tyr Asp Gly Ser Tyr Gly Pro Trp Phe Ala Tyr Trp
100 105 110

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

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<223> BSO-9A7

<400> 16

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

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

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

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

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

Val Thr Val Ser Ala
115

<210> 17
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<212> PRT
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<400> 17

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

Ser Val Lys Met Ser Cys Lys Ala Ala Gly Tyr Thr Phe Thr Asp Tyr

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20

25

30

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

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

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

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

Ala Arg Arg Ser Thr Thr Ile Arg Phe Gly Ala Met Asp Asn Trp Gly
100 105 110

Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

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

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

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

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Gly Gly Ile Trp Thr Gly Gly Gly Thr Asn Tyr Asn Ser Ala Leu Lys
 50 55 60

Pro Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
 65 70 75 80

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

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

Leu Val Thr Val Ser Ala
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Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
 1 5 10

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<400> 20

Lys Val Ser
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<400> 21

Ser Gln Ser Thr His Val Pro Leu Thr
1 5

<210> 22
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<400> 22

Glu Asn Val Gly Thr Tyr
1 5

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<400> 23

Gly Ala Ser
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<400> 24

Gly Gln Gly Tyr Ser Tyr Pro Tyr Thr
1 5

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<223> BSO-2E5 CDR1 Light Chain

<400> 25

Gln Asp Ile Gly Ser Ser
1 5

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<400> 26

Ala Thr Ala
1

<210> 27

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<223> BSO-2E5 CDR3 Light Chain

<400> 27

Gln Gln Tyr Ala Ser Ser Pro Pro Thr

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1 5

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<400> 28

Glu Ser Val Glu Tyr Ser Gly Thr Thr Leu
 1 5 10

<210> 29
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<400> 29

Gln Gln Ser Arg Lys Val Pro Tyr Thr
 1 5

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<400> 30

Gln Ser Leu Leu Tyr Gly Ser Asn Gln Lys Asn Tyr
 1 5 10

<210> 31
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<400> 31

Trp Ala Ser

1

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> BSO-5E5 CDR3 Light Chain

<400> 32

Gln Gln Tyr Tyr Ser Tyr Pro Arg Thr

1

5

<210> 33

<211> 6

<212> PRT

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<223> BSO-9A7 CDR1 Light Chain

<400> 33

Gln Ser Ile Ser Asn Asn

1

5

<210> 34

<211> 3

<212> PRT

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<223> BSO-9A7 CDR2 Light Chain

<400> 34

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Tyr Ala Ser
1

<210> 35
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<400> 35

Gln Gln Arg Tyr Ser Trp Pro Leu Thr
1 5

<210> 36
<211> 6
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<223> BSO-10D11 CDR1 Light Chain

<400> 36

Gln Glu Ile Ser Ala Tyr
1 5

<210> 37
<211> 3
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<223> BSO-10D11 CDR2 Light Chain

<400> 37

Ser Thr Ser
1

<210> 38

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<211> 9
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<400> 38

Leu Gln Tyr Ala Ser Ser Pro Leu Thr
1 5

<210> 39
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<400> 39

Gln Asn Val Gly Ser Asn
1 5

<210> 40
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<223> BSO-13B10 CDR2 Light Chain

<400> 40

Ser Ala Ser
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<400> 41

Gln Gln Tyr Asn Ser Tyr Pro Leu Thr
1 5

<210> 42

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<400> 42

Gly Phe Thr Phe Thr Asn Asn Trp
1 5

<210> 43

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<223> BSO-1E3_1 CDR2 Heavy Chain

<400> 43

Ile His Pro Asn Ser Gly Ile Thr
1 5

<210> 44

<211> 12

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<223> BSO-1E3_1 CDR3 Heavy Chain

<400> 44

Arg Ser Asp Gly Thr Tyr Glu Gly Tyr Phe Asp Tyr
1 5 10

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<210> 45
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<400> 45

Gly Tyr Asn Phe Asn Asp Tyr Tyr
1 5

<210> 46
<211> 8
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<223> BSO-1E3_2 CDR2 Heavy Chain

<400> 46

Ile Phe Pro Gly Arg Ile Ile Thr
1 5

<210> 47
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<223> BSO-1E3_1 CDR3 Heavy Chain

<400> 47

Ala Arg Gly Val Gly Glu Gly Phe Asp Tyr
1 5 10

<210> 48
<211> 8
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<220>

<223> BSO 2E5 CDR1 Heavy Chain

<400> 48

Gly Phe Thr Phe Ser Thr Ser Tyr
1 5

<210> 49

<211> 8

<212> PRT

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<223> BSO-2E5 CDR2 Heavy Chain

<400> 49

Ile Tyr Ala Gly Thr Gly Ser Thr
1 5

<210> 50

<211> 6

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<223> BSO-2E5 CDR3 Heavy Chain

<400> 50

Ala Arg His Trp Ala Tyr
1 5

<210> 51

<211> 8

<212> PRT

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<220>

<223> BSO-4G3 CDR1 Heavy Chain

<400> 51

Gly Phe Thr Phe Ser Thr Tyr Ala

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1 5

<210> 52
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 <223> BS0-4G3 CDR2 Heavy Chain

<400> 52

Ile Lys Ser Asn Gly Gly Ser Thr
 1 5

<210> 53
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<400> 53

Ala His Gly Leu Leu Phe Ala His
 1 5

<210> 54
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 <223> BS0-5E5 CDR1 Heavy Chain

<400> 54

Gly Tyr Ser Ile Thr Ser Asp Tyr Tyr
 1 5

<210> 55
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<220>

<223> BSO-5E5 CDR2 Heavy Chain

<400> 55

Ile Ser Tyr Asp Ser Ser Asn
1 5

<210> 56

<211> 15

<212> PRT

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<223> BSO-5E5 CDR3 Heavy Chain

<400> 56

Ala Ser Val Gly Tyr Tyr Tyr Val Ser Asp Trp Tyr Phe Asp Val
1 5 10 15

<210> 57

<211> 8

<212> PRT

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<223> BSO-7G9 CDR1 Heavy Chain

<400> 57

Gly Tyr Thr Phe Thr Ser Tyr Trp
1 5

<210> 58

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<400> 58

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Ile His Pro Asn Ser Gly Tyr Thr
1 5

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<400> 59

Ala Arg Gly Gly Tyr Asp Gly Ser Tyr Gly Pro Trp Phe Ala Tyr
1 5 10 15

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<400> 60

Gly Tyr Thr Phe Thr Asn Tyr Trp
1 5

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<400> 61

Ile Gly Pro Ser Asp Ser Lys Thr
1 5

<210> 62

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<400> 62

Ala Arg Gly Asp Tyr Val Leu Phe Thr Tyr
 1 5 10

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<400> 63

Gly Tyr Thr Phe Thr Asp Tyr Trp
 1 5

<210> 64
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<400> 64

Ile Phe Pro Gly Gly Asp Tyr Thr
 1 5

<210> 65
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<400> 65

Ala Arg Arg Ser Thr Thr Ile Arg Phe Gly Ala Met Asp Asn
1 5 10

<210> 66

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<223> BSO-13B10 CDR1 Heavy Chain

<400> 66

Gly Phe Ser Leu Thr Ser Phe Ser
1 5

<210> 67

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> BSO-13B10 CDR2 Heavy Chain

<400> 67

Ile Trp Thr Gly Gly Gly Thr
1 5

<210> 68

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> BSO-13B10 CDR3 Heavy Chain

<400> 68

Ala Arg Asn Ser Asn Tyr Pro Ser Gly Phe Ala Tyr
1 5 10

eolf-seql

<210> 69
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> BSO-9A7, BSO-10D11, BSO-13B10, BSO-2E5 LC-CDR1-1 Family consensus

<220>
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<222> (2)..(2)
<223> X = N, S, E or D

<220>
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<222> (3)..(3)
<223> X = I or V

<220>
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<222> (4)..(4)
<223> X = G or S

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<222> (5)..(5)
<223> X = S, N or A

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X = N, Y or S

<400> 69

Gln Xaa Xaa Xaa Xaa Xaa
1 5

<210> 70
<211> 12
<212> PRT
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<220>
<223> BSO-5E5, BSO-1E3_1, BSO-7G9 LC-CDR1-2 Family Consensus

eolf-seql

<220>
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<223> X = Absent or L

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X = V or Y

<220>
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<222> (6)..(6)
<223> X = H or G

<220>
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<223> X = G or Q

<220>
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<222> (10)..(10)
<223> X = N or K

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<222> (11)..(11)
<223> X = T or N

<400> 70

Gln Ser Leu Xaa Xaa Xaa Ser Asn Xaa Xaa Xaa Tyr
1 5 10

<210> 71
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> BSO-4G3, BSO-1E3_2, BSO-5E5, BSO-9A7, BSO-13B10 LC-CDR2-1 Family Consensus

eolf-seql

<220>
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<222> (1)..(1)
<223> X = G, W, Y or S

<400> 71

Xaa Ala Ser
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<210> 72
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> BSO-10D11, BSO-1E3_1, BSO-7G9 LC-CDR2-2 Family Consensus

<220>
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<222> (1)..(1)
<223> X = S or K

<220>
<221> MISC_FEATURE
<222> (2)..(2)
<223> X = T or V

<400> 72

Xaa Xaa Ser
1

<210> 73
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> BSO-1E3_1, BSO-7G9, BSO-1E3_2, BSO-2E5, BSO-4G3, BSO-5E5,
BSO-9A7, BSO-10D11, BSo-13B10 LC-CDR3-1 Family Consensus

<220>
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eolf-seql

<222> (1)..(1)
 <223> X = Q, S, G or L

<220>
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 <222> (3)..(3)
 <223> X = Y, S, G or R

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 <222> (4)..(4)
 <223> X = Y, A, T, N or R

<220>
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 <223> X = S, H or K

<220>
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 <222> (6)..(6)
 <223> X = V, Y, S or W

<220>
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 <223> X = L, Y, R or P

<400> 73

Xaa Gln Xaa Xaa Xaa Xaa Pro Xaa Thr
 1 5

<210> 74
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BSO-7G9, BSO-9A7, BSO-10D11 HC-CDR1-1 Family Consensus

<220>
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 <222> (6)..(6)
 <223> X = S, N or D

eolf-seql

<400> 74

Gly Tyr Thr Phe Thr Xaa Tyr Trp
1 5

<210> 75

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> BSO-2E5, BSO-4G3, BSO-1E3_1 HC-CDR1-2 Family Consensus

<220>

<221> MISC_FEATURE

<222> (5)..(5)

<223> X = S or T

<220>

<221> MISC_FEATURE

<222> (6)..(6)

<223> X = T or N

<220>

<221> MISC_FEATURE

<222> (7)..(7)

<223> X = S, Y or N

<220>

<221> MISC_FEATURE

<222> (8)..(8)

<223> X = Y, A or W

<400> 75

Gly Phe Thr Phe Xaa Xaa Xaa Xaa
1 5

<210> 76

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> BSO-5E5, BSO-1E3_2 HC-CDR1-3 Family Consensus

eolf-seql

<220>
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 <222> (3)..(3)
 <223> X = S or N

<220>
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 <222> (4)..(4)
 <223> X = I or F

<220>
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 <222> (5)..(5)
 <223> X = T or N

<220>
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 <223> X = Absent or S

<400> 76

Gly Tyr Xaa Xaa Xaa Xaa Asp Tyr Tyr
 1 5

<210> 77
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BSO-1E3_1, BSO-4G3, BSO-2E5, BSO-7G9 HC-CDR2-1 Family Consensus

<220>
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 <222> (2)..(2)
 <223> X = H, K or Y

<220>
 <221> MISC_FEATURE
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 <223> X = P, S or A

<220>

eolf-seql

<221> MISC_FEATURE
 <222> (4)..(4)
 <223> X = N or G

<220>
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 <222> (5)..(5)
 <223> X = S, G or T

<220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> X = S, I or Y

<400> 77

Ile Xaa Xaa Xaa Xaa Gly Xaa Thr
 1 5

<210> 78
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> BSO-1E3_2, BSO-10D11 HC-CDR2-2 Family Consensus

<220>
 <221> MISC_FEATURE
 <222> (5)..(5)
 <223> X = R or G

<220>
 <221> MISC_FEATURE
 <222> (6)..(6)
 <223> X = I or D

<220>
 <221> MISC_FEATURE
 <222> (7)..(7)
 <223> X = I or Y

<400> 78

Ile Phe Pro Gly Xaa Xaa Xaa Thr
 1 5

eolf-seql

<210> 79
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> BSO-7G9, BSO-1E3_2, BSO-9A7 HC-CDR3-1 Family Consensus

<220>
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<222> (4)..(4)
<223> X = Absent, D or G

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> X = Absent or Y

<220>
<221> MISC_FEATURE
<222> (6)..(6)
<223> X = V or D

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> X = G or L

<220>
<221> MISC_FEATURE
<222> (8)..(8)
<223> X = Absent, E or S

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> X = Absent or Y

<220>
<221> MISC_FEATURE
<222> (10)..(10)
<223> X = Absent or G

<220>
<221> MISC_FEATURE

eolf-seql

<222> (11)..(11)
<223> X = Absent or P

<220>
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<222> (12)..(12)
<223> X = Absent or W

<220>
<221> MISC_FEATURE
<222> (14)..(14)
<223> X = D, T or A

<400> 79

Ala	Arg	Gly	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Tyr
1			5					10						15	

<210> 80
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> BSO-1E3_1

<400> 80
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atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg 120
tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300
ctcacgttcg gtgctgggac caagctggag ctgaaa 336

<210> 81
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> BSO-1E5_2

eolf-seql

<400> 81
aacattgttaa tgacccaatc tcccaaattcc atgtccatgt cagtaggaga gagggtcacc 60
ttgagctgca aggccagtga gaatgtgggt acttatgtat cctgggtatca acagaaacca 120
gagcagtctc ctaaactgct gatatacggg gcatccaacc ggtacactgg ggtccccgat 180
cgcttcacag gcagtggatc tgcaacagat ttcactctga ccatcagcag tgtgcaggct 240
gaagaccttg cagattatca ctgtggacag ggttacagct atccgtacac gttcggaggg 300
gggaccaagc tggaaataaa a 321

<210> 82
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> BSO-2E5

<400> 82
gacatccaga tgacccagtc tccatcctcc ttatctgcct ctctgggaga aagagtcagt 60
ctcacttgtc gggcaagtca ggacattggg agtagcttaa actggcttca gcaggaacca 120
gatggaacta ttaaagcct gatctacgcc acagccagtt tagaatctgg tgtccccaaa 180
aggttcagtgc gcagtaggtc tgggtcagac tattctctca ccatcagcag acttgagtct 240
gaagattttg tagactatta ctgtcaacaa tatgctagct ctctcccccac gttcgggtgct 300
gggaccaagc tggagctgaa a 321

<210> 83
<211> 333
<212> DNA
<213> Artificial Sequence

<220>
<223> BSO-4G3

<400> 83
gacattgtgc tcacccaatc tccagcttct ttggctgtgt ctctagggca gagtgtcacc 60

eolf-seql

atctcctgca gagccagtga aagtgttgaa tattctggca ctactttaat gcagtggtag	120
caacagaaac caggacagcc acccaaactc ctcatctatg gtgcatccaa cgtagaatct	180
gggggtccctg ccagggttag tggcagtggg tctgggacag acttcagcct caacatccat	240
cctgtggagg aggatgatat tgcaatgtat ttctgtcagc aaagtaggaa ggttccgtat	300
acgttcggat cggggaccaa gctggaaata aaa	333

<210> 84
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BSO-5E5

<400> 84 gacattgtga tgtcacagtc tccatcctcc ctacctgtgt cagttggaga gaatgttact	60
atgagctgca agtccagtca gagcctttta tatggtagca atcaaaagaa ctacttggcc	120
tggtaccagc agaaaccagg gcagtctcct aaactgctga ttactgggc atccactagg	180
gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagattt cactctcacc	240
atcagcagtg tgaaggctga agacctggca gtttatttct gtcagcaata ttatagctat	300
cctcggacgt tcggtggagg caccaagctg gaaatcaaa	339

<210> 85
 <211> 336
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BSO-7G9

<400> 85 gatgttgta tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc	60
atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg	120
tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt	180

eolf-seq1

tctgggggtcc cagacagggtt cagtggcagt ggatcaggga cagatttcac actcaagatc	240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg	300
ctcacgttcg gtgctgggac caagctggag ctgaaa	336

<210> 86
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BSO-9A7

<400> 86	
gatattgtgc taactcagtc tccagccacc ctgtctatga ctccaggaga tagcgtcagt	60
ctttcctgca gggccagcca aagtattagc aacaacctac actgggtatca acaaaaatca	120
catgagtctc caaggcttct catcaagtat gcttcccagt ccatctctgg gatccccctcc	180
aggttcagtg gcagtggatc ggggacagat ttactctca gtttcaacag tgtggagact	240
gaagattttg gagtgtatct ctgtcaacag agatacagct ggcctctcac gttcggtgct	300
gggaccaagc tggaaatgaa a	321

<210> 87
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BSO-10D11

<400> 87	
gacatccaga tgacccagtc tccatcctcc ttatctgcct ctctgggaga aagagtcagt	60
ctcacttgtc gggcaagtca ggaaattagt gcttacttaa gctggcttca gcagaaacca	120
gatggaacta ttaaagcct gatctacagc acatccactt tagattctgg tgtcccaaaa	180
aggttcagtg gcagtaggtc tgggtcagat tattctctca ccatcagcag ccttgagtct	240
gaagattttg cagactatct ctgtctccaa tatgctagtt ctccgctcac gttcggtgct	300

eolf-seql

gggaccaagc tggagctgaa a 321

<210> 88
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> BSO-13B10

<400> 88
gacattgtga tgaccagtc tcaaaaattc atgtccacat cagtaggaga cagggtcagc 60
gtcacctgca aggccagtca gaatgtgggt agtaatgtag cctggatatca acagaaagca 120
gggcaatctc cttaaagcact gatttactcg gcatcctacc ggtacagtgg agtccctgat 180
cgcttcacag gcagtggatc tgggacagat ttcactctca ccatcagcaa tgtgcagtct 240
gaagacttgg cagagtatct ctgtcagcaa tataacagct atccgctcac gttcgggtgct 300
gggaccaagc tggagctgaa a 321

<210> 89
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> BSO-1E3_1

<400> 89
cagggtccaac tgcagcagcc tggggctgaa ctgggtcacgc ctggggcttc agtgaagttg 60
tcctgcaagg cttctggctt cactttcacc aacaactgga tgactgggt gaagcagaga 120
cctggacaag gccttgagtg gattggaatg attcatccta atagtgggat tactaacatc 180
aatgagaagt tcaagaacaa ggccacagtg actgtagaca aatcctccag cacagtctac 240
atacaactca gcagcctgac atctgaggac tctgcgggtct attactgtcg ctccgatggg 300
acctacgagg gctactttga ctactggggc caaggcaccc ctctcacagt ctctca 357

<210> 90

eolf-seql

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

<220>
 <223> BSO-1E3_2

<400> 90
 cagggtccaac tacagcagtc tggacctgaa ctggtgaagc ctggggcttc agtgaagata 60
 tcctgcaagg cttctggcta caatttcaat gactactata taaactgggt gaaccagagg 120
 cctggacagg gacttgagtg gattggatgg atttttcctg gaagaattat tacttactac 180
 aatgagaaat tcaagggcaa ggccacactt actgtagaca catcctccaa cacagcctac 240
 atgttgctca gcagcctgac ctctgaggac tctgcggctt atttctgtgc aagaggggta 300
 ggagagggct ttgactactg gggccaaggc accactctca cagtctcctc a 351

<210> 91
 <211> 339
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BSO-2E5

<400> 91
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 tcctgcaaga cttctggctt caccttcagt actagttata taagttgggt gaagcagaag 120
 cctcgacaga gtcttgagtg gattgcatgg atttatgctg gaactggtag tactagctat 180
 aatcagaaat tcacaggcaa ggcccaactg actgtagaca catcctccag cacagcctac 240
 atgcaactca gcagcctgac atctgaggac tctgccatct attactgtgc aagacactgg 300
 gcttactggg gccaagggac tctggtcact gtctctgca 339

<210> 92
 <211> 345
 <212> DNA
 <213> Artificial Sequence

eolf-seql

<220>

<223> BSO-4G3

<400> 92

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tcctgtgcag	cctctggatt	cactttcagt	acctatgcc	tgtcttgggt	tcgccagact	120
ccagagaaga	ggctggagtg	ggcgcagcc	attaaaagta	atggtggttag	cacctactat	180
ccagacactg	tgaaggaccg	attcaccatt	tccagagaca	atgccaagaa	caccctgtac	240
ctgcaaatga	gcagtctgag	gcctgaggac	acagccttgt	attactgtgc	acatgggtctc	300
ctgtttgctc	actggggcca	agggactctg	gtcactgtct	ctgca		345

<210> 93

<211> 366

<212> DNA

<213> Artificial Sequence

<220>

<223> BSO-5E5

<220>

<221> misc_feature

<222> (352)..(352)

<223> n is a, c, g, or t

<400> 93

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acctgctctg	tactggcta	ctccatcacc	agtgattatt	actggaactg	gatccggcag	120
tttccaggaa	acaaactgga	atggatgggc	tacataagct	acgatagtag	caataactac	180
aacccatctc	tcaaaaatcg	aatctccatc	actcgtgaca	catctaagaa	ccagtttttc	240
ctgaagttga	attctgtgac	tactgaggac	acagccacat	attactgtgc	ttcagtgggt	300
tattactacg	ttagtgactg	gtacttcgat	gtctggggca	cagggaccac	gntcaccgtc	360
tcctca						366

<210> 94

eolf-seql

<211> 366
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BSO-7G9

<400> 94
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 tcctgcaagg cttctggcta cactttcacc agctactgga tgcactgggt gaagcagagg 120
 cctggacaag gccttgagtg gattggaatg attcatccta atagtgggta tactaattac 180
 aatgagaagt tcaagatcaa ggccacactg actgtagaca aatcctccag cacagcccac 240
 atgcaactca gcagcctgac atctgaggat tctgcggtct atcactgtgc aagagggggg 300
 tatgatgggt cctacgggcc ctggtttgct tactggggcc aagggactct ggtcactgtc 360
 tctgca 366

<210> 95
 <211> 351
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> BSO-9A7

<400> 95
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 tcctgcaagg cttctggcta caccttcacc aactactgga tgcattgggt gaagcagagg 120
 cctgtacaag gccttgagtg gattggtaac attggccctt ctgatagtaa aactcactac 180
 aatcaaaaaat tcaaggacaa ggccacattg actgtagaca aatcctccag cacagcctac 240
 atgcaactca acagcctgac atctgaggac tctgcggtct attactgtgc aaggggtgat 300
 tacgtcctgt ttacttactg gggccaaggg actctgggtca ctgtctctgc a 351

<210> 96
 <211> 363
 <212> DNA

eolf-seql

<213> Artificial Sequence

<220>

<223> BSO-10D11

<400> 96

caggtccagc tgcagcagtc tggaactgag ctggtaaggc ctgggacttc agtgaagatg	60
tcctgcaagg ctgctggata caccttcact gactactgga taggttggat aaagcagagg	120
cctggacatg gccttgagtg gattggagat attttccctg gaggtgatta tactaagtgc	180
agtgagaggt tcaagggcaa ggccaaactg actgcagaca catcctccag cactgcctac	240
atgcagctca gcagactgac atctgaggac tctgccatct attactgtgc aagaaggagt	300
actacgatac gcttcggggc tatggacaac tgggggtcaag gaacctcagt caccgtctcc	360
tca	363

<210> 97

<211> 354

<212> DNA

<213> Artificial Sequence

<220>

<223> BSO-13B10

<400> 97

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acatgcactg tctctggggt ctcattaacc agcttttcta taagctgggt tcgccagcca	120
ccaggaaagg gtctggagtg gcttggagga atatggactg gtggaggcac aaattataat	180
tcagctctca aaccagact gagcatcagc aaagacaact ccaagagtca agttttctta	240
aaaatgaaca gtctgcaaac tgatgacaca gccagggtact actgtgccag aaatagtaac	300
tacccttccg ggtttgctta ctggggccaa gggactctgg tcaactgtctc tgca	354

<210> 98

<211> 1575

<212> DNA

<213> Artificial Sequence

eolf-seql

<220>

<223> IL-11:IL-11Ralpha fusion protein

<400> 98

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ccggcgtgca	ctctccacag	gcttggggac	ctccaggcgt	gcagtatggc	cagcctggca		120
gatccgtgaa	gctgtgctgt	cctggcgtga	cagctggcga	ccctgtgtcc	tggttcagag		180
atggcgagcc	caagctgctg	cagggcccag	attctggact	gggccacgaa	ctggtgctgg		240
cccaggccga	ttctaccgac	gagggcacct	acatctgcca	gaccctggat	ggcgccctgg		300
gcggaacagt	gacactgcag	ctgggctacc	ctcccgccag	acctgtggtg	tcttgtcagg		360
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eolf-seql

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

Pro Val Ser Trp Phe Arg Asp Gly Glu Pro Lys Leu Leu Gln Gly Pro
 50 55 60

Asp Ser Gly Leu Gly His Glu Leu Val Leu Ala Gln Ala Asp Ser Thr
 65 70 75 80

Asp Glu Gly Thr Tyr Ile Cys Gln Thr Leu Asp Gly Ala Leu Gly Gly
 85 90 95

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

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Cys Gln Ala Ala Asp Tyr Glu Asn Phe Ser Cys Thr Trp Ser Pro Ser
115 120 125

Gln Ile Ser Gly Leu Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys Lys
130 135 140

Thr Val Leu Gly Ala Asp Ser Gln Arg Arg Ser Pro Ser Thr Gly Pro
145 150 155 160

Trp Pro Cys Pro Gln Asp Pro Leu Gly Ala Ala Arg Cys Val Val His
165 170 175

Gly Ala Glu Phe Trp Ser Gln Tyr Arg Ile Asn Val Thr Glu Val Asn
180 185 190

Pro Leu Gly Ala Ser Thr Arg Leu Leu Asp Val Ser Leu Gln Ser Ile
195 200 205

Leu Arg Pro Asp Pro Pro Gln Gly Leu Arg Val Glu Ser Val Pro Gly
210 215 220

Tyr Pro Arg Arg Leu Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro
225 230 235 240

Cys Gln Pro His Phe Leu Leu Lys Phe Arg Leu Gln Tyr Arg Pro Ala
245 250 255

Gln His Pro Ala Trp Ser Thr Val Glu Pro Ala Gly Leu Glu Glu Val
260 265 270

Ile Thr Asp Ala Val Ala Gly Leu Pro His Ala Val Arg Val Ser Ala
275 280 285

Arg Asp Phe Leu Asp Ala Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala
290 295 300

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Trp Gly Thr Pro Ser Thr Gly Gly Pro Ala Gly Gln Ser Gly Gly Gly
305 310 315 320

Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Val Pro Gly Pro Pro
325 330 335

Pro Gly Pro Pro Arg Val Ser Pro Asp Pro Arg Ala Glu Leu Asp Ser
340 345 350

Thr Val Leu Leu Thr Arg Ser Leu Leu Ala Asp Thr Arg Gln Leu Ala
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Ala Gln Leu Arg Asp Lys Phe Pro Ala Asp Gly Asp His Asn Leu Asp
370 375 380

Ser Leu Pro Thr Leu Ala Met Ser Ala Gly Ala Leu Gly Ala Leu Gln
385 390 395 400

Leu Pro Gly Val Leu Thr Arg Leu Arg Ala Asp Leu Leu Ser Tyr Leu
405 410 415

Arg His Val Gln Trp Leu Arg Arg Ala Gly Gly Ser Ser Leu Lys Thr
420 425 430

Leu Glu Pro Glu Leu Gly Thr Leu Gln Ala Arg Leu Asp Arg Leu Leu
435 440 445

Arg Arg Leu Gln Leu Leu Met Ser Arg Leu Ala Leu Pro Gln Pro Pro
450 455 460

Pro Asp Pro Pro Ala Pro Pro Leu Ala Pro Pro Ser Ser Ala Trp Gly
465 470 475 480

Gly Ile Arg Ala Ala His Ala Ile Leu Gly Gly Leu His Leu Thr Leu
485 490 495

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Asp Trp Ala Val Arg Gly Leu Leu Leu Leu Lys Thr Arg Leu His His
500 505 510

His His His His
515