

eolf-othd-000001
SEQUENCE LISTING

<110> H. Lundbeck A/S

<120> Sortilin D region antibodies

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<160> 188

<170> PatentIn version 3.5

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<223> 5E1 CDR1 Light Chain

<400> 1

Lys	Ser	Ser	Gln	Ser	Leu	Leu	Asp	Ser	Asn	Gly	Lys	Thr	Tyr	Leu	Asn
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Leu	Val	Ser	Lys	Leu	Asp	Ser
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<400> 3

Cys Gln Gly Thr His Phe Pro Leu Thr
1 5

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Gly Phe Ile Phe Ser Ile Tyr Gly Met Ser
1 5 10

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<223> 5E1 CDR 2 Heavy Chain

<400> 5

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

Gly

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<400> 6

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His Asp Asp Ser Trp Phe Ala Tyr
1 5

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<400> 7

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

Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
20 25 30

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

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

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

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

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

Arg

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<400> 8

Glu Val His Leu Val Glu Ser Gly Gly Asp Leu Val Asn Pro Gly Gly
1 5 10 15

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

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

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

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

Leu Gln Met Ser Gly Leu Lys Ser Glu Asp Thr Gly Thr Tyr His Cys
85 90 95

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

Val Thr Val Ser Ala
115

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<400> 9

Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

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<223> 1F2 (Lambda) CDR2 Light Chain

<400> 10

Gly Thr Asn Asn Arg Ala Pro
1 5

<210> 11

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<400> 11

Ala Leu Trp Tyr Ser Asn His Phe Trp Val
1 5 10

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Gly Phe Thr Phe Ser Ser Tyr Gly Met Ser
1 5 10

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

Gly

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<223> 1F2 (Lambda) CDR3 Heavy Chain

<400> 14

Leu	Cys	Gly	Pro	Leu	Cys	Ser	Gly	Tyr
1				5				

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<400> 15

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 Gly Arg
100 105 110

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Glu Val Gln Leu Val Glu Ser Gly Gly Asp 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

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

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

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

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

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

Ser Val Thr Val Ser Ser
115

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<223> 068 CDR1 Light Chain

<400> 17

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

<210> 18
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<223> 068 CDR2 Light Chain

<400> 18

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 19
<211> 9
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<220>

<223> 068 CDR3 Light Chain

<400> 19

Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 20

<211> 10

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<223> 068 CDR1 Heavy Chain

<400> 20

Gly Phe Thr Phe Ser Ile Tyr Gly Met His
1 5 10

<210> 21

<211> 17

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<223> 068 CDR2 Heavy Chain

<400> 21

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

Gly

<210> 22

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<223> 068 CDR3 Heavy Chain

<400> 22

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

<210> 23

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<220>

<223> 068 VL

<400> 23

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

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

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

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

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

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

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

<210> 24

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<400> 24

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

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

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

Ala Val Ile Ser Tyr Asp Gly Ser Ser Lys Tyr Tyr Ala Asp Ser Val
50 55 60

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

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

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<400> 25

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

<210> 26

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<212> PRT

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<223> 1320 CDR2 Light Chain

<400> 26

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 27

<211> 9

<212> PRT

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<223> 1320 CDR3 Light Chain

<400> 27

Gln Gln Arg Thr Asn Trp Ser Ile Thr
1 5

<210> 28

<211> 10

<212> PRT

<213> Artificial

<220>

<223> 1320 CDR1 Heavy Chain

<400> 28

Gly Phe Thr Phe Ser Ser Tyr Val Met Ser
1 5 10

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<210> 29
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<220>
<223> 1320 CDR2 Heavy Chain

<400> 29

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

Gly

<210> 30
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<212> PRT
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<223> 1320 CDR3 Heavy Chain

<400> 30

Leu Ile Trp Gly Trp Asp Ile
1 5

<210> 31
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<212> PRT
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<220>
<223> 1320 VL

<400> 31

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Ser Ser Leu Glu Pro
65 70 75 80

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

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

<210> 32
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<212> PRT
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<220>
<223> 1320 VH

<400> 32

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

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

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

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

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

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

Ala Lys Leu Ile Trp Gly Trp Asp Ile Trp Gly Gln Gly Thr Met Val
100 105 110

Thr Val Ser Ser
115

<210> 33
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<400> 33

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

<210> 34
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<400> 34

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 35
<211> 9
<212> PRT
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<220>

<223> 93-05 CDR3 Light Chain

<400> 35

Gln Gln Tyr Gly Ser Ser Pro Phe Thr
1 5

<210> 36

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<223> 93-05 CDR1 Heavy Chain

<400> 36

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5 10

<210> 37

<211> 17

<212> PRT

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<223> 93-05 CDR2 Heavy Chain

<400> 37

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

Gly

<210> 38

<211> 11

<212> PRT

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<223> 93-05 CDR3 Heavy Chain

<400> 38

Ile Ala Ala Ala Gly Thr Asn Tyr Phe Asp Tyr
1 5 10

<210> 39

<211> 108

<212> PRT

<213> Artificial

<220>

<223> 93-05 VL

<400> 39

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

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

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 40

<211> 120

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<212> PRT
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<400> 40

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

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

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

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

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

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

Val Ala Ile Ala Ala Ala Gly Thr Asn Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 41
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<400> 41

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

<210> 42

<211> 7

<212> PRT

<213> Artificial

<220>

<223> 93-01 CDR2 Light Chain

<400> 42

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 43

<211> 9

<212> PRT

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<220>

<223> 93-01 CDR3 Light Chain

<400> 43

Gln Gln Tyr Gly Ser Ser Pro Phe Thr
1 5

<210> 44

<211> 10

<212> PRT

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<223> 93-01 CDR1 Heavy Chain

<400> 44

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5 10

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<210> 45
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<400> 45

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

Gly

<210> 46
<211> 11
<212> PRT
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<220>
<223> 93-01 CDR3 Heavy Chain

<400> 46

Ile Ala Ala Ala Gly Thr Asn Tyr Phe Asp Tyr
1 5 10

<210> 47
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<212> PRT
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<220>
<223> 93-01 VL

<400> 47

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

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

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

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

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

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

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 48
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<212> PRT
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<220>
<223> 93-01 VH

<400> 48

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

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

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

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

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

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

Val Ala Ile Ala Ala Ala Gly Thr Asn Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 49
<211> 12
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<220>
<223> 924 CDR1 Light Chain

<400> 49

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

<210> 50
<211> 7
<212> PRT
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<220>
<223> 924 CDR2 Light Chain

<400> 50

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 51
<211> 9
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<220>

<223> 924 CDR3 Light Chain

<400> 51

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> 52

<211> 12

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<220>

<223> 924 CDR1 Heavy Chain

<400> 52

Gly Gly Ser Ile Ser Ser Gly Asn Tyr Tyr Trp Asn
1 5 10

<210> 53

<211> 16

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<220>

<223> 924 CDR2 Heavy Chain

<400> 53

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

<210> 54

<211> 11

<212> PRT

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<220>

<223> 924 CDR3 Heavy Chain

<400> 54

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Leu Ile Thr Ser Gln Asn Phe Phe Phe Asp Tyr
1 5 10

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<220>
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<400> 55

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

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

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

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

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

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

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

<210> 56
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<223> 924 VH

<400> 56

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

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

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

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

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

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

Cys Ala Ala Leu Ile Thr Ser Gln Asn Phe Phe Phe Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 57

<211> 12

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<400> 57

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

<210> 58
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 <212> PRT
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<220>
 <223> 1276 CDR2 Light Chain

<400> 58

Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 59
 <211> 9
 <212> PRT
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<220>
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<400> 59

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
 1 5

<210> 60
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<400> 60

Gly Phe Thr Phe Asn Thr Phe Ala Met Asn
 1 5 10

<210> 61
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<220>

<223> 1276 CDR2 Heavy Chain

<400> 61

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

Gly

<210> 62

<211> 13

<212> PRT

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<220>

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<400> 62

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

<210> 63

<211> 108

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<220>

<223> 1276 VL

<400> 63

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

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

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

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

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

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

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

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<400> 64

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Phe
20 25 30

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

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

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

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

Ala Thr Pro Ile Thr Val Val Arg Gly Val Ser Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 65
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<220>
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<400> 65

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

<210> 66
<211> 7
<212> PRT
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<220>
<223> 849 CDR2 Light Chain

<400> 66

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 67
<211> 9
<212> PRT
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<220>
<223> 849 CDR3 Light Chain

<400> 67

Gln Gln Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 68

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<223> 849 CDR1 Heavy Chain

<400> 68

Gly Phe Thr Phe Asn Thr Phe Ala Met Asn
1 5 10

<210> 69

<211> 17

<212> PRT

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<220>

<223> 849 CDR2 Heavy Chain

<400> 69

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

Gly

<210> 70

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<400> 70

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Leu Val Arg Gly Val Arg Asp Ala Phe Asp Ile
1 5 10

<210> 71
<211> 108
<212> PRT
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<220>
<223> 849 VL

<400> 71

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

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

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

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

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

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

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

<210> 72
<211> 120
<212> PRT
<213> Artificial

<220>

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<223> 849 VH

<400> 72

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Phe
20 25 30

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

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

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

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

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

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 73

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 531-02 CDR1 Light Chain

<400> 73

Arg Ala Ser Gln Ser Val Ser Ser Ser Asp Leu Ala
1 5 10

<210> 74
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> 531-02 CDR2 Light Chain

<400> 74

Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 75
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> 531-02 CDR3 Light Chain

<400> 75

Gln Gln Tyr Gly Ser Ser Pro Leu Thr
 1 5

<210> 76
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> 531-02 CDR1 Heavy Chain

<400> 76

Gly Phe Thr Phe Ser Arg Tyr Val Met Ser
 1 5 10

<210> 77
 <211> 17
 <212> PRT
 <213> Artificial

eolf-othd-000001

<220>

<223> 531-02 CDR2 Heavy Chain

<400> 77

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

Gly

<210> 78

<211> 8

<212> PRT

<213> Artificial

<220>

<223> 531-02 CDR3 Heavy Chain

<400> 78

Gly Ala Phe Gly Ala Phe Asp Ile
1 5

<210> 79

<211> 108

<212> PRT

<213> Artificial

<220>

<223> 531-02 VL

<400> 79

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

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

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

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

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

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

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

<210> 80
<211> 117
<212> PRT
<213> Artificial

<220>
<223> 531-02 VH

<400> 80

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

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

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

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

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

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

Ala Glu Gly Ala Phe Gly Ala Phe Asp Ile Trp Gly Gln Gly Thr Met
100 105 110

Val Thr Val Ser Ser
115

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

<220>
<223> 548-01 CDR1 Light Chain

<400> 81

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

<210> 82
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 548-01 CDR2 Light Chain

<400> 82

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 83
<211> 9
<212> PRT
<213> Artificial

<220>
<223> 548-01 CDR3 Light Chain

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<400> 83

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> 84

<211> 10

<212> PRT

<213> Artificial

<220>

<223> 548-01 CDR1 Heavy Chain

<400> 84

Lys Phe Thr Phe Asn Thr Tyr Ala Met Asn
1 5 10

<210> 85

<211> 17

<212> PRT

<213> Artificial

<220>

<223> 548-01 CDR2 Heavy Chain

<400> 85

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

Gly

<210> 86

<211> 13

<212> PRT

<213> Artificial

<220>

<223> 548-01 CDR3 Heavy Chain

<400> 86

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

<210> 87
<211> 108
<212> PRT
<213> Artificial

<220>
<223> 548-01 VL

<400> 87

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

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

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

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

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

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

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

<210> 88
<211> 122
<212> PRT
<213> Artificial

<220>

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<223> 548-01 VH

<400> 88

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

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

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

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

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

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

Ala Thr Pro Ile Val Val Val Ser Ile Asp Met Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 89

<211> 11

<212> PRT

<213> Artificial

<220>

<223> 548-02 CDR1 Light Chain

<400> 89

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

<210> 90
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> 548-02 CDR2 Light Chain

<400> 90

Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 91
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> 548-02 CDR3 Light Chain

<400> 91

Gln Gln Arg Ser Asn Trp Pro Leu Thr
 1 5

<210> 92
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> 548-02 CDR1 Heavy Chain

<400> 92

Lys Phe Thr Phe Asn Thr Tyr Ala Met Asn
 1 5 10

<210> 93
 <211> 17
 <212> PRT
 <213> Artificial

<220>

<223> 548-02 CDR2 Heavy Chain

<400> 93

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

Gly

<210> 94

<211> 13

<212> PRT

<213> Artificial

<220>

<223> 548-02 CDR3 Heavy Chain

<400> 94

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

<210> 95

<211> 107

<212> PRT

<213> Artificial

<220>

<223> 548-02 VL

<400> 95

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

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

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

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

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

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

<210> 96
<211> 122
<212> PRT
<213> Artificial

<220>
<223> 548-02 VH

<400> 96

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

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

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

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

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

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

Ala Thr Pro Ile Val Val Val Ser Ile Asp Met Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 97
<211> 12
<212> PRT
<213> Artificial

<220>
<223> 1289-02 CDR1 Light Chain

<400> 97

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

<210> 98
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 1289-02 CDR2 Light Chain

<400> 98

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 99
<211> 9
<212> PRT
<213> Artificial

<220>
<223> 1289-02 CDR3 Light Chain

eolf-othd-000001

<400> 99

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> 100

<211> 10

<212> PRT

<213> Artificial

<220>

<223> 1289-02 CDR1 Heavy Chain

<400> 100

Gly Phe Thr Phe Ser Ser Phe Ala Met Ser
1 5 10

<210> 101

<211> 17

<212> PRT

<213> Artificial

<220>

<223> 1289-02 CDR2 Heavy Chain

<400> 101

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

Gly

<210> 102

<211> 13

<212> PRT

<213> Artificial

<220>

<223> 1289-02 CDR3 Heavy Chain

<400> 102

eolf-othd-000001

Pro Ile Thr Leu Val Arg Gly Val Gly Ala Phe Asp Ile
1 5 10

<210> 103
<211> 108
<212> PRT
<213> Artificial

<220>
<223> 1289-02 VL

<400> 103

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

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

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

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

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

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

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

<210> 104
<211> 122
<212> PRT
<213> Artificial

<220>

eolf-othd-000001

<223> 1289-02 VH

<400> 104

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

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

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

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

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

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

Ala Thr Pro Ile Thr Leu Val Arg Gly Val Gly Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 105

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 811-02 CDR1 Light Chain

<400> 105

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

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

<220>
 <223> 811-02 CDR2 Light Chain

<400> 106

Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 107
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> 811-02 CDR3 Light Chain

<400> 107

Gln Gln Tyr Gly Ser Ser Pro Pro Trp Thr
 1 5 10

<210> 108
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> 811-02 CDR1 Heavy Chain

<400> 108

Gly Phe Thr Phe Ser Thr Phe Ala Met Asn
 1 5 10

<210> 109
 <211> 17
 <212> PRT
 <213> Artificial

eolf-othd-000001

<220>

<223> 811-02 CDR2 Heavy Chain

<400> 109

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

Gly

<210> 110

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 811-02 CDR3 Heavy Chain

<400> 110

Ile Pro Val Lys Leu Gly Asp Asp Ala Phe Asp Ile
1 5 10

<210> 111

<211> 109

<212> PRT

<213> Artificial

<220>

<223> 811-02 VL

<400> 111

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

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

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

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

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

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

Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 112
<211> 121
<212> PRT
<213> Artificial

<220>
<223> 811-02 VH

<400> 112

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

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

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

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

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

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

Ala Thr Ile Pro Val Lys Leu Gly Asp Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 113
<211> 12
<212> PRT
<213> Artificial

<220>
<223> 566-01 CDR1 Light Chain

<400> 113

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

<210> 114
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 566-01 CDR2 Light Chain

<400> 114

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 115
<211> 9
<212> PRT
<213> Artificial

<220>
<223> 566-01 CDR3 Light Chain

eolf-othd-000001

<400> 115

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
1 5

<210> 116

<211> 10

<212> PRT

<213> Artificial

<220>

<223> 566-01 CDR1 Heavy Chain

<400> 116

Gly Phe Thr Phe Ser Thr Phe Ala Met Ser
1 5 10

<210> 117

<211> 17

<212> PRT

<213> Artificial

<220>

<223> 566-01 CDR2 Heavy Chain

<400> 117

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

Gly

<210> 118

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 566-01 CDR3 Heavy Chain

<400> 118

eolf-othd-000001

Pro Ile Thr Met Val Arg Gly Glu Ala Phe Asp Ile
1 5 10

<210> 119
<211> 108
<212> PRT
<213> Artificial

<220>
<223> 566-01 VL

<400> 119

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

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

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

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

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

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

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

<210> 120
<211> 121
<212> PRT
<213> Artificial

<220>

eolf-othd-000001

<223> 566-01 VH

<400> 120

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

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

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

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

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

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

Ala Ser Pro Ile Thr Met Val Arg Gly Glu Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 121

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 562 CDR1 Light Chain

<400> 121

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

<210> 122
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> 562 CDR2 Light Chain

<400> 122

Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 123
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> 562 CDR3 Light Chain

<400> 123

Gln Gln Tyr Gly Ser Ser Pro Ile Thr
 1 5

<210> 124
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> 562 CDR1 Heavy Chain

<400> 124

Gly Phe Thr Phe Ser Thr Phe Ala Met Ser
 1 5 10

<210> 125
 <211> 17
 <212> PRT
 <213> Artificial

<220>

<223> 562 CDR2 Heavy Chain

<400> 125

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

Gly

<210> 126

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 562 CDR3 Heavy Chain

<400> 126

Pro	Ile	Thr	Val	Val	Arg	Gly	Glu	Ala	Phe	Asp	Ile
1				5					10		

<210> 127

<211> 108

<212> PRT

<213> Artificial

<220>

<223> 562 VL

<400> 127

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

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

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

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

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

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

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

<210> 128
<211> 121
<212> PRT
<213> Artificial

<220>
<223> 562 VH

<400> 128

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

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

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

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

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

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

Ala Ser Pro Ile Thr Val Val Arg Gly Glu Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 129
<211> 12
<212> PRT
<213> Artificial

<220>
<223> 193 CDR1 Light Chain

<400> 129

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Ile Ala
1 5 10

<210> 130
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 193 CDR2 Light Chain

<400> 130

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 131
<211> 9
<212> PRT
<213> Artificial

<220>
<223> 193 CDR3 Light Chain

eolf-othd-000001

<400> 131

Gln Gln Tyr Val Asn Ser Pro Leu Thr
1 5

<210> 132

<211> 10

<212> PRT

<213> Artificial

<220>

<223> 193 CDR1 Heavy Chain

<400> 132

Gly Phe Thr Phe Thr Ser Phe Ala Met Ser
1 5 10

<210> 133

<211> 17

<212> PRT

<213> Artificial

<220>

<223> 193 CDR2 Heavy Chain

<400> 133

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

Gly

<210> 134

<211> 11

<212> PRT

<213> Artificial

<220>

<223> 193 CDR3 Heavy Chain

<400> 134

eolf-othd-000001

Leu Val Arg Gly Val Ile Ile Val Phe Asp Ile
1 5 10

<210> 135
<211> 108
<212> PRT
<213> Artificial

<220>
<223> 193 VL

<400> 135

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

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

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

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

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

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

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

<210> 136
<211> 120
<212> PRT
<213> Artificial

<220>

eolf-othd-000001

<223> 193 VH

<400> 136

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

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

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

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

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

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

Ala Ser Leu Val Arg Gly Val Ile Ile Val Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 137

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 88 CDR1 Light Chain

<400> 137

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

<210> 138
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> 88 CDR2 Light Chain

<400> 138

Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 139
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> 88 CDR3 Light Chain

<400> 139

Gln Gln Tyr Gly Ser Ser Pro Leu Thr
 1 5

<210> 140
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> 88 CDR1 Heavy Chain

<400> 140

Gly Phe Thr Phe Ser Thr Phe Ala Met Ser
 1 5 10

<210> 141
 <211> 17
 <212> PRT
 <213> Artificial

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<220>

<223> 88 CDR2 Heavy Chain

<400> 141

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

Gly

<210> 142

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 88 CDR3 Heavy Chain

<400> 142

Tyr Ile Val Ala Thr Ile Ala Asp Ala Phe Asp Ile
1 5 10

<210> 143

<211> 108

<212> PRT

<213> Artificial

<220>

<223> 88 VL

<400> 143

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

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

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

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

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

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

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

<210> 144
<211> 121
<212> PRT
<213> Artificial

<220>
<223> 88 VH

<400> 144

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

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

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

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

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

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

Ala Thr Tyr Ile Val Ala Thr Ile Ala Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 145
<211> 12
<212> PRT
<213> Artificial

<220>
<223> 045 CDR1 Light Chain

<400> 145

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

<210> 146
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 045 CDR2 Light Chain

<400> 146

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 147
<211> 9
<212> PRT
<213> Artificial

<220>
<223> 045 CDR3 Light Chain

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<400> 147

Gln His Tyr Gly Ser Ser Pro Leu Thr
1 5

<210> 148

<211> 10

<212> PRT

<213> Artificial

<220>

<223> 045 CDR1 Heavy Chain

<400> 148

Gly Phe Thr Phe Asn Ser Tyr Ala Met Ser
1 5 10

<210> 149

<211> 17

<212> PRT

<213> Artificial

<220>

<223> 045 CDR2 Heavy Chain

<400> 149

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

Gly

<210> 150

<211> 11

<212> PRT

<213> Artificial

<220>

<223> 045 CDR3 Heavy Chain

<400> 150

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Met Val Arg Gly Val Ile Val Asn Phe Asp Tyr
1 5 10

<210> 151
<211> 108
<212> PRT
<213> Artificial

<220>
<223> 045 VL

<400> 151

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

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

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

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

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

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

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

<210> 152
<211> 120
<212> PRT
<213> Artificial

<220>

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<223> 045 VH

<400> 152

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

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

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

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

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

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

Ala Ser Met Val Arg Gly Val Ile Val Asn Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 153

<211> 12

<212> PRT

<213> Artificial

<220>

<223> 044 CDR1 Light Chain

<400> 153

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

<210> 154
 <211> 7
 <212> PRT
 <213> Artificial

<220>
 <223> 044 CDR2 Light Chain

<400> 154

Gly Ala Ser Ser Arg Ala Thr
 1 5

<210> 155
 <211> 9
 <212> PRT
 <213> Artificial

<220>
 <223> 044 CDR3 Light Chain

<400> 155

Gln Gln Tyr Gly Ser Ser Pro Leu Thr
 1 5

<210> 156
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> 044 CDR1 Heavy Chain

<400> 156

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
 1 5 10

<210> 157
 <211> 17
 <212> PRT
 <213> Artificial

eolf-othd-000001

<220>

<223> 044 CDR2 Heavy Chain

<400> 157

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

Gly

<210> 158

<211> 11

<212> PRT

<213> Artificial

<220>

<223> 044 CDR3 Heavy Chain

<400> 158

Met Val Arg Gly Val Phe Ile Asn Phe Asp Tyr
1 5 10

<210> 159

<211> 108

<212> PRT

<213> Artificial

<220>

<223> 044 VL

<400> 159

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

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

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

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

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

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

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

<210> 160
<211> 120
<212> PRT
<213> Artificial

<220>
<223> 044 VH

<400> 160

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

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

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

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

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

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

Ala Ser Met Val Arg Gly Val Phe Ile Asn Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 161
<211> 12
<212> PRT
<213> Artificial

<220>
<223> 002 CDR1 Light Chain

<400> 161

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

<210> 162
<211> 7
<212> PRT
<213> Artificial

<220>
<223> 002 CDR2 Light Chain

<400> 162

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 163
<211> 8
<212> PRT
<213> Artificial

<220>
<223> 002 CDR3 Light Chain

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<400> 163

Gln Gln Tyr Gly Ser Ser Leu Thr
1 5

<210> 164

<211> 10

<212> PRT

<213> Artificial

<220>

<223> 002 CDR1 Heavy Chain

<400> 164

Gly Phe Thr Phe Ser Ser Tyr Ala Met Ser
1 5 10

<210> 165

<211> 17

<212> PRT

<213> Artificial

<220>

<223> 002 CDR2 Heavy Chain

<400> 165

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

Gly

<210> 166

<211> 11

<212> PRT

<213> Artificial

<220>

<223> 002 CDR3 Heavy Chain

<400> 166

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Met Val Arg Gly Val Ile Ile Asn Phe Asp Tyr
1 5 10

<210> 167
<211> 107
<212> PRT
<213> Artificial

<220>
<223> 002 VL

<400> 167

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

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

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

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

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

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

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

<210> 168
<211> 120
<212> PRT
<213> Artificial

<220>

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<223> 002 VH

<400> 168

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

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

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

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

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

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

Ala Val Met Val Arg Gly Val Ile Ile Asn Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 169

<211> 831

<212> PRT

<213> Artificial

<220>

<223> full human Sortilin sequence isoform 1

<400> 169

Met Glu Arg Pro Trp Gly Ala Ala Asp Gly Leu Ser Arg Trp Pro His
1 5 10 15

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Gly Leu Gly Leu Leu Leu Leu Leu Gln Leu Leu Pro Pro Ser Thr Leu
20 25 30

Ser Gln Asp Arg Leu Asp Ala Pro Pro Pro Pro Ala Ala Pro Leu Pro
35 40 45

Arg Trp Ser Gly Pro Ile Gly Val Ser Trp Gly Leu Arg Ala Ala Ala
50 55 60

Ala Gly Gly Ala Phe Pro Arg Gly Gly Arg Trp Arg Arg Ser Ala Pro
65 70 75 80

Gly Glu Asp Glu Glu Cys Gly Arg Val Arg Asp Phe Val Ala Lys Leu
85 90 95

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

Ser Leu Ser Trp Val Gly Asp Ser Thr Gly Val Ile Leu Val Leu Thr
115 120 125

Thr Phe His Val Pro Leu Val Ile Met Thr Phe Gly Gln Ser Lys Leu
130 135 140

Tyr Arg Ser Glu Asp Tyr Gly Lys Asn Phe Lys Asp Ile Thr Asp Leu
145 150 155 160

Ile Asn Asn Thr Phe Ile Arg Thr Glu Phe Gly Met Ala Ile Gly Pro
165 170 175

Glu Asn Ser Gly Lys Val Val Leu Thr Ala Glu Val Ser Gly Gly Ser
180 185 190

Arg Gly Gly Arg Ile Phe Arg Ser Ser Asp Phe Ala Lys Asn Phe Val
195 200 205

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Gln Thr Asp Leu Pro Phe His Pro Leu Thr Gln Met Met Tyr Ser Pro
210 215 220

Gln Asn Ser Asp Tyr Leu Leu Ala Leu Ser Thr Glu Asn Gly Leu Trp
225 230 235 240

Val Ser Lys Asn Phe Gly Gly Lys Trp Glu Glu Ile His Lys Ala Val
245 250 255

Cys Leu Ala Lys Trp Gly Ser Asp Asn Thr Ile Phe Phe Thr Thr Tyr
260 265 270

Ala Asn Gly Ser Cys Lys Ala Asp Leu Gly Ala Leu Glu Leu Trp Arg
275 280 285

Thr Ser Asp Leu Gly Lys Ser Phe Lys Thr Ile Gly Val Lys Ile Tyr
290 295 300

Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe Ala Ser Val Met Ala Asp
305 310 315 320

Lys Asp Thr Thr Arg Arg Ile His Val Ser Thr Asp Gln Gly Asp Thr
325 330 335

Trp Ser Met Ala Gln Leu Pro Ser Val Gly Gln Glu Gln Phe Tyr Ser
340 345 350

Ile Leu Ala Ala Asn Asp Asp Met Val Phe Met His Val Asp Glu Pro
355 360 365

Gly Asp Thr Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp Arg Gly Ile
370 375 380

Val Tyr Ser Lys Ser Leu Asp Arg His Leu Tyr Thr Thr Thr Gly Gly
385 390 395 400

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Glu Thr Asp Phe Thr Asn Val Thr Ser Leu Arg Gly Val Tyr Ile Thr
405 410 415

Ser Val Leu Ser Glu Asp Asn Ser Ile Gln Thr Met Ile Thr Phe Asp
420 425 430

Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn Ser Glu Cys
435 440 445

Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys Ser Leu His Ile His Ala
450 455 460

Ser Tyr Ser Ile Ser Gln Lys Leu Asn Val Pro Met Ala Pro Leu Ser
465 470 475 480

Glu Pro Asn Ala Val Gly Ile Val Ile Ala His Gly Ser Val Gly Asp
485 490 495

Ala Ile Ser Val Met Val Pro Asp Val Tyr Ile Ser Asp Asp Gly Gly
500 505 510

Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro His Tyr Tyr Thr Ile Leu
515 520 525

Asp Ser Gly Gly Ile Ile Val Ala Ile Glu His Ser Ser Arg Pro Ile
530 535 540

Asn Val Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp Gln Thr Tyr
545 550 555 560

Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr Gly Leu Ala Ser Glu Pro
565 570 575

Gly Ala Arg Ser Met Asn Ile Ser Ile Trp Gly Phe Thr Glu Ser Phe
580 585 590

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Leu Thr Ser Gln Trp Val Ser Tyr Thr Ile Asp Phe Lys Asp Ile Leu
595 600 605

Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu Ala His Ser
610 615 620

Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly Tyr Lys Glu
625 630 635 640

Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn Gly Arg Asp
645 650 655

Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser Leu Glu Asp
660 665 670

Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp Ser Lys Cys
675 680 685

Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe Cys Leu Tyr
690 695 700

Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys Ile Pro Gly
705 710 715 720

Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val Lys Asp Leu
725 730 735

Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys Gln Asn Ser
740 745 750

Lys Ser Asn Ser Val Pro Ile Ile Leu Ala Ile Val Gly Leu Met Leu
755 760 765

Val Thr Val Val Ala Gly Val Leu Ile Val Lys Lys Tyr Val Cys Gly
770 775 780

Gly Arg Phe Leu Val His Arg Tyr Ser Val Leu Gln Gln His Ala Glu
785 790 795 800

Ala Asn Gly Val Asp Gly Val Asp Ala Leu Asp Thr Ala Ser His Thr
805 810 815

Asn Lys Ser Gly Tyr His Asp Asp Ser Asp Glu Asp Leu Leu Glu
820 825 830

<210> 170

<211> 88

<212> PRT

<213> Artificial

<220>

<223> D region as identified by present invention

<400> 170

His Tyr Tyr Thr Ile Leu Asp Ser Gly Gly Ile Ile Val Ala Ile Glu
1 5 10 15

His Ser Ser Arg Pro Ile Asn Val Ile Lys Phe Ser Thr Asp Glu Gly
20 25 30

Gln Cys Trp Gln Thr Tyr Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr
35 40 45

Gly Leu Ala Ser Glu Pro Gly Ala Arg Ser Met Asn Ile Ser Ile Trp
50 55 60

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

Asp Phe Lys Asp Ile Leu Glu Arg
85

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<210> 171

<211> 700

<212> PRT

<213> Artificial

<220>

<223> Sortilin hSORTECDBAP

<400> 171

Ser Ala Pro Gly Glu Asp Glu Glu Cys Gly Arg Val Arg Asp Phe Val
1 5 10 15

Ala Lys Leu Ala Asn Asn Thr His Gln His Val Phe Asp Asp Leu Arg
20 25 30

Gly Ser Val Ser Leu Ser Trp Val Gly Asp Ser Thr Gly Val Ile Leu
35 40 45

Val Leu Thr Thr Phe His Val Pro Leu Val Ile Met Thr Phe Gly Gln
50 55 60

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

Thr Asp Leu Ile Asn Asn Thr Phe Ile Arg Thr Glu Phe Gly Met Ala
85 90 95

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

Gly Gly Ser Arg Gly Gly Arg Ile Phe Arg Ser Ser Asp Phe Ala Lys
115 120 125

Asn Phe Val Gln Thr Asp Leu Pro Phe His Pro Leu Thr Gln Met Met
130 135 140

Tyr Ser Pro Gln Asn Ser Asp Tyr Leu Leu Ala Leu Ser Thr Glu Asn
145 150 155 160

Gly Leu Trp Val Ser Lys Asn Phe Gly Gly Lys Trp Glu Glu Ile His
165 170 175

Lys Ala Val Cys Leu Ala Lys Trp Gly Ser Asp Asn Thr Ile Phe Phe
180 185 190

Thr Thr Tyr Ala Asn Gly Ser Cys Lys Ala Asp Leu Gly Ala Leu Glu
195 200 205

Leu Trp Arg Thr Ser Asp Leu Gly Lys Ser Phe Lys Thr Ile Gly Val
210 215 220

Lys Ile Tyr Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe Ala Ser Val
225 230 235 240

Met Ala Asp Lys Asp Thr Thr Arg Arg Ile His Val Ser Thr Asp Gln
245 250 255

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

Phe Tyr Ser Ile Leu Ala Ala Asn Asp Asp Met Val Phe Met His Val
275 280 285

Asp Glu Pro Gly Asp Thr Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp
290 295 300

Arg Gly Ile Val Tyr Ser Lys Ser Leu Asp Arg His Leu Tyr Thr Thr
305 310 315 320

Thr Gly Gly Glu Thr Asp Phe Thr Asn Val Thr Ser Leu Arg Gly Val
325 330 335

Tyr Ile Thr Ser Val Leu Ser Glu Asp Asn Ser Ile Gln Thr Met Ile
340 345 350

Thr Phe Asp Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn
355 360 365

Ser Glu Cys Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys Ser Leu His
370 375 380

Ile His Ala Ser Tyr Ser Ile Ser Gln Lys Leu Asn Val Pro Met Ala
385 390 395 400

Pro Leu Ser Glu Pro Asn Ala Val Gly Ile Val Ile Ala His Gly Ser
405 410 415

Val Gly Asp Ala Ile Ser Val Met Val Pro Asp Val Tyr Ile Ser Asp
420 425 430

Asp Gly Gly Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro His Tyr Tyr
435 440 445

Thr Ile Leu Asp Ser Gly Gly Ile Ile Val Ala Ile Glu His Ser Ser
450 455 460

Arg Pro Ile Asn Val Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp
465 470 475 480

Gln Thr Tyr Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr Gly Leu Ala
485 490 495

Ser Glu Pro Gly Ala Arg Ser Met Asn Ile Ser Ile Trp Gly Phe Thr
500 505 510

Glu Ser Phe Leu Thr Ser Gln Trp Val Ser Tyr Thr Ile Asp Phe Lys
515 520 525

Asp Ile Leu Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu
530 535 540

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Ala His Ser Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly
545 550 555 560

Tyr Lys Glu Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn
565 570 575

Gly Arg Asp Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser
580 585 590

Leu Glu Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp
595 600 605

Ser Lys Cys Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe
610 615 620

Cys Leu Tyr Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys
625 630 635 640

Ile Pro Gly Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val
645 650 655

Lys Asp Leu Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys
660 665 670

Gln Asn Ser Lys Ser Asn Gly Ser Ala Gly Gly Ser Gly Gly Leu Asn
675 680 685

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695 700

<210> 172
<211> 700
<212> PRT
<213> Artificial

<220>

<223> Sortilin SORTECDBAP_hBACK

<400> 172

Ser Ala Pro Gly Glu Asp Glu Glu Cys Gly Arg Val Arg Asp Phe Val
 1 5 10 15

Ala Lys Leu Ala Asn Asn Thr His Gln His Ile Phe Asn Asp Leu Ser
 20 25 30

Gly Ser Val Ser Leu Ser Trp Val Gly Asp Ser Thr Gly Val Ile Leu
 35 40 45

Val Leu Thr Thr Phe Gln Val Pro Ile Phe Met Ile Thr Ile Gly Gln
 50 55 60

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

Thr Asp Leu Ile Asn Asn Thr Phe Ile Arg Ser Asp Phe Gly Ile Ala
 85 90 95

Ile Gly Pro Glu Asn Ser Gly Lys Val Val Leu Thr Ala Asp Val Ser
 100 105 110

Gly Ser His Gly Ser Arg Ile Phe Arg Ser Ser Asp Phe Ala Lys Asn
 115 120 125

Phe Val Gln Gln Glu Leu Pro Phe Val Pro Leu Met Gln Ile Met Tyr
 130 135 140

Ser Pro Gln Asn Ser Asp Tyr Leu Leu Ala Leu Ser Asn Lys Asn Glu
 145 150 155 160

Leu Trp Val Ser Lys Asn Phe Gly Gly Lys Trp Glu Lys Leu Tyr Asp
 165 170 175

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Thr Val Cys Leu Ala Lys Trp Gly Ser Asp Asn Thr Ile Phe Phe Thr
180 185 190

Ala Asn His Asn Gly Ser Cys Ser Asn Asp Arg Gly Met Leu Glu Leu
195 200 205

Trp Arg Thr Ser Asp Leu Gly Lys Ser Phe Lys Thr Ile Gly Ser Lys
210 215 220

Ile Tyr Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe Ala Ser Val Met
225 230 235 240

Thr Gly Lys Gly Thr Leu Arg Ala Ile His Val Ser Thr Asp Gln Gly
245 250 255

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

Tyr Ser Ile Leu Ala Ala Asn Asp Asp Met Val Phe Met His Val Asp
275 280 285

Glu Pro Gly Asp Ser Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp Arg
290 295 300

Gly Ile Val Tyr Ser Lys Ser Leu Glu Arg His Leu Tyr Thr Thr Thr
305 310 315 320

Gly Gly Glu Thr Asp Phe Thr Asn Val Thr Ser Leu Arg Gly Val Tyr
325 330 335

Ile Thr Ser Ile Leu Ala Glu Asp Lys Ser Val Gln Ser Met Ile Thr
340 345 350

Phe Asp Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn Ser
355 360 365

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Lys Cys Asp Ala Thr Ala Arg Asp Pro Glu Lys Cys Ser Leu His Ile
370 375 380

His Ala Ala Tyr Ser Ile Ala Thr Gly Leu Asn Val Pro Met Leu Pro
385 390 395 400

Leu Ser Glu Pro Asn Ala Val Gly Ile Val Ile Ala His Gly Ser Val
405 410 415

Gly Asp Ala Ile Ser Val Met Arg Pro Asp Val Tyr Ile Ser Asp Asp
420 425 430

Gly Gly Tyr Ser Trp Thr Lys Ala Leu Glu Gly Pro His His Tyr Thr
435 440 445

Ile Leu Asp Ser Gly Gly Ile Ile Val Ala Val Glu Gln Asn Ala His
450 455 460

Gln Gly Val Asn Gln Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp
465 470 475 480

Gln Thr Tyr Asn Phe Thr Lys Asp Pro Ile Phe Phe Thr Gly Leu Ala
485 490 495

Ser Glu Pro Gly Ala Arg Ser Met Asn Ile Ser Ile Trp Gly Tyr Arg
500 505 510

Ser Ser Leu Phe His Gln Tyr Trp Ile Ser Tyr Thr Ile Asp Phe Lys
515 520 525

Asp Ile Leu Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu
530 535 540

Ala His Ser Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly
545 550 555 560

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Tyr Lys Glu Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn
565 570 575

Gly Arg Asp Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser
580 585 590

Leu Glu Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp
595 600 605

Ser Lys Cys Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe
610 615 620

Cys Leu Tyr Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys
625 630 635 640

Ile Pro Gly Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val
645 650 655

Lys Asp Leu Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys
660 665 670

Gln Asn Ser Lys Ser Asn Gly Ser Ala Gly Gly Ser Gly Gly Leu Asn
675 680 685

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695 700

<210> 173

<211> 700

<212> PRT

<213> Artificial

<220>

<223> Sortilin SORTECDBAP_tetra

<400> 173

Arg Ser Thr Glu Gln Gly Glu Ser Cys Ser Gly Leu Leu Gly Ala Asp
1 5 10 15

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

Gly Ser Val Ser Leu Ala Trp Val Gly Asp Gly Thr Gly Val Ile Leu
35 40 45

Ala Leu Thr Thr Phe Gln Val Pro Ile Phe Met Ile Thr Ile Gly Gln
50 55 60

Ser Lys Leu Tyr Arg Ser Glu Asp Tyr Gly Lys Ser Phe Glu Asp Val
65 70 75 80

Thr Asn Leu Ile Asn Asn Thr Phe Ile Arg Ser Asp Phe Gly Ile Ala
85 90 95

Ile Gly Pro Glu Asn Ser Gly Lys Val Ile Leu Thr Ala Asp Val Ser
100 105 110

Gly Ser His Gly Ser Arg Ile Phe Val Ser Ser Asp Phe Gly Lys Ser
115 120 125

Phe Thr His Gln Glu Leu Pro Phe Val Pro Leu Met Gln Ile Thr Tyr
130 135 140

Asn Pro Glu Asn Ser Asn Val Leu Leu Ala Leu Ser Asn Lys Asn Glu
145 150 155 160

Leu Trp Leu Ser Glu Asp Phe Gly Thr Asn Trp Lys Lys Leu Tyr Asp
165 170 175

Thr Val Cys Leu Ala Lys Trp Gly Arg Lys Gly Thr Ile Phe Phe Thr
180 185 190

Ala Asn His Asn Gly Ser Cys Ser Asn Asp Arg Gly Met Leu Glu Leu
195 200 205

Glu Arg Thr Thr Asp Tyr Gly Lys Ser Phe Lys Thr Val Ala Ser Lys
 210 215 220

Ile Tyr Ser Phe Gly Leu Gly Gly Lys Phe Leu Phe Ala Ser Val Met
 225 230 235 240

Thr Gly Lys Gly Thr Leu Arg Ala Ile His Val Ser Val Asp Asp Gly
 245 250 255

Asp Thr Trp Asn Met Ala Gln Leu Pro Pro Val Gly His Glu Gln Phe
 260 265 270

Tyr Ser Ile Leu Ala Ala Asn Asp Glu Met Val Phe Met His Val Asp
 275 280 285

Glu Pro Gly Asp Ser Gly Phe Gly Thr Ile Tyr Val Ser Asp Asp Arg
 290 295 300

Gly Thr Val Tyr Ser Lys Ser Leu Glu Arg His Leu Tyr Thr Thr Thr
 305 310 315 320

Gly Gly Glu Thr Asp Phe Ile Asn Val Thr Ser Leu Arg Gly Val Phe
 325 330 335

Thr Thr Ser Ile Leu Ala Glu Asp Lys Ser Val Gln Ser Val Ile Ser
 340 345 350

Phe Asp Gln Gly Gly Glu Trp Val Pro Leu Arg Lys Pro Ala Asp Ser
 355 360 365

Lys Cys Asp Ala Thr Ala Arg Asp Pro Glu Lys Cys Ser Leu His Ile
 370 375 380

His Ala Ala Tyr Ser Ile Ala Thr Gly Leu Asn Val Pro Met Leu Pro
 385 390 395 400

Leu Ser Glu Pro Asn Ala Val Gly Leu Val Leu Ala His Gly Ser Val
405 410 415

Gly Asp Ala Ile Ser Val Met Arg Pro Asp Val Tyr Val Ser Asp Asp
420 425 430

Gly Gly Tyr Thr Trp Ile Lys Ala Leu Glu Gly Pro His His Tyr Ala
435 440 445

Ile Leu Asp Ser Gly Gly Leu Leu Val Ala Val Glu Gln Asn Ala His
450 455 460

Gln Gly Val Asn Gln Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp
465 470 475 480

Gly Val Tyr Asn Phe Thr Lys Asp Pro Ile Phe Phe Thr Gly Leu Ala
485 490 495

Ser Glu Pro Gly Ala Arg Ser Met Asn Val Ser Leu Trp Gly Tyr Arg
500 505 510

Ser Ser Leu Phe His Gln Tyr Trp Ile Ser Phe Thr Ile Asp Phe Arg
515 520 525

Asp Leu Ile Thr Arg Asn Cys Thr Asp Lys Asp Tyr Val Gln Trp Leu
530 535 540

Ala His Ser Asp Asp Ile Ser Asp Pro Asn Asp Gly Cys Met Leu Gly
545 550 555 560

Tyr Lys Glu Lys Phe Leu Arg Leu Lys Lys Asp Ser Val Cys Leu Asn
565 570 575

Gly Arg Asp Tyr Glu Val Asn Thr Gln Pro Thr Pro Cys Leu Cys Thr
580 585 590

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Leu Asp Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Lys Glu Asn Ser
595 600 605

Ser Glu Cys Val Glu Gln Pro Asp Leu Lys Gly Lys Val Leu Glu Phe
610 615 620

Cys Leu His Gly Thr Glu Glu Glu Leu Leu Thr Asn Gly Tyr Arg Lys
625 630 635 640

Ile Pro Gly Asp Lys Cys Glu Gly Gly Gln Ile Pro Glu Arg Lys Glu
645 650 655

Ile Asn Leu Arg Arg Arg Cys Val Ser Asp Leu Leu Gly Pro Glu Phe
660 665 670

Leu Val Lys Lys Ser Ser Gly Ser Ala Gly Gly Ser Gly Gly Leu Asn
675 680 685

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695 700

<210> 174
<211> 701
<212> PRT
<213> Artificial

<220>
<223> Sortilin SORTECDBAP_hB01-05

<400> 174

Ser Ala Pro Gly Glu Asp Glu Glu Cys Gly Arg Val Arg Asp Phe Val
1 5 10 15

Ala Lys Leu Ala Asn Asn Thr His Gln His Val Phe Asp Asp Leu Arg
20 25 30

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Gly	Ser	Val	Ser	Leu	Ser	Trp	Val	Gly	Asp	Ser	Thr	Gly	Val	Ile	Leu
		35					40					45			
Val	Leu	Thr	Thr	Phe	His	Val	Pro	Leu	Val	Ile	Met	Thr	Phe	Gly	Gln
		50				55					60				
Ser	Lys	Leu	Tyr	Arg	Ser	Glu	Asp	Tyr	Gly	Lys	Asn	Phe	Lys	Asp	Ile
65					70					75					80
Thr	Asp	Leu	Ile	Asn	Asn	Thr	Phe	Ile	Arg	Thr	Glu	Phe	Gly	Met	Ala
				85					90					95	
Ile	Gly	Pro	Glu	Asn	Ser	Gly	Lys	Val	Val	Leu	Thr	Ala	Glu	Val	Ser
			100					105						110	
Gly	Gly	Ser	Arg	Gly	Gly	Arg	Ile	Phe	Arg	Ser	Ser	Asp	Phe	Ala	Lys
		115					120					125			
Asn	Phe	Val	Gln	Thr	Asp	Leu	Pro	Phe	His	Pro	Leu	Thr	Gln	Met	Met
		130					135					140			
Tyr	Ser	Pro	Gln	Asn	Ser	Asp	Tyr	Leu	Leu	Ala	Leu	Ser	Thr	Glu	Asn
145					150					155					160
Gly	Leu	Trp	Val	Ser	Lys	Asn	Phe	Gly	Gly	Lys	Trp	Glu	Glu	Ile	His
				165					170					175	
Lys	Ala	Val	Cys	Leu	Ala	Lys	Trp	Gly	Ser	Asp	Asn	Thr	Ile	Phe	Phe
			180					185					190		
Thr	Thr	Tyr	Ala	Asn	Gly	Ser	Cys	Lys	Ala	Asp	Leu	Gly	Ala	Leu	Glu
		195					200					205			
Leu	Trp	Arg	Thr	Ser	Asp	Leu	Gly	Lys	Ser	Phe	Lys	Thr	Ile	Gly	Val
		210					215				220				

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Lys Ile Tyr Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe Ala Ser Val
225 230 235 240

Met Ala Asp Lys Asp Thr Thr Arg Arg Ile His Val Ser Thr Asp Gln
245 250 255

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

Phe Tyr Ser Ile Leu Ala Ala Asn Asp Glu Met Val Phe Met His Val
275 280 285

Asp Glu Pro Gly Asp Ser Gly Phe Gly Thr Ile Tyr Val Ser Asp Asp
290 295 300

Arg Gly Thr Val Tyr Ser Lys Ser Leu Glu Arg His Leu Tyr Thr Thr
305 310 315 320

Thr Gly Gly Glu Thr Asp Phe Ile Asn Val Thr Ser Leu Arg Gly Val
325 330 335

Phe Thr Thr Ser Ile Leu Ala Glu Asp Lys Ser Val Gln Ser Val Ile
340 345 350

Ser Phe Asp Gln Gly Gly Glu Trp Val Pro Leu Arg Lys Pro Ala Asp
355 360 365

Ser Lys Cys Asp Ala Thr Ala Arg Asp Pro Glu Lys Cys Ser Leu His
370 375 380

Ile His Ala Ala Tyr Ser Ile Ala Thr Gly Leu Asn Val Pro Met Leu
385 390 395 400

Pro Leu Ser Glu Pro Asn Ala Val Gly Leu Val Leu Ala His Gly Ser
405 410 415

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Val Gly Asp Ala Ile Ser Val Met Arg Pro Asp Val Tyr Val Ser Asp
420 425 430

Asp Gly Gly Tyr Thr Trp Ile Lys Ala Leu Glu Gly Pro His His Tyr
435 440 445

Ala Ile Leu Asp Ser Gly Gly Leu Leu Val Ala Val Glu Gln Asn Ala
450 455 460

His Gln Gly Val Asn Gln Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys
465 470 475 480

Trp Gly Val Tyr Asn Phe Thr Lys Asp Pro Ile Phe Phe Thr Gly Leu
485 490 495

Ala Ser Glu Pro Gly Ala Arg Ser Met Asn Val Ser Leu Trp Gly Tyr
500 505 510

Arg Ser Ser Leu Phe His Gln Tyr Trp Ile Ser Phe Thr Ile Asp Phe
515 520 525

Arg Asp Leu Ile Thr Arg Asn Cys Thr Asp Lys Asp Tyr Val Gln Trp
530 535 540

Leu Ala His Ser Asp Asp Ile Ser Asp Pro Asn Asp Gly Cys Met Leu
545 550 555 560

Gly Tyr Lys Glu Lys Phe Leu Arg Leu Lys Lys Asp Ser Val Cys Leu
565 570 575

Asn Gly Arg Asp Tyr Glu Val Asn Thr Gln Pro Thr Pro Cys Leu Cys
580 585 590

Thr Leu Asp Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Lys Glu Asn
595 600 605

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Ser Ser Glu Cys Val Glu Gln Pro Asp Leu Lys Gly Lys Val Leu Glu
610 615 620

Phe Cys Leu His Gly Thr Glu Glu Glu Leu Leu Thr Asn Gly Tyr Arg
625 630 635 640

Lys Ile Pro Gly Asp Lys Cys Glu Gly Gly Gln Ile Pro Glu Arg Lys
645 650 655

Glu Ile Asn Leu Arg Arg Arg Cys Val Ser Asp Leu Leu Gly Pro Glu
660 665 670

Phe Leu Val Lys Lys Ser Ser Gly Ser Ala Gly Gly Ser Gly Gly Leu
675 680 685

Asn Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695 700

<210> 175

<211> 700

<212> PRT

<213> Artificial

<220>

<223> Sortilin SORTECDBAP_hRIM

<400> 175

Ser Ala Pro Gly Glu Asp Glu Glu Cys Gly Arg Val Arg Asp Phe Val
1 5 10 15

Ala Lys Leu Ala Asn Asn Thr His Gln His Val Phe Asp Asp Leu Arg
20 25 30

Gly Ser Val Ser Leu Ala Trp Val Gly Asp Gly Thr Gly Val Ile Leu
35 40 45

Ala Leu Thr Thr Phe Gln Val Pro Ile Phe Met Ile Thr Ile Gly Gln
50 55 60

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

Thr Asp Leu Ile Asn Asn Thr Phe Ile Arg Ser Asp Phe Gly Ile Ala
85 90 95

Ile Gly Pro Glu Asn Ser Gly Lys Val Ile Leu Thr Ala Asp Val Ser
100 105 110

Gly Ser His Gly Ser Arg Ile Phe Arg Ser Ser Asp Phe Ala Lys Asn
115 120 125

Phe Val Gln Thr Asp Leu Pro Phe Val Pro Leu Met Gln Ile Thr Tyr
130 135 140

Asn Pro Glu Asn Ser Asn Val Leu Leu Ala Leu Ser Asn Lys Asn Glu
145 150 155 160

Leu Trp Val Ser Lys Asn Phe Gly Gly Lys Trp Glu Glu Ile His Asp
165 170 175

Thr Val Cys Leu Ala Lys Trp Gly Arg Lys Gly Thr Ile Phe Phe Thr
180 185 190

Ala Asn His Asn Gly Ser Cys Ser Asn Asp Arg Gly Met Leu Glu Leu
195 200 205

Trp Arg Thr Ser Asp Leu Gly Lys Ser Phe Lys Thr Ile Gly Val Lys
210 215 220

Ile Tyr Ser Phe Gly Leu Gly Gly Lys Phe Leu Phe Ala Ser Val Met
225 230 235 240

Thr Gly Lys Gly Thr Leu Arg Arg Ile His Val Ser Thr Asp Gln Gly
245 250 255

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

Tyr Ser Ile Leu Ala Ala Asn Asp Glu Met Val Phe Met His Val Asp
275 280 285

Glu Pro Gly Asp Ser Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp Arg
290 295 300

Gly Ile Val Tyr Ser Lys Ser Leu Asp Arg His Leu Tyr Thr Thr Thr
305 310 315 320

Gly Gly Glu Thr Asp Phe Ile Asn Val Thr Ser Leu Arg Gly Val Phe
325 330 335

Thr Thr Ser Ile Leu Ala Glu Asp Lys Ser Ile Gln Thr Met Ile Thr
340 345 350

Phe Asp Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn Ser
355 360 365

Glu Cys Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys Ser Leu His Ile
370 375 380

His Ala Ala Tyr Ser Ile Ala Thr Gly Leu Asn Val Pro Met Leu Pro
385 390 395 400

Leu Ser Glu Pro Asn Ala Val Gly Leu Val Leu Ala His Gly Ser Val
405 410 415

Gly Asp Ala Ile Ser Val Met Arg Pro Asp Val Tyr Ile Ser Asp Asp
420 425 430

Gly Gly Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro His His Tyr Ala
435 440 445

Ile Leu Asp Ser Gly Gly Leu Leu Val Ala Val Glu Gln Asn Ala His
450 455 460

Gln Gly Val Asn Val Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp
465 470 475 480

Gln Thr Tyr Thr Phe Thr Arg Asp Pro Ile Phe Phe Thr Gly Leu Ala
485 490 495

Ser Glu Pro Gly Ala Arg Ser Met Asn Val Ser Leu Trp Gly Tyr Arg
500 505 510

Ser Ser Leu Phe His Gln Gln Trp Val Ser Tyr Thr Ile Asp Phe Lys
515 520 525

Asp Ile Leu Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu
530 535 540

Ala His Ser Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly
545 550 555 560

Tyr Lys Glu Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn
565 570 575

Gly Arg Asp Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser
580 585 590

Leu Glu Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp
595 600 605

Ser Lys Cys Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe
610 615 620

Cys Leu Tyr Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys
625 630 635 640

Ile Pro Gly Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val
645 650 655

Lys Asp Leu Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys
660 665 670

Gln Asn Ser Lys Ser Asn Gly Ser Ala Gly Gly Ser Gly Gly Leu Asn
675 680 685

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695 700

<210> 176
<211> 699
<212> PRT
<213> Artificial

<220>
<223> Sortilin SORTECDBAP_hB06-10

<400> 176

Arg Ser Thr Glu Gln Gly Glu Ser Cys Ser Gly Leu Leu Gly Ala Asp
1 5 10 15

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

Gly Ser Val Ser Leu Ala Trp Val Gly Asp Gly Thr Gly Val Ile Leu
35 40 45

Ala Leu Thr Thr Phe Gln Val Pro Ile Phe Met Ile Thr Ile Gly Gln
50 55 60

Ser Lys Leu Tyr Arg Ser Glu Asp Tyr Gly Lys Ser Phe Glu Asp Val
65 70 75 80

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Thr Asn Leu Ile Asn Asn Thr Phe Ile Arg Ser Asp Phe Gly Ile Ala
85 90 95

Ile Gly Pro Glu Asn Ser Gly Lys Val Ile Leu Thr Ala Asp Val Ser
100 105 110

Gly Ser His Gly Ser Arg Ile Phe Val Ser Ser Asp Phe Gly Lys Ser
115 120 125

Phe Thr His Gln Glu Leu Pro Phe Val Pro Leu Met Gln Ile Thr Tyr
130 135 140

Asn Pro Glu Asn Ser Asn Val Leu Leu Ala Leu Ser Asn Lys Asn Glu
145 150 155 160

Leu Trp Leu Ser Glu Asp Phe Gly Thr Asn Trp Lys Lys Leu Tyr Asp
165 170 175

Thr Val Cys Leu Ala Lys Trp Gly Arg Lys Gly Thr Ile Phe Phe Thr
180 185 190

Ala Asn His Asn Gly Ser Cys Ser Asn Asp Arg Gly Met Leu Glu Leu
195 200 205

Glu Arg Thr Thr Asp Tyr Gly Lys Ser Phe Lys Thr Val Ala Ser Lys
210 215 220

Ile Tyr Ser Phe Gly Leu Gly Gly Lys Phe Leu Phe Ala Ser Val Met
225 230 235 240

Thr Gly Lys Gly Thr Leu Arg Ala Ile His Val Ser Val Asp Asp Gly
245 250 255

Asp Thr Trp Asn Met Ala Gln Leu Pro Ser Val Gly Gln Glu Gln Phe
260 265 270

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Tyr Ser Ile Leu Ala Ala Asn Asp Asp Met Val Phe Met His Val Asp
 275 280 285

Glu Pro Gly Asp Thr Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp Arg
 290 295 300

Gly Ile Val Tyr Ser Lys Ser Leu Asp Arg His Leu Tyr Thr Thr Thr
 305 310 315 320

Gly Gly Glu Thr Asp Phe Thr Asn Val Thr Ser Leu Arg Gly Val Tyr
 325 330 335

Ile Thr Ser Val Leu Ser Glu Asp Asn Ser Ile Gln Thr Met Ile Thr
 340 345 350

Phe Asp Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn Ser
 355 360 365

Glu Cys Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys Ser Leu His Ile
 370 375 380

His Ala Ser Tyr Ser Ile Ser Gln Lys Leu Asn Val Pro Met Ala Pro
 385 390 395 400

Leu Ser Glu Pro Asn Ala Val Gly Ile Val Ile Ala His Gly Ser Val
 405 410 415

Gly Asp Ala Ile Ser Val Met Val Pro Asp Val Tyr Ile Ser Asp Asp
 420 425 430

Gly Gly Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro His Tyr Tyr Thr
 435 440 445

Ile Leu Asp Ser Gly Gly Ile Ile Val Ala Ile Glu His Ser Ser Arg
 450 455 460

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Pro Ile Asn Val Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp Gln
465 470 475 480

Thr Tyr Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr Gly Leu Ala Ser
485 490 495

Glu Pro Gly Ala Arg Ser Met Asn Ile Ser Ile Trp Gly Phe Thr Glu
500 505 510

Ser Phe Leu Thr Ser Gln Trp Val Ser Tyr Thr Ile Asp Phe Lys Asp
515 520 525

Ile Leu Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu Ala
530 535 540

His Ser Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly Tyr
545 550 555 560

Lys Glu Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn Gly
565 570 575

Arg Asp Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser Leu
580 585 590

Glu Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp Ser
595 600 605

Lys Cys Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe Cys
610 615 620

Leu Tyr Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys Ile
625 630 635 640

Pro Gly Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val Lys
645 650 655

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Asp Leu Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys Gln
660 665 670

Asn Ser Lys Ser Asn Gly Ser Ala Gly Gly Ser Gly Gly Leu Asn Asp
675 680 685

Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695

<210> 177
<211> 700
<212> PRT
<213> Artificial

<220>
<223> Sortilin SORTECDBAP_hB12390

<400> 177

Ser Ala Pro Gly Glu Asp Glu Glu Cys Gly Arg Val Arg Asp Phe Val
1 5 10 15

Ala Lys Leu Ala Asn Asn Thr His Gln His Val Phe Asp Asp Leu Arg
20 25 30

Gly Ser Val Ser Leu Ser Trp Val Gly Asp Ser Thr Gly Val Ile Leu
35 40 45

Val Leu Thr Thr Phe His Val Pro Leu Val Ile Met Thr Phe Gly Gln
50 55 60

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

Thr Asp Leu Ile Asn Asn Thr Phe Ile Arg Thr Glu Phe Gly Met Ala
85 90 95

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

Gly Gly Ser Arg Gly Gly Arg Ile Phe Arg Ser Ser Asp Phe Ala Lys
115 120 125

Asn Phe Val Gln Thr Asp Leu Pro Phe His Pro Leu Thr Gln Met Met
130 135 140

Tyr Ser Pro Gln Asn Ser Asp Tyr Leu Leu Ala Leu Ser Thr Glu Asn
145 150 155 160

Gly Leu Trp Val Ser Lys Asn Phe Gly Gly Lys Trp Glu Glu Ile His
165 170 175

Lys Thr Val Cys Leu Ala Lys Trp Gly Arg Lys Gly Thr Ile Phe Phe
180 185 190

Thr Ala Asn His Asn Gly Ser Cys Ser Asn Asp Arg Gly Met Leu Glu
195 200 205

Leu Glu Arg Thr Thr Asp Tyr Gly Lys Ser Phe Lys Thr Val Ala Ser
210 215 220

Lys Ile Tyr Ser Phe Gly Leu Gly Gly Lys Phe Leu Phe Ala Ser Val
225 230 235 240

Met Thr Gly Lys Gly Thr Leu Arg Ala Ile His Val Ser Val Asp Asp
245 250 255

Gly Asp Thr Trp Asn Met Ala Gln Leu Pro Pro Val Gly His Glu Gln
260 265 270

Phe Tyr Ser Ile Leu Ala Ala Asn Asp Glu Met Val Phe Met His Val
275 280 285

Asp Glu Pro Gly Asp Ser Gly Phe Gly Thr Ile Tyr Val Ser Asp Asp
290 295 300

Arg Gly Thr Val Tyr Ser Lys Ser Leu Glu Arg His Leu Tyr Thr Thr
305 310 315 320

Thr Gly Gly Glu Thr Asp Phe Ile Asn Val Thr Ser Leu Arg Gly Val
325 330 335

Phe Thr Thr Ser Ile Leu Ala Glu Asp Lys Ser Val Gln Ser Val Ile
340 345 350

Ser Phe Asp Gln Gly Gly Glu Trp Val Pro Leu Arg Lys Pro Ala Asp
355 360 365

Ser Lys Cys Asp Ala Thr Ala Arg Asp Pro Glu Lys Cys Ser Leu His
370 375 380

Ile His Ala Ala Tyr Ser Ile Ala Thr Gly Leu Asn Val Pro Met Leu
385 390 395 400

Pro Leu Ser Glu Pro Asn Ala Val Gly Leu Val Leu Ala His Gly Ser
405 410 415

Val Gly Asp Ala Ile Ser Val Met Arg Pro Asp Val Tyr Val Ser Asp
420 425 430

Asp Gly Gly Tyr Thr Trp Ile Lys Ala Leu Glu Gly Pro His Tyr Tyr
435 440 445

Thr Ile Leu Asp Ser Gly Gly Ile Ile Val Ala Ile Glu His Ser Ser
450 455 460

Arg Pro Ile Asn Val Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp
465 470 475 480

Gln Thr Tyr Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr Gly Leu Ala
485 490 495

Ser Glu Pro Gly Ala Arg Ser Met Asn Ile Ser Ile Trp Gly Phe Thr
500 505 510

Glu Ser Phe Leu Thr Ser Gln Trp Val Ser Tyr Thr Ile Asp Phe Lys
515 520 525

Asp Ile Leu Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu
530 535 540

Ala His Ser Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly
545 550 555 560

Tyr Lys Glu Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn
565 570 575

Gly Arg Asp Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser
580 585 590

Leu Glu Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp
595 600 605

Ser Lys Cys Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe
610 615 620

Cys Leu Tyr Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys
625 630 635 640

Ile Pro Gly Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val
645 650 655

Lys Asp Leu Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys
660 665 670

Gln Asn Ser Lys Ser Asn Gly Ser Ala Gly Gly Ser Gly Gly Leu Asn
675 680 685

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695 700

<210> 178
<211> 700
<212> PRT
<213> Artificial

<220>
<223> Sortilin SORTECDBAP_hB45678

<400> 178

Arg Ser Thr Glu Gln Gly Glu Ser Cys Ser Gly Leu Leu Gly Ala Asp
1 5 10 15

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

Gly Ser Val Ser Leu Ala Trp Val Gly Asp Gly Thr Gly Val Ile Leu
35 40 45

Ala Leu Thr Thr Phe Gln Val Pro Ile Phe Met Ile Thr Ile Gly Gln
50 55 60

Ser Lys Leu Tyr Arg Ser Glu Asp Tyr Gly Lys Ser Phe Glu Asp Val
65 70 75 80

Thr Asn Leu Ile Asn Asn Thr Phe Ile Arg Ser Asp Phe Gly Ile Ala
85 90 95

Ile Gly Pro Glu Asn Ser Gly Lys Val Ile Leu Thr Ala Asp Val Ser
100 105 110

Gly Ser His Gly Ser Arg Ile Phe Val Ser Ser Asp Phe Gly Lys Ser
115 120 125

eolf-othd-000001

Phe Thr His Gln Glu Leu Pro Phe Val Pro Leu Met Gln Ile Thr Tyr
 130 135 140

Asn Pro Glu Asn Ser Asn Val Leu Leu Ala Leu Ser Asn Lys Asn Glu
 145 150 155 160

Leu Trp Leu Ser Glu Asp Phe Gly Thr Asn Trp Lys Lys Leu Tyr Asp
 165 170 175

Ala Val Cys Leu Ala Lys Trp Gly Ser Asp Asn Thr Ile Phe Phe Thr
 180 185 190

Thr Tyr Ala Asn Gly Ser Cys Lys Ala Asp Leu Gly Ala Leu Glu Leu
 195 200 205

Trp Arg Thr Ser Asp Leu Gly Lys Ser Phe Lys Thr Ile Gly Val Lys
 210 215 220

Ile Tyr Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe Ala Ser Val Met
 225 230 235 240

Ala Asp Lys Asp Thr Thr Arg Arg Ile His Val Ser Thr Asp Gln Gly
 245 250 255

Asp Thr Trp Ser Met Ala Gln Leu Pro Ser Val Gly Gln Glu Gln Phe
 260 265 270

Tyr Ser Ile Leu Ala Ala Asn Asp Asp Met Val Phe Met His Val Asp
 275 280 285

Glu Pro Gly Asp Thr Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp Arg
 290 295 300

Gly Ile Val Tyr Ser Lys Ser Leu Asp Arg His Leu Tyr Thr Thr Thr
 305 310 315 320

eolf-othd-000001

Gly Gly Glu Thr Asp Phe Thr Asn Val Thr Ser Leu Arg Gly Val Tyr
 325 330 335

Ile Thr Ser Val Leu Ser Glu Asp Asn Ser Ile Gln Thr Met Ile Thr
 340 345 350

Phe Asp Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn Ser
 355 360 365

Glu Cys Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys Ser Leu His Ile
 370 375 380

His Ala Ser Tyr Ser Ile Ser Gln Lys Leu Asn Val Pro Met Ala Pro
 385 390 395 400

Leu Ser Glu Pro Asn Ala Val Gly Ile Val Ile Ala His Gly Ser Val
 405 410 415

Gly Asp Ala Ile Ser Val Met Val Pro Asp Val Tyr Ile Ser Asp Asp
 420 425 430

Gly Gly Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro His His Tyr Ala
 435 440 445

Ile Leu Asp Ser Gly Gly Leu Leu Val Ala Val Glu Gln Asn Ala His
 450 455 460

Gln Gly Val Asn Gln Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp
 465 470 475 480

Gly Val Tyr Asn Phe Thr Lys Asp Pro Ile Phe Phe Thr Gly Leu Ala
 485 490 495

Ser Glu Pro Gly Ala Arg Ser Met Asn Val Ser Leu Trp Gly Tyr Arg
 500 505 510

eolf-othd-000001

Ser Ser Leu Phe His Gln Tyr Trp Ile Ser Phe Thr Ile Asp Phe Arg
515 520 525

Asp Leu Ile Thr Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu
530 535 540

Ala His Ser Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly
545 550 555 560

Tyr Lys Glu Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn
565 570 575

Gly Arg Asp Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser
580 585 590

Leu Glu Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp
595 600 605

Ser Lys Cys Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe
610 615 620

Cys Leu Tyr Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys
625 630 635 640

Ile Pro Gly Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val
645 650 655

Lys Asp Leu Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys
660 665 670

Gln Asn Ser Lys Ser Asn Gly Ser Ala Gly Gly Ser Gly Gly Leu Asn
675 680 685

Asp Ile Phe Glu Ala Gln Lys Ile Glu Trp His Glu
690 695 700

eolf-othd-000001

<210> 179

<211> 763

<212> PRT

<213> Artificial

<220>

<223> Sortilin SORTECD_HIS

<400> 179

Met Glu Arg Pro Trp Gly Ala Ala Asp Gly Leu Ser Arg Trp Pro His
1 5 10 15

Gly Leu Gly Leu Leu Leu Leu Leu Gln Leu Leu Pro Pro Ser Thr Leu
20 25 30

Ser Gln Asp Arg Leu Asp Ala Pro Pro Pro Pro Ala Ala Pro Leu Pro
35 40 45

Arg Trp Ser Gly Pro Ile Gly Val Ser Trp Gly Leu Arg Ala Ala Ala
50 55 60

Ala Gly Gly Ala Phe Pro Arg Gly Gly Arg Trp Arg Arg Ser Ala Pro
65 70 75 80

Gly Glu Asp Glu Glu Cys Gly Arg Val Arg Asp Phe Val Ala Lys Leu
85 90 95

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

Ser Leu Ser Trp Val Gly Asp Ser Thr Gly Val Ile Leu Val Leu Thr
115 120 125

Thr Phe His Val Pro Leu Val Ile Met Thr Phe Gly Gln Ser Lys Leu
130 135 140

Tyr Arg Ser Glu Asp Tyr Gly Lys Asn Phe Lys Asp Ile Thr Asp Leu
145 150 155 160

Ile Asn Asn Thr Phe Ile Arg Thr Glu Phe Gly Met Ala Ile Gly Pro
165 170 175

Glu Asn Ser Gly Lys Val Val Leu Thr Ala Glu Val Ser Gly Gly Ser
180 185 190

Arg Gly Gly Arg Ile Phe Arg Ser Ser Asp Phe Ala Lys Asn Phe Val
195 200 205

Gln Thr Asp Leu Pro Phe His Pro Leu Thr Gln Met Met Tyr Ser Pro
210 215 220

Gln Asn Ser Asp Tyr Leu Leu Ala Leu Ser Thr Glu Asn Gly Leu Trp
225 230 235 240

Val Ser Lys Asn Phe Gly Gly Lys Trp Glu Glu Ile His Lys Ala Val
245 250 255

Cys Leu Ala Lys Trp Gly Ser Asp Asn Thr Ile Phe Phe Thr Thr Tyr
260 265 270

Ala Asn Gly Ser Cys Lys Ala Asp Leu Gly Ala Leu Glu Leu Trp Arg
275 280 285

Thr Ser Asp Leu Gly Lys Ser Phe Lys Thr Ile Gly Val Lys Ile Tyr
290 295 300

Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe Ala Ser Val Met Ala Asp
305 310 315 320

Lys Asp Thr Thr Arg Arg Ile His Val Ser Thr Asp Gln Gly Asp Thr
325 330 335

Trp Ser Met Ala Gln Leu Pro Ser Val Gly Gln Glu Gln Phe Tyr Ser
340 345 350

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Ile Leu Ala Ala Asn Asp Asp Met Val Phe Met His Val Asp Glu Pro
 355 360 365

Gly Asp Thr Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp Arg Gly Ile
 370 375 380

Val Tyr Ser Lys Ser Leu Asp Arg His Leu Tyr Thr Thr Thr Gly Gly
 385 390 395 400

Glu Thr Asp Phe Thr Asn Val Thr Ser Leu Arg Gly Val Tyr Ile Thr
 405 410 415

Ser Val Leu Ser Glu Asp Asn Ser Ile Gln Thr Met Ile Thr Phe Asp
 420 425 430

Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn Ser Glu Cys
 435 440 445

Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys Ser Leu His Ile His Ala
 450 455 460

Ser Tyr Ser Ile Ser Gln Lys Leu Asn Val Pro Met Ala Pro Leu Ser
 465 470 475 480

Glu Pro Asn Ala Val Gly Ile Val Ile Ala His Gly Ser Val Gly Asp
 485 490 495

Ala Ile Ser Val Met Val Pro Asp Val Tyr Ile Ser Asp Asp Gly Gly
 500 505 510

Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro His Tyr Tyr Thr Ile Leu
 515 520 525

Asp Ser Gly Gly Ile Ile Val Ala Ile Glu His Ser Ser Arg Pro Ile
 530 535 540

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Asn Val Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp Gln Thr Tyr
545 550 555 560

Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr Gly Leu Ala Ser Glu Pro
565 570 575

Gly Ala Arg Ser Met Asn Ile Ser Ile Trp Gly Phe Thr Glu Ser Phe
580 585 590

Leu Thr Ser Gln Trp Val Ser Tyr Thr Ile Asp Phe Lys Asp Ile Leu
595 600 605

Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu Ala His Ser
610 615 620

Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly Tyr Lys Glu
625 630 635 640

Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn Gly Arg Asp
645 650 655

Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser Leu Glu Asp
660 665 670

Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp Ser Lys Cys
675 680 685

Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe Cys Leu Tyr
690 695 700

Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys Ile Pro Gly
705 710 715 720

Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val Lys Asp Leu
725 730 735

Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys Gln Asn Ser
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Lys Ser Asn His His His His His His His His
755 760

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Ala Lys Leu Ala Asn Asn Thr His Gln His Val Phe Asp Asp Leu Arg
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Gly Ser Val Ser Leu Ser Trp Val Gly Asp Ser Thr Gly Val Ile Leu
35 40 45

Val Leu Thr Thr Phe His Val Pro Leu Val Ile Met Thr Phe Gly Gln
50 55 60

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

Thr Asp Leu Ile Asn Asn Thr Phe Ile Arg Thr Glu Phe Gly Met Ala
85 90 95

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

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Gly Gly Ser Arg Gly Gly Arg Ile Phe Arg Ser Ser Asp Phe Ala Lys
115 120 125

Asn Phe Val Gln Thr Asp Leu Pro Phe His Pro Leu Thr Gln Met Met
130 135 140

Tyr Ser Pro Gln Asn Ser Asp Tyr Leu Leu Ala Leu Ser Thr Glu Asn
145 150 155 160

Gly Leu Trp Val Ser Lys Asn Phe Gly Gly Lys Trp Glu Glu Ile His
165 170 175

Lys

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Val Leu Thr Thr Phe His Val Pro Leu Val Ile Met Thr Phe Gly Gln
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Ser Lys Leu Tyr Arg Ser Glu Asp Tyr Gly Lys Asn
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Ser Lys Leu

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Phe Lys Asp Ile Thr Asp
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Thr Gly Leu
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Gly	Ser	Val	Ser	Leu	Ser	Trp	Val	Gly	Asp	Ser	Thr	Gly	Val	Ile	Leu
		35					40					45			
Val	Leu	Thr	Thr	Phe	His	Val	Pro	Leu	Val	Ile	Met	Thr	Phe	Gly	Gln
		50				55					60				
Ser	Lys	Leu	Tyr	Arg	Ser	Glu	Asp	Tyr	Gly	Lys	Asn	Phe	Lys	Asp	Ile
65					70					75					80
Thr	Asp	Leu	Ile	Asn	Asn	Thr	Phe	Ile	Arg	Thr	Glu	Phe	Gly	Met	Ala
				85					90					95	
Ile	Gly	Pro	Glu	Asn	Ser	Gly	Lys	Val	Val	Leu	Thr	Ala	Glu	Val	Ser
			100					105						110	
Gly	Gly	Ser	Arg	Gly	Gly	Arg	Ile	Phe	Arg	Ser	Ser	Asp	Phe	Ala	Lys
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Asn	Phe	Val	Gln	Thr	Asp	Leu	Pro	Phe	His	Pro	Leu	Thr	Gln	Met	Met
		130					135					140			
Tyr	Ser	Pro	Gln	Asn	Ser	Asp	Tyr	Leu	Leu	Ala	Leu	Ser	Thr	Glu	Asn
145					150					155					160
Gly	Leu	Trp	Val	Ser	Lys	Asn	Phe	Gly	Gly	Lys	Trp	Glu	Glu	Ile	His
				165					170					175	
Lys	Ala	Val	Cys	Leu	Ala	Lys	Trp	Gly	Ser	Asp	Asn	Thr	Ile	Phe	Phe
			180					185					190		
Thr	Thr	Tyr	Ala	Asn	Gly	Ser	Cys	Lys	Ala	Asp	Leu	Gly	Ala	Leu	Glu
		195					200					205			
Leu	Trp	Arg	Thr	Ser	Asp	Leu	Gly	Lys	Ser	Phe	Lys	Thr	Ile	Gly	Val
		210					215				220				

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Lys Ile Tyr Ser Phe Gly Leu Gly Gly Arg Phe Leu Phe Ala Ser Val
 225 230 235 240

Met Ala Asp Lys Asp Thr Thr Arg Arg Ile His Val Ser Thr Asp Gln
 245 250 255

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

Phe Tyr Ser Ile Leu Ala Ala Asn Asp Asp Met Val Phe Met His Val
 275 280 285

Asp Glu Pro Gly Asp Thr Gly Phe Gly Thr Ile Phe Thr Ser Asp Asp
 290 295 300

Arg Gly Ile Val Tyr Ser Lys Ser Leu Asp Arg His Leu Tyr Thr Thr
 305 310 315 320

Thr Gly Gly Glu Thr Asp Phe Thr Asn Val Thr Ser Leu Arg Gly Val
 325 330 335

Tyr Ile Thr Ser Val Leu Ser Glu Asp Asn Ser Ile Gln Thr Met Ile
 340 345 350

Thr Phe Asp Gln Gly Gly Arg Trp Thr His Leu Arg Lys Pro Glu Asn
 355 360 365

Ser Glu Cys Asp Ala Thr Ala Lys Asn Lys Asn Glu Cys Ser Leu His
 370 375 380

Ile His Ala Ser Tyr Ser Ile Ser Gln Lys Leu Asn Val Pro Met Ala
 385 390 395 400

Pro Leu Ser Glu Pro Asn Ala Val Gly Ile Val Ile Ala His Gly Ser
 405 410 415

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Val Gly Asp Ala Ile Ser Val Met Val Pro Asp Val Tyr Ile Ser Asp
420 425 430

Asp Gly Gly Tyr Ser Trp Thr Lys Met Leu Glu Gly Pro His Tyr Tyr
435 440 445

Thr Ile Leu Asp Ser Gly Gly Ile Ile Val Ala Ile Glu His Ser Ser
450 455 460

Arg Pro Ile Asn Val Ile Lys Phe Ser Thr Asp Glu Gly Gln Cys Trp
465 470 475 480

Gln Thr Tyr Thr Phe Thr Arg Asp Pro Ile Tyr Phe Thr Gly Leu Ala
485 490 495

Ser Glu Pro Gly Ala Arg Ser Met Asn Ile Ser Ile Trp Gly Phe Thr
500 505 510

Glu Ser Phe Leu Thr Ser Gln Trp Val Ser Tyr Thr Ile Asp Phe Lys
515 520 525

Asp Ile Leu Glu Arg Asn Cys Glu Glu Lys Asp Tyr Thr Ile Trp Leu
530 535 540

Ala His Ser Thr Asp Pro Glu Asp Tyr Glu Asp Gly Cys Ile Leu Gly
545 550 555 560

Tyr Lys Glu Gln Phe Leu Arg Leu Arg Lys Ser Ser Val Cys Gln Asn
565 570 575

Gly Arg Asp Tyr Val Val Thr Lys Gln Pro Ser Ile Cys Leu Cys Ser
580 585 590

Leu Glu Asp Phe Leu Cys Asp Phe Gly Tyr Tyr Arg Pro Glu Asn Asp
595 600 605

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Ser Lys Cys Val Glu Gln Pro Glu Leu Lys Gly His Asp Leu Glu Phe
610 615 620

Cys Leu Tyr Gly Arg Glu Glu His Leu Thr Thr Asn Gly Tyr Arg Lys
625 630 635 640

Ile Pro Gly Asp Lys Cys Gln Gly Gly Val Asn Pro Val Arg Glu Val
645 650 655

Lys Asp Leu Lys Lys Lys Cys Thr Ser Asn Phe Leu Ser Pro Glu Lys
660 665 670

Gln Asn Ser Lys Ser Asn Ser Gly Ser Ala Met Ile Glu Gly Arg Gly
675 680 685

Val Gly His His His His His His
690 695