

OP19-0160-Sequence Listing

<110> ONCOTAG DIAGNOSTICS CO., LTD.

<120> MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO MRS

<130> OP19-0160/PCT/SG

<150> KR 10-2017-0058896

<151> 2017-05-11

<150> PCT/KR2018/005442

<151> 2018-05-11

<160> 49

<170> KopatentIn 2.0

<210> 1

<211> 900

<212> PRT

<213> Homo sapiens MRS protein (NP_004981.2)

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Met Arg Leu Phe Val Ser Asp Gly Val Pro Gly Cys Leu Pro Val Leu
1 5 10 15

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

Val Gly Pro Glu Asp Cys Val Val Pro Phe Leu Thr Arg Pro Lys Val
35 40 45

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

Ile Cys Arg Tyr Phe Phe Leu Leu Ser Gly Trp Glu Gln Asp Asp Leu
65 70 75 80

Thr Asn Gln Trp Leu Glu Trp Glu Ala Thr Glu Leu Gln Pro Ala Leu
85 90 95

Ser Ala Ala Leu Tyr Tyr Leu Val Val Gln Gly Lys Lys Gly Glu Asp
100 105 110

Val Leu Gly Ser Val Arg Arg Ala Leu Thr His Ile Asp His Ser Leu
115 120 125

Ser Arg Gln Asn Cys Pro Phe Leu Ala Gly Glu Thr Glu Ser Leu Ala
130 135 140

Asp Ile Val Leu Trp Gly Ala Leu Tyr Pro Leu Leu Gln Asp Pro Ala
145 150 155 160

Tyr Leu Pro Glu Glu Leu Ser Ala Leu His Ser Trp Phe Gln Thr Leu
165 170 175

Ser Thr Gln Glu Pro Cys Gln Arg Ala Ala Glu Thr Val Leu Lys Gln
180 185 190

Gln Gly Val Leu Ala Leu Arg Pro Tyr Leu Gln Lys Gln Pro Gln Pro
195 200 205

Ser Pro Ala Glu Gly Arg Ala Val Thr Asn Glu Pro Glu Glu Glu Glu
210 215 220

Leu Ala Thr Leu Ser Glu Glu Glu Ile Ala Met Ala Val Thr Ala Trp
225 230 235 240

Glu Lys Gly Leu Glu Ser Leu Pro Pro Leu Arg Pro Gln Gln Asn Pro

255

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Asp Thr Gly Ile Pro Ala Asp Ile Trp Arg Phe Tyr Leu Leu Tyr Ile
610 615 620

Arg Pro Glu Gly Gln Asp Ser Ala Phe Ser Trp Thr Asp Leu Leu Leu
625 630 635 640

Lys Asn Asn Ser Glu Leu Leu Asn Asn Leu Gly Asn Phe Ile Asn Arg
645 650 655

Ala Gly Met Phe Val Ser Lys Phe Phe Gly Gly Tyr Val Pro Glu Met
660 665 670

Val Leu Thr Pro Asp Asp Gln Arg Leu Leu Ala His Val Thr Leu Glu
675 680 685

Leu Gln His Tyr His Gln Leu Leu Glu Lys Val Arg Ile Arg Asp Ala
690 695 700

Leu Arg Ser Ile Leu Thr Ile Ser Arg His Gly Asn Gln Tyr Ile Gln
705 710 715 720

Val Asn Glu Pro Trp Lys Arg Ile Lys Gly Ser Glu Ala Asp Arg Gln
725 730 735

Arg Ala Gly Thr Val Thr Gly Leu Ala Val Asn Ile Ala Ala Leu Leu
740 745 750

Ser Val Met Leu Gln Pro Tyr Met Pro Thr Val Ser Ala Thr Ile Gln
755 760 765

Ala Gln Leu Gln Leu Pro Pro Pro Ala Cys Ser Ile Leu Leu Thr Asn
770 775 780

Phe Leu Cys Thr Leu Pro Ala Gly His Gln Ile Gly Thr Val Ser Pro
785 790 795 800

Leu Phe Gln Lys Leu Glu Asn Asp Gln Ile Glu Ser Leu Arg Gln Arg
805 810 815

Phe Gly Gly Gly Gln Ala Lys Thr Ser Pro Lys Pro Ala Val Val Glu
820 825 830

Thr Val Thr Thr Ala Lys Pro Gln Gln Ile Gln Ala Leu Met Asp Glu
835 840 845

Val Thr Lys Gln Gly Asn Ile Val Arg Glu Leu Lys Ala Gln Lys Ala
850 855 860

Asp Lys Asn Glu Val Ala Ala Glu Val Ala Lys Leu Leu Asp Leu Lys
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Lys Gln Leu Ala Val Ala Glu Gly Lys Pro Pro Glu Ala Pro Lys Gly
885 890 895

Lys Lys Lys Lys
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<210> 2
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<212> DNA
<213> Homo sapiens MRS mRNA (NM_004990.3)

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agagcccggg gcagagcaga ggtgctcatc agcactgtag gcccggaaga ttgtgtggtc 120

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ccgttcctga	cccggcctaa	ggtcctctgtc	ttgcagctgg	atagcggcaa	ctacctcttc	180
tccactagt	caatctgccg	atattttttt	ttgttatctg	gctgggagca	agatgacctc	240
actaaccagt	ggctggaatg	ggaagcgaca	gagctgcagc	cagctttgtc	tgctgccctg	300
tactatttag	tggtccaagg	caagaagggg	gaagatgttc	ttggttcagt	gcggagagcc	360
ctgactcaca	ttgaccacag	cttgagtcgt	cagaactgtc	ctttcctggc	tggggagaca	420
gaatctctag	ccgacattgt	tttgtgggga	gccctatacc	cattactgca	agatcccgcc	480
tacctccctg	aggagctgag	tgccctgcac	agctggttcc	agacactgag	taccaggaa	540
ccatgtcagc	gagctgcaga	gactgtactg	aaacagcaag	gtgtcctggc	tctccggcct	600
tacctcaaaa	agcagcccca	gcccagcccc	gctgagggaa	gggctgtcac	caatgagcct	660
gaggaggagg	agctggctac	cctatctgag	gaggagattg	ctatggctgt	tactgcttgg	720
gagaagggcc	tagaaagt	gtt	gccccgctg	cgccccagc	agaatccagt	780
gctggagaaa	ggaatgtgct	catcaccagt	gccctccctt	acgtcaacaa	tgtccccac	840
cttgggaaca	tcattggttg	tgtgctcagt	gccgatgtct	ttgccaggta	ctctgcctc	900
cgccagtgga	acaccctcta	tctgtgtggg	acagatgagt	atggtacagc	aacagagacc	960
aaggctctgg	aggagggact	aacccccag	gagatctgcg	acaagtacca	catcatccat	1020
gctgacatct	accgctgggt	taacatttcg	tttgatattt	ttggtcgcac	caccactcca	1080
cagcagacca	aaatcaccca	ggacattttc	cagcagttgc	tgaaacgagg	ttttgtgctg	1140
caagatactg	tgagcaact	gcatgtgag	cactgtgctc	gcttcctggc	tgaccgcttc	1200
gtggagggcg	tgtgtccctt	ctgtggctat	gaggaggctc	ggggtgacca	gtgtgacaag	1260
tgtggcaagc	tcatcaatgc	tgtcgagctt	aagaagcctc	agtgtaaagt	ctgccgatca	1320
tgccctgtgg	tgagtcgag	ccagcacctg	tttctggacc	tgccctaagct	ggagaagcga	1380
ctggaggagt	ggttggggag	gacattgcct	ggcagtgact	ggacacccaa	tgcccagttt	1440
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tggggaaccc	ctgtaccctt	agaagggttt	gaagacaagg	tattctatgt	ctggtttgat	1560
gccactattg	gctatctgtc	catcacagcc	aactacacag	accagtggga	gagatggtgg	1620
aagaaccag	agcaagtggg	cctgtatcag	ttcatggcca	aagacaatgt	tcctttccat	1680
agcttagtct	ttccttgctc	agccctagga	gctgaggata	actatacctt	ggtcagccac	1740
ctcattgcta	cagagtacct	gaactatgag	gatgggaaat	tctctaagag	ccgcggtgtg	1800
ggagtgtttg	gggacatggc	ccaggacacg	gggatccctg	ctgacatctg	gcgcttctat	1860
ctgctgtaca	ttcggcctga	gggccaggac	agtgttttct	cctggacgga	cctgctgctg	1920
aagaataatt	ctgagctgct	taacaacctg	ggcaacttca	tcaacagagc	tgggatgttt	1980
gtgtctaagt	tctttggggg	ctatgtgcct	gagatggtgc	tcaccctga	tgatcagcgc	2040
ctgctggccc	atgtcacctt	ggagctccag	cactatcacc	agctacttga	gaagggttcgg	2100
atccgggatg	ccttgccgag	tatcctcacc	atatctcgac	atggcaacca	atatattcag	2160

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gtgaatgagc cctggaagcg gattaaaggc agtgaggctg acaggcaacg ggcaggaaca 2220
 gtgactggct tggcagtga ttagctgcc ttgctctctg tcatgcttca gccttacatg 2280
 cccacggtta gtgccacaat ccaggcccag ctgcagctcc cacctccagc ctgcagtatc 2340
 ctgctgacaa acttcctgtg taccttacca gcaggacacc agattggcac agtcagtccc 2400
 ttgttccaaa aattggaaaa tgaccagatt gaaagttaa ggcagcgctt tggagggggc 2460
 caggcaaaaa cgtccccgaa gccagcagtt gtagagactg ttacaacagc caagccacag 2520
 cagatacaag cgctgatgga tgaagtgaca aaacaaggaa acattgtccg agaactgaaa 2580
 gcacaaaagg cagacaagaa cgaggttgct gcggagggtg cgaaactctt ggatctaaag 2640
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 taa 2703

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

<220>
 <223> 1E8 VL CDR1

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 Lys Ser Ser Gln Ser Leu Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
 1 5 10 15

Ala

<210> 4
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1E8 VL CDR1

<400> 4
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<210> 5
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1E8 VL CDR2

<400> 5
 Trp Ala Ser Thr Arg Glu Ser
 1 5

<210> 6
 <211> 21
 <212> DNA

OP19-0160-Sequence Listing

<213> Artificial Sequence

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<223> 1E8 VL CDR2

<400> 6
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<210> 7
<211> 8
<212> PRT
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<220>
<223> 1E8 VL CDR3

<400> 7
Gln Gln Tyr Tyr Ser Tyr Pro Thr
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<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

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<223> 1E8 VL CDR3

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<210> 9
<211> 6
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<220>
<223> 1E8 VH CDR1

<400> 9
Ser Asp Tyr Ala Trp Asn
1 5

<210> 10
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> 1E8 VH CDR1

<400> 10
agtgattatg cctggaac 18

<210> 11
<211> 16
<212> PRT
<213> Artificial Sequence

OP19-0160-Sequence Listing

<220>

<223> 1E8 VH CDR2

<400> 11

Tyr Ile Ser Tyr Ser Gly Arg Thr Ser Tyr Lys Ser Ser Leu Lys Ser
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<210> 12

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> 1E8 VH CDR2

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<210> 13

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 1E8 VH CDR3

<400> 13

Asp Tyr Gly Asn Phe Val Gly Tyr Phe Asp Val
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<210> 14

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> 1E8 VH CDR3

<400> 14

gactatggtgta acttcgtagg ttacttcgat gtc

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<210> 15

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> 8A12 VL CDR1

<400> 15

Lys Ala Ser Gln Asp Ile Asn Ser Tyr Leu Ser
1 5 10

<210> 16

<211> 33

OP19-0160-Sequence Listing

<212> DNA
<213> Artificial Sequence

<220>
<223> 8A12 VL CDR1

<400> 16
aaggcgagtc aggacattaa tagctattta agc

33

<210> 17
<211> 7
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<223> 8A12 VL CDR2

<400> 17
Arg Ala Asn Arg Leu Val Asp
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<210> 18
<211> 21
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<213> Artificial Sequence

<220>
<223> 8A12 VL CDR2

<400> 18
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<211> 9
<212> PRT
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<220>
<223> 8A12 VL CDR3

<400> 19
Leu Gln Tyr Asp Glu Phe Pro Arg Thr
1 5

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> 8A12 VL CDR3

<400> 20
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27

<210> 21
<211> 6
<212> PRT

OP19-0160-Sequence Listing

<213> Artificial Sequence

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<223> 8A12 VH CDR1

<400> 21

Ser Glu Tyr Ala Trp Thr
1 5

<210> 22

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> 8A12 VH CDR1

<400> 22

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<210> 23

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> 8A12 VH CDR2

<400> 23

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<210> 24

<211> 48

<212> DNA

<213> Artificial Sequence

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<223> 8A12 VH CDR2

<400> 24

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<210> 25

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> 8A12 VH CDR3

<400> 25

Ser Leu Trp Pro Arg Gly Trp Phe Ala Tyr
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<210> 26

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<211> 30
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<213> Artificial Sequence

<220>
<223> 8A12 VH CDR3

<400> 26
tcactttggc ccaggggctg gtttgcttac

30

<210> 27
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<223> 1E8 VL

<400> 27
Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
1 5 10 15
Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
20 25 30
Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45
Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60
Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
65 70 75 80
Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
85 90 95
Tyr Tyr Ser Tyr Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 28
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> 1E8 VL

<400> 28
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tggtaccagc agaaaccagg gcagtctcct aaactgctga ttactgggc atccactagg 180
gaatctgggg tccctgatcg cttcacaggc agtggatctg ggacagaatt cactctcacc 240
atcagcagtg tgaaggctga agacctggca gtttattact gtcagcaata ttatagctat 300
ccgacgttcg gtggaggcac caagctggaa atcaaa 336

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<210> 29
 <211> 120
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 1E8 VH

<400> 29
 Asp Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Asn Pro Ser Gln
 1 5 10 15
 Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
 20 25 30
 Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
 35 40 45
 Met Gly Tyr Ile Ser Tyr Ser Gly Arg Thr Ser Tyr Lys Ser Ser Leu
 50 55 60
 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
 65 70 75 80
 Leu Glu Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95
 Ala Arg Asp Tyr Gly Asn Phe Val Gly Tyr Phe Asp Val Trp Gly Ala
 100 105 110
 Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 30
 <211> 360
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 1E8 VH

<400> 30
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 acctgcactg tcaactggcta ttcaatcacc agtgattatg cctggaactg gatccggcag 120
 ttccaggaa acaaactgga gtggatgggc tacataagct acagtggctg cactagctac 180
 aaatcatctc tcaaaagtcg aatctctatc actcgagaca catccaagaa ccagttcttc 240
 ctggagttga attctgtgac tactgaggac acagccacat attactgtgc aagagactat 300
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<210> 31
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 8A12 VL

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<400> 31
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Met Tyr Ala Ser Leu Gly
 1 5 10 15
 Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
 20 25 30
 Leu Ser Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Thr Leu Met
 35 40 45
 Tyr Arg Ala Asn Arg Leu Val Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Tyr
 65 70 75 80
 Glu Asp Met Gly Ile Tyr Tyr Cys Leu Gln Tyr Asp Glu Phe Pro Arg
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 32
 <211> 321
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 8A12 VL

<400> 32
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 gggaaatctc ctaagacct gatgtatcgt gcaaacagat tggtagatgg ggtcccatca 180
 aggttcagtg gcagtggatc tggccaagat tattctctca ccatcagcag cctggaatat 240
 gaagatatgg gaatttatta ttgtctacag tatgatgagt ttcctcggac gttcgggtgga 300
 ggcaccaagc tggaaatcaa a 321

<210> 33
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> 8A12 VH

<400> 33
 Asp Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
 1 5 10 15
 Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Glu
 20 25 30
 Tyr Ala Trp Thr Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
 35 40 45
 Met Gly Tyr Ile Asn Tyr Asn Gly Asn Thr Asn Leu Asn Pro Ser Leu

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50 55 60
 Lys Ser Arg Ile Ser Ile Ile Arg Asp Thr Ser Lys Asn Gln Phe Phe
 65 70 75 80
 Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95
 Ala Arg Ser Leu Trp Pro Arg Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110
 Thr Leu Val Thr Val Ser Ala
 115

<210> 34
 <211> 357
 <212> DNA
 <213> Artificial sequence

<220>
 <223> 8A12 VH

<400> 34
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 tttccaggaa acaaaactgga atggatgggc tacataaact acaatggcaa cactaactta 180
 aatccatctc tcaaaagtcg aatctctatc attcgagaca catccaagaa ccagttcttc 240
 ctgcagttga attctgtgac aactgaggac acagccacat attactgtgc aagatcactt 300
 tggcccaggg gctgggtttgc ttactggggc caaggggactc tgggtcactgt ctctgca 357

<210> 35
 <211> 218
 <212> PRT
 <213> Artificial sequence

<220>
 <223> 1E8 light chain

<400> 35
 Asp Ile Val Met Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Val Gly
 1 5 10 15
 Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser Leu Leu Tyr Ser
 20 25 30
 Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 35 40 45
 Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
 50 55 60
 Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
 65 70 75 80
 Ile Ser Ser Val Lys Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
 85 90 95
 Tyr Tyr Ser Tyr Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

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Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Glu Gln
115 120 125
Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu Asn Asn Phe Tyr
130 135 140
Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln
145 150 155 160
Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr
165 170 175
Tyr Ser Met Ser Arg Thr Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg
180 185 190
His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr Ser Thr Ser Pro
195 200 205
Ile Val Lys Ser Phe Asn Arg Asn Glu Cys
210 215

<210> 36
<211> 450
<212> PRT
<213> Artificial Sequence
<220>
<223> 1E8 Heavy chain

<400> 36
Asp Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Asn Pro Ser Gln
1 5 10 15
Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30
Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45
Met Gly Tyr Ile Ser Tyr Ser Gly Arg Thr Ser Tyr Lys Ser Ser Leu
50 55 60
Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80
Leu Glu Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95
Ala Arg Asp Tyr Gly Asn Phe Val Gly Tyr Phe Asp Val Trp Gly Ala
100 105 110
Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr Ala Pro Ser Val
115 120 125
Tyr Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr
130 135 140
Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr
145 150 155 160
Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
165 170 175
Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Thr Ser
180 185 190

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Ser Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala
195 200 205

Ser Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile
210 215 220

Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly
225 230 235 240

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile
245 250 255

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp
260 265 270

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His
275 280 285

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg
290 295 300

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys
305 310 315 320

Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu
325 330 335

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr
340 345 350

Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu
355 360 365

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp
370 375 380

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val
385 390 395 400

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu
405 410 415

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His
420 425 430

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro
435 440 445

Gly Lys
450

<210> 37
<211> 213
<212> PRT
<213> Artificial Sequence

<220>
<223> 8A12 light chain

<400> 37
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Glu Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Ser Tyr
20 25 30

OP19-0160-Sequence Listing

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

<210> 38
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<223> 8A12 Heavy chain

<400> 38
Asp Val Lys Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15
Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Glu
20 25 30
Tyr Ala Trp Thr Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45
Met Gly Tyr Ile Asn Tyr Asn Gly Asn Thr Asn Leu Asn Pro Ser Leu
50 55 60
Lys Ser Arg Ile Ser Ile Ile Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80
Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95
Ala Arg Ser Leu Trp Pro Arg Gly Trp Phe Ala Tyr Trp Gly Gln Gly
100 105 110

OP19-0160-Sequence Listing

Thr Leu Val Thr Val Ser Ala Ala Lys Thr Thr Ala Pro Ser Val Tyr
 115 120 125
 Pro Leu Ala Pro Val Cys Gly Asp Thr Thr Gly Ser Ser Val Thr Leu
 130 135 140
 Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Leu Thr Trp
 145 150 155 160
 Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175
 Gln Ser Asp Leu Tyr Thr Leu Ser Ser Val Thr Val Thr Ser Ser
 180 185 190
 Thr Trp Pro Ser Gln Ser Ile Thr Cys Asn Val Ala His Pro Ala Ser
 195 200 205
 Ser Thr Lys Val Asp Lys Lys Ile Glu Pro Arg Gly Pro Thr Ile Lys
 210 215 220
 Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro
 225 230 235 240
 Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser
 245 250 255
 Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp Asp
 260 265 270
 Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His Thr
 275 280 285
 Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val
 290 295 300
 Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys Glu
 305 310 315 320
 Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg
 325 330 335
 Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val
 340 345 350
 Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr
 355 360 365
 Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr
 370 375 380
 Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu
 385 390 395 400
 Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys
 405 410 415
 Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu
 420 425 430
 Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly
 435 440 445
 Lys

OP19-0160-Sequence Listing

<210> 39
 <211> 40
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> main binding site of Ab

 <400> 39
 Ala Gln Lys Ala Asp Lys Asn Glu Val Ala Ala Glu Val Ala Lys Leu
 1 5 10 15
 Leu Asp Leu Lys Lys Gln Leu Ala Val Ala Glu Gly Lys Pro Pro Glu
 20 25 30
 Ala Pro Lys Gly Lys Lys Lys Lys
 35 40

 <210> 40
 <211> 266
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> MRS fragment 1(1-256 aa)

 <400> 40
 Met Arg Leu Phe Val Ser Asp Gly Val Pro Gly Cys Leu Pro Val Leu
 1 5 10 15
 Ala Ala Ala Gly Arg Ala Arg Gly Arg Ala Glu Val Leu Ile Ser Thr
 20 25 30
 Val Gly Pro Glu Asp Cys Val Val Pro Phe Leu Thr Arg Pro Lys Val
 35 40 45
 Pro Val Leu Gln Leu Asp Ser Gly Asn Tyr Leu Phe Ser Thr Ser Ala
 50 55 60
 Ile Cys Arg Tyr Phe Phe Leu Leu Ser Gly Trp Glu Gln Asp Asp Leu
 65 70 75 80
 Thr Asn Gln Trp Leu Glu Trp Glu Ala Thr Glu Leu Gln Pro Ala Leu
 85 90 95
 Ser Ala Ala Leu Tyr Tyr Leu Val Val Gln Gly Lys Lys Gly Glu Asp
 100 105 110
 Val Leu Gly Ser Val Arg Arg Ala Leu Thr His Ile Asp His Ser Leu
 115 120 125
 Ser Arg Gln Asn Cys Pro Phe Leu Ala Gly Glu Thr Glu Ser Leu Ala
 130 135 140
 Asp Ile Val Leu Trp Gly Ala Leu Tyr Pro Leu Leu Gln Asp Pro Ala
 145 150 155 160
 Tyr Leu Pro Glu Glu Leu Ser Ala Leu His Ser Trp Phe Gln Thr Leu
 165 170 175
 Ser Thr Gln Glu Pro Cys Gln Arg Ala Ala Glu Thr Val Leu Lys Gln
 180 185 190
 Gln Gly Val Leu Ala Leu Arg Pro Tyr Leu Gln Lys Gln Pro Gln Pro
 195 200 205

OP19-0160-Sequence Listing

Ser Pro Ala Glu Gly Arg Ala Val Thr Asn Glu Pro Glu Glu Glu Glu
210 215 220
Leu Ala Thr Leu Ser Glu Glu Glu Ile Ala Met Ala Val Thr Ala Trp
225 230 235 240
Glu Lys Gly Leu Glu Ser Leu Pro Pro Leu Arg Pro Gln Gln Asn Pro
245 250 255
Val Leu Pro Val Ala Gly Glu Arg Asn Val
260 265

<210> 41
<211> 151
<212> PRT
<213> Artificial Sequence

<220>
<223> MRS fragment 2(267-417 aa)

<400> 41
Leu Ile Thr Ser Ala Leu Pro Tyr Val Asn Asn Val Pro His Leu Gly
1 5 10 15
Asn Ile Ile Gly Cys Val Leu Ser Ala Asp Val Phe Ala Arg Tyr Ser
20 25 30
Arg Leu Arg Gln Trp Asn Thr Leu Tyr Leu Cys Gly Thr Asp Glu Tyr
35 40 45
Gly Thr Ala Thr Glu Thr Lys Ala Leu Glu Glu Gly Leu Thr Pro Gln
50 55 60
Glu Ile Cys Asp Lys Tyr His Ile Ile His Ala Asp Ile Tyr Arg Trp
65 70 75 80
Phe Asn Ile Ser Phe Asp Ile Phe Gly Arg Thr Thr Thr Pro Gln Gln
85 90 95
Thr Lys Ile Thr Gln Asp Ile Phe Gln Gln Leu Leu Lys Arg Gly Phe
100 105 110
Val Leu Gln Asp Thr Val Glu Gln Leu Arg Cys Glu His Cys Ala Arg
115 120 125
Phe Leu Ala Asp Arg Phe Val Glu Gly Val Cys Pro Phe Cys Gly Tyr
130 135 140
Glu Glu Ala Arg Gly Asp Gln
145 150

<210> 42
<211> 331
<212> PRT
<213> Artificial Sequence

<220>
<223> MRS fragment 3(267-597 aa)

<400> 42
Leu Ile Thr Ser Ala Leu Pro Tyr Val Asn Asn Val Pro His Leu Gly
1 5 10 15

OP19-0160-Sequence Listing

Asn Ile Ile Gly Cys Val Leu Ser Ala Asp Val Phe Ala Arg Tyr Ser
20 25 30
Arg Leu Arg Gln Trp Asn Thr Leu Tyr Leu Cys Gly Thr Asp Glu Tyr
35 40 45
Gly Thr Ala Thr Glu Thr Lys Ala Leu Glu Glu Gly Leu Thr Pro Gln
50 55 60
Glu Ile Cys Asp Lys Tyr His Ile Ile His Ala Asp Ile Tyr Arg Trp
65 70 75 80
Phe Asn Ile Ser Phe Asp Ile Phe Gly Arg Thr Thr Thr Pro Gln Gln
85 90 95
Thr Lys Ile Thr Gln Asp Ile Phe Gln Gln Leu Leu Lys Arg Gly Phe
100 105 110
Val Leu Gln Asp Thr Val Glu Gln Leu Arg Cys Glu His Cys Ala Arg
115 120 125
Phe Leu Ala Asp Arg Phe Val Glu Gly Val Cys Pro Phe Cys Gly Tyr
130 135 140
Glu Glu Ala Arg Gly Asp Gln Cys Asp Lys Cys Gly Lys Leu Ile Asn
145 150 155 160
Ala Val Glu Leu Lys Lys Pro Gln Cys Lys Val Cys Arg Ser Cys Pro
165 170 175
Val Val Gln Ser Ser Gln His Leu Phe Leu Asp Leu Pro Lys Leu Glu
180 185 190
Lys Arg Leu Glu Glu Trp Leu Gly Arg Thr Leu Pro Gly Ser Asp Trp
195 200 205
Thr Pro Asn Ala Gln Phe Ile Thr Arg Ser Trp Leu Arg Asp Gly Leu
210 215 220
Lys Pro Arg Cys Ile Thr Arg Asp Leu Lys Trp Gly Thr Pro Val Pro
225 230 235 240
Leu Glu Gly Phe Glu Asp Lys Val Phe Tyr Val Trp Phe Asp Ala Thr
245 250 255
Ile Gly Tyr Leu Ser Ile Thr Ala Asn Tyr Thr Asp Gln Trp Glu Arg
260 265 270
Trp Trp Lys Asn Pro Glu Gln Val Asp Leu Tyr Gln Phe Met Ala Lys
275 280 285
Asp Asn Val Pro Phe His Ser Leu Val Phe Pro Cys Ser Ala Leu Gly
290 295 300
Ala Glu Asp Asn Tyr Thr Leu Val Ser His Leu Ile Ala Thr Glu Tyr
305 310 315 320
Leu Asn Tyr Glu Asp Gly Lys Phe Ser Lys Ser
325 330

<210> 43
<211> 597
<212> PRT
<213> Artificial Sequence
<220>
<223> MRS fragment 4(1-597 aa)

OP19-0160-Sequence Listing

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<400>      43
Met  Arg  Leu  Phe  Val  Ser  Asp  Gly  Val  Pro  Gly  Cys  Leu  Pro  Val  Leu
 1          5          10          15

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

Val  Gly  Pro  Glu  Asp  Cys  Val  Val  Pro  Phe  Leu  Thr  Arg  Pro  Lys  Val
      35          40          45

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

Ile  Cys  Arg  Tyr  Phe  Phe  Leu  Leu  Ser  Gly  Trp  Glu  Gln  Asp  Asp  Leu
      65          70          75          80

Thr  Asn  Gln  Trp  Leu  Glu  Trp  Glu  Ala  Thr  Glu  Leu  Gln  Pro  Ala  Leu
      85          90          95

Ser  Ala  Ala  Leu  Tyr  Tyr  Leu  Val  Val  Gln  Gly  Lys  Lys  Gly  Glu  Asp
      100          105          110

Val  Leu  Gly  Ser  Val  Arg  Arg  Ala  Leu  Thr  His  Ile  Asp  His  Ser  Leu
      115          120          125

Ser  Arg  Gln  Asn  Cys  Pro  Phe  Leu  Ala  Gly  Glu  Thr  Glu  Ser  Leu  Ala
      130          135          140

Asp  Ile  Val  Leu  Trp  Gly  Ala  Leu  Tyr  Pro  Leu  Leu  Gln  Asp  Pro  Ala
      145          150          155          160

Tyr  Leu  Pro  Glu  Glu  Leu  Ser  Ala  Leu  His  Ser  Trp  Phe  Gln  Thr  Leu
      165          170          175

Ser  Thr  Gln  Glu  Pro  Cys  Gln  Arg  Ala  Ala  Glu  Thr  Val  Leu  Lys  Gln
      180          185          190

Gln  Gly  Val  Leu  Ala  Leu  Arg  Pro  Tyr  Leu  Gln  Lys  Gln  Pro  Gln  Pro
      195          200          205

Ser  Pro  Ala  Glu  Gly  Arg  Ala  Val  Thr  Asn  Glu  Pro  Glu  Glu  Glu  Glu
      210          215          220

Leu  Ala  Thr  Leu  Ser  Glu  Glu  Glu  Ile  Ala  Met  Ala  Val  Thr  Ala  Trp
      225          230          235          240

Glu  Lys  Gly  Leu  Glu  Ser  Leu  Pro  Pro  Leu  Arg  Pro  Gln  Gln  Asn  Pro
      245          250          255

Val  Leu  Pro  Val  Ala  Gly  Glu  Arg  Asn  Val  Leu  Ile  Thr  Ser  Ala  Leu
      260          265          270

Pro  Tyr  Val  Asn  Asn  Val  Pro  His  Leu  Gly  Asn  Ile  Ile  Gly  Cys  Val
      275          280          285

Leu  Ser  Ala  Asp  Val  Phe  Ala  Arg  Tyr  Ser  Arg  Leu  Arg  Gln  Trp  Asn
      290          295          300

Thr  Leu  Tyr  Leu  Cys  Gly  Thr  Asp  Glu  Tyr  Gly  Thr  Ala  Thr  Glu  Thr
      305          310          315          320

Lys  Ala  Leu  Glu  Glu  Gly  Leu  Thr  Pro  Gln  Glu  Ile  Cys  Asp  Lys  Tyr
      325          330          335

His  Ile  Ile  His  Ala  Asp  Ile  Tyr  Arg  Trp  Phe  Asn  Ile  Ser  Phe  Asp
      340          345          350

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OP19-0160-Sequence Listing

Ile Phe Gly Arg Thr Thr Thr Pro Gln Gln Thr Lys Ile Thr Gln Asp
355 360 365

Ile Phe Gln Gln Leu Leu Lys Arg Gly Phe Val Leu Gln Asp Thr Val
370 375 380

Glu Gln Leu Arg Cys Glu His Cys Ala Arg Phe Leu Ala Asp Arg Phe
385 390 395 400

Val Glu Gly Val Cys Pro Phe Cys Gly Tyr Glu Glu Ala Arg Gly Asp
405 410 415

Gln Cys Asp Lys Cys Gly Lys Leu Ile Asn Ala Val Glu Leu Lys Lys
420 425 430

Pro Gln Cys Lys Val Cys Arg Ser Cys Pro Val Val Gln Ser Ser Gln
435 440 445

His Leu Phe Leu Asp Leu Pro Lys Leu Glu Lys Arg Leu Glu Glu Trp
450 455 460

Leu Gly Arg Thr Leu Pro Gly Ser Asp Trp Thr Pro Asn Ala Gln Phe
465 470 475 480

Ile Thr Arg Ser Trp Leu Arg Asp Gly Leu Lys Pro Arg Cys Ile Thr
485 490 495

Arg Asp Leu Lys Trp Gly Thr Pro Val Pro Leu Glu Gly Phe Glu Asp
500 505 510

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

Thr Ala Asn Tyr Thr Asp Gln Trp Glu Arg Trp Trp Lys Asn Pro Glu
530 535 540

Gln Val Asp Leu Tyr Gln Phe Met Ala Lys Asp Asn Val Pro Phe His
545 550 555 560

Ser Leu Val Phe Pro Cys Ser Ala Leu Gly Ala Glu Asp Asn Tyr Thr
565 570 575

Leu Val Ser His Leu Ile Ala Thr Glu Tyr Leu Asn Tyr Glu Asp Gly
580 585 590

Lys Phe Ser Lys Ser
595

<210> 44
<211> 303
<212> PRT
<213> Artificial Sequence

<220>
<223> MRS fragment 5(598-900 aa)

<400> 44
Arg Gly Val Gly Val Phe Gly Asp Met Ala Gln Asp Thr Gly Ile Pro
1 5 10 15

Ala Asp Ile Trp Arg Phe Tyr Leu Leu Tyr Ile Arg Pro Glu Gly Gln
20 25 30

Asp Ser Ala Phe Ser Trp Thr Asp Leu Leu Leu Lys Asn Asn Ser Glu
35 40 45

OP19-0160-Sequence Listing

Leu Leu Asn Asn Leu Gly Asn Phe Ile Asn Arg Ala Gly Met Phe Val
50 55 60
Ser Lys Phe Phe Gly Gly Tyr Val Pro Glu Met Val Leu Thr Pro Asp
65 70 75 80
Asp Gln Arg Leu Leu Ala His Val Thr Leu Glu Leu Gln His Tyr His
85 90 95
Gln Leu Leu Glu Lys Val Arg Ile Arg Asp Ala Leu Arg Ser Ile Leu
100 105 110
Thr Ile Ser Arg His Gly Asn Gln Tyr Ile Gln Val Asn Glu Pro Trp
115 120 125
Lys Arg Ile Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala Gly Thr Val
130 135 140
Thr Gly Leu Ala Val Asn Ile Ala Ala Leu Leu Ser Val Met Leu Gln
145 150 155 160
Pro Tyr Met Pro Thr Val Ser Ala Thr Ile Gln Ala Gln Leu Gln Leu
165 170 175
Pro Pro Pro Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu Cys Thr Leu
180 185 190
Pro Ala Gly His Gln Ile Gly Thr Val Ser Pro Leu Phe Gln Lys Leu
195 200 205
Glu Asn Asp Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly Gly Gly Gln
210 215 220
Ala Lys Thr Ser Pro Lys Pro Ala Val Val Glu Thr Val Thr Thr Ala
225 230 235 240
Lys Pro Gln Gln Ile Gln Ala Leu Met Asp Glu Val Thr Lys Gln Gly
245 250 255
Asn Ile Val Arg Glu Leu Lys Ala Gln Lys Ala Asp Lys Asn Glu Val
260 265 270
Ala Ala Glu Val Ala Lys Leu Leu Asp Leu Lys Lys Gln Leu Ala Val
275 280 285
Ala Glu Gly Lys Pro Pro Glu Ala Pro Lys Gly Lys Lys Lys
290 295 300

<210> 45
<211> 603
<212> PRT
<213> Artificial Sequence
<220>
<223> MRS fragment 6(298-900 aa)

<400> 45
Ser Arg Leu Arg Gln Trp Asn Thr Leu Tyr Leu Cys Gly Thr Asp Glu
1 5 10 15
Tyr Gly Thr Ala Thr Glu Thr Lys Ala Leu Glu Glu Gly Leu Thr Pro
20 25 30

OP19-0160-Sequence Listing

Gln Glu Ile Cys Asp Lys Tyr His Ile Ile His Ala Asp Ile Tyr Arg
35 40 45

Trp Phe Asn Ile Ser Phe Asp Ile Phe Gly Arg Thr Thr Thr Pro Gln
50 55 60

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

Phe Val Leu Gln Asp Thr Val Glu Gln Leu Arg Cys Glu His Cys Ala
85 90 95

Arg Phe Leu Ala Asp Arg Phe Val Glu Gly Val Cys Pro Phe Cys Gly
100 105 110

Tyr Glu Glu Ala Arg Gly Asp Gln Cys Asp Lys Cys Gly Lys Leu Ile
115 120 125

Asn Ala Val Glu Leu Lys Lys Pro Gln Cys Lys Val Cys Arg Ser Cys
130 135 140

Pro Val Val Gln Ser Ser Gln His Leu Phe Leu Asp Leu Pro Lys Leu
145 150 155 160

Glu Lys Arg Leu Glu Glu Trp Leu Gly Arg Thr Leu Pro Gly Ser Asp
165 170 175

Trp Thr Pro Asn Ala Gln Phe Ile Thr Arg Ser Trp Leu Arg Asp Gly
180 185 190

Leu Lys Pro Arg Cys Ile Thr Arg Asp Leu Lys Trp Gly Thr Pro Val
195 200 205

Pro Leu Glu Gly Phe Glu Asp Lys Val Phe Tyr Val Trp Phe Asp Ala
210 215 220

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

Arg Trp Trp Lys Asn Pro Glu Gln Val Asp Leu Tyr Gln Phe Met Ala
245 250 255

Lys Asp Asn Val Pro Phe His Ser Leu Val Phe Pro Cys Ser Ala Leu
260 265 270

Gly Ala Glu Asp Asn Tyr Thr Leu Val Ser His Leu Ile Ala Thr Glu
275 280 285

Tyr Leu Asn Tyr Glu Asp Gly Lys Phe Ser Lys Ser Arg Gly Val Gly
290 295 300

Val Phe Gly Asp Met Ala Gln Asp Thr Gly Ile Pro Ala Asp Ile Trp
305 310 315 320

Arg Phe Tyr Leu Leu Tyr Ile Arg Pro Glu Gly Gln Asp Ser Ala Phe
325 330 335

Ser Trp Thr Asp Leu Leu Leu Lys Asn Asn Ser Glu Leu Leu Asn Asn
340 345 350

Leu Gly Asn Phe Ile Asn Arg Ala Gly Met Phe Val Ser Lys Phe Phe
355 360 365

Gly Gly Tyr Val Pro Glu Met Val Leu Thr Pro Asp Asp Gln Arg Leu
370 375 380

Leu Ala His Val Thr Leu Glu Leu Gln His Tyr His Gln Leu Leu Glu
385 390 395 400

OP19-0160-Sequence Listing

Lys Val Arg Ile Arg Asp Ala Leu Arg Ser Ile Leu Thr Ile Ser Arg
405 410 415
His Gly Asn Gln Tyr Ile Gln Val Asn Glu Pro Trp Lys Arg Ile Lys
420 425 430
Gly Ser Glu Ala Asp Arg Gln Arg Ala Gly Thr Val Thr Gly Leu Ala
435 440 445
Val Asn Ile Ala Ala Leu Leu Ser Val Met Leu Gln Pro Tyr Met Pro
450 455 460
Thr Val Ser Ala Thr Ile Gln Ala Gln Leu Gln Leu Pro Pro Pro Ala
465 470 475 480
Cys Ser Ile Leu Leu Thr Asn Phe Leu Cys Thr Leu Pro Ala Gly His
485 490 495
Gln Ile Gly Thr Val Ser Pro Leu Phe Gln Lys Leu Glu Asn Asp Gln
500 505 510
Ile Glu Ser Leu Arg Gln Arg Phe Gly Gly Gly Gln Ala Lys Thr Ser
515 520 525
Pro Lys Pro Ala Val Val Glu Thr Val Thr Thr Ala Lys Pro Gln Gln
530 535 540
Ile Gln Ala Leu Met Asp Glu Val Thr Lys Gln Gly Asn Ile Val Arg
545 550 555 560
Glu Leu Lys Ala Gln Lys Ala Asp Lys Asn Glu Val Ala Ala Glu Val
565 570 575
Ala Lys Leu Leu Asp Leu Lys Lys Gln Leu Ala Val Ala Glu Gly Lys
580 585 590
Pro Pro Glu Ala Pro Lys Gly Lys Lys Lys
595 600

<210> 46
<211> 201
<212> PRT
<213> Artificial sequence
<220>
<223> MRS fragment 7(660-860 aa)

<400> 46
Phe Val Ser Lys Phe Phe Gly Gly Tyr Val Pro Glu Met Val Leu Thr
1 5 10 15
Pro Asp Asp Gln Arg Leu Leu Ala His Val Thr Leu Glu Leu Gln His
20 25 30
Tyr His Gln Leu Leu Glu Lys Val Arg Ile Arg Asp Ala Leu Arg Ser
35 40 45
Ile Leu Thr Ile Ser Arg His Gly Asn Gln Tyr Ile Gln Val Asn Glu
50 55 60
Pro Trp Lys Arg Ile Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala Gly
65 70 75 80
Thr Val Thr Gly Leu Ala Val Asn Ile Ala Ala Leu Leu Ser Val Met
85 90 95

OP19-0160-Sequence Listing

Leu Gln Pro Tyr Met Pro Thr Val Ser Ala Thr Ile Gln Ala Gln Leu
100 105 110
Gln Leu Pro Pro Pro Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu Cys
115 120 125
Thr Leu Pro Ala Gly His Gln Ile Gly Thr Val Ser Pro Leu Phe Gln
130 135 140
Lys Leu Glu Asn Asp Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly Gly
145 150 155 160
Gly Gln Ala Lys Thr Ser Pro Lys Pro Ala Val Val Glu Thr Val Thr
165 170 175
Thr Ala Lys Pro Gln Gln Ile Gln Ala Leu Met Asp Glu Val Thr Lys
180 185 190
Gln Gly Asn Ile Val Arg Glu Leu Lys
195 200

<210> 47
<211> 241
<212> PRT
<213> Artificial Sequence
<220>
<223> MRS fragment 8(660-900 aa)

<400> 47
Phe Val Ser Lys Phe Phe Gly Gly Tyr Val Pro Glu Met Val Leu Thr
1 5 10 15
Pro Asp Asp Gln Arg Leu Leu Ala His Val Thr Leu Glu Leu Gln His
20 25 30
Tyr His Gln Leu Leu Glu Lys Val Arg Ile Arg Asp Ala Leu Arg Ser
35 40 45
Ile Leu Thr Ile Ser Arg His Gly Asn Gln Tyr Ile Gln Val Asn Glu
50 55 60
Pro Trp Lys Arg Ile Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala Gly
65 70 75 80
Thr Val Thr Gly Leu Ala Val Asn Ile Ala Ala Leu Leu Ser Val Met
85 90 95
Leu Gln Pro Tyr Met Pro Thr Val Ser Ala Thr Ile Gln Ala Gln Leu
100 105 110
Gln Leu Pro Pro Pro Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu Cys
115 120 125
Thr Leu Pro Ala Gly His Gln Ile Gly Thr Val Ser Pro Leu Phe Gln
130 135 140
Lys Leu Glu Asn Asp Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly Gly
145 150 155 160
Gly Gln Ala Lys Thr Ser Pro Lys Pro Ala Val Val Glu Thr Val Thr
165 170 175
Thr Ala Lys Pro Gln Gln Ile Gln Ala Leu Met Asp Glu Val Thr Lys
180 185 190

OP19-0160-Sequence Listing

Gln Gly Asn Ile Val Arg Glu Leu Lys Ala Gln Lys Ala Asp Lys Asn
195 200 205
Glu Val Ala Ala Glu Val Ala Lys Leu Leu Asp Leu Lys Lys Gln Leu
210 215 220
Ala Val Ala Glu Gly Lys Pro Pro Glu Ala Pro Lys Gly Lys Lys Lys
225 230 235 240
Lys

<210> 48
<211> 171
<212> PRT
<213> Artificial Sequence

<220>
<223> MRS fragment 9(730-900 aa)

<400> 48
Gly Ser Glu Ala Asp Arg Gln Arg Ala Gly Thr Val Thr Gly Leu Ala
1 5 10 15
Val Asn Ile Ala Ala Leu Leu Ser Val Met Leu Gln Pro Tyr Met Pro
20 25 30
Thr Val Ser Ala Thr Ile Gln Ala Gln Leu Gln Leu Pro Pro Pro Ala
35 40 45
Cys Ser Ile Leu Leu Thr Asn Phe Leu Cys Thr Leu Pro Ala Gly His
50 55 60
Gln Ile Gly Thr Val Ser Pro Leu Phe Gln Lys Leu Glu Asn Asp Gln
65 70 75 80
Ile Glu Ser Leu Arg Gln Arg Phe Gly Gly Gly Gln Ala Lys Thr Ser
85 90 95
Pro Lys Pro Ala Val Val Glu Thr Val Thr Thr Ala Lys Pro Gln Gln
100 105 110
Ile Gln Ala Leu Met Asp Glu Val Thr Lys Gln Gly Asn Ile Val Arg
115 120 125
Glu Leu Lys Ala Gln Lys Ala Asp Lys Asn Glu Val Ala Ala Glu Val
130 135 140
Ala Lys Leu Leu Asp Leu Lys Lys Gln Leu Ala Val Ala Glu Gly Lys
145 150 155 160
Pro Pro Glu Ala Pro Lys Gly Lys Lys Lys Lys
165 170

<210> 49
<211> 174
<212> PRT
<213> Artificial Sequence

<220>
<223> Homo sapiens AIMP3 protein

<400> 49

OP19-0160-Sequence Listing

Met Ala Ala Ala Ala Glu Leu Ser Leu Leu Glu Lys Ser Leu Gly Leu
1 5 10 15
Ser Lys Gly Asn Lys Tyr Ser Ala Gln Gly Glu Arg Gln Ile Pro Val
20 25 30
Leu Gln Thr Asn Asn Gly Pro Ser Leu Thr Gly Leu Thr Thr Ile Ala
35 40 45
Ala His Leu Val Lys Gln Ala Asn Lys Glu Tyr Leu Leu Gly Ser Thr
50 55 60
Ala Glu Glu Lys Ala Ile Val Gln Gln Trp Leu Glu Tyr Arg Val Thr
65 70 75 80
Gln Val Asp Gly His Ser Ser Lys Asn Asp Ile His Thr Leu Leu Lys
85 90 95
Asp Leu Asn Ser Tyr Leu Glu Asp Lys Val Tyr Leu Thr Gly Tyr Asn
100 105 110
Phe Thr Leu Ala Asp Ile Leu Leu Tyr Tyr Gly Leu His Arg Phe Ile
115 120 125
Val Asp Leu Thr Val Gln Glu Lys Glu Lys Tyr Leu Asn Val Ser Arg
130 135 140
Trp Phe Cys His Ile Gln His Tyr Pro Gly Ile Arg Gln His Leu Ser
145 150 155 160
Ser Val Val Phe Ile Lys Asn Arg Leu Tyr Thr Asn Ser His
165 170