

SEQUENCE LISTING

<110> The Brigham and Women's Hospital, Inc.

<120> ANTI-PERIPHERAL LYMPH NODE ADDRESSIN ANTIBODIES AND USES THEREOF

<130> 29618-0208W01

<140> PCT/US2020/017879

<141> 2020-02-12

<150> 62/804,797

<151> 2019-02-13

<160> 18

<170> PatentIn version 3.5

<210> 1

<211> 351

<212> DNA

<213> Artificial Sequence

<220>

<223> Sequence encoding MHA112 Heavy Chain

<400> 1

cagggtgcagc tgaaggagtc aggacctggc ctggtggcgc cctcacagag cctgtccatc 60

acttgcaactg tctctggggtt ttcattaacc agctatgggtg tagactgggt tcgccagcct 120

ccaggaaagg gtctggagtg gctgggagta atatgggggtg gtggaagcac aaattataat 180

tcagctctca tgtccagact gagcatcagc aaagacaact ccaagagcca agttttctta 240

aaaatgaaca gtctgcaaac tgatgacaca gccatgtact actgtgccaa acatagtaaa 300

gggggggtact tcgatgtctg gggcacaggg accacgtca ccgtctcctc a 351

<210> 2

<211> 117

<212> PRT

<213> Artificial Sequence

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<223> MHA112 Heavy chain

<400> 2

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

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

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

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

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

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

Lys His Ser Lys Gly Gly Tyr Phe Asp Val Trp Gly Thr Gly Thr Thr
100 105 110

Val Thr Val Ser Ser
115

<210> 3
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MHA112 Heavy chain CDR1

<400> 3

Gly Phe Ser Leu Thr Ser Tyr
1 5

<210> 4
<211> 5
<212> PRT
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<220>
<223> MHA112 Heavy chain CDR2

<400> 4

Trp Gly Gly Gly Ser
1 5

<210> 5
<211> 9
<212> PRT
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<220>
<223> MHA112 Heavy chain CDR3

<400> 5

His Ser Lys Gly Gly Tyr Phe Asp Val
1 5

<210> 6
<211> 318
<212> DNA
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<220>
<223> Sequence encoding MHA112 light Chain

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gaaattgtgc tcactcagtc tccagccatc acagctgcat ctctggggca aaaggtcacc 60
atcacctgca gtgccagctc aagtgttaagt tacatgcact ggtaccagca gaagtcaggc 120
acctccccca aaccatggat ttatgaaata tccaaactgg cttctggagt cccagctcgc 180
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagcat ggaggctgaa 240
gatgctgcca tttattactg ccagcagtgg aattatcctc ttatcacgtt cggtgctggg 300
accaagctgg agctgaaa 318

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

<220>
<223> MHA112 Light chain

<400> 7

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

Gln Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
 20 25 30

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

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

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu
 65 70 75 80

Asp Ala Ala Ile Tyr Tyr Cys Gln Gln Trp Asn Tyr Pro Leu Ile Thr
 85 90 95

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

<210> 8
 <211> 10
 <212> PRT
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<220>
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<400> 8

Ser Ala Ser Ser Ser Val Ser Tyr Met His
 1 5 10

<210> 9
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<220>
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<400> 9

Glu Ile Ser Lys Leu Ala Ser
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<210> 10
<211> 9
<212> PRT
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<220>
<223> MHA112 Light chain CDR3

<400> 10

Gln Gln Trp Asn Tyr Pro Leu Ile Thr
1 5

<210> 11
<211> 25
<212> PRT
<213> Artificial Sequence

<220>
<223> MHA112 Heavy chain framework region 1

<400> 11

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

Ser Leu Ser Ile Thr Cys Thr Val Ser
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<210> 12
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> MHA112 Heavy chain framework region 2

<400> 12

Gly Val Asp Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
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Gly Val Ile

<210> 13
<211> 41
<212> PRT

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<223> MHA112 Heavy chain framework region 3

<400> 13

Thr Asn Tyr Asn Ser Ala Leu Met Ser Arg Leu Ser Ile Ser Lys Asp
1 5 10 15

Asn Ser Lys Ser Gln Val Phe Leu Lys Met Asn Ser Leu Gln Thr Asp
20 25 30

Asp Thr Ala Met Tyr Tyr Cys Ala Lys
35 40

<210> 14

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<212> PRT

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<223> MHA112 Heavy chain framework

<400> 14

Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser
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<210> 15

<211> 23

<212> PRT

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<223> MHA112 Light chain framework region 1

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Glu Ile Val Leu Thr Gln Ser Pro Ala Ile Thr Ala Ala Ser Leu Gly
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Gln Lys Val Thr Ile Thr Cys
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<210> 16

<211> 15

<212> PRT
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<220>
<223> MHA112 Light chain framework region 2

<400> 16

Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
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<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> MHA112 Light chain framework region 3

<400> 17

Gly	Val	Pro	Ala	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser
1				5					10					15	

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

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

<220>
<223> MHA112 Light chain framework region 4

<400> 18

Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys
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