

SEQUENCE LISTING

<110> Albert Einstein College of Medicine
 Zang, Xingxing
 <120> MONOCLONAL ANTIBODIES AGAINST HUMAN TIM-3
 <130> 129807-8004.W000
 <150> US 62/720,234
 <151> 2018-08-21
 <160> 22
 <170> PatentIn version 3.5
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 Gly Tyr Ser Phe Thr Gly Tyr Thr Ile Asn
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Ala Arg Arg Tyr Tyr Gly Tyr Asp Ala Met Asp Tyr
1 5 10

<210> 4
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<223> 50B5 LCDR1

<400> 4

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

Ala

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<400> 5

Trp Ala Ser Thr Arg Glu Ser
1 5

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<400> 6

His Gln Tyr Leu Ser Ser Tyr Thr
1 5

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<223> 15B4 HCDR1

<400> 7

Gly	Phe	Asn	Ile	Lys	Asp	Tyr	Tyr	Met	His
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<400> 8

Trp	Ile	Asp	Pro	Glu	Asn	Asp	Asn	Thr	Ile	Tyr
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<400> 9

Ala	Arg	Asp	Phe	Gly	Tyr	Val	Ala	Trp	Leu	Val	Tyr
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<400> 10

Lys	Ala	Ser	Gln	Asn	Val	Asp	Thr	Ala	Val	Ala
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<212> PRT
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<400> 11

Ser Ala Ser Asn Arg Tyr Thr
1 5

<210> 12
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<400> 12

Gln Gln Tyr Ser Ser Tyr Pro Thr
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<400> 13

Met Phe Ser His Leu Pro Phe Asp Cys Val Leu Leu Leu Leu Leu Leu
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Leu Leu Thr Arg Ser Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln
20 25 30

Asn Ala Tyr Leu Pro Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu
35 40 45

Val Pro Val Cys Trp Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly
50 55 60

Asn Val Val Leu Arg Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser
65 70 75 80

Arg Tyr Trp Leu Asn Gly Asp Phe Arg Lys Gly Asp Val Ser Leu Thr

85

90

95

Ile Glu Asn Val Thr Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile
 100 105 110

Gln Ile Pro Gly Ile Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val
 115 120 125

Ile Lys Pro Ala Lys Val Thr Pro Ala Pro Thr Arg Gln Arg Asp Phe
 130 135 140

Thr Ala Ala Phe Pro Arg Met Leu Thr Thr Arg Gly His Gly Pro Ala
 145 150 155 160

Glu Thr Gln Thr Leu Gly Ser Leu Pro Asp Ile Asn Leu Thr Gln Ile
 165 170 175

Ser Thr Leu Ala Asn Glu Leu Arg Asp Ser Arg Leu Ala Asn Asp Leu
 180 185 190

Arg Asp Ser Gly Ala Thr Ile Arg Ile Gly Ile Tyr Ile Gly Ala Gly
 195 200 205

Ile Cys Ala Gly Leu Ala Leu Ala Leu Ile Phe Gly Ala Leu Ile Phe
 210 215 220

Lys Trp Tyr Ser His Ser Lys Glu Lys Ile Gln Asn Leu Ser Leu Ile
 225 230 235 240

Ser Leu Ala Asn Leu Pro Pro Ser Gly Leu Ala Asn Ala Val Ala Glu
 245 250 255

Gly Ile Arg Ser Glu Glu Asn Ile Tyr Thr Ile Glu Glu Asn Val Tyr
 260 265 270

Glu Val Glu Glu Pro Asn Glu Tyr Tyr Cys Tyr Val Ser Ser Arg Gln
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Gln Pro Ser Gln Pro Leu Gly Cys Arg Phe Ala Met Pro
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gtccagctgc aacagtctgg acctgagctg gtgaagcctg gagcttcaat gaagatatcc 120
tgcaaggctt ctggttactc attcactggc tacaccataa actgggtgaa gcagagccat 180
ggaaagaacc ttgagtggat tggacttttt aatccttaca atggtggtac taccttcaac 240
cagaagttca agggcaaggc cacattaact gttgacaagt catccagcac agcctacatg 300
gagctcctca gtctgacatc tgaggactct gcagtctatt actgtgcaag acgatactac 360
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<220>
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<400> 15

Met Gly Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
1 5 10 15

Val His Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe
35 40 45

Thr Gly Tyr Thr Ile Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu
50 55 60

Glu Trp Ile Gly Leu Phe Asn Pro Tyr Asn Gly Gly Thr Thr Phe Asn
65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Arg Tyr Tyr Gly Tyr Asp Ala Met Asp Tyr Trp
115 120 125

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
130 135

<210> 16
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<223> 50B5 light chain

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<223> LCDR2

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<223> LCDR3

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atgagctgta agtccagtca aagtgtttta tacagttcaa atcagaagaa ccacttggcc 180
tggtaccagc agaaaccagg gcagtctcct aaactgctaa tctactgggc atccactagg 240
gaatctggtg tccctgatcg cttcacaggc agtggatctg ggacagattt tactcttacc 300
atcagcagtg tacaagctga agacctggca gtttattact gtcataata cctctcctcg 360
tacacgttcg gagggggggac caagctggaa attaag 396

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<400> 17

Met Glu Ser Gln Thr Gln Val Phe Leu Ser Leu Leu Leu Trp Val Ser
1 5 10 15

Gly Thr Cys Gly Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala
20 25 30

Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser Gln Ser
35 40 45

Val Leu Tyr Ser Ser Asn Gln Lys Asn His Leu Ala Trp Tyr Gln Gln
50 55 60

Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg
65 70 75 80

Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp
85 90 95

Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr
100 105 110

Tyr Cys His Gln Tyr Leu Ser Ser Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125

Leu Glu Ile Lys
130

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tgcaaagctt ctggcttcaa cattaaagac tactatatgc actgggtgag gcagaggcct 180
gaacagggcc tggagtggat tggatggatt gatcctgaga atgacaatac tatatatgac 240
ccgaagttcc aggacagggc cagtataaca gcagacacat cctccaacac agcctacctg 300
cagctcagca gcctgacatc tgaggacact gccgtctatt actgtgctag ggacttcggc 360
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<222> (116)..(127)
<223> HCDR3

<400> 19

Met Glu Trp Ser Trp Val Phe Leu Phe Leu Met Ala Val Val Thr Gly
1 5 10 15

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Val Val Arg
20 25 30

Pro Gly Ala Leu Val Lys Leu Ser Cys Lys Ala Ser Gly Phe Asn Ile
35 40 45

Lys Asp Tyr Tyr Met His Trp Val Arg Gln Arg Pro Glu Gln Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Asp Pro Glu Asn Asp Asn Thr Ile Tyr Asp
65 70 75 80

Pro Lys Phe Gln Asp Arg Ala Ser Ile Thr Ala Asp Thr Ser Ser Asn
85 90 95

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
100 105 110

Tyr Tyr Cys Ala Arg Asp Phe Gly Tyr Val Ala Trp Leu Val Tyr Trp
115 120 125

Gly Gln Gly Thr Leu Val Thr Val Ser Ala
130 135

<210> 20
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<223> LCDR3

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acctgcaagg ccagtcagaa tgtggatact gctgtagcct ggtatcaaca gaaaccagga 180
caatctccta aactactgat ttactcggca tccaatcggg acactggagt ccctgatcgc 240
ttcacaggca ctggatctgg gacagatttc actctcacca tcaacaatat gcagtctgaa 300
gacctggcag attatttctg ccagcaatat agcagctatc ccacgttcgg agggaggacc 360

aagctggaaa taaaacgg

378

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<223> LCDR3

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Met Ser Gln Ser Gln Val Phe Val Phe Ala Phe Leu Trp Leu Ser Gly
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Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Glu Phe Met Ser Thr
20 25 30

Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asn Val
35 40 45

Asp Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
50 55 60

Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg
65 70 75 80

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

Met Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Ser Ser
100 105 110

Tyr Pro Thr Phe Gly Gly Arg Thr Lys Leu Glu Ile Lys Arg
115 120 125

<210> 22
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<212> PRT
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<400> 22

Ser Glu Val Glu Tyr Arg Ala Glu Val Gly Gln Asn Ala Tyr Leu Pro
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Cys Phe Tyr Thr Pro Ala Ala Pro Gly Asn Leu Val Pro Val Cys Trp
20 25 30

Gly Lys Gly Ala Cys Pro Val Phe Glu Cys Gly Asn Val Val Leu Arg
35 40 45

Thr Asp Glu Arg Asp Val Asn Tyr Trp Thr Ser Arg Tyr Trp Leu Asn
50 55 60

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

Leu Ala Asp Ser Gly Ile Tyr Cys Cys Arg Ile Gln Ile Pro Gly Ile
85 90 95

Met Asn Asp Glu Lys Phe Asn Leu Lys Leu Val Ile Lys Pro Ala
100 105 110