

311SG438-seq1-000001
SEQUENCE LISTING

<110> Agency for Science, Technology and Research

<120> Anti-TIM-3 Antibodies

<130> RIC/FP7158009

<150> GB 1419092.0

<151> 2014-10-27

<150> GB 1419089.6

<151> 2014-10-27

<160> 61

<170> PatentIn version 3.3

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<212> PRT

<213> Homo sapiens

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Asp Ile Gln Met Thr Gln Ser Pro Ser Phe Met Ser Ala Ser Val Gly
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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

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

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Gln Pro
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Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Pro Pro
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Thr Phe Gly Pro Gly Thr Thr Leu Glu Ile Lys
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Leu Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Pro Leu Ile
35 40 45

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

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

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

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

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

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

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

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
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Tyr Leu Ala Trp Tyr Gln Gln Thr 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

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20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Ile 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
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Arg Ala Ser Gln Asp Ile Gly Ser Tyr Leu Ala
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Arg Ala Ser Gln Ser Val Gly Ser Tyr Leu Ala
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Asp Ala Thr Asn Arg Ala Thr
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Gln His Arg Arg Thr
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Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
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Leu Gly Ser Asn Arg Ala Ser
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Met Gln Gly Thr His Trp Pro Pro Thr
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Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
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Gly Ala Ser Ser Arg Ala Thr
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

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

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

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

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

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

Cys Ala Arg Gly Glu His Arg Gly Glu Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

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

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

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

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

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

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

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

Ala Arg Asp Leu Tyr Ser Tyr Gly Phe Tyr Tyr Tyr Gly Met Asp Val
100 105 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

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Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His
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Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe Gln
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Ser Pro Gly Val Val Thr Ala Leu Phe Asp Tyr
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<210> 27
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 <212> PRT
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<400> 27

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

<210> 28
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<400> 28

Ser Ile Tyr Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Lys Ser
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<210> 29
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 <212> PRT
 <213> Homo sapiens

<400> 29

Gly Glu His Arg Gly Glu Phe Asp Tyr
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<210> 30
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Gly Gly Ser Ile Ser Ser Ser Asn Trp Trp Ser
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Glu Ile Tyr His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
1 5 10 15

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Val Val Ala Val Ala Gly Thr Val Asp Tyr
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<210> 33
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Asp Gln Tyr Ser Ser Gly Trp Tyr Tyr Tyr Gly Met Asp Val
1 5 10

<210> 34
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Asp Leu Tyr Ser Tyr Gly Phe Tyr Tyr Tyr Gly Met Asp Val
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atcacttgcc gggccagtca ggacattggc agttatttag cctggtatca gcaaaaacca 120
gggaaagccc ctaaactcct gatctatgct gcatccactt tgcaaagtgg ggtcccatca 180
aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcaacag tctgcaacct 240
gaagattttg caacttacta ctgtcaacag agttacagtt cccctccgac tttcgggcct 300
gggaccacat tggagatcaa a 321

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<212> DNA
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<400> 36
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ctctcctgca gggccagtca gagtgttggc agctacttag cctggtacca gcagagacct 120
ggccaggctc ccaggcccct catctatgat gcaaccaaca gggccactgg catcccaacc 180

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aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 240
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gagatcaaa 309

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<212> DNA
<213> Homo sapiens

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tccgggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240
agcaggggtg aggctgagga tgttgggggt tattactgca tgcaaggtac aacttggcct 300
ccgacgttcg gccaaaggac caaggtggaa ctcaaa 336

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cctggccagg ctcccaggct cctcatctat ggtgcatcca gcagggccac tggcatccca 180
gacaggttca gtggcagtg gtctgggaca gacttcactc tcaccatcag cagactggag 240
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caaggacac gactggagat taaa 324

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<213> Homo sapiens

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gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240
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ccccaggga aggggctgga gtggattggg gaaatctatc atagtgggag caccaactac 180
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gcagtggctg gtacggttga ctactggggc caggaaccc tggtcaccgt ctcaagc 357

<210> 43
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cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggtag cacaagctac 180
gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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gtctcaagc 369

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Gln Ser Val Val Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln
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Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn
20 25 30

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Ala Ile Ser Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Glu Thr Trp Asp Ser Ser Leu
85 90 95

Ser Ala Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

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<213> Artificial sequence

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<220>

<223> Synthetic sequence: Light chain variable domain sequence for anti-TIM-3 antibody A11_gI

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

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

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

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Gly Ile Thr Gly Leu Gln
65 70 75 80

Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Glu Thr Trp Asp Ser Ser Leu
85 90 95

Ser Ala Gly Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu
100 105 110

<210> 47

<211> 13

<212> PRT

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

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Gly Asn Asn Trp Arg Pro Ser
1 5

<210> 49

<211> 11

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<213> Homo sapiens

<400> 49

Glu Thr Trp Asp Ser Ser Leu Ser Ala Gly Val
1 5 10

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<211> 116
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<400> 50

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 Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe Ser Gly Tyr
 20 25 30
 Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
 50 55 60
 Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
 65 70 75 80
 Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
 85 90 95
 Arg Gly Tyr Val Ala Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser
 115

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 <213> Artificial sequence

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 <223> synthetic sequence: Heavy chain variable domain sequence for
 anti-TIM-3 antibody clone A11_gI

<400> 51

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

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

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

Thr Val Ser Ser
115

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Gly Gly Ser Phe Ser Gly Tyr Tyr Trp Ser
1 5 10

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<400> 53

Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser
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Gly Tyr Val Ala Gly Phe Asp Tyr
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ccaggaacag cccccaaact cctcatTTat ggcaataatt ggcgaccctc agggattcct 180
gaccgcttct ctggctccaa gtctggcacc tcagccaccc tggccatcag cggacttcag 240
actggggacg aggccgatta ttactgcgaa acatgggata gcagcctgag tgctggggta 300
ttcggcggag ggaccaagct gaccgtccta 330

<210> 56
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<213> Artificial sequence

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<223> synthetic sequence: Nucleotide sequence of heavy chain variable domain sequence for anti-TIM-3 antibody clone A11_gI

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ccaggaacag cccccaaact cctcatttat ggcaataatt ggcgaccctc agggattcct 180
gaccgcttct ctggctccaa gtctggcacc tcagccaccc tgggcatcac cggacttcag 240
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