

311SG445-seq1-000001
SEQUENCE LISTING

<110> Agency for Science, Technology and Research

<120> Anti-PD-L1 Antibodies

<130> RIC/FP7082969

<160> 36

<170> PatentIn version 3.3

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<212> PRT

<213> Homo sapiens

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

Met Tyr Glu Thr Asn Lys Arg Pro Trp Gly Ile Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Thr Leu Asp Ile Ala Gly Leu Gln
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Thr Gly Asp Glu Ala Asp Tyr Tyr Cys Gly Ala Trp Asp Ser Gly Leu
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Thr Gly Met Leu Phe Gly Gly Gly Thr Lys Val Thr Val Leu
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<213> Homo sapiens

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20 25 30

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

Asp Asp Gly Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
50 55 60

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

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

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

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

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

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

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

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

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Tyr Asp Ser Ser
85 90 95

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

Leu

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

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

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

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

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala 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 Gly His Gly Tyr Ser Tyr Gly Ala Phe Asp Tyr Trp Gly
 100 105 110

Gln Gly Thr Leu
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Glu Thr Asn Lys Arg Pro Trp
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Gln Ala Trp Asp Ser Thr Val Val
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Asp Asn Asn Glu Arg Leu Ser
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Gly Thr Trp Asp Ser Ser Leu Ser Val Val Val

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Gly Asn Ser Asn Arg Pro Ser
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Ser Tyr Ala Ile Ser
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<210> 22
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Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

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Gly Gly Ser Tyr Gly Ser Leu Tyr Ala Phe Asp Ile
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Gly Gly Tyr Gly Gly Asn Ser Leu Tyr Ala Phe Asp Ile
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Ser Gly His Gly Tyr Ser Tyr Gly Ala Phe Asp Tyr
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<223> Xaa = Leu or Tyr

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<221> VARIANT

<222> (9)..(9)

<223> Xaa = Tyr or Gly

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<222> (13)..(13)

<223> Xaa = Ile or Tyr

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<213> Homo sapiens

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ccaggaacag	ccccaaaat	cgatcatgat	gaaactaata	aacgtccctg	ggggattcct	180
gaccgattct	ccggctccaa	gtctggcacg	tccgccaccc	tggacatcgc	cggactccag	240
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<212> DNA

<213> Homo sapiens

<400> 28

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ccaggaacag	ccccaaact	cctcatttat	gacaataatg	agcgactctc	agggattcct	180

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gaccgattct ctggttccaa gtctggcacg tcagccaccc tgggcatcag cggactccag	240
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ttcggcggag ggaccaagct gaccgtccta	330

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cttcaggaa cagccccaa actcctcatc tatggtaaca gcaatcggcc ctcaggggtc	180
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<400> 31	
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gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagggggc	300
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agc	363

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gcacagaagt tccagggcag agtcacgatt accgcggaca aatccacgag cacagcctac	240
atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagggggc	300
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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

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

Gly Arg Ile Ile Pro Ile Leu Gly Ile Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

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Gln Gly Thr Leu Val Thr Val Ser Ser				
	115		120	
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