

Sequence Listing

<110> SHANGHAI JUNSHI BIOSCIENCES CO., LTD.
SUZHOU JUNMENG BIOSCIENCES CO., LTD.

<120> ANTI-BTLA ANTIBODY

<130> 184868

<150> CN 201810870514.0

<151> 2018-08-02

<160> 51

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<213> Artificial Sequence

<220>

<223> HCDR1

<400> 1

Asp Thr Tyr Leu His

1 5

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<400> 2

Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Arg Phe Gln

1 5 10 15

Gly

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Asp Tyr Tyr Gly Ser Ser Leu Phe Asp Tyr
1 5 10

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<400> 4

Asp Ser Tyr Ile His
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<400> 5

Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe Arg
1 5 10 15
Gly

<210> 6

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<400> 6

Asp His Tyr Gly Ser Ser Leu Phe Asp Tyr
1 5 10

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<400> 7

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 8

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<400> 8

Val Leu Ser Lys Leu Glu Ser
1 5

<210> 9

<211> 9

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<400> 9

Trp Gln Gly Thr His Phe Pro Tyr Thr
1 5

<210> 10

<211> 16

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<400> 10

Lys Ser Ser Gln Ser Leu Leu Asp Ser Asp Gly Lys Thr Tyr Leu Asn
1 5 10 15

<210> 11

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<400> 11

Leu Val Ser Lys Leu Asp Ser

1 5

<210> 12
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<220>
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<400> 12
 Trp Gln Gly Thr Tyr Phe Pro Tyr Thr
 1 5

<210> 13
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<400> 13
 His Thr Tyr Ala His
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<400> 14
 Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe Gln
 1 5 10 15
 Gly

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<400> 15
 Asp His Tyr Gly Ser Ser Leu Leu Asp Tyr

1 5 10

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<400> 16
 Lys Ala Ser Gln Asp Ile Asn Lys Tyr Ile Ala
 1 5 10

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<220>
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<400> 17
 Tyr Thr Ser Thr Leu Gln Pro
 1 5

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<220>
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<400> 18
 Leu Gln Tyr Ala Thr Tyr Ala Pro Pro Ala Val Ser Ile
 1 5 10

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<400> 19
 Asp Thr Tyr Val His
 1 5

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<400> 20
 Arg Ile Asp Pro Ala Asn Gly His Thr Lys Phe Asp Pro Lys Phe Gln
 1 5 10 15
 Gly

<210> 21
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<400> 21
 Asp Tyr Tyr Gly Ser Ser Leu Leu Asp Tyr
 1 5 10

<210> 22
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 <212> PRT
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<220>
 <223> LCDR1

<400> 22
 Ser Glu Pro Pro Ser Glu Asp Gly Lys Thr Tyr
 1 5 10

<210> 23
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 <212> PRT
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<400> 23
 Val Val Ser
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<210> 24
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 <212> PRT
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<400> 24
 Trp Gln Gly Thr His Phe Pro Tyr Thr
 1 5

<210> 25
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<400> 25
 Asp Thr Tyr Val His
 1 5

<210> 26
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 <213> Artificial Sequence

<220>
 <223> HCDR2

<400> 26
 Arg Ile Asp Pro Ala Asn Gly His Thr Lys Tyr Asp Pro Lys Leu Gln
 1 5 10 15
 Gly

<210> 27
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 <212> PRT
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<220>
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<400> 27
 Asp Tyr Tyr Gly Ser Ser Leu Leu Asp Tyr
 1 5 10

<210> 28
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<400> 28
 Asp Thr Tyr Met His
 1 5

<210> 29
 <211> 17
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<220>
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<400> 29
 Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Phe Asp Pro Lys Phe Gln
 1 5 10 15
 Gly

<210> 30
 <211> 10
 <212> PRT
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<220>
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<400> 30
 Asp His Tyr Gly Ser Ser Leu Leu Asp Tyr
 1 5 10

<210> 31
 <211> 11
 <212> PRT
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<220>
 <223> LCDR1

<400> 31
 Lys Ala Ser Gln Asp Ile Lys Ser Tyr Leu Ser
 1 5 10

<210> 32
 <211> 7
 <212> PRT
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<220>
 <223> LCDR2

<400> 32
 Tyr Ala Thr Ser Leu Ala Asp
 1 5

<210> 33
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> LCDR3

<400> 33
 Leu Gln His Gly Ala Asp Ala Ala Pro Thr Val Ser Ile
 1 5 10

<210> 34
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain variable region

<400> 34
 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Asn Leu Ser Cys Thr Ala Ser Gly Phe Ala Ile Arg Asp Thr
 20 25 30
 Tyr Leu His Trp Val Lys Gln Arg Pro Glu Gln Val Leu Glu Trp Thr
 35 40 45
 Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Arg Phe
 50 55 60
 Gln Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
 65 70 75 80
 Leu His Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Ala Asp Tyr Tyr Gly Ser Ser Leu Phe Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser
 115

<210> 35
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain variable region

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

<210> 36
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

<400> 36
 Asp Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Lys Arg Leu Ile Tyr Val Leu Ser Lys Leu Glu Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Thr Gly Val Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Val Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95
 Thr His Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 37
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

<400> 37
 Glu Val Val Met Thr Gln Thr Pro Leu Thr Leu Ser Val Thr Ile Gly
 1 5 10 15
 Gln Ser Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Lys Arg Leu Met His Leu Val Ser Lys Leu Asp Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Gly Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Trp Gln Gly
 85 90 95
 Thr Tyr Phe Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Thr Lys
 100 105 110

<210> 38
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain variable region

<400> 38
 Glu Val Gln Leu Gln Gln Ser Gly Ala Asp Leu Val Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Phe Lys His Thr
 20 25 30
 Tyr Ala His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
 50 55 60
 Gln Gly Lys Ala Thr Met Thr Ala Asp Thr Ala Ser Asn Ala Ala Phe
 65 70 75 80
 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Val Ala Asp His Tyr Gly Ser Ser Leu Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Ser Leu Thr Val Ser Ser
 115

<210> 39
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

<400> 39
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15
 Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Lys Tyr
 20 25 30
 Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg Leu Leu Ile
 35 40 45
 His Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser Ser Leu Glu Ser
 65 70 75 80
 Glu Asp Ser Ala Asn Tyr Tyr Cys Leu Gln Tyr Ala Thr Tyr Ala Pro
 85 90 95
 Pro Ala Val Ser Ile Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 100 105 110

<210> 40
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain variable region

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

<210> 41
 <211> 108
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

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

<210> 42
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain variable region

<400> 42
 Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 1 5 10 15
 Ser Val Lys Leu Ser Cys Thr Val Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30
 Tyr Val His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asp Pro Ala Asn Gly His Thr Lys Tyr Asp Pro Lys Leu
 50 55 60
 Gln Gly Thr Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
 65 70 75 80
 Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Thr Asp Tyr Tyr Gly Ser Ser Leu Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser
 115

<210> 43
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain variable region

<400> 43
 Glu Val His Leu Gln Gln Ser Gly Thr Glu Leu Met Lys Pro Gly Ala
 1 5 10 15
 Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Leu Asn Ile Arg Asp Thr
 20 25 30
 Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Phe Asp Pro Lys Phe
 50 55 60
 Gln Gly Lys Ala Thr Leu Thr Ser Asp Thr Ser Ser Asn Thr Ala Tyr
 65 70 75 80
 Leu His Phe Ser Ser Leu Thr Ser Glu Asp Ala Ala Val Tyr Tyr Cys
 85 90 95
 Val Ser Asp His Tyr Gly Ser Ser Leu Leu Asp Tyr Trp Gly Gln Gly
 100 105 110
 Thr Ser Leu Thr Val Ser Ser
 115

<210> 44
 <211> 111
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

<400> 44
 Asp Ile Lys 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 Lys Ser Tyr
 20 25 30
 Leu Ser Trp Tyr Gln Gln Lys Pro Trp Lys Ser Pro Lys Thr Leu Ile
 35 40 45
 Tyr Tyr Ala Thr Ser Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Gln Asp Tyr Ser Leu Thr Ile Thr Ser Leu Glu Ser
 65 70 75 80
 Asp Asp Thr Ala Thr Tyr Tyr Cys Leu Gln His Gly Ala Asp Ala Ala
 85 90 95
 Pro Thr Val Ser Ile Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 45
 <211> 119
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Heavy chain variable region

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

<210> 46
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

<400> 46
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 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 Trp Gln Gly
 85 90 95
 Thr Tyr Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 47
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

<400> 47
 Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Arg Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp 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 Trp Gln Gly
 85 90 95
 Thr Tyr Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 48
 <211> 112
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Light chain variable region

<400> 48
 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
 1 5 10 15
 Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu Leu Asp Ser
 20 25 30
 Asp Gly Lys Thr Tyr Leu Asn Trp Phe Gln Gln Arg Pro Gly Gln Ser
 35 40 45
 Pro Arg Arg Leu Met His Leu Val Ser Lys Leu Asp 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 Trp Gln Gly
 85 90 95
 Thr Tyr Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 49

<211> 384
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Human BTLA extracellular domain

<400> 49
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 ggagatccct ttgaactaga atgccctgtg aaatactgtg ctaacaggcc tcatgtgact 120
 tggtgcaagc tcaatggaac aacatgtgta aaacttgaag atagacaaac aagttggaag 180
 gaagagaaga acatttcatt ttctattcta cattttgaac cagtgccttc taatgacaat 240
 gggtcatacc gctgttctgc aaattttcag tctaattctca ttgaaagcca ctcaacaact 300
 ctttatgtga cagatgtaaa aagtcctca gaacgaccct ccaaggacga aatggcaagc 360
 agaccctggc tcctgtatag tgct 384

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 <211> 41
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 <213> Artificial Sequence

<220>
 <223> Primer

<400> 50
 gtacgctctt catgtaaaga atcatgtgat gtacagcttt a 41

<210> 51
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 51
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