

<110> INSTITUTE FOR BASIC SCIENCE
 POSTECH ACADEMY-INDUSTRY FOUNDATION
 <120> ANTI-HUMAN INTERLEUKIN-2 ANTIBODIES AND USES THEREOF
 <130> PP-B2037
 <150> KR 10-2017-0064815
 <151> 2017-05-25
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 <170> KoPatentIn 3.0
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 cctggacagg gtctggaatg gattggggct atttatcctg gagatgggtga tactaggtac 180
 attcagaatt tcaagggcaa ggccacattg actgcagata aatcctccag cacagcctac 240
 atgcaactca gcagcttggc atctgaggac tctgcggtct attactgtgc aagatccctg 300
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 ggggaacctc ctaagctcct tatttcagaa ggcaatactc ttcgtcctgg agtcccatcc 180
 cgattctcca gcagtggcta tggtagatg tttgttttta caattgaaaa catgctctca 240
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<223> TCB2 Heavy chain variable region

<400> 3
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Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
20 25 30
Trp Ile Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Glu Trp Ile Gly
35 40 45
Ala Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Ile Gln Asn Phe Lys
50 55 60
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met
65 70 75 80
Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala
85 90 95
Arg Ser Leu Ala Thr Arg Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
100 105 110
Gly Thr Ser Val Thr Val Ser Ser
115 120

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<223> TCB2 Light chain variable region

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

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1 5

<210> 12
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<223> TCB2 Heavy chain CDR2

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

<210> 13
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<220>
<223> TCB2 Heavy chain CDR3

<400> 13
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<210> 14
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<212> PRT
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<223> TCB2 Light chain CDR2

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Glu Gly Asn Thr Leu Arg Pro
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<400> 16
Leu Gln Ser Asp Asn Leu Pro Tyr Thr
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<210> 17
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<220>
<223> Nara1 Heavy chain CDR1

<400> 17
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<220>
<223> Nara1 Heavy chain CDR2

<400> 18
Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys
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Gly

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<220>
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<400> 19
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<220>
 <223> Nara1 Light chain CDR1

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<210> 21
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<220>
 <223> Nara1 Light chain CDR2

<400> 21
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<210> 22
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Nara1 Light chain CDR3

<400> 22
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<210> 23
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> human chimeric TCB2 Heavy chain Variable region

<400> 23
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 1 5 10 15
 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
 20 25 30
 Trp Ile Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Ala Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Ile Gln Asn Phe
 50 55 60
 Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser Leu Ala Thr Arg Gly Phe Tyr Ala Met Asp Tyr Trp Gly
100 105 110
Gln Gly Thr Ser Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125
Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
130 135 140
Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175
Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190
Pro Ser Ser Asn Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His
195 200 205
Lys Pro Ser Asn Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys
210 215 220
Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val
225 230 235 240
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
260 265 270
Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285
Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser
290 295 300
Val Leu Thr Val Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320
Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile
325 330 335
Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser
385 390 395 400
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
405 410 415
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440 445

<210> 24
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 <213> Artificial Sequence

<220>
 <223> human chimeric TCB2 Light chain Variable region

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 Glu Lys Val Thr Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp
 20 25 30
 Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile
 35 40 45
 Ser Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser
 50 55 60
 Ser Gly Tyr Gly Thr Asp Phe Val Phe Thr Ile Glu Asn Met Leu Ser
 65 70 75 80
 Glu Asp Val Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
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<210> 25
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<220>
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gggaaagccc ccaagctgct gatctatgag ggaaatactc tgcggcccgg cgtgcctagc      180
agattcagct cctctggctc tgggaccgat ttcaccttta caatcagttc actgcagccc      240
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gggaccaaac tggaatcaa a                                              321

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<210>      26
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<212>      PRT
<213>      Artificial Sequence

<220>
<223>      humanized TCB2_VL03463

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Asp Arg Val Thr Ile Thr Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp
          20           25           30
Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35           40           45
Tyr Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser
 50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65           70           75           80
Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Tyr
          85           90           95
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
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<210>      27
<211>      363
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<220>
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ccaggacagg gactggagtg gatgggagca atctaccctg gagacggcga tacacgatat      180
attcagaact tcaaaggccg ggtgactatg accagagaca catctactag taccgtctat      240
atggagctga gctccctgag gagcgaagat accgctgtct actattgcgc ccgctctctg      300
gctacaagag ggttctacgc tatggattat tggggacagg ggacactggg caccgtcagc      360
agc                                              363

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<210>      28

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<211> 121
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 <213> Artificial Sequence

<220>
 <223> humanized TCB2_VH03463

<400> 28
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 1 5 10 15
 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
 20 25 30
 Trp Ile Gln Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Ala Ile Tyr Pro Gly Asp Gly Asp Thr Arg Tyr Ile Gln Asn Phe
 50 55 60
 Lys 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 Leu Ala Thr Arg Gly Phe Tyr Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 29
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 <212> DNA
 <213> Artificial Sequence

<220>
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 ggcaaagccc ccaagctgct gatcagcgag ggaaatactc tgcgaccagg agtgccttct 180
 agattctctg gcagtgggta tggaaccgat ttcaccttta caatcagctc cctgcagccc 240
 gaagatattg ctgactacta ttgcctgcag agcgataacc tgccatacac cttcggcggg 300
 gggaccaaac tggaatcaa a 321

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 <212> PRT
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<220>
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1 5 10 15
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 20 25 30
 Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45
 Ser Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80
 Glu Asp Ile Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro Tyr
 85 90 95
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 31
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 <212> DNA
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<220>
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 ccaggacagg gactggagtg gatgggagca atctaccctg gagacggcga tacaagatat 180
 attcagaact tcaagggccg ggtgactatg accagagaca catctactag taccgtctat 240
 atggagctga gctccctgag gagcgaagat accgctgtct actattgcgc ccgctctctg 300
 gctacaaggg ggttctacgc aatggattac tgggggcagg ggacactggg caccgtctca 360
 tca 363

<210> 32
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized TCB2_VH1

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

Lys 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 Leu Ala Thr Arg Gly Phe Tyr Ala Met Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 33
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 <212> DNA
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<220>
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 ccaggacagg gactggagtg gatcggagca atctaccctg gagacggcga tacacggtat 180
 attcagaact tcaaaggcag agtgactatg accgctgaca catctactag taccgtctat 240
 atggagctga gctccctgag gagcgaagat accgccgtct actattgcg cccgtctctg 300
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<210> 34
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> humanized TCB2_VH2

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

Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser
		115					120	