

# SEQUENCE LISTING

<110> UNIVERSITY HEALTH NETWORK

<120> T CELL RECEPTORS AND METHODS OF USE THEREOF

<130> 4285.007PC01/C-K/BMD

<150> US 62/813,651

<151> 2019-03-04

<160> 56

<170> PatentIn version 3.5

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<211> 273

<212> PRT

<213> Artificial Sequence

<220>

<223> alpha chain amino acid sequence

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Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp  
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Val Ser Ser Lys Gln Glu Val Thr Gln Ile Pro Ala Ala Leu Ser Val  
20 25 30

Pro Glu Gly Glu Asn Leu Val Leu Asn Cys Ser Phe Thr Asp Ser Ala  
35 40 45

Ile Tyr Asn Leu Gln Trp Phe Arg Gln Asp Pro Gly Lys Gly Leu Thr  
50 55 60

Ser Leu Leu Leu Ile Gln Ser Ser Gln Arg Glu Gln Thr Ser Gly Arg  
65 70 75 80

Leu Asn Ala Ser Leu Asp Lys Ser Ser Gly Arg Ser Thr Leu Tyr Ile  
85 90 95

Ala Ala Ser Gln Pro Gly Asp Ser Ala Thr Tyr Leu Cys Ala Val Ala  
100 105 110

Thr Asp Ser Trp Gly Lys Leu Gln Phe Gly Ala Gly Thr Gln Val Val

115

120

125

Val Thr Pro Asp Ile Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg  
 130 135 140

Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp  
 145 150 155 160

Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr  
 165 170 175

Asp Lys Thr Val Leu Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser  
 180 185 190

Ala Val Ala Trp Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe  
 195 200 205

Asn Asn Ser Ile Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser  
 210 215 220

Ser Cys Asp Val Lys Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn  
 225 230 235 240

Leu Asn Phe Gln Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu  
 245 250 255

Lys Val Ala Gly Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser  
 260 265 270

Glx

&lt;210&gt; 2

&lt;211&gt; 324

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; beta chain amino acid sequence

&lt;400&gt; 2

Met Leu Ser Pro Asp Leu Pro Asp Ser Ala Trp Asn Thr Arg Leu Leu

|     |     |     |     |
|-----|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Cys | His | Val | Met |
|     | 20  |     |     |
| Leu | Cys | Leu | Leu |
|     |     | 25  |     |
| Gly | Ala | Val | Ser |
|     |     |     | 30  |
| Ala | Ala | Gly |     |
| Val | Ile | Gln | Ser |
|     | 35  |     |     |
| Pro | Arg | His | Leu |
|     |     | 40  |     |
| Ile | Lys | Glu | Lys |
|     |     |     | 45  |
| Arg | Glu | Thr | Ala |
| Thr | Leu | Lys | Cys |
|     | 50  |     |     |
| Tyr | Pro | Ile | Pro |
|     |     | 55  |     |
| Arg | His | Asp | Thr |
|     |     |     | 60  |
| Val | Tyr | Trp | Tyr |
| Gln | Gln | Gly | Pro |
|     |     |     | 70  |
| Gln | Asp | Pro | Gln |
|     |     |     | 75  |
| Phe | Leu | Ile | Ser |
|     |     |     | 80  |
| Phe | Tyr | Glu |     |
| Lys | Met | Gln | Ser |
|     |     | 85  |     |
| Asp | Lys | Gly | Ser |
|     |     |     | 90  |
| Ile | Pro | Asp | Arg |
|     |     |     | 95  |
| Phe | Ser | Ala | Gln |
| Gln | Phe | Ser | Asp |
|     |     | 100 |     |
| Tyr | His | Ser | Glu |
|     |     |     | 105 |
| Leu | Asn | Met | Ser |
|     |     |     | 110 |
| Ser | Ser | Leu | Glu |
|     |     |     | 115 |
| Ala | Leu | Tyr | Phe |
|     |     |     | 120 |
| Cys | Ala | Ser | Ser |
|     |     |     | 125 |
| Leu | Leu | Pro | Glu |
|     |     |     | 130 |
| Gly | Asp | Ser | Ala |
|     |     |     | 135 |
| Thr | Gly | Arg | Val |
|     | 130 |     |     |
| Ser | Gly | Tyr | Thr |
|     |     | 135 |     |
| Phe | Gly | Ser | Gly |
|     |     |     | 140 |
| Thr | Arg | Leu | Thr |
| Val | Val | Glu | Asp |
|     |     |     | 145 |
| Leu | Asn | Lys | Val |
|     |     |     | 150 |
| Phe | Pro | Pro | Glu |
|     |     |     | 155 |
| Val | Ala | Val | Phe |
|     |     |     | 160 |
| Glu | Pro | Ser | Glu |
|     |     |     | 165 |
| Ala | Glu | Ile | Ser |
|     |     |     | 170 |
| His | Thr | Gln | Lys |
|     |     |     | 175 |
| Ala | Thr | Leu | Val |
| Cys | Leu | Ala | Thr |
|     |     | 180 |     |
| Gly | Phe | Phe | Pro |
|     |     |     | 185 |
| Asp | His | Val | Glu |
|     |     |     | 190 |
| Leu | Ser | Trp | Trp |
| Val | Asn | Gly | Lys |
|     |     |     | 195 |
| Glu | Val | His | Ser |
|     |     |     | 200 |
| Gly | Val | Ser | Thr |
|     |     |     | 205 |
| Asp | Pro | Gln | Pro |
| Leu | Lys | Glu | Gln |
|     |     |     | 210 |
| Pro | Ala | Leu | Asn |
|     |     |     | 215 |
| Asp | Ser | Arg | Tyr |
|     |     |     | 220 |
| Cys | Leu | Ser | Ser |

Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe  
225 230 235 240

Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr  
245 250 255

Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp  
260 265 270

Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr Gln Gln Gly Val  
275 280 285

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu  
290 295 300

Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg  
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Lys Asp Phe Glx

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Asp Ser Ala Ile Tyr Asn  
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Pro Arg His Asp Thr  
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Cys Ala Val Ala Thr Asp Ser Trp Gly Lys Leu Gln Phe  
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Ile Gln Ser Ser Gln Arg Glu  
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Phe Tyr Glu Lys Met Gln  
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| Cys | Ala | Ser | Ser | Leu | Leu | Pro | Glu | Gly | Thr | Gly | Arg | Val | Ser | Gly | Tyr |
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Thr Phe

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Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser  
1 5 10 15

Gly Leu Glu Ala Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg  
20 25 30

His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser  
35 40 45

Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly Glu  
50 55 60

Arg Ile Glu Lys Val Glu His Ser Asp Leu Ser Phe Ser Lys Asp Trp  
65 70 75 80

Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp  
85 90 95

Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys Ile  
100 105 110

Val Lys Trp Asp Arg Asp Met  
115

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<212> DNA  
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caggaggtga cgcagattcc tgcagctctg agtgtcccag aaggagaaaa cttggttctc 120

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| aactgcagtt tcactgatag cgctattttac aacctccagt ggtttaggca ggaccctggg | 180 |
| aaaggtctca catctctgtt gcttattcag tcaagtcaga gagagcaaac aagtgggaaga | 240 |
| cttaatgcct cgctggataa atcatcagga cgtagtactt tatacattgc agcttctcag  | 300 |
| cctggtgact cagccaccta cctctgtgct gtcgcaactg acagctgggg gaaattgcag  | 360 |
| tttgagcag ggaccaggt tgtggtcacc ccagatatcc agaaccctga ccctgccgtg    | 420 |
| taccagctga gagactctaa atccagtgac aagtctgtct gcctattcac cgattttgat  | 480 |
| tctcaaaca atgtgtcaca aagtaaggat tctgatgtgt atatcacaga caaaactgtg   | 540 |
| ctagacatga ggtctatgga cttcaagagc aacagtgtg tggcctggag caacaaatct   | 600 |
| gactttgcat gtgcaaacgc cttcaacaac agcattattc cagaagacac cttcttcccc  | 660 |
| agcccagaaa gttcctgtga tgtcaagctg gtcgagaaaa gctttgaaac agatacgaac  | 720 |
| ctaaactttc aaaacctgtc agtgattggg ttccgaatcc tcctcctgaa agtggccggg  | 780 |
| tttaatctgc tcatgacgct gcggctgtgg tccagctga                         | 819 |

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<212> DNA

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<223> beta chain nucleotide sequence

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| ctttgtctcc tgggagcagt ttcagtggt gctggagtca tccagtcccc aagacatctg  | 120 |
| atcaaagaaa agagggaaac agccactctg aaatgctatc ctatccctag acacgacact | 180 |
| gtctactggt accagcaggg tccaggtcag gacccccagt tcctcatttc gttttatgaa | 240 |
| aagatgcaga gcgataaagg aagcatccct gatcgattct cagctcaaca gttcagtgac | 300 |
| tatcattctg aactgaacat gagctccttg gagctggggg actcagccct gtacttctgt | 360 |
| gccagcagcc tcctaccgga agggacaggc cgtgtaagt gctacacctt cggttcgggg  | 420 |
| accagggttaa ccgtttaga ggacctgaac aagggtgttc caccgaggt cgctgtgttt  | 480 |
| gagccatcag aagcagagat ctcccacacc caaaaggcca cactggtgtg cctggccaca | 540 |
| ggcttcttcc ctgaccacgt ggagctgagc tggtgggtga atgggaagga ggtgcacagt | 600 |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| ggggtcagca cggacccgca gcccctcaag gagcagcccg ccctcaatga ctccagatac | 660 |
| tgcctgagca gccgcctgag ggtctcggcc accttctggc agaacccccg caaccacttc | 720 |
| cgctgtcaag tccagttcta cgggctctcg gagaatgacg agtggaccca ggatagggcc | 780 |
| aaacccgtca cccagatcgt cagcgccgag gcctggggta gagcagactg tggctttacc | 840 |
| tcggtgtcct accagcaagg ggtcctgtct gccaccatcc tctatgagat cctgctaggg | 900 |
| aaggccaccc tgtatgctgt gctggtcagc gcccttgtgt tgatggccat ggtcaagaga | 960 |
| aaggatttct ga                                                     | 972 |

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Met Asp Leu Val Leu Lys Arg Cys Leu Leu His Leu Ala Val Ile Gly  
1 5 10 15

Ala Leu Leu Ala Val Gly Ala Thr Lys Val Pro Arg Asn Gln Asp Trp  
20 25 30

Leu Gly Val Ser Arg Gln Leu Arg Thr Lys Ala Trp Asn Arg Gln Leu  
35 40 45

Tyr Pro Glu Trp Thr Glu Ala Gln Arg Leu Asp Cys Trp Arg Gly Gly  
50 55 60

Gln Val Ser Leu Lys Val Ser Asn Asp Gly Pro Thr Leu Ile Gly Ala  
65 70 75 80

Asn Ala Ser Phe Ser Ile Ala Leu Asn Phe Pro Gly Ser Gln Lys Val  
85 90 95

Leu Pro Asp Gly Gln Val Ile Trp Val Asn Asn Thr Ile Ile Asn Gly  
100 105 110

Ser Gln Val Trp Gly Gly Gln Pro Val Tyr Pro Gln Glu Thr Asp Asp  
115 120 125

Ala Cys Ile Phe Pro Asp Gly Gly Pro Cys Pro Ser Gly Ser Trp Ser  
130 135 140

Gln Lys Arg Ser Phe Val Tyr Val Trp Lys Thr Trp Gly Gln Tyr Trp  
145 150 155 160

Gln Val Leu Gly Gly Pro Val Ser Gly Leu Ser Ile Gly Thr Gly Arg  
165 170 175

Ala Met Leu Gly Thr His Thr Met Glu Val Thr Val Tyr His Arg Arg  
180 185 190

Gly Ser Arg Ser Tyr Val Pro Leu Ala His Ser Ser Ser Ala Phe Thr  
195 200 205

Ile Thr Asp Gln Val Pro Phe Ser Val Ser Val Ser Gln Leu Arg Ala  
210 215 220

Leu Asp Gly Gly Asn Lys His Phe Leu Arg Asn Gln Pro Leu Thr Phe  
225 230 235 240

Ala Leu Gln Leu His Asp Pro Ser Gly Tyr Leu Ala Glu Ala Asp Leu  
245 250 255

Ser Tyr Thr Trp Asp Phe Gly Asp Ser Ser Gly Thr Leu Ile Ser Arg  
260 265 270

Ala Leu Val Val Thr His Thr Tyr Leu Glu Pro Gly Pro Val Thr Ala  
275 280 285

Gln Val Val Leu Gln Ala Ala Ile Pro Leu Thr Ser Cys Gly Ser Ser  
290 295 300

Pro Val Pro Gly Thr Thr Asp Gly His Arg Pro Thr Ala Glu Ala Pro  
305 310 315 320

Asn Thr Thr Ala Gly Gln Val Pro Thr Thr Glu Val Val Gly Thr Thr  
325 330 335

Pro Gly Gln Ala Pro Thr Ala Glu Pro Ser Gly Thr Thr Ser Val Gln  
340 345 350

Val Pro Thr Thr Glu Val Ile Ser Thr Ala Pro Val Gln Met Pro Thr  
355 360 365

Ala Glu Ser Thr Gly Met Thr Pro Glu Lys Val Pro Val Ser Glu Val  
370 375 380

Met Gly Thr Thr Leu Ala Glu Met Ser Thr Pro Glu Ala Thr Gly Met  
385 390 395 400

Thr Pro Ala Glu Val Ser Ile Val Val Leu Ser Gly Thr Thr Ala Ala  
405 410 415

Gln Val Thr Thr Thr Glu Trp Val Glu Thr Thr Ala Arg Glu Leu Pro  
420 425 430

Ile Pro Glu Pro Glu Gly Pro Asp Ala Ser Ser Ile Met Ser Thr Glu  
435 440 445

Ser Ile Thr Gly Ser Leu Gly Pro Leu Leu Asp Gly Thr Ala Thr Leu  
450 455 460

Arg Leu Val Lys Arg Gln Val Pro Leu Asp Cys Val Leu Tyr Arg Tyr  
465 470 475 480

Gly Ser Phe Ser Val Thr Leu Asp Ile Val Gln Gly Ile Glu Ser Ala  
485 490 495

Glu Ile Leu Gln Ala Val Pro Ser Gly Glu Gly Asp Ala Phe Glu Leu  
500 505 510

Thr Val Ser Cys Gln Gly Gly Leu Pro Lys Glu Ala Cys Met Glu Ile  
515 520 525

Ser Ser Pro Gly Cys Gln Pro Pro Ala Gln Arg Leu Cys Gln Pro Val  
530 535 540

Leu Pro Ser Pro Ala Cys Gln Leu Val Leu His Gln Ile Leu Lys Gly  
 545 550 555 560

Gly Ser Gly Thr Tyr Cys Leu Asn Val Ser Leu Ala Asp Thr Asn Ser  
 565 570 575

Leu Ala Val Val Ser Thr Gln Leu Ile Met Pro Gly Gln Glu Ala Gly  
 580 585 590

Leu Gly Gln Val Pro Leu Ile Val Gly Ile Leu Leu Val Leu Met Ala  
 595 600 605

Val Val Leu Ala Ser Leu Ile Tyr Arg Arg Arg Leu Met Lys Gln Asp  
 610 615 620

Phe Ser Val Pro Gln Leu Pro His Ser Ser Ser His Trp Leu Arg Leu  
 625 630 635 640

Pro Arg Ile Phe Cys Ser Cys Pro Ile Gly Glu Asn Ser Pro Leu Leu  
 645 650 655

Ser Gly Gln Gln Val  
 660

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 <223> siRNA-TCRa-1

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 guaaggauuc ugauguguat t

21

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uacacaucag aauccuuact t 21

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ccaccauccu cuaugagaut t 21

<210> 56  
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