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SEQUENCE LISTING

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<120> ENGINEERED HIGH-AFFINITY HUMAN T CELL RECEPTORS

<130> IMMU-003/01WO

<150> US 61/907,887
<151> 2013-11-22

<160> 16

<170> PatentIn version 3.5

<210> 1
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified variable alpha region of the TCR (Survivin - K2.4.1) with high affinity to Survivin/HLA-A2

<400> 1

Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro Glu Gly
1 5 10 15

Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln Ser
20 25 30

Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile Met
35 40 45

Ser Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala Gln
50 55 60

Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile Arg Asp Ser Gln
65 70 75 80

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

Met Phe Gly Asp Gly Thr Gln Leu Val Val Lys Pro Asn Ile
100 105 110

<210> 2
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<223> Modified variable alpha region of the TCR (Survivin - K2.4.6) with high affinity to Survivin/HLA-A2

<400> 2

Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro Glu Gly
1 5 10 15

Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln Ser
20 25 30

Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile Met
35 40 45

Ser Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala Gln
50 55 60

Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile Arg Asp Ser Gln
65 70 75 80

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val His Gly Trp Tyr Thr
85 90 95

Met Phe Gly Asp Gly Thr Gln Leu Val Val Lys Pro Asn Ile
100 105 110

<210> 3
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Single-chain TCR (Survivin-K2.4.1) that binds with high-affinity to Survivin/HLA-A2

<400> 3

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Ser Gln Thr Ile His Gln Trp Pro Ala Thr Leu Val Gln Pro Val Gly
1               5                  10                  15

Ser Pro Leu Ser Leu Glu Cys Thr Val Glu Gly Thr Ser Asn Pro Asn
            20                  25                  30

Leu Tyr Trp Tyr Arg Gln Ala Ala Gly Arg Gly Leu Glu Leu Leu Phe
        35                  40                  45

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

Phe Ala Ser Arg Pro Gln Asp Arg Gln Phe Ile Leu Ser Ser Lys Lys
65                  70                  75                  80

Leu Leu Leu Ser Asp Ser Gly Phe Tyr Leu Cys Ala Trp Ser Ile Gly
                85                  90                  95

Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp
            100                 105                 110

Leu Lys Asn Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys
        115                 120                 125

Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser
    130                 135                 140

Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg
145                 150                 155                 160

Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro
                165                 170                 175

Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg
            180                 185                 190

Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile
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195 200 205

Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val Ser
210 215 220

Lys Gly Tyr Lys Met Phe Gly Asp Gly Thr Gln Leu Val Val Lys Pro
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Asn Ile

<210> 4
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> Single-chain TCR (Survivin-K2.4.6) that binds with high-affinity to Survivin/HLA-A2

<400> 4

Ser Gln Thr Ile His Gln Trp Pro Ala Thr Leu Val Gln Pro Val Gly
1 5 10 15

Ser Pro Leu Ser Leu Glu Cys Thr Val Glu Gly Thr Ser Asn Pro Asn
20 25 30

Leu Tyr Trp Tyr Arg Gln Ala Ala Gly Arg Gly Leu Glu Leu Leu Phe
35 40 45

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

Phe Ala Ser Arg Pro Gln Asp Arg Gln Phe Ile Leu Ser Ser Lys Lys
65 70 75 80

Leu Leu Leu Ser Asp Ser Gly Phe Tyr Leu Cys Ala Trp Ser Ile Gly
85 90 95

Ala Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp
100 105 110

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Leu Lys Asn Gly Ser Ala Asp Asp Ala Lys Lys Asp Ala Ala Lys Lys
        115                 120                 125


Asp Gly Lys Ser Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser
    130                 135                 140


Val Pro Glu Gly Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg
145                 150                 155                 160


Gly Ser Gln Ser Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro
                165                 170                 175


Glu Leu Ile Met Ser Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg
            180                 185                 190


Phe Thr Ala Gln Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile
        195                 200                 205


Arg Asp Ser Gln Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Val His
    210                 215                 220


Gly Trp Tyr Thr Met Phe Gly Asp Gly Thr Gln Leu Val Val Lys Pro
225                 230                 235                 240


Asn Ile
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<210> 5
<211> 9
<212> PRT
<213> Homo sapiens

<400> 5

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Leu Met Leu Gly Glu Phe Leu Lys Leu
1               5
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<210> 6
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<213> Human T cell lymphotrophic virus

<400> 6

Leu Leu Phe Gly Tyr Pro Val Tyr Val
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<210> 7
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<213> Artificial Sequence

<220>
<223> Amino acid linker sequence

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Ser

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer Splice 4L

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ggcagcccca taaacacaca gtat 24

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer T7

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taatacgact cactataggg 20

<210> 10
<211> 21

<212> DNA
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<220>
<223> Reverse primer used to generate the Surv CDR3alpha library

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cacagcgcac agataggtag c 21

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ctcagctggt tgtg 74

<210> 12
<211> 114
<212> PRT
<213> Homo sapiens

<400> 12

Ser Gln Thr Ile His Gln Trp Pro Ala Thr Leu Val Gln Pro Val Gly
1 5 10 15

Ser Pro Leu Ser Leu Glu Cys Thr Val Glu Gly Thr Ser Asn Pro Asn
20 25 30

Leu Trp Tyr Arg Gln Ala Ala Gly Arg Gly Leu Glu Leu Leu Phe Tyr
35 40 45

Ser Val Gly Ile Gly Gln Ile Ser Ser Glu Val Pro Gln Asn Leu Phe
50 55 60

Ala Ser Arg Pro Gln Asp Arg Gln Phe Ile Leu Ser Ser Lys Lys Leu
65 70 75 80

Leu Leu Ser Asp Ser Gly Phe Tyr Leu Cys Ala Trp Ser Ile Gly Ala
85 90 95

Glu Gln Phe Phe Gly Pro Gly Thr Arg Leu Thr Val Leu Glu Asp Leu
100 105 110

Lys Asn

<210> 13
<211> 110
<212> PRT
<213> Homo sapiens

<400> 13

Gln Lys Glu Val Glu Gln Asn Ser Gly Pro Leu Ser Val Pro Glu Gly
1 5 10 15

Ala Ile Ala Ser Leu Asn Cys Thr Tyr Ser Asp Arg Gly Ser Gln Ser
20 25 30

Phe Phe Trp Tyr Arg Gln Tyr Ser Gly Lys Ser Pro Glu Leu Ile Met
35 40 45

Ser Ile Tyr Ser Asn Gly Asp Lys Glu Asp Gly Arg Phe Thr Ala Gln
50 55 60

Leu Asn Lys Ala Ser Gln Tyr Val Ser Leu Leu Ile Arg Asp Ser Gln
65 70 75 80

Pro Ser Asp Ser Ala Thr Tyr Leu Cys Ala Ala Asn Asn Ala Arg Leu
85 90 95

Met Phe Gly Asp Gly Thr Gln Leu Val Val Lys Pro Asn Ile
100 105 110

<210> 14
<211> 9
<212> PRT
<213> Homo sapiens

<400> 14

Arg Met Phe Pro Asn Ala Pro Tyr Leu
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<210> 15

<211> 9
<212> PRT
<213> Influenza A

<400> 15

Ala Ser Asn Glu Asn Met Asp Ala Met
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<210> 16
<211> 9
<212> PRT
<213> Influenza A

<400> 16

Ala Ser Asn Glu Asn Met Glu Thr Met
1 5