

SEQUENCE LISTING

<110> UNIVERSITY HEALTH NETWORK

<120> T CELL RECEPTORS AND METHODS OF USE THEREOF

<130> 4285.008PC01/C-K/BMD

<150> US 62/823,487

<151> 2019-03-25

<160> 93

<170> PatentIn version 3.5

<210> 1

<211> 271

<212> PRT

<213> Artificial Sequence

<220>

<223> Tyr-alpha chain amino acid sequence

<400> 1

Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu
1 5 10 15

Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly
20 25 30

Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp
35 40 45

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile
50 55 60

Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe
65 70 75 80

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser
85 90 95

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

Ser Gln Gly Asn Leu Ile Phe Gly Lys Gly Thr Lys Leu Ser Val Lys

115

120

125

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

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

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

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

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

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

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

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

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

<210> 2

<211> 314

<212> PRT

<213> Artificial Sequence

<220>

<223> Tyr-beta chain amino acid sequence

<400> 2

Met Ser Ile Gly Leu Leu Cys Cys Ala Ala Leu Ser Leu Leu Trp Ala
 1 5 10 15

Gly Pro Val Asn Ala Gly Val Thr Gln Thr Pro Lys Phe Gln Val Leu

20

25

30

Lys Thr Gly Gln Ser Met Thr Leu Gln Cys Ala Gln Asp Met Asn His
 35 40 45

Glu Tyr Met Ser Trp Tyr Arg Gln Asp Pro Gly Met Gly Leu Arg Leu
 50 55 60

Ile His Tyr Ser Val Gly Ala Gly Ile Thr Asp Gln Gly Glu Val Pro
 65 70 75 80

Asn Gly Tyr Asn Val Ser Arg Ser Thr Thr Glu Asp Phe Pro Leu Arg
 85 90 95

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

Ser His His Ser Gly Gly Ile Tyr Asn Glu Gln Phe Phe Gly Pro Gly
 115 120 125

Thr Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu
 130 135 140

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
 145 150 155 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu
 165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
 180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
 195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
 210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
 225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr
260 265 270

Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
290 295 300

Met Val Lys Arg Lys Asp Ser Arg Gly Glx
305 310

<210> 3
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Tyr-alpha chain nucleotide sequence

<400> 3
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accacccagc ccatctccat ggactcatat gaaggacaag aagtgaacat aacctgtagc 120
cacaacaaca ttgctacaaa tgattatatac acgtgggtacc aacagtttcc cagccaagga 180
ccacgattta ttattcaagg atacaagaca aaagttacaa acgaagtggc ctccctgttt 240
atccctgccg acagaaagtc cagcactctg agcctgcccc gggtttccct gagcgacact 300
gctgtgtact actgcctcgt gggtgacgta gaaggaagcc aaggaaatct catctttgga 360
aaaggcacta aactctctgt taaaccaa atccagaacc ctgaccctgc cgtgtaccag 420
ctgagagact ctaaattccag tgacaagtct gtctgcctat tcaccgattt tgatttctcaa 480
acaaatgtgt cacaaagtaa ggattctgat gtgtatatca cagacaaaac tgtgtctagac 540
atgaggtcta tggacttcaa gagcaacagt gctgtggcct ggagcaacaa atctgacttt 600
gcatgtgcaa acgccttcaa caacagcatt attccagaag acaccttctt cccagccca 660
gaaagttcct gtgatgtcaa gctggtcgag aaaagctttg aaacagatac gaacctaaac 720

tttcaaaacc tgtcagtgat tgggttccga atcctcctcc tgaaagtggc cgggtttaat	780
ctgctcatga cgctgcggct gtggtccagc tga	813

<210> 4
 <211> 942
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Tyr-beta chain nucleotide sequence

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cagtgtgccc aggatatgaa ccatgaatac atgtcctggc atcgacaaga cccaggcatg	180
gggctgaggc tgattcatta ctgagttggc gctggtatca ctgaccaagg agaagtcccc	240
aatggctaca atgtctccag atcaaccaca gaggatttcc cgctcaggct gctgtcggct	300
gctccctccc agacatctgt gtacttctgt gccagcagtc accattcggg ggggatctac	360
aatgagcagt tcttcgggcc agggacacgg ctaccgtgc tagaggacct gaaaaacgtg	420
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctcca caccctaaag	480
gccacactgg tatgcctggc cacaggcttc taccgacg accgtggagct gagctggtgg	540
gtgaatggga aggaggtgca cagtgggggc agcacagacc cgagcccct caaggagcag	600
cccgccctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc	660
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcggagaat	720
gacgagtgga cccaggatag ggccaaacct gtcaccaga tcgtcagcgc cgaggcctgg	780
ggtagagcag actgtggctt cacctccgag tcttaccagc aaggggtcct gtctgccacc	840
atcctctatg agatcttgct agggaaggcc accttgatg ccgtgctggc cagtgccttc	900
gtgctgatgg ccatggtcaa gagaaaggat tccagaggct ag	942

<210> 5
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Tyr-alpha CDR1

<400> 5

Asn Ile Ala Thr Asn Asp Tyr
1 5

<210> 6

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Tyr-alpha CDR2

<400> 6

Gly Tyr Lys Thr Lys
1 5

<210> 7

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Tyr-alpha CDR3

<400> 7

Cys Leu Val Gly Asp Val Glu Gly Ser Gln Gly Asn Leu Ile Phe
1 5 10 15

<210> 8

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Tyr-beta CDR1

<400> 8

Met Asn His Glu Tyr
1 5

<210> 9

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Tyr-beta CDR2

<400> 9

Ser Val Gly Ala Gly Ile

1 5

<210> 10

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Tyr-beta CDR3

<400> 10

Cys Ala Ser Ser His His Ser Gly Gly Ile Tyr Asn Glu Gln Phe Phe

1 5 10 15

<210> 11

<211> 280

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A1-alpha chain amino acid sequence

<400> 11

Met Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val

1 5 10 15

Val Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser

20 25 30

Val Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg

35 40 45

Asp Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu

50 55 60

Leu Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile

65 70 75 80

Ser Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn

85

90

95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
 100 105 110

Ala Leu Ser Glu Ser Tyr Ser Gly Ala Gly Ser Tyr Gln Leu Thr Phe
 115 120 125

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

Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val
 145 150 155 160

Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys
 165 170 175

Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu Asp Met Arg Ser
 180 185 190

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

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

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

Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn Leu Ser Val Ile
 245 250 255

Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe Asn Leu Leu Met
 260 265 270

Thr Leu Arg Leu Trp Ser Ser Glx
 275 280

<210> 12

<211> 312

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A1-beta chain amino acid sequence

<400> 12

Met Gly Thr Ser Leu Leu Cys Trp Met Ala Leu Cys Leu Leu Gly Ala
1 5 10 15

Asp His Ala Asp Thr Gly Val Ser Gln Asn Pro Arg His Lys Ile Thr
20 25 30

Lys Arg Gly Gln Asn Val Thr Phe Arg Cys Asp Pro Ile Ser Glu His
35 40 45

Asn Arg Leu Tyr Trp Tyr Arg Gln Thr Leu Gly Gln Gly Pro Glu Phe
50 55 60

Leu Thr Tyr Phe Gln Asn Glu Ala Gln Leu Glu Lys Ser Arg Leu Leu
65 70 75 80

Ser Asp Arg Phe Ser Ala Glu Arg Pro Lys Gly Ser Phe Ser Thr Leu
85 90 95

Glu Ile Gln Arg Thr Glu Gln Gly Asp Ser Ala Met Tyr Leu Cys Ala
100 105 110

Ser Ser Leu Ala Ser Gly Ser Asn Gln Pro Gln His Phe Gly Asp Gly
115 120 125

Thr Arg Leu Ser Ile Leu Glu Asp Leu Asn Lys Val Phe Pro Pro Glu
130 135 140

Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys
145 150 155 160

Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val Glu
165 170 175

Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr
180 185 190

Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr
195 200 205

Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro
210 215 220

Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn
225 230 235 240

Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser
245 250 255

Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser Tyr
260 265 270

Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly
275 280 285

Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala
290 295 300

Met Val Lys Arg Lys Asp Phe Glx
305 310

<210> 13
<211> 840
<212> DNA
<213> Artificial Sequence

<220>
<223> MAGE-A1-alpha chain nucleotide sequence

<400> 13
atgctgactg ccagcctggt gagggcagtc atagcctcca tctgtgttgt atccagcatg 60
gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc 120
ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca 180
ccaagtggag aattggtttt cttatttcgt cggaactctt ttgatgagca aaatgaaata 240
agtggtcggt attcttgga cttccagaaa tccaccagtt cttcaactt caccatcaca 300
gcctcacaag tcgtggactc agcagtatac ttctgtgctc tgagtgagtc atactctggg 360

gctgggagtt accaactcac tttcgggaag gggaccaaac tctcggtcat accaaatatt	420
cagaaccctg accctgccgt gtaccagctg agagactcta aatccagtga caagtctgtc	480
tgcctattca ccgattttga ttctcaaaca aatgtgtcac aaagtaagga ttctgatgtg	540
tatatcacag acaaaaactgt gctagacatg aggtctatgg acttcaagag caacagtgtc	600
gtggcctgga gcaacaaatc tgactttgca tgtgcaaacg ctttcaacaa cagcattatt	660
ccagaagaca ctttcttccc cagcccagaa agttcctgtg atgtcaagct ggtcgagaaa	720
agctttgaaa cagatacgaa cctaaacttt caaaacctgt cagtgattgg gttccgaatc	780
ctcctcctga aagtggccgg gtttaatctg ctcatgacgc tgcggctgtg gtccagctga	840

<210> 14

<211> 936

<212> DNA

<213> Artificial Sequence

<220>

<223> MAGE-A1-beta chain nucleotide sequence

<400> 14

atgggcacca gcctcctctg ctggatggcc ctgtgtctcc tgggggcaga tcacgcagat	60
actggagtct cccagaaccc cagacacaag atcacaaaga ggggacagaa tgtaactttc	120
aggtgtgatc caatttctga acacaaccgc ctttattggc accgacagac cctggggcag	180
ggcccagagt ttctgactta cttccagaat gaagctcaac tagaaaaatc aaggctgctc	240
agtgatcggc tctctgcaga gaggcctaag ggatctttct ccaccttgga gatccagcgc	300
acagagcagg gggactcggc catgtatctc tgtgccagca gcttagcttc gggcagcaat	360
cagccccagc attttggtga tgggactcga ctctccatcc tagaggacct gaacaaggctg	420
ttcccacccg aggtcgctgt gtttgagcca tcagaagcag agatctccca caccctaaag	480
gccacactgg tgtgcctggc cacaggcttc ttccccgacc acgtggagct gagctggtgg	540
gtgaatggga aggaggtgca cagtggggtc agcacggacc cgcagcccct caaggagcag	600
cccgccctca atgactccag atactgcctg agcagccgcc tgagggtctc ggccaccttc	660
tggcagaacc cccgcaacca cttccgctgt caagtccagt tctacgggct ctcggagaat	720
gacgagtgga cccaggatag ggccaaaccc gtcaccaga tcgtcagcgc cgaggcctgg	780
ggtagagcag actgtggctt tacctcggct tcctaccagc aaggggctct gtctgccacc	840

atcctctatg agatcctgct agggaaggcc accctgtatg ctgtgctggt cagcgccctt 900
gtgttgatgg ccatgggtcaa gagaaaggat ttctga 936

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A1-alpha CDR1

<400> 15

Thr Arg Asp Thr Thr Tyr Tyr Leu
1 5

<210> 16
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A1-alpha CDR2

<400> 16

Arg Asn Ser Phe Asp Glu Gln Asn
1 5

<210> 17
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A1-alpha CDR3

<400> 17

Cys Ala Leu Ser Glu Ser Tyr Ser Gly Ala Gly Ser Tyr Gln Leu Thr
1 5 10 15

Phe

<210> 18
<211> 5
<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A1-beta CDR1

<400> 18

Ser Glu His Asn Arg
1 5

<210> 19

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A1-beta CDR2

<400> 19

Phe Gln Asn Glu Ala Gln
1 5

<210> 20

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A1-beta CDR3

<400> 20

Cys Ala Ser Ser Leu Ala Ser Gly Ser Asn Gln Pro Gln His Phe
1 5 10 15

<210> 21

<211> 269

<212> PRT

<213> Artificial Sequence

<220>

<223> MART1-alpha chain amino acid sequence

<400> 21

Met Trp Gly Val Phe Leu Leu Tyr Val Ser Met Lys Met Gly Gly Thr
1 5 10 15

Thr Gly Gln Asn Ile Asp Gln Pro Thr Glu Met Thr Ala Thr Glu Gly

20

25

30

Ala Ile Val Gln Ile Asn Cys Thr Tyr Gln Thr Ser Gly Phe Asn Gly
 35 40 45

Leu Phe Trp Tyr Gln Gln His Ala Gly Glu Ala Pro Thr Phe Leu Ser
 50 55 60

Tyr Asn Val Leu Asp Gly Leu Glu Glu Lys Gly Arg Phe Ser Ser Phe
 65 70 75 80

Leu Ser Arg Ser Lys Gly Tyr Ser Tyr Leu Leu Leu Lys Glu Leu Gln
 85 90 95

Met Lys Asp Ser Ala Ser Tyr Leu Cys Ala Val Tyr Gly Gly Ala Thr
 100 105 110

Asn Lys Leu Ile Phe Gly Thr Gly Thr Leu Leu Ala Val Gln Pro Asn
 115 120 125

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

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

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

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

Ser Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile
 195 200 205

Ile Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val
 210 215 220

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

Asn Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly
245 250 255

Phe Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser Glx
260 265

<210> 22
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-beta chain amino acid sequence

<400> 22

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

Gly Leu Ser Asn Ala Gly Val Met Gln Asn Pro Arg His Leu Val Arg
20 25 30

Arg Arg Gly Gln Glu Ala Arg Leu Arg Cys Ser Pro Met Lys Gly His
35 40 45

Ser His Val Tyr Trp Tyr Arg Gln Leu Pro Glu Glu Gly Leu Lys Phe
50 55 60

Met Val Tyr Leu Gln Lys Glu Asn Ile Ile Asp Glu Ser Gly Met Pro
65 70 75 80

Lys Glu Arg Phe Ser Ala Glu Phe Pro Lys Glu Gly Pro Ser Ile Leu
85 90 95

Arg Ile Gln Gln Val Val Arg Gly Asp Ser Ala Ala Tyr Phe Cys Ala
100 105 110

Ser Ser Pro His Ala Gly Gly Val Asp Glu Lys Leu Phe Phe Gly Ser
115 120 125

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

Glu Val Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ala Thr Gly Phe Phe Pro Asp His Val
165 170 175

Glu Leu Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser
180 185 190

Thr Asp Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg
195 200 205

Tyr Cys Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn
210 215 220

Pro Arg Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu
225 230 235 240

Asn Asp Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val
245 250 255

Ser Ala Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Val Ser
260 265 270

Tyr Gln Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu
275 280 285

Gly Lys Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met
290 295 300

Ala Met Val Lys Arg Lys Asp Phe Glx
305 310

<210> 23
<211> 807
<212> DNA
<213> Artificial Sequence

<220>
<223> MART1-alpha chain nucleotide sequence

<400> 23

atgtggggag ttttccttct ttatgtttcc atgaagatgg gaggcactac aggacaaaac	60
attgaccagc ccactgagat gacagctacg gaaggtgcc a ttgtccagat caactgcacg	120
taccagacat ctgggttcaa cgggctgttc tgggtaccagc aacatgctgg cgaagcaccc	180
acatttctgt cttacaatgt tctggatggg ttggaggaga aaggtcgttt ttcttcattc	240
cttagtcggg ctaaagggt a cagttacctc cttttgaagg agctccagat gaaagactct	300
gcctcttacc tctgtgctgt gtatgggtgg gctacaaaca agctcatctt tggaactggc	360
actctgcttg ctgtccagcc aaatatccag aaccctgacc ctgccgtgta ccagctgaga	420
gactctaaat ccagtgacaa gtctgtctgc ctattcacgc attttgattc tcaaacaat	480
gtgtcacaaa gtaaggattc tgatgtgtat atcacagaca aaactgtgct agacatgagg	540
tctatggact tcaagagcaa cagtgtgtg gcctggagca acaaactctga ctttgcatgt	600
gcaaacgcct tcaacaacag cattattcca gaagacacct tcttcccag cccagaaagt	660
tcctgtgatg tcaagctggg cgagaaaagc tttgaaacag atacgaacct aaactttcaa	720
aacctgtcag tgattgggtt ccgaatctc ctctgaaag tggccgggtt taatctgctc	780
atgacgctgc ggctgtgggc cagctga	807

<210> 24
 <211> 939
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MART1-beta chain nucleotide sequence

<400> 24	
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gccggcgtca tgcagaacct aagacacctg gtcaggagga ggggacagga ggcaagactg	120
agatgcagcc caatgaaagg acacagtcac gtttactggg atcggcagct cccagaggaa	180
ggtctgaaat tcatggttta tctccagaaa gaaaatatca tagatgagtc aggaatgcc a	240
aaggaacgat tttctgctga atttccaaa gagggcccca gcacctgag gatccagcag	300
gtagtgcgag gagattcggc agcttatttc tgtgccagct caccacacgc ggggggagtt	360
gatgaaaaac tgttttttgg cagtgaacc cagctctctg tcttgaggga cctgaacaag	420
gtgttccac ccgaggctgc tgtgtttgag ccatcagaag cagagatctc ccacacccaa	480

aaggccacac tgggtgtgcct ggccacaggc ttcttcctg accacgtgga gctgagctgg	540
tgggtgaatg ggaaggaggt gcacagtggg gtcagcacgg acccgagcc cctcaaggag	600
cagcccggcc tcaatgactc cagatactgc ctgagcagcc gcctgagggt ctcggccacc	660
ttctggcaga acccccgcaa ccacttcgc tgtcaagtcc agttctacgg gctctcggag	720
aatgacgagt ggaccagga tagggccaaa cccgtcacc agatcgtcag cgccgaggcc	780
tggggtagag cagactgtgg ctttacctcg gtgtcctacc agcaaggggt cctgtctgcc	840
accatcctct atgagatcct gctaggggaag gccaccctgt atgctgtgct ggtcagcgcc	900
cttgtgttga tggccatgg caagagaaag gatttctga	939

<210> 25
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MART1-alpha CDR1

<400> 25

Thr	Ser	Gly	Phe	Asn	Gly
1				5	

<210> 26
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MART1-alpha CDR2

<400> 26

Asn	Val	Leu	Asp	Gly	Leu
1				5	

<210> 27
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MART1-alpha CDR3

<400> 27

Cys Ala Val Tyr Gly Gly Ala Thr Asn Lys Leu Ile Phe
1 5 10

<210> 28
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-beta CDR1

<400> 28

Lys Gly His Ser His
1 5

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-beta CDR2

<400> 29

Leu Gln Lys Glu Asn Ile
1 5

<210> 30
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-beta CDR3

<400> 30

Cys Ala Ser Ser Pro His Ala Gly Gly Val Asp Glu Lys Leu Phe Phe
1 5 10 15

<210> 31
<211> 277
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3-alpha chain amino acid sequence

<400> 31

Met Leu Thr Ala Ser Leu Leu Arg Ala Val Ile Ala Ser Ile Cys Val
1 5 10 15

Val Ser Ser Met Ala Gln Lys Val Thr Gln Ala Gln Thr Glu Ile Ser
20 25 30

Val Val Glu Lys Glu Asp Val Thr Leu Asp Cys Val Tyr Glu Thr Arg
35 40 45

Asp Thr Thr Tyr Tyr Leu Phe Trp Tyr Lys Gln Pro Pro Ser Gly Glu
50 55 60

Leu Val Phe Leu Ile Arg Arg Asn Ser Phe Asp Glu Gln Asn Glu Ile
65 70 75 80

Ser Gly Arg Tyr Ser Trp Asn Phe Gln Lys Ser Thr Ser Ser Phe Asn
85 90 95

Phe Thr Ile Thr Ala Ser Gln Val Val Asp Ser Ala Val Tyr Phe Cys
100 105 110

Ala Leu Glu Val Arg Ser Ser Ala Ser Lys Ile Ile Phe Gly Ser Gly
115 120 125

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

Tyr Gln Leu Arg Asp Ser Lys Ser Ser Asp Lys Ser Val Cys Leu Phe
145 150 155 160

Thr Asp Phe Asp Ser Gln Thr Asn Val Ser Gln Ser Lys Asp Ser Asp
165 170 175

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

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

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

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

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

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

Leu Trp Ser Ser Glx
275

<210> 32
<211> 310
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3-beta chain amino acid sequence

<400> 32

Met Leu Leu Leu Leu Leu Leu Leu Gly Pro Gly Ser Gly Leu Gly Ala
1 5 10 15

Val Val Ser Gln His Pro Ser Trp Val Ile Cys Lys Ser Gly Thr Ser
20 25 30

Val Lys Ile Glu Cys Arg Ser Leu Asp Phe Gln Ala Thr Thr Met Phe
35 40 45

Trp Tyr Arg Gln Phe Pro Lys Gln Ser Leu Met Leu Met Ala Thr Ser
50 55 60

Asn Glu Gly Ser Lys Ala Thr Tyr Glu Gln Gly Val Glu Lys Asp Lys
65 70 75 80

Phe Leu Ile Asn His Ala Ser Leu Thr Leu Ser Thr Leu Thr Val Thr
85 90 95

Ser Ala His Pro Glu Asp Ser Ser Phe Tyr Ile Cys Ser Ala Asn Pro
100 105 110

Arg Thr Thr Leu Tyr Glu Gln Tyr Phe Gly Pro Gly Thr Arg Leu Thr
115 120 125

Val Thr Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val Ala Val Phe
130 135 140

Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala Thr Leu Val
145 150 155 160

Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu Ser Trp Trp
165 170 175

Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp Pro Gln Pro
180 185 190

Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys Leu Ser Ser
195 200 205

Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn His Phe
210 215 220

Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu Trp Thr
225 230 235 240

Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu Ala Trp
245 250 255

Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln Gly Val
260 265 270

Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala Thr Leu
275 280 285

Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val Lys Arg
290 295 300

Lys Asp Ser Arg Gly Glx

<210> 33
 <211> 831
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MAGE-A3-alpha chain nucleotide sequence

<400> 33
 atgctgactg ccagcctgtt gagggcagtc atagcctcca tctgtgttgt atccagcatg 60
 gctcagaagg taactcaagc gcagactgaa atttctgtgg tggagaagga ggatgtgacc 120
 ttggactgtg tgtatgaaac ccgtgatact acttattact tattctggta caagcaacca 180
 ccaagtggag aattggtttt cttatttcgt cggaactctt ttgatgagca aaatgaaata 240
 agtggtcggt attcttgaa cttccagaaa tccaccagtt cttcaactt caccatcaca 300
 gcctcacaag tcgtggactc agcagtatac ttctgtgctc tggaagtgag aagcagtgct 360
 tccaagataa tctttggatc agggaccaga ctacagcatcc ggccaaatat ccagaaccct 420
 gaccctgccg tgtaccagct gagagactct aaatccagtg acaagtctgt ctgcctattc 480
 accgattttg attctcaaac aaatgtgtca caaagtaagg attctgatgt gtatatcaca 540
 gacaaaactg tgctagacat gaggtctatg gacttcaaga gcaacagtgc tgtggcctgg 600
 agcaacaaat ctgactttgc atgtgcaaac gccttcaaca acagcattat tccagaagac 660
 accttcttcc ccagcccaga aagttcctgt gatgtcaagc tggtcgagaa aagctttgaa 720
 acagatacga acctaaactt tcaaaacctg tcagtgattg ggttccgaat cctcctcctg 780
 aaagtggccg ggtttaatct gctcatgacg ctgcggctgt ggtccagctg a 831

<210> 34
 <211> 930
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> MAGE-A3-beta chain nucleotide sequence

<400> 34
 atgctgtgctg ttctgctgct tctggggcca ggctccgggc ttggtgctgt cgtctctcaa 60
 catccgagct gggttatctg taagagtgga acctctgtga agatcgagtg ccgttcctg 120

gactttcagg ccacaactat gttttggtat cgtcagttcc cgaaacagag tctcatgctg	180
atggcaactt ccaatgaggg ctccaaggcc acatacgagc aaggcgtcga gaaggacaag	240
tttctcatca accatgcaag cctgaccttg tccactctga cagtgaccag tgcccatcct	300
gaagacagca gcttctacat ctgcagtgc aacccccgga ctaccctcta cgagcagtac	360
ttcgggccgg gcaccaggct cacggtcaca gaggacctga aaaacgtgtt cccacccgag	420
gtcgctgtgt ttgagccatc agaagcagag atctcccaca cccaaaaggc cacactgggtg	480
tgcttgccca caggcttcta ccccgaccac gtggagctga gctgggtgggt gaatgggaag	540
gaggtgcaca gtgggggtcag cacagacccg cagcccctca aggagcagcc cgccctcaat	600
gactccagat actgcctgag cagccgcctg agggctctcg ccaccttctg gcagaacccc	660
cgcaaccact tccgctgtca agtccagttc tacgggctct cggagaatga cgagtggacc	720
caggataggg ccaaacctgt caccagatc gtcagcgccg aggcctgggg tagagcagac	780
tgtggcttca cctccgagtc ttaccagcaa ggggtcctgt ctgccaccat cctctatgag	840
atcttgctag ggaaggccac cttgtatgcc gtgctggtca gtgcccttgt gctgatggcc	900
atggtcaaga gaaaggattc cagaggctag	930

<210> 35
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MAGE-A3-alpha CDR1

<400> 35

Thr	Arg	Asp	Thr	Thr	Tyr	Tyr
1				5		

<210> 36
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> MAGE-A3-alpha CDR2

<400> 36

Arg Asn Ser Phe Asp Glu Gln Asn

1 5

<210> 37
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3-alpha CDR3

<400> 37

Cys Ala Leu Glu Val Arg Ser Ser Ala Ser Lys Ile Ile Phe
1 5 10

<210> 38
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3-beta CDR1

<400> 38

Asp Phe Gln Ala Thr Thr
1 5

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3-beta CDR2

<400> 39

Ser Asn Glu Gly Ser Lys Ala
1 5

<210> 40
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3-beta CDR3

<400> 40

Cys Ser Ala Asn Pro Arg Thr Thr Leu Tyr Glu Gln Tyr Phe
1 5 10

<210> 41
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-alpha chain amino acid sequence

<400> 41

Met Glu Thr Leu Leu Gly Leu Leu Ile Leu Trp Leu Gln Leu Gln Trp
1 5 10 15

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 Glu
100 105 110

Pro Met Glu Tyr Gly Asn Lys Leu Val Phe Gly Ala Gly Thr Ile Leu
115 120 125

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

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

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

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

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

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

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

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

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

Ser Glx

<210> 42
<211> 313
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-beta chain amino acid sequence

<400> 42

Met Ser Asn Gln Val Leu Cys Cys Val Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Asn Thr Val Asp Gly Gly Ile Thr Gln Ser Pro Lys Tyr Leu Phe Arg
20 25 30

Lys Glu Gly Gln Asn Val Thr Leu Ser Cys Glu Gln Asn Leu Asn His
35 40 45

Asp Ala Met Tyr Trp Tyr Arg Gln Asp Pro Gly Gln Gly Leu Arg Leu
50 55 60

Ile Tyr Tyr Ser Gln Ile Val Asn Asp Phe Gln Lys Gly Asp Ile Ala
65 70 75 80

Glu Gly Tyr Ser Val Ser Arg Glu Lys Lys Glu Ser Phe Pro Leu Thr
85 90 95

Val Thr Ser Ala Gln Lys Asn Pro Thr Ala Phe Tyr Leu Cys Ala Ser
100 105 110

Ser Ala Leu Phe Ser Gly Ala Asn Val Leu Thr Phe Gly Ala Gly Ser
115 120 125

Arg Leu Thr Val Leu Glu Asp Leu Lys Asn Val Phe Pro Pro Glu Val
130 135 140

Ala Val Phe Glu Pro Ser Glu Ala Glu Ile Ser His Thr Gln Lys Ala
145 150 155 160

Thr Leu Val Cys Leu Ala Thr Gly Phe Tyr Pro Asp His Val Glu Leu
165 170 175

Ser Trp Trp Val Asn Gly Lys Glu Val His Ser Gly Val Ser Thr Asp
180 185 190

Pro Gln Pro Leu Lys Glu Gln Pro Ala Leu Asn Asp Ser Arg Tyr Cys
195 200 205

Leu Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg
210 215 220

Asn His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp
225 230 235 240

Glu Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala
245 250 255

Glu Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln

260

265

270

Gln Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys
 275 280 285

Ala Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met
 290 295 300

Val Lys Arg Lys Asp Ser Arg Gly Glx
 305 310

<210> 43

<211> 822

<212> DNA

<213> Artificial Sequence

<220>

<223> SSX2-alpha chain nucleotide sequence

<400> 43

atggagaccc tcttgggcct gcttattcctt tggctgcagc tgcaatgggt gagcagcaaa 60

caggaggtga cacagattcc tgcagctctg agtgtcccag aaggagaaaa cttggttctc 120

aactgcagtt tctactgatag cgctattttac aacctccagt ggtttaggca ggaccctggg 180

aaaggtctca catctctgtt gcttattcag tcaagtcaga gagagcaaac aagtggaaga 240

cttaatgcct cgctggataa atcatcagga cgtagtactt tatacattgc agctttctcag 300

cctggtgact cagccaccta cctctgtgct gtggaaccca tggaatatgg aaacaaactg 360

gtctttggcg caggaaccat tctgagagtc aagtcctata tccagaaccc tgaccctgcc 420

gtgtaccagc tgagagactc taaatccagt gacaagtctg tctgcctatt caccgatttt 480

gatttctcaa ccaatgtgtc acaaagtaag gattctgatg tgtatatcac agacaaaact 540

gtgctagaca tgaggtctat ggacttcaag agcaacagtg ctgtggcctg gagcaacaaa 600

tctgactttg catgtgcaaa cgccttcaac aacagcatta ttccagaaga caccttcttc 660

cccagcccag aaagttcctg tgatgtcaag ctggctcgaga aaagctttga aacagatacg 720

aacctaaact ttcaaaacct gtcagtgatt gggttccgaa tcctcctcct gaaagtggcc 780

gggtttaatc tgctcatgac gctgcggctg tggtccagct ga 822

<210> 44

<211> 939
<212> DNA
<213> Artificial Sequence

<220>
<223> SSX2-beta chain nucleotide sequence

<400> 44
atgagcaacc aggtgctctg ctgtgtggtc ctttgtctcc tgggagcaaa caccgtggat 60
ggtggaatca ctcagtcccc aaagtacctg ttcagaaagg aaggacagaa tgtgaccctg 120
agttgtgaac agaatttgaa ccacgatgcc atgtactggt accgacagga cccagggcaa 180
gggctgagat tgatctacta ctcacagata gtaaattgact ttcagaaagg agatatagct 240
gaagggtaca gcgtctctcg ggagaagaag gaatcctttc ctctcactgt gacatcggcc 300
caaaagaacc cgacagcttt ctatctctgt gccagtagtg cgttattctc tggggccaac 360
gtcctgactt tcggggccgg cagcaggctg accgtgctgg aggacctgaa aaacgtgttc 420
ccacccgagg tcgctgtggt tgagccatca gaagcagaga tctccacac caaaaggcc 480
acactggtgt gcctggccac aggcttctac cccgaccacg tggagctgag ctggtgggtg 540
aatgggaagg aggtgcacag tggggtcagc acagaccgc agcccctcaa ggagcagccc 600
gccctcaatg actccagata ctgcctgagc agccgcctga gggctctggc caccttctgg 660
cagaaccccc gcaaccactt ccgctgtcaa gtccagttct acgggctctc ggagaatgac 720
gagtggaccc aggatagggc caaacctgtc acccagatcg tcagcgccga ggcctgggggt 780
agagcagact gtggcttcac ctccgagtct taccagcaag gggctcctgtc tgccaccatc 840
ctctatgaga tcttgctagg gaaggccacc ttgtatgccg tgctggtcag tgccctcgtg 900
ctgatggcca tgggtcaagag aaaggattcc agaggctga 939

<210> 45
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-alpha CDR1

<400> 45

Asp Ser Ala Ile Tyr Asn
1 5

<210> 46
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-alpha CDR2

<400> 46

Ile Gln Ser Ser Gln Arg Glu
1 5

<210> 47
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-alpha CDR3

<400> 47

Cys Ala Val Glu Pro Met Glu Tyr Gly Asn Lys Leu Val Phe
1 5 10

<210> 48
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-beta CDR1

<400> 48

Leu Asn His Asp Ala
1 5

<210> 49
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-beta CDR2

<400> 49

Ser Gln Ile Val Asn Asp

1

5

<210> 50
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-beta CDR3

<400> 50

Cys Ala Ser Ser Ala Leu Phe Ser Gly Ala Asn Val Leu Thr Phe
1 5 10 15

<210> 51
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Tyr-epitope (460-468)

<400> 51

Phe Gln Asp Tyr Ile Lys Ser Tyr Leu
1 5

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A1-epitope (289-297)

<400> 52

Arg Val Arg Phe Phe Phe Pro Ser Leu
1 5

<210> 53
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-epitope (25-33)

<400> 53

Glu Glu Ala Ala Gly Ile Gly Ile Leu
1 5

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3-epitope (167-176)

<400> 54

Met Glu Val Asp Pro Ile Gly His Leu Tyr
1 5 10

<210> 55
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2-epitope (41-49)

<400> 55

Lys Ala Ser Glu Lys Ile Phe Tyr Val
1 5

<210> 56
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> B2m amino acid sequence

<400> 56

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

<210> 57
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA-TCRa-1 Nucleotides 1 to 19 are ribonucleotides-other nucle
otides are deoxyribonucleotides

<400> 57
guaaggauuc ugauguguat t 21

<210> 58
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA-TCRa-2 Nucleotides 1 to 19 are ribonucleotides-other nucle
otides are deoxyribonucleotides

<400> 58
uacacaucag aauccuuact t 21

<210> 59
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA-TCRb-1 Nucleotides 1 to 19 are ribonucleotides-other nucle

otides are deoxyribonucleotides

<400> 59
ccaccauccu cuaugagaut t 21

<210> 60
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA-TCRb-2 Nucleotides 1 to 19 are ribonucleotides-other nucle
otides are deoxyribonucleotides

<400> 60
aucucauaga ggaugguggt t 21

<210> 61
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 1

<400> 61
Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly
1 5 10 15

His Gly His Ser
20

<210> 62
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 6

<400> 62
Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly His Gly His Ser Tyr
1 5 10 15

Thr Thr Ala Glu
20

<210> 63
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 11

<400> 63

Gly Tyr Pro Lys Lys Gly His Gly His Ser Tyr Thr Thr Ala Glu Glu
1 5 10 15

Ala Ala Gly Ile
20

<210> 64
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 16

<400> 64

Gly His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile Gly
1 5 10 15

Ile Leu Thr Val
20

<210> 65
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 21

<400> 65

Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile Leu Thr Val Ile
1 5 10 15

Leu Gly Val Leu
20

<210> 66
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 26

<400> 66

Glu Ala Ala Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu
1 5 10 15

Leu Ile Gly Cys
20

<210> 67
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 31

<400> 67

Gly Ile Leu Thr Val Ile Leu Gly Val Leu Leu Leu Ile Gly Cys Trp
1 5 10 15

Tyr Cys Arg Arg
20

<210> 68
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 36

<400> 68

Ile Leu Gly Val Leu Leu Leu Ile Gly Cys Trp Tyr Cys Arg Arg Arg
1 5 10 15

Asn Gly Tyr Arg
20

<210> 69
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 41

<400> 69

Leu Leu Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala
1 5 10 15

Leu Met Asp Lys
20

<210> 70
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 46

<400> 70

Trp Tyr Cys Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser
1 5 10 15

Leu His Val Gly
20

<210> 71
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 51

<400> 71

Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val Gly Thr
1 5 10 15

Gln Cys Ala Leu
20

<210> 72
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 56

<400> 72

Ala	Leu	Met	Asp	Lys	Ser	Leu	His	Val	Gly	Thr	Gln	Cys	Ala	Leu	Thr
1				5					10					15	

Arg	Arg	Cys	Pro
			20

<210> 73
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 61

<400> 73

Ser	Leu	His	Val	Gly	Thr	Gln	Cys	Ala	Leu	Thr	Arg	Arg	Cys	Pro	Gln
1				5					10					15	

Glu	Gly	Phe	Asp
			20

<210> 74
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 66

<400> 74

Thr	Gln	Cys	Ala	Leu	Thr	Arg	Arg	Cys	Pro	Gln	Glu	Gly	Phe	Asp	His
1				5					10					15	

Arg	Asp	Ser	Lys
			20

<210> 75
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 71

<400> 75

Thr	Arg	Arg	Cys	Pro	Gln	Glu	Gly	Phe	Asp	His	Arg	Asp	Ser	Lys	Val
1				5					10					15	

Ser	Leu	Gln	Glu
			20

<210> 76
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 76

<400> 76

Gln	Glu	Gly	Phe	Asp	His	Arg	Asp	Ser	Lys	Val	Ser	Leu	Gln	Glu	Lys
1				5					10					15	

Asn	Cys	Glu	Pro
			20

<210> 77
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 81

<400> 77

His	Arg	Asp	Ser	Lys	Val	Ser	Leu	Gln	Glu	Lys	Asn	Cys	Glu	Pro	Val
1				5					10					15	

Val	Pro	Asn	Ala
			20

<210> 78
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 86

<400> 78

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

Pro Ala Tyr Glu
20

<210> 79
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 91

<400> 79

Lys Asn Cys Glu Pro Val Val Pro Asn Ala Pro Pro Ala Tyr Glu Lys
1 5 10 15

Leu Ser Ala Glu
20

<210> 80
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 96

<400> 80

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

Ser Pro Pro Pro
20

<210> 81
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1-derived overlapping peptide position 99

<400> 81

Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser Pro Pro
1 5 10 15

Pro Tyr Ser Pro
20

<210> 82
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> HIV rev67-75

<400> 82

Ser Ala Glu Pro Val Pro Leu Gln Leu
1 5

<210> 83
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NY-ESO-1 60-72

<400> 83

Ala Pro Arg Gly Pro His Gly Gly Ala Ala Ser Gly Leu
1 5 10

<210> 84
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> EBV EBNA3A379-387

<400> 84

Arg Pro Pro Ile Phe Ile Arg Arg Leu
1 5

<210> 85

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV nef128-137

<400> 85

Thr Pro Gly Pro Gly Val Arg Tyr Pro Leu
1 5 10

<210> 86

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> HIV gag161-170

<400> 86

Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
1 5 10

<210> 87

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> NY-ESO-1 157-165

<400> 87

Ser Leu Leu Met Trp Ile Thr Gln Val
1 5

<210> 88

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HTLV-1 tax11-19

<400> 88

Leu Leu Phe Gly Tyr Pro Val Tyr Val
1 5

<210> 89

<211> 529

<212> PRT

<213> Artificial Sequence

<220>

<223> Tyr - Full Length Amino Acid Sequence

<400> 89

Met Leu Leu Ala Val Leu Tyr Cys Leu Leu Trp Ser Phe Gln Thr Ser
1 5 10 15

Ala Gly His Phe Pro Arg Ala Cys Val Ser Ser Lys Asn Leu Met Glu
20 25 30

Lys Glu Cys Cys Pro Pro Trp Ser Gly Asp Arg Ser Pro Cys Gly Gln
35 40 45

Leu Ser Gly Arg Gly Ser Cys Gln Asn Ile Leu Leu Ser Asn Ala Pro
50 55 60

Leu Gly Pro Gln Phe Pro Phe Thr Gly Val Asp Asp Arg Glu Ser Trp
65 70 75 80

Pro Ser Val Phe Tyr Asn Arg Thr Cys Gln Cys Ser Gly Asn Phe Met
85 90 95

Gly Phe Asn Cys Gly Asn Cys Lys Phe Gly Phe Trp Gly Pro Asn Cys
100 105 110

Thr Glu Arg Arg Leu Leu Val Arg Arg Asn Ile Phe Asp Leu Ser Ala
115 120 125

Pro Glu Lys Asp Lys Phe Phe Ala Tyr Leu Thr Leu Ala Lys His Thr
130 135 140

Ile Ser Ser Asp Tyr Val Ile Pro Ile Gly Thr Tyr Gly Gln Met Lys
145 150 155 160

Asn Gly Ser Thr Pro Met Phe Asn Asp Ile Asn Ile Tyr Asp Leu Phe
165 170 175

Val Trp Met His Tyr Tyr Val Ser Met Asp Ala Leu Leu Gly Gly Ser
180 185 190

Glu Ile Trp Arg Asp Ile Asp Phe Ala His Glu Ala Pro Ala Phe Leu
195 200 205

Pro Trp His Arg Leu Phe Leu Leu Arg Trp Glu Gln Glu Ile Gln Lys
210 215 220

Leu Thr Gly Asp Glu Asn Phe Thr Ile Pro Tyr Trp Asp Trp Arg Asp
225 230 235 240

Ala Glu Lys Cys Asp Ile Cys Thr Asp Glu Tyr Met Gly Gly Gln His
245 250 255

Pro Thr Asn Pro Asn Leu Leu Ser Pro Ala Ser Phe Phe Ser Ser Trp
260 265 270

Gln Ile Val Cys Ser Arg Leu Glu Glu Tyr Asn Ser His Gln Ser Leu
275 280 285

Cys Asn Gly Thr Pro Glu Gly Pro Leu Arg Arg Asn Pro Gly Asn His
290 295 300

Asp Lys Ser Arg Thr Pro Arg Leu Pro Ser Ser Ala Asp Val Glu Phe
305 310 315 320

Cys Leu Ser Leu Thr Gln Tyr Glu Ser Gly Ser Met Asp Lys Ala Ala
325 330 335

Asn Phe Ser Phe Arg Asn Thr Leu Glu Gly Phe Ala Ser Pro Leu Thr
340 345 350

Gly Ile Ala Asp Ala Ser Gln Ser Ser Met His Asn Ala Leu His Ile

355

360

365

Tyr Met Asn Gly Thr Met Ser Gln Val Gln Gly Ser Ala Asn Asp Pro
 370 375 380

Ile Phe Leu Leu His His Ala Phe Val Asp Ser Ile Phe Glu Gln Trp
 385 390 395 400

Leu Arg Arg His Arg Pro Leu Gln Glu Val Tyr Pro Glu Ala Asn Ala
 405 410 415

Pro Ile Gly His Asn Arg Glu Ser Tyr Met Val Pro Phe Ile Pro Leu
 420 425 430

Tyr Arg Asn Gly Asp Phe Phe Ile Ser Ser Lys Asp Leu Gly Tyr Asp
 435 440 445

Tyr Ser Tyr Leu Gln Asp Ser Asp Pro Asp Ser Phe Gln Asp Tyr Ile
 450 455 460

Lys Ser Tyr Leu Glu Gln Ala Ser Arg Ile Trp Ser Trp Leu Leu Gly
 465 470 475 480

Ala Ala Met Val Gly Ala Val Leu Thr Ala Leu Leu Ala Gly Leu Val
 485 490 495

Ser Leu Leu Cys Arg His Lys Arg Lys Gln Leu Pro Glu Glu Lys Gln
 500 505 510

Pro Leu Leu Met Glu Lys Glu Asp Tyr His Ser Leu Tyr Gln Ser His
 515 520 525

Leu

<210> 90

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<223> MAGE-A1 - Full Length Amino Acid Sequence

<400> 90

Met Ser Leu Glu Gln Arg Ser Leu His Cys Lys Pro Glu Glu Ala Leu
1 5 10 15

Glu Ala Gln Gln Glu Ala Leu Gly Leu Val Cys Val Gln Ala Ala Thr
20 25 30

Ser Ser Ser Ser Pro Leu Val Leu Gly Thr Leu Glu Glu Val Pro Thr
35 40 45

Ala Gly Ser Thr Asp Pro Pro Gln Ser Pro Gln Gly Ala Ser Ala Phe
50 55 60

Pro Thr Thr Ile Asn Phe Thr Arg Gln Arg Gln Pro Ser Glu Gly Ser
65 70 75 80

Ser Ser Arg Glu Glu Glu Gly Pro Ser Thr Ser Cys Ile Leu Glu Ser
85 90 95

Leu Phe Arg Ala Val Ile Thr Lys Lys Val Ala Asp Leu Val Gly Phe
100 105 110

Leu Leu Leu Lys Tyr Arg Ala Arg Glu Pro Val Thr Lys Ala Glu Met
115 120 125

Leu Glu Ser Val Ile Lys Asn Tyr Lys His Cys Phe Pro Glu Ile Phe
130 135 140

Gly Lys Ala Ser Glu Ser Leu Gln Leu Val Phe Gly Ile Asp Val Lys
145 150 155 160

Glu Ala Asp Pro Thr Gly His Ser Tyr Val Leu Val Thr Cys Leu Gly
165 170 175

Leu Ser Tyr Asp Gly Leu Leu Gly Asp Asn Gln Ile Met Pro Lys Thr
180 185 190

Gly Phe Leu Ile Ile Val Leu Val Met Ile Ala Met Glu Gly Gly His
195 200 205

Ala Pro Glu Glu Glu Ile Trp Glu Glu Leu Ser Val Met Glu Val Tyr
210 215 220

Asp Gly Arg Glu His Ser Ala Tyr Gly Glu Pro Arg Lys Leu Leu Thr
225 230 235 240

Gln Asp Leu Val Gln Glu Lys Tyr Leu Glu Tyr Arg Gln Val Pro Asp
245 250 255

Ser Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala Leu Ala
260 265 270

Glu Thr Ser Tyr Val Lys Val Leu Glu Tyr Val Ile Lys Val Ser Ala
275 280 285

Arg Val Arg Phe Phe Phe Pro Ser Leu Arg Glu Ala Ala Leu Arg Glu
290 295 300

Glu Glu Glu Gly Val
305

<210> 91
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> MART1 - Full Length Amino Acid Sequence

<400> 91

Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro Lys Lys Gly
1 5 10 15

His Gly His Ser Tyr Thr Thr Ala Glu Glu Ala Ala Gly Ile Gly Ile
20 25 30

Leu Thr Val Ile Leu Gly Val Leu Leu Leu Ile Gly Cys Trp Tyr Cys
35 40 45

Arg Arg Arg Asn Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val
50 55 60

Gly Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly Phe Asp
65 70 75 80

His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys Asn Cys Glu Pro Val
85 90 95

Val Pro Asn Ala Pro Pro Ala Tyr Glu Lys Leu Ser Ala Glu Gln Ser
100 105 110

Pro Pro Pro Tyr Ser Pro
115

<210> 92
<211> 314
<212> PRT
<213> Artificial Sequence

<220>
<223> MAGE-A3 - Full Length Amino Acid Sequence

<400> 92

Met Pro Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Glu Gly Leu
1 5 10 15

Glu Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala
20 25 30

Thr Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val
35 40 45

Thr Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser
50 55 60

Pro Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp
65 70 75 80

Ser Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser
85 90 95

Thr Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys
100 105 110

Val Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu
115 120 125

Pro Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln
130 135 140

Tyr Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu
145 150 155 160

Val Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr
165 170 175

Ile Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp
180 185 190

Asn Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile
195 200 205

Ile Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu
210 215 220

Leu Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly
225 230 235 240

Asp Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu
245 250 255

Glu Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu
260 265 270

Trp Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His
275 280 285

His Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu
290 295 300

His Glu Trp Val Leu Arg Glu Gly Glu Glu
305 310

<211> 188
<212> PRT
<213> Artificial Sequence

<220>
<223> SSX2 - Full Length Amino Acid Sequence

<400> 93

Met Asn Gly Asp Asp Ala Phe Ala Arg Arg Pro Thr Val Gly Ala Gln
1 5 10 15

Ile Pro Glu Lys Ile Gln Lys Ala Phe Asp Asp Ile Ala Lys Tyr Phe
20 25 30

Ser Lys Glu Glu Trp Glu Lys Met Lys Ala Ser Glu Lys Ile Phe Tyr
35 40 45

Val Tyr Met Lys Arg Lys Tyr Glu Ala Met Thr Lys Leu Gly Phe Lys
50 55 60

Ala Thr Leu Pro Pro Phe Met Cys Asn Lys Arg Ala Glu Asp Phe Gln
65 70 75 80

Gly Asn Asp Leu Asp Asn Asp Pro Asn Arg Gly Asn Gln Val Glu Arg
85 90 95

Pro Gln Met Thr Phe Gly Arg Leu Gln Gly Ile Ser Pro Lys Ile Met
100 105 110

Pro Lys Lys Pro Ala Glu Glu Gly Asn Asp Ser Glu Glu Val Pro Glu
115 120 125

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

Pro Thr Thr Ser Glu Lys Ile His Glu Arg Ser Gly Pro Lys Arg Gly
145 150 155 160

Glu His Ala Trp Thr His Arg Leu Arg Glu Arg Lys Gln Leu Val Ile
165 170 175

Tyr Glu Glu Ile Ser Asp Pro Glu Glu Asp Asp Glu

