

SEQUENCE LISTING

<110> DUKE UNIVERSITY
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WANG, Guoping

<120> ANTI-LMP2 TCR-T CELL THERAPY FOR THE TREATMENT OF EBV-ASSOCIATED
CANCERS

<130> 19-2104-WO

<150> US 62/771,653
<151> 2018-11-27

<160> 14

<170> PatentIn version 3.5

<210> 1
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> LMP2 antigen

<400> 1

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<210> 2
<211> 497
<212> PRT
<213> Human herpesvirus 4

<400> 2

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Gly	Gly	Asp	Pro	Asp	Gly	Tyr	Asp	Gly	Gly	Asn	Asn	Ser	Gln	Tyr	Pro
			20					25					30		

Ser	Ala	Ser	Gly	Ser	Ser	Gly	Asn	Thr	Pro	Thr	Pro	Pro	Asn	Asp	Glu
		35					40					45			

Glu Arg Glu Ser Asn Glu Glu Pro Pro Pro Pro Tyr Glu Asp Pro Tyr
50 55 60

Trp Gly Asn Gly Asp Arg His Ser Asp Tyr Gln Pro Leu Gly Thr Gln
65 70 75 80

Asp Gln Ser Leu Tyr Leu Gly Leu Gln His Asp Gly Asn Asp Gly Leu
85 90 95

Pro Pro Pro Pro Tyr Ser Pro Arg Asp Asp Ser Ser Gln His Ile Tyr
100 105 110

Glu Glu Ala Gly Arg Gly Ser Met Asn Pro Val Cys Leu Pro Val Ile
115 120 125

Val Ala Pro Tyr Leu Phe Trp Leu Ala Ala Ile Ala Ala Ser Cys Phe
130 135 140

Thr Ala Ser Val Ser Thr Val Val Thr Ala Thr Gly Leu Ala Leu Ser
145 150 155 160

Leu Leu Leu Leu Ala Ala Val Ala Ser Ser Tyr Ala Ala Ala Gln Arg
165 170 175

Lys Leu Leu Thr Pro Val Thr Val Leu Thr Ala Val Val Thr Phe Phe
180 185 190

Ala Ile Cys Leu Thr Trp Arg Ile Glu Asp Pro Pro Phe Asn Ser Leu
195 200 205

Leu Phe Ala Leu Leu Ala Ala Ala Gly Gly Leu Gln Gly Ile Tyr Val
210 215 220

Leu Val Met Leu Val Leu Leu Ile Leu Ala Tyr Arg Arg Arg Trp Arg
225 230 235 240

Arg Leu Thr Val Cys Gly Gly Ile Met Phe Leu Ala Cys Val Leu Val
245 250 255

Leu Ile Val Asp Ala Val Leu Gln Leu Ser Pro Leu Leu Gly Ala Val

260

265

270

Thr Val Val Ser Met Thr Leu Leu Leu Leu Ala Phe Val Leu Trp Leu
 275 280 285

Ser Ser Pro Gly Gly Leu Gly Thr Leu Gly Ala Ala Leu Leu Thr Leu
 290 295 300

Ala Ala Ala Leu Ala Leu Leu Ala Ser Leu Ile Leu Gly Thr Leu Asn
 305 310 315 320

Leu Thr Thr Met Phe Leu Leu Met Leu Leu Trp Thr Leu Val Val Leu
 325 330 335

Leu Ile Cys Ser Ser Cys Ser Ser Cys Pro Leu Ser Lys Ile Leu Leu
 340 345 350

Ala Arg Leu Phe Leu Tyr Ala Leu Ala Leu Leu Leu Leu Ala Ser Ala
 355 360 365

Leu Ile Ala Gly Gly Ser Ile Leu Gln Thr Asn Phe Lys Ser Leu Ser
 370 375 380

Ser Thr Glu Phe Ile Pro Asn Leu Phe Cys Met Leu Leu Leu Ile Val
 385 390 395 400

Ala Gly Ile Leu Phe Ile Leu Ala Ile Leu Thr Glu Trp Gly Ser Gly
 405 410 415

Asn Arg Thr Tyr Gly Pro Val Phe Met Cys Leu Gly Gly Leu Leu Thr
 420 425 430

Met Val Ala Gly Ala Val Trp Leu Thr Val Met Ser Asn Thr Leu Leu
 435 440 445

Ser Ala Trp Ile Leu Thr Ala Gly Phe Leu Ile Phe Leu Ile Gly Phe
 450 455 460

Ala Leu Phe Gly Val Ile Arg Cys Cys Arg Tyr Cys Cys Tyr Tyr Cys
 465 470 475 480

Leu Thr Leu Glu Ser Glu Glu Arg Pro Pro Thr Pro Tyr Arg Asn Thr
485 490 495

Val

<210> 3
<211> 421
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR A11-003

<400> 3

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser
65 70 75 80

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

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

Asn Asp Met Arg Phe Gly Ala Gly Thr Arg Leu Thr Val Lys Pro Asp
115 120 125

Ile Gln Asn Pro Glu Pro Ala Val Tyr Gln Leu Lys Asp Pro Arg Ser

130

135

140

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

Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val
 165 170 175

Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
 180 185 190

Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
 195 200 205

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

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

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

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

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
 275 280 285

Gly Pro Met Gly Cys Arg Leu Leu Cys Cys Ala Val Leu Cys Leu Leu
 290 295 300

Gly Ala Val Pro Ile Asp Thr Glu Val Thr Gln Thr Pro Lys His Leu
 305 310 315 320

Val Met Gly Met Thr Asn Lys Lys Ser Leu Lys Cys Glu Gln His Met
 325 330 335

Gly His Arg Ala Met Tyr Trp Tyr Lys Gln Lys Ala Lys Lys Pro Pro
 340 345 350

Glu Leu Met Phe Val Tyr Ser Tyr Glu Lys Leu Ser Ile Asn Glu Ser
355 360 365

Val Pro Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser Leu Leu Asn
370 375 380

Leu His Leu His Ala Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys
385 390 395 400

Ala Ser Ser Pro Gly Arg Trp Tyr Glu Gln Phe Phe Gly Pro Gly Thr
405 410 415

Arg Leu Thr Val Leu
420

<210> 4
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR A11-003 Variable alpha chain

<400> 4

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser
65 70 75 80

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser

85

90

95

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

Asn Asp Met Arg Phe Gly Ala Gly Thr Arg Leu Thr Val Lys Pro
 115 120 125

<210> 5

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR A11-003 Variable CDR3 alpha

<400> 5

Ala Val Val Asn Asn Asn Asp Met Arg Phe Gly
 1 5 10

<210> 6

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR A11-003 Variable beta chain

<400> 6

Met Gly Cys Arg Leu Leu Cys Cys Ala Val Leu Cys Leu Leu Gly Ala
 1 5 10 15

Val Pro Ile Asp Thr Glu Val Thr Gln Thr Pro Lys His Leu Val Met
 20 25 30

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

Arg Ala Met Tyr Trp Tyr Lys Gln Lys Ala Lys Lys Pro Pro Glu Leu
 50 55 60

Met Phe Val Tyr Ser Tyr Glu Lys Leu Ser Ile Asn Glu Ser Val Pro
 65 70 75 80

Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser Leu Leu Asn Leu His
85 90 95

Leu His Ala Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

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

Thr Val Leu
130

<210> 7
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> TCR A11-003 Variable CDR3 beta

<400> 7

Ala Ser Ser Pro Gly Arg Trp Tyr Glu Gln Phe
1 5 10

<210> 8
<211> 1263
<212> DNA
<213> Artificial Sequence

<220>
<223> TCR A11-003

<400> 8
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ctgcggtgca acttttagcga cagcgtgaac aacctgcagt gggtccacca gaatccttgg 180
ggccagctga tcaacctgtt ctacatcccc agcggcacca agcagaacgg cagactgtct 240
gctaccaccg tggccaccga gagatacagc ctgctgtaca tcagcagcag ccagaccaca 300
gacagcggcg tgtacttttg cgccgtggtc aacaacaacg acatgagatt cggagccggc 360

accagactga ccgtgaagcc cgatatccag aatccagagc ctgccgtgta ccagctgaag	420
gaccctagaa gccaggacag caccctgtgc ctgttcaccg acttcgacag ccagatcaac	480
gtgccaaga ccatggaaag cggcaccttc atcaccgaca agaccgtgct ggacatgaag	540
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caggacatct tcaaagagac aaacgcctgc tatcccagca gcgacgtgcc ctgtgatgcc	660
acactgaccg agaagtcctt cgagacagac atgaacctga acttccagaa cctgagcgtg	720
atgggcctgc gcatcctgct gcttaaagtg gccggcttca acctgctgat gaccctgaga	780
ctgtggtcca gcagggccaa gagaggaagc ggcgccacaa actttagcct gctgaaacag	840
gccggcgacg tggaagaaaa ccctggacct atgggctgca gactgctgtg ttgtgccgtg	900
ctgtgtctgc tgggcgccgt gcctattgac accgaagtga cccagacacc taagcacctg	960
gtcatgggca tgacaaacaa gaaaagcctg aagtgcgagc agcacatggg ccacagagcc	1020
atgtactggg acaagcagaa ggccaagaaa cctccagagc tgatgttcgt gtacagctac	1080
gagaagctga gcatcaacga gagcgtgccc agcaggttca gccctgagtg tcctaatagc	1140
tccctgctga atctgcatct gcacgccctg cagcctgagg attctgccct gtacctgtgt	1200
gccagctctc ccggacgttg gtacgagcag tttttcggcc ctggcacacg gctgacagtt	1260
ctg	1263

<210> 9
 <211> 421
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR A11-125

<400> 9

Met	Lys	Arg	Ile	Leu	Gly	Ala	Leu	Leu	Gly	Leu	Leu	Ser	Ala	Gln	Val
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Cys	Cys	Val	Arg	Gly	Ile	Gln	Val	Glu	Gln	Ser	Pro	Pro	Asp	Leu	Ile
			20					25					30		

Leu	Gln	Glu	Gly	Ala	Asn	Ser	Thr	Leu	Arg	Cys	Asn	Phe	Ser	Asp	Ser
		35					40					45			

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser
65 70 75 80

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

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

Asn Asp Met Arg Phe Gly Ala Gly Thr Arg Leu Thr Val Lys Pro Asp
115 120 125

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

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

Val Pro Lys Thr Met Glu Ser Gly Thr Phe Ile Thr Asp Lys Thr Val
165 170 175

Leu Asp Met Lys Ala Met Asp Ser Lys Ser Asn Gly Ala Ile Ala Trp
180 185 190

Ser Asn Gln Thr Ser Phe Thr Cys Gln Asp Ile Phe Lys Glu Thr Asn
195 200 205

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

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

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

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

Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn Pro
 275 280 285

Gly Pro Met Gly Cys Arg Leu Leu Cys Cys Ala Val Leu Cys Leu Leu
 290 295 300

Gly Ala Val Pro Ile Asp Thr Glu Val Thr Gln Thr Pro Lys His Leu
 305 310 315 320

Val Met Gly Met Thr Asn Lys Lys Ser Leu Lys Cys Glu Gln His Met
 325 330 335

Gly His Arg Ala Met Tyr Trp Tyr Lys Gln Lys Ala Lys Lys Pro Pro
 340 345 350

Glu Leu Met Phe Val Tyr Ser Tyr Glu Lys Leu Ser Ile Asn Glu Ser
 355 360 365

Val Pro Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser Leu Leu Asn
 370 375 380

Leu His Leu His Ala Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys
 385 390 395 400

Ala Ser Ser Gln Gly Arg Trp Tyr Glu Ala Phe Phe Gly Gln Gly Thr
 405 410 415

Arg Leu Thr Val Val
 420

<210> 10
 <211> 127
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> TCR A11-125 Variable alpha chain

<400> 10

Met Lys Arg Ile Leu Gly Ala Leu Leu Gly Leu Leu Ser Ala Gln Val
1 5 10 15

Cys Cys Val Arg Gly Ile Gln Val Glu Gln Ser Pro Pro Asp Leu Ile
20 25 30

Leu Gln Glu Gly Ala Asn Ser Thr Leu Arg Cys Asn Phe Ser Asp Ser
35 40 45

Val Asn Asn Leu Gln Trp Phe His Gln Asn Pro Trp Gly Gln Leu Ile
50 55 60

Asn Leu Phe Tyr Ile Pro Ser Gly Thr Lys Gln Asn Gly Arg Leu Ser
65 70 75 80

Ala Thr Thr Val Ala Thr Glu Arg Tyr Ser Leu Leu Tyr Ile Ser Ser
85 90 95

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

Asn Asp Met Arg Phe Gly Ala Gly Thr Arg Leu Thr Val Lys Pro
115 120 125

<210> 11

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR A11-125 Variable CDR3 alpha

<400> 11

Ala Val Leu Asn Asn Asn Asp Met Arg Phe Gly
1 5 10

<210> 12

<211> 131

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR A11-125 Variable beta chain

<400> 12

Met Gly Cys Arg Leu Leu Cys Cys Ala Val Leu Cys Leu Leu Gly Ala
1 5 10 15

Val Pro Ile Asp Thr Glu Val Thr Gln Thr Pro Lys His Leu Val Met
20 25 30

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

Arg Ala Met Tyr Trp Tyr Lys Gln Lys Ala Lys Lys Pro Pro Glu Leu
50 55 60

Met Phe Val Tyr Ser Tyr Glu Lys Leu Ser Ile Asn Glu Ser Val Pro
65 70 75 80

Ser Arg Phe Ser Pro Glu Cys Pro Asn Ser Ser Leu Leu Asn Leu His
85 90 95

Leu His Ala Leu Gln Pro Glu Asp Ser Ala Leu Tyr Leu Cys Ala Ser
100 105 110

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

Thr Val Val
130

<210> 13

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> TCR A11-125 Variable CDR3 beta

<400> 13

Ala Ser Ser Gln Gly Arg Trp Tyr Glu Ala Phe
1 5 10

<210> 14
 <211> 1263
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> TCR A11-125

<400> 14
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 ctgcggtgca acttttagcga cagcgtgaac aacctgcagt ggttccacca gaatccttgg 180
 ggccagctga tcaacctggt ctacatcccc agcggcacca agcagaacgg cagactgtct 240
 gctaccaccg tggccaccga gagatacagc ctgctgtaca tcagcagcag ccagaccaca 300
 gacagcggcg tgtacttttg cgccgtgctg aacaacaacg acatgagatt cggagccggc 360
 accagactga ccgtgaagcc cgatatccag aatccagagc ctgccgtgta ccagctgaag 420
 gaccctagaa gccaggacag caccctgtgc ctgttcaccg acttcgacag ccagatcaac 480
 gtgccaaga ccatggaaag cggcaccttc atcaccgaca agaccgtgct ggacatgaag 540
 gccatggaca gcaagagcaa cggcgccatt gcctgggtcca accagaccag cttcacatgc 600
 caggacatct tcaaagagac aaacgcctgc tatcccagca gcgacgtgcc ctgtgatgcc 660
 aactgaccg agaagtcctt cgagacagac atgaacctga acttcagaa cctgagcgtg 720
 atgggcctgc gcatcctgct gcttaaagtg gccggcttca acctgctgat gaccctgaga 780
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 ctgtgtctgc tggg'gcgctg gcctattgac accgaagtga cccagacacc taagcacctg 960
 gtcattgggca tgacaaacaa gaaaagcctg aagtgcgagc agcacatggg ccacagagcc 1020
 atgtactggg acaagcagaa ggccaagaaa cctcctgagc tgatgttcgt gtacagctac 1080
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gtg

1263