

SEQUENCE LISTING

<110> BAYLOR COLLEGE OF MEDICINE

<120> REPROGRAMMING CD4 T CELLS INTO CYTOTOXIC CD8 CELLS BY FORCED
EXPRESSION OF CD8AB AND CLASS 1 RESTRICTED T CELL RECEPTORS

<130> BAYM.P0258WO-1001068755

<140> PCT/US2019/028202

<141> 2019-04-18

<150> 62/659,971

<151> 2018-04-19

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 20

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 1

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<210> 2

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 2

Glu Leu Thr Leu Gly Glu Phe Leu Lys Leu
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<210> 3

<211> 9

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
peptide

<400> 3

Asn Leu Thr His Val Leu Tyr Pro Val
1 5

<210> 4

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<212> PRT

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<223> Description of Artificial Sequence: Synthetic
peptide

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Leu Met Leu Gly Glu Phe Leu Lys Leu
1 5

<210> 5

<211> 9

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<223> Description of Artificial Sequence: Synthetic
peptide

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Asn Leu Thr His Val Leu Tyr Pro Val
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<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (1)..(3)

<223> This region may or may not be present

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Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
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Glu Asn Pro Gly Pro
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<210> 7
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peptide

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<223> This region may or may not be present

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Glu Glu Asn Pro Gly Pro
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<210> 8
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<223> This region may or may not be present

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Val Glu Ser Asn Pro Gly Pro
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<210> 9
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<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<220>

<221> MOD_RES

<222> (1)..(3)

<223> This region may or may not be present

<400> 9

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Gly	Asp	Val	Glu	Ser	Asn	Pro	Gly	Pro
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<210> 10

<211> 2150

<212> DNA

<213> Homo sapiens

<400> 10

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tggagctgaa	gtgccaggt	ctgctgtcc	acccgacgt	gggctgctc	tggctcttc		180
agccgcgcgg	cgccgccgc	agtcccact	tcctcctat	cctctccaa	aacaagcca		240
aggcggccga	ggggctgg	accagcgg	tctcgggca	gaggttg	gacaccttc		300
tcctcaccct	gagcgactt	cgccgagag	acgagggt	ctatttctg	tcggccctg		360
gcaactccat	catgtactt	agccacttc	tgccggtct	cctgccagc	aagcccacca		420
cgacgccagc	gccgcgacc	ccaacaccg	cgcccaccat	cgcgtcgc	cccctgtccc		480
tgcgcccaga	ggcgtgccg	ccagcggcg	ggggcg	gcacacgag	gggctggact		540
tcgcctgtga	tatctacat	tgggcgcct	tggccggg	ttgtggggt	cttctcctgt		600
cactggttat	caccctttac	tgcaaccaca	ggaaccga	acgtgtttg	aaatgtcccc		660
ggcctgtgg	caaatcgga	gacaagcca	gcctttcgg	gagatacgt	taaccctgtg		720
caacagccac	tacattact	caaactgag	tccttcctt	tgagggag	agtccttccc		780

tttcattttt tccagtcttc ctccctgtgt attcattctc atgattatta ttttagtggg	840
ggcggggtgg gaaagattac tttttcttta tgtgtttgac gggaaacaaa actaggtaaa	900
atctacagta caccacaagg gtcacaatac tgttgtgcgc acatcgcggt agggcgtgga	960
aaggggcagg ccagagctac ccgcagagtt ctcagaatca tgctgagaga gctggaggca	1020
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tgtaaaatat gtctttcttt tttaaatagg gttgtactat gctgttatga gtggctttta	1980
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	2150

<210> 11

<211> 235

<212> PRT

<213> Homo sapiens

<400> 11

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

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			20					25					30				
Trp	Asn	Leu	Gly	Glu	Thr	Val	Glu	Leu	Lys	Cys	Gln	Val	Leu	Leu	Ser		
		35					40					45					
Asn	Pro	Thr	Ser	Gly	Cys	Ser	Trp	Leu	Phe	Gln	Pro	Arg	Gly	Ala	Ala		
	50					55					60						
Ala	Ser	Pro	Thr	Phe	Leu	Leu	Tyr	Leu	Ser	Gln	Asn	Lys	Pro	Lys	Ala		
65					70					75					80		
Ala	Glu	Gly	Leu	Asp	Thr	Gln	Arg	Phe	Ser	Gly	Lys	Arg	Leu	Gly	Asp		
				85					90					95			
Thr	Phe	Val	Leu	Thr	Leu	Ser	Asp	Phe	Arg	Arg	Glu	Asn	Glu	Gly	Cys		
			100					105					110				
Tyr	Phe	Cys	Ser	Ala	Leu	Ser	Asn	Ser	Ile	Met	Tyr	Phe	Ser	His	Phe		
		115					120					125					
Val	Pro	Val	Phe	Leu	Pro	Ala	Lys	Pro	Thr	Thr	Thr	Pro	Ala	Pro	Arg		
	130					135					140						
Pro	Pro	Thr	Pro	Ala	Pro	Thr	Ile	Ala	Ser	Gln	Pro	Leu	Ser	Leu	Arg		
145					150					155					160		
Pro	Glu	Ala	Cys	Arg	Pro	Ala	Ala	Gly	Gly	Ala	Val	His	Thr	Arg	Gly		
				165					170					175			
Leu	Asp	Phe	Ala	Cys	Asp	Ile	Tyr	Ile	Trp	Ala	Pro	Leu	Ala	Gly	Thr		
			180					185					190				
Cys	Gly	Val	Leu	Leu	Leu	Ser	Leu	Val	Ile	Thr	Leu	Tyr	Cys	Asn	His		
		195					200					205					
Arg	Asn	Arg	Arg	Arg	Val	Cys	Lys	Cys	Pro	Arg	Pro	Val	Val	Lys	Ser		
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Gly Asp Lys Pro Ser Leu Ser Ala Arg Tyr Val
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agaccctgc	atacataaag	gtgcaaacca	acaagatggg	gatgctgtcc	tgcgaggcta	180
aaatctccct	cagtaacatg	cgcattctact	ggctgagaca	gcgccaggca	ccgagcagtg	240
acagtcacca	cgagttcctg	gccctctggg	attccgcaaa	agggactatc	cacggtgaag	300
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caagcgtgaa	gccggaagac	agtggcatct	acttctgcat	gatcgtcggg	agccccgagc	420
tgaccttcgg	gaagggaact	cagctgagtg	tggttgattt	ccttcccacc	actgcccagc	480
ccaccaagaa	gtccaccctc	aagaagagag	tgtgccgggt	accaggcca	gagaccaga	540
agggcctcaa	ggggaaggtg	tatcaggaac	ctttgtcccc	caatgcctgc	atggatacta	600
cagcaatact	acaacctcac	agaagctgct	taacccatgg	atcctgaaaa	cataggcaag	660
aagcacaggt	cctgatgagt	ggatctttac	tacttttacc	agatt		705

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<210> 13
<211> 198
<212> PRT
<213> Homo sapiens
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<400> 13
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20 25 30

Thr Asn Lys Met Val Met Leu Ser Cys Glu Ala Lys Ile Ser Leu Ser
35 40 45

Asn Met Arg Ile Tyr Trp Leu Arg Gln Arg Gln Ala Pro Ser Ser Asp
50 55 60

Ser His His Glu Phe Leu Ala Leu Trp Asp Ser Ala Lys Gly Thr Ile
65 70 75 80

His Gly Glu Glu Val Glu Gln Glu Lys Ile Ala Val Phe Arg Asp Ala
85 90 95

Ser Arg Phe Ile Leu Asn Leu Thr Ser Val Lys Pro Glu Asp Ser Gly
100 105 110

Ile Tyr Phe Cys Met Ile Val Gly Ser Pro Glu Leu Thr Phe Gly Lys
115 120 125

Gly Thr Gln Leu Ser Val Val Asp Phe Leu Pro Thr Thr Ala Gln Pro
130 135 140

Thr Lys Lys Ser Thr Leu Lys Lys Arg Val Cys Arg Leu Pro Arg Pro
145 150 155 160

Glu Thr Gln Lys Gly Leu Lys Gly Lys Val Tyr Gln Glu Pro Leu Ser
165 170 175

Pro Asn Ala Cys Met Asp Thr Thr Ala Ile Leu Gln Pro His Arg Ser
180 185 190

Cys Leu Thr His Gly Ser
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<210> 14

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<220>

<221> MOD_RES

<222> (5)..(5)

<223> Any amino acid

<400> 14

Gly Asp Val Glu Xaa Asn Pro Gly Pro

1

5