

1849675_1
SEQUENCE LISTING

<110> National University of Singapore

<120> CHIMERIC RECEPTOR THAT TRIGGERS ANTIBODY-DEPENDENT CELL
CYTOTOXICITY AGAINST MULTIPLE TUMORS

<130> N0565.70000WO00

<150> US 62/026,243
<151> 2014-07-18

<150> US 61/892,218
<151> 2013-10-17

<160> 18

<170> PatentIn version 3.5

<210> 1
<211> 436
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Polypeptide

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Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
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His Ala Ala Arg Pro Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val
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Val Phe Leu Glu Pro Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val
35 40 45

Thr Leu Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln
50 55 60

Trp Phe His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe
65 70 75 80

Ile Asp Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr
85 90 95

Asn Leu Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly
100 105 110

Trp Leu Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro
115 120 125

Ile His Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val
130 135 140

Thr Tyr Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser
145 150 155 160

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Asp Phe Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe
 165 170 175
 Cys Arg Gly Leu Val Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn
 180 185 190
 Ile Thr Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe
 195 200 205
 Pro Pro Gly Tyr Gln Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
 210 215 220
 Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 225 230 235 240
 Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
 245 250 255
 Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
 260 265 270
 Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
 275 280 285
 Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
 290 295 300
 Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
 305 310 315 320
 Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
 325 330 335
 Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 340 345 350
 Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 355 360 365
 Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 370 375 380
 Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 385 390 395 400
 Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
 405 410 415
 Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
 420 425 430

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Leu Pro Pro Arg
435

<210> 2
<211> 192
<212> PRT
<213> Artificial Sequence

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<223> Synthetic Polypeptide
<400> 2

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
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Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
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Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
35 40 45

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
50 55 60

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
65 70 75 80

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
85 90 95

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
100 105 110

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
115 120 125

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
130 135 140

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

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
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Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
180 185 190

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<213> Artificial Sequence

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<220>

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Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
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Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
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Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
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Ile Thr Leu Tyr Cys
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Arg Pro Val Gln Thr Thr Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe
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Pro Glu Glu Glu Glu Gly Gly Cys Glu Leu
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<223> Synthetic Polypeptide

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Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
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Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

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Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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His Ala Ala Arg Pro
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<400> 9

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aattccacac	agtggtttca	caatgagagc	ctcatctcaa	gccaggcctc	gagctacttc	240
attgacgctg	ccacagtcga	cgacagtgga	gagtacaggt	gccagacaaa	cctctccacc	300
ctcagtgacc	cggtgcagct	agaagtccat	atcggctggc	tgttgctcca	ggccccctcg	360
tgggtgttca	aggaggaaga	ccctattcac	ctgaggtgtc	acagctggaa	gaacactgct	420
ctgcataagg	tcacatattt	acagaatggc	aaaggcagga	agtattttca	tcataattct	480
gacttctaca	ttccaaaagc	cacactcaaa	gacagcggct	cctacttctg	cagggggcct	540
gttgggagta	aaaatgtgtc	ttcagagact	gtgaacatca	ccatcactca	aggtttggca	600
gtgtcaacca	tctcatcatt	ctttccacct	gggtaccaa	ccacgacgcc	agcgccgcga	660
ccaccaacac	cggcgcccac	catcgcgtcg	cagcccctgt	ccctgcgccc	agaggcgtgc	720
cggccagcgg	cggggggcgc	agtgcacacg	agggggctgg	acttcgcctg	tgatatctac	780
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tactgcaaac	ggggcagaaa	gaaactcctg	tatatattca	aacaaccatt	tatgagacca	900
gtacaaacta	ctcaagagga	agatggctgt	agctgccgat	ttccagaaga	agaagaagga	960
ggatgtgaac	tgagagtga	gttcagcagg	agcgagagc	ccccgcgta	ccagcagggc	1020
cagaaccagc	tctataacga	gctcaatcta	ggacgaagag	aggagtacga	tgttttggac	1080
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ggcctgtaca	atgaactgca	gaaagataag	atggcggagg	cctacagtga	gattgggatg	1200
aaaggcgagc	gccggagggg	caaggggcac	gatggccttt	accagggctc	cagtacagcc	1260
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tccacacagt	ggtttcacaa tgagagcctc atctcaagcc aggcctcgag ctacttcatt 180
gacgctgcca	cagtgcagca cagtggagag tacaggtgcc agacaaacct ctccaccctc 240
agtgacccgg	tgagctaga agtccatatc ggctggctgt tgctccaggc ccctcggtgg 300
gtgttcaagg	aggaagaccc tattcacctg aggtgtcaca gctggaagaa cactgctctg 360
cataagggtca	catatttaca gaatggcaaa ggcaggaagt attttcatca taattctgac 420

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ttctacattc caaaagccac actcaaagac agcggctcct acttctgcag ggggcttgtt 480
 gggagtaaaa atgtgtcttc agagactgtg aacatcacca tcaactcaagg tttggcagtg 540
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 tccctgcgcc cagaggcgtg ccggccagcg gcggggggcg cagtgcacac gagggggctg 120
 gacttcgcct gtgatatcta catctgggcg cccttggccg ggacttgtgg ggtccttctc 180
 ctgtcactgg ttatcacctt ttactgc 207

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 actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120
 gaactg 126

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 cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180
 gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240
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 tacgacgccc ttcacatgca ggccctgccc cctcgctaa 339

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<223> Synthetic Polynucleotide

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<212> PRT

<213> Artificial Sequence

<220>

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<400> 15

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35 40 45Thr Leu Lys Cys Gln Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln
50 55 60Trp Phe His Asn Glu Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe
65 70 75 80Ile Asp Ala Ala Thr Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr
85 90 95Asn Leu Ser Thr Leu Ser Asp Pro Val Gln Leu Glu Val His Ile Gly
100 105 110Trp Leu Leu Leu Gln Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro
115 120 125Ile His Leu Arg Cys His Ser Trp Lys Asn Thr Ala Leu His Lys Val
130 135 140Thr Tyr Leu Gln Asn Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser
145 150 155 160Asp Phe Tyr Ile Pro Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe
165 170 175Cys Arg Gly Leu Phe Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn
180 185 190Ile Thr Ile Thr Gln Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe
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Pro Pro Gly Tyr Gln Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
 210 215 220
 Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
 225 230 235 240
 Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
 245 250 255
 Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
 260 265 270
 Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Lys Arg Gly Arg Lys Lys
 275 280 285
 Leu Leu Tyr Ile Phe Lys Gln Pro Phe Met Arg Pro Val Gln Thr Thr
 290 295 300
 Gln Glu Glu Asp Gly Cys Ser Cys Arg Phe Pro Glu Glu Glu Glu Gly
 305 310 315 320
 Gly Cys Glu Leu Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
 325 330 335
 Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
 340 345 350
 Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
 355 360 365
 Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
 370 375 380
 Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
 385 390 395 400
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 Leu Pro Pro Arg
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<210> 16
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<400> 16

Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
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Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
 20 25 30

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
 35 40 45

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
 50 55 60

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
 65 70 75 80

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
 85 90 95

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
 100 105 110

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
 115 120 125

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
 130 135 140

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Phe
 145 150 155 160

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
 165 170 175

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
 180 185 190

<210> 17

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agggtgctcg agaaggacag tgtgactctg aagtgccagg gagcctactc ccctgaggac 180

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