

SEQUENCE LISTING

<110> RAMOT AT TEL-AVIV UNIVERSITY LTD.  
ICHILOV TECH LTD  
YEDA RESEARCH AND DEVELOPMENT CO. LTD

<120> CHIMERIC ANTIGEN RECEPTORS TO SIALYL-TN GLYCAN ANTIGEN

<130> RAMOT/0102 PCT

<150> 63176894

<151> 2021-04-20

<160> 26

<170> PatentIn version 3.5

<210> 1

<211> 113

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized sequence

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Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln  
1 5 10 15

Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Ile Ser Tyr  
20 25 30

Gly Val Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu  
35 40 45

Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr His Ser Thr Leu Ile  
50 55 60

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

Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Val  
85 90 95

Gly Pro Arg Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser  
100 105 110

Ala

<210> 2  
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<400> 2

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

Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met  
20 25 30

His Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr  
35 40 45

Asp Thr Ser Lys Leu Thr Ser Gly Val Pro Ala Arg Phe Ser Gly Ser  
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu  
65 70 75 80

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Thr Leu Thr  
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
100 105

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<400> 3

Ser Tyr Gly Val Ser  
1 5

<210> 4  
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Val	Ile	Trp	Gly	Asp	Gly	Ser	Thr	Asn	Tyr	His	Ser	Thr	Leu	Ile	Ser
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Pro	Arg	Phe	Ala	Tyr
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Ser	Ala	Ser	Ser	Ser	Val	Ser	Tyr	Met	His
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<400> 7

Asp	Thr	Ser	Lys	Leu	Thr	Ser
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Gln Gln Trp Ser Ser Asn Thr Leu Thr  
1 5

<210> 9  
<211> 5  
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<400> 9

Gly Gly Gly Gly Ser  
1 5

<210> 10  
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<400> 10

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
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<211> 234  
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<400> 11

Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln

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Thr	Cys	Thr	Val
		25	
Ser	Gly	Phe	Ser
			30
Leu	Ile	Ser	Tyr
Gly	Val	Ser	Trp
	35		
Val	Arg	Gln	Pro
		40	
Pro	Gly	Lys	Gly
			45
Leu	Glu	Trp	Leu
Gly	Val	Ile	Trp
	50		
Gly	Asp	Gly	Ser
		55	
Thr	Asn	Tyr	His
			60
Ser	Thr	Leu	Ile
Ser	Arg	Leu	Ser
Ile	Asn	Lys	Asp
	70		
Asn	Ser	Lys	Ser
		75	
Gln	Val	Phe	Leu
			80
Lys	Leu	Asn	Ser
Leu	Gln	Thr	Asp
	85		
Asp	Asp	Thr	Ala
		90	
Thr	Ala	Thr	Tyr
Tyr	Tyr	Cys	Val
		95	
Gly	Pro	Arg	Phe
Ala	Tyr	Trp	Gly
Gln	Gly	Gly	Thr
	100		
Gly	Thr	Leu	Val
Thr	Val	Ser	
Ala	Gly	Gly	Gly
	115		
Ser	Gly	Gly	Gly
		120	
Ser	Gly	Gly	Gly
			125
Gln	Ile	Val	Leu
	130		
Thr	Gln	Ser	Pro
		135	
Ala	Ile	Met	Ser
			140
Ser	Ala	Ser	Pro
Glu	Lys	Val	Thr
Met	Thr	Cys	Ser
	150		
Ala	Ser	Ser	Ser
		155	
Val	Ser	Tyr	Met
			160
His	Trp	Tyr	Gln
Gln	Lys	Ser	Gly
	165		
Thr	Ser	Gly	Thr
		170	
Pro	Lys	Arg	Trp
Ile	Tyr		
			175
Asp	Thr	Ser	Lys
Leu	Thr	Ser	Gly
	180		
Val	Pro	Ala	Arg
Phe	Ser	Gly	Ser
			190
Gly	Ser	Gly	Thr
Ser	Tyr	Ser	Leu
Thr	Ile	Ser	Ser
Met	Glu	Ala	Glu
			205
Asp	Ala	Ala	Thr
Tyr	Tyr	Cys	Gln
		215	
Gln	Gln	Trp	Ser
Ser	Ser	Asn	Thr
Leu	Thr		
			220

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
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<400> 12

Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu  
1 5 10 15

Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro  
20 25 30

Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val  
35 40 45

Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe  
50 55 60

Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp  
65 70 75 80

Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr  
85 90 95

Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser  
100 105 110

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<400> 13

Gln Val Arg Lys Ala Ala Ile Thr Ser Tyr Glu Lys Ser Asp Gly Val  
1 5 10 15

Tyr Thr Gly Leu Ser Thr Arg Asn Gln Glu Thr Tyr Glu Thr Leu Lys  
20 25 30

His Glu Lys Pro Pro Gln  
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<400> 14

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

Val Ile Met Ser Arg Gly  
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<400> 15

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

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

Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly  
35 40 45

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

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Asp Gly Ser Thr Asn  
65 70 75 80

Tyr His Ser Thr Leu Ile Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser  
85 90 95

Lys Ser Gln Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr  
100 105 110

Ala Thr Tyr Tyr Cys Val Gly Pro Arg Phe Ala Tyr Trp Gly Gln Gly  
115 120 125

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly  
130 135 140

Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile  
145 150 155 160

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser  
165 170 175

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser  
180 185 190

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Thr Ser Gly Val Pro  
195 200 205

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
210 215 220

Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
225 230 235 240

Ser Ser Asn Thr Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
245 250 255

Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Gly Ser Gly Gly Gly  
260 265 270

Gly Ser Ala Ala Ala Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp  
275 280 285

Asn Glu Lys Ser Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu



290

295

300

Cys Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu  
305 310 315 320

Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val  
325 330 335

Ala Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His  
340 345 350

Ser Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys  
355 360 365

His Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser  
370 375 380

Gln Val Arg Lys Ala Ala Ile Thr Ser Tyr Glu Lys Ser Asp Gly Val  
385 390 395 400

Tyr Thr Gly Leu Ser Thr Arg Asn Gln Glu Thr Tyr Glu Thr Leu Lys  
405 410 415

His Glu Lys Pro Pro Gln  
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<210> 16

<211> 414

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthesized sequence

<400> 16

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

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

Leu Val Ala Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly  
35 40 45

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

Lys Gly Leu Glu Trp Leu Gly Val Ile Trp Gly Asp Gly Ser Thr Asn  
65 70 75 80

Tyr His Ser Thr Leu Ile Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser  
85 90 95

Lys Ser Gln Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr  
100 105 110

Ala Thr Tyr Tyr Cys Val Gly Pro Arg Phe Ala Tyr Trp Gly Gln Gly  
115 120 125

Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Gly Gly  
130 135 140

Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile  
145 150 155 160

Met Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser  
165 170 175

Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser  
180 185 190

Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Thr Ser Gly Val Pro  
195 200 205

Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
210 215 220

Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp  
225 230 235 240

Ser Ser Asn Thr Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys  
245 250 255

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ala Ala Ala Ile Glu Val



aaactgaaca gtctgcaaac tgatgacaca gccacgtact actgtgtcgg accccggttt 300  
gcttactggg gccaaggac tctggtcact gtctctgca 339

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acctcccca aaagatggat ttatgacaca tccaaactga cttctggagt ccctgctcgc 180  
ttcagtggca gtgggtctgg gacctcttac tctctcacia tcagcagcat ggaggctgaa 240  
gatgctgcca cttattactg ccagcagtgg agtagtaata cgctcacgtt cggtgctggg 300  
accaagctgg agctgaaa 318

<210> 19  
<211> 45  
<212> DNA  
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<400> 19  
ggaggtggcg gtagcggagg cggcggttct ggaggtggcg ggagc 45

<210> 20  
<211> 702  
<212> DNA  
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ccaggaaagg gtctggagtg gctgggagta atatgggggt acgggagcac aaattatcat 180

tcaactctca tatccagact gagcatcaac aaggataact ccaagagcca agttttctta	240
aaactgaaca gtctgcaaac tgatgacaca gccacgtact actgtgtcgg accccgggtt	300
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ctgacttctg gagtccttgc tcgcttcagt ggaggtgggt ctgggacctc ttactctctc	600
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aagccctttt ggggtgctgg ggtggttgg ggagtcctgg cttgctatag cttgctagta	180
acagtggcct ttattatattt ctgggtgagg agtaagagga gcaggctcct gcacagtgc	240
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ccaccacgcg acttcgcagc ctatagatct	330

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agagga 66

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<211> 1269  
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