

SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

<120> PEPTIDES DERIVED FROM CDCA1 AND VACCINES CONTAINING THE SAME

<130> ONC-A1801P

<150> JP 2018-145607

<151> 2018-08-02

<160> 48

<170> PatentIn version 3.5

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<212> PRT

<213> Artificial Sequence

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<223> a peptide derived from CDCA1

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Tyr Met Glu Phe Leu Trp Gln Tyr
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Leu Ser Asp Gly Ile Gln Glu Leu Gln
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Tyr Met Arg Ala Leu Gln Ile Val Tyr
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Met	Met	Pro	Val	Asn	Ser	Glu	Val	Met	Tyr
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<210> 32

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Thr	Ala	Asp	Ile	Leu	Cys	Pro	Lys	Ala	Lys
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Phe	Arg	Glu	Ala	Cys	Arg	Glu	Thr	Tyr
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<210> 39

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<212> DNA

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<223> a PCR primer for the TCR analysis

<400> 43

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<213> Homo sapiens

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180

ctccatcca aggcgcgggc aggtgccggg acgctgggc tggcgggtgtt ttcgtcgtgc

240

tcagcgggtgg gaggaggcgg aagaaaccag agcctgggag attaacagga aacttccaag

300

atg gaa act ttg tct ttc ccc aga tat aat gta gct gag att gtg att

348

Met Glu Thr Leu Ser Phe Pro Arg Tyr Asn Val Ala Glu Ile Val Ile

1

5

10

15

cat att cgc aat aag atc tta aca gga gct gat ggt aaa aac ctc acc

396

His Ile Arg Asn Lys Ile Leu Thr Gly Ala Asp Gly Lys Asn Leu Thr

20

25

30

aag aat gat ctt tat cca aat cca aag cct gaa gtc ttg cac atg atc Lys Asn Asp Leu Tyr Pro Asn Pro Lys Pro Glu Val Leu His Met Ile 35 40 45	444
tac atg aga gcc tta caa ata gta tat gga att cga ctg gaa cat ttt Tyr Met Arg Ala Leu Gln Ile Val Tyr Gly Ile Arg Leu Glu His Phe 50 55 60	492
tac atg atg cca gtg aac tct gaa gtc atg tat cca cat tta atg gaa Tyr Met Met Pro Val Asn Ser Glu Val Met Tyr Pro His Leu Met Glu 65 70 75 80	540
ggc ttc tta cca ttc agc aat tta gtt act cat ctg gac tca ttt ttg Gly Phe Leu Pro Phe Ser Asn Leu Val Thr His Leu Asp Ser Phe Leu 85 90 95	588
cct atc tgc cgg gtg aat gac ttt gag act gct gat att cta tgt cca Pro Ile Cys Arg Val Asn Asp Phe Glu Thr Ala Asp Ile Leu Cys Pro 100 105 110	636
aaa gca aaa cgg aca agt cgg ttt tta agt ggc att atc aac ttt att Lys Ala Lys Arg Thr Ser Arg Phe Leu Ser Gly Ile Ile Asn Phe Ile 115 120 125	684
cac ttc aga gaa gca tgc cgt gaa acg tat atg gaa ttt ctt tgg caa His Phe Arg Glu Ala Cys Arg Glu Thr Tyr Met Glu Phe Leu Trp Gln 130 135 140	732
tat aaa tcc tct gcg gac aaa atg caa cag tta aac gcc gca cac cag Tyr Lys Ser Ser Ala Asp Lys Met Gln Gln Leu Asn Ala Ala His Gln 145 150 155 160	780
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att aaa ctt gga att caa caa cta aaa gat gct gct gaa agg gag aaa Ile Lys Leu Gly Ile Gln Gln Leu Lys Asp Ala Ala Glu Arg Glu Lys 405 410 415	1548
ctg aag tcc cag gaa ata ttt cta aac ttg aaa act gct ttg gag aaa	1596

Leu Lys Ser Gln Glu Ile Phe Leu Asn Leu Lys Thr Ala Leu Glu Lys
 420 425 430
 tac cac gac ggt att gaa aag gca gca gag gac tcc tat gct aag ata 1644
 Tyr His Asp Gly Ile Glu Lys Ala Ala Glu Asp Ser Tyr Ala Lys Ile
 435 440 445
 gat gag aag aca gct gaa ctg aag agg aag atg ttc aaa atg tca acc 1692
 Asp Glu Lys Thr Ala Glu Leu Lys Arg Lys Met Phe Lys Met Ser Thr
 450 455 460
 tga ttaacaaaat tacatgtctt ttgttaaag gcttgccatc ttttaatttt 1745
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His Ile Arg Asn Lys Ile Leu Thr Gly Ala Asp Gly Lys Asn Leu Thr
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Lys Asn Asp Leu Tyr Pro Asn Pro Lys Pro Glu Val Leu His Met Ile
 35 40 45

Tyr Met Arg Ala Leu Gln Ile Val Tyr Gly Ile Arg Leu Glu His Phe
 50 55 60

Tyr Met Met Pro Val Asn Ser Glu Val Met Tyr Pro His Leu Met Glu
 65 70 75 80

Gly Phe Leu Pro Phe Ser Asn Leu Val Thr His Leu Asp Ser Phe Leu
 85 90 95

Pro Ile Cys Arg Val Asn Asp Phe Glu Thr Ala Asp Ile Leu Cys Pro
 100 105 110

Lys Ala Lys Arg Thr Ser Arg Phe Leu Ser Gly Ile Ile Asn Phe Ile
 115 120 125

His Phe Arg Glu Ala Cys Arg Glu Thr Tyr Met Glu Phe Leu Trp Gln
 130 135 140

Tyr Lys Ser Ser Ala Asp Lys Met Gln Gln Leu Asn Ala Ala His Gln
 145 150 155 160

Glu Ala Leu Met Lys Leu Glu Arg Leu Asp Ser Val Pro Val Glu Glu
 165 170 175

Gln Glu Glu Phe Lys Gln Leu Ser Asp Gly Ile Gln Glu Leu Gln Gln
 180 185 190

Ser Leu Asn Gln Asp Phe His Gln Lys Thr Ile Val Leu Gln Glu Gly
 195 200 205

Asn Ser Gln Lys Lys Ser Asn Ile Ser Glu Lys Thr Lys Arg Leu Asn
 210 215 220

Glu Leu Lys Leu Ser Val Val Ser Leu Lys Glu Ile Gln Glu Ser Leu
 225 230 235 240

Lys Thr Lys Ile Val Asp Ser Pro Glu Lys Leu Lys Asn Tyr Lys Glu
 245 250 255

Lys Met Lys Asp Thr Val Gln Lys Leu Lys Asn Ala Arg Gln Glu Val
 260 265 270

Val Glu Lys Tyr Glu Ile Tyr Gly Asp Ser Val Asp Cys Leu Pro Ser
 275 280 285

Cys Gln Leu Glu Val Gln Leu Tyr Gln Lys Lys Ile Gln Asp Leu Ser
 290 295 300

Asp Asn Arg Glu Lys Leu Ala Ser Ile Leu Lys Glu Ser Leu Asn Leu
 305 310 315 320

Glu Asp Gln Ile Glu Ser Asp Glu Ser Glu Leu Lys Lys Leu Lys Thr
 325 330 335

Glu Glu Asn Ser Phe Lys Arg Leu Met Ile Val Lys Lys Glu Lys Leu
 340 345 350

Ala Thr Ala Gln Phe Lys Ile Asn Lys Lys His Glu Asp Val Lys Gln
 355 360 365

Tyr Lys Arg Thr Val Ile Glu Asp Cys Asn Lys Val Gln Glu Lys Arg
 370 375 380

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

Ile Lys Leu Gly Ile Gln Gln Leu Lys Asp Ala Ala Glu Arg Glu Lys
 405 410 415

Leu Lys Ser Gln Glu Ile Phe Leu Asn Leu Lys Thr Ala Leu Glu Lys
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Tyr His Asp Gly Ile Glu Lys Ala Ala Glu Asp Ser Tyr Ala Lys Ile
 435 440 445

Asp Glu Lys Thr Ala Glu Leu Lys Arg Lys Met Phe Lys Met Ser Thr
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$\langle 212 \rangle$	DNA
$\langle 213 \rangle$	Homo sapiens

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atg caa cag tta aac gcc gca cac cag gag gca tta atg aaa ctg gag				655
Met Gln Gln Leu Asn Ala Ala His Gln Glu Ala Leu Met Lys Leu Glu				
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Arg Leu Asp Ser Val Pro Val Glu Glu Gln Glu Glu Phe Lys Gln Leu				
	170	175	180	
tca gat gga att cag gag cta caa caa tca cta aat cag gat ttt cat				751
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Pro Glu Lys Leu Lys Asn Tyr Lys Glu Lys Met Lys Asp Thr Val Gln				
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Lys Leu Lys Asn Ala Arg Gln Glu Val Val Glu Lys Tyr Glu Ile Tyr				
	265	270	275	
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Ser Ile Leu Lys Glu Ser Leu Asn Leu Glu Asp Gln Ile Glu Ser Asp				
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<211> 464
 <212> PRT
 <213> Homo sapiens

<400> 47

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

Tyr Met Arg Ala Leu Gln Ile Val Tyr Gly Ile Arg Leu Glu His Phe
 50 55 60

Tyr Met Met Pro Val Asn Ser Glu Val Met Tyr Pro His Leu Met Glu
 65 70 75 80

Gly Phe Leu Pro Phe Ser Asn Leu Val Thr His Leu Asp Ser Phe Leu
 85 90 95

Pro Ile Cys Arg Val Asn Asp Phe Glu Thr Ala Asp Ile Leu Cys Pro
 100 105 110

Lys Ala Lys Arg Thr Ser Arg Phe Leu Ser Gly Ile Ile Asn Phe Ile
 115 120 125

His Phe Arg Glu Ala Cys Arg Glu Thr Tyr Met Glu Phe Leu Trp Gln
 130 135 140

Tyr Lys Ser Ser Ala Asp Lys Met Gln Gln Leu Asn Ala Ala His Gln
 145 150 155 160

Glu Ala Leu Met Lys Leu Glu Arg Leu Asp Ser Val Pro Val Glu Glu
 165 170 175

Gln Glu Glu Phe Lys Gln Leu Ser Asp Gly Ile Gln Glu Leu Gln Gln
 180 185 190

Ser Leu Asn Gln Asp Phe His Gln Lys Thr Ile Val Leu Gln Glu Gly
 195 200 205

Asn Ser Gln Lys Lys Ser Asn Ile Ser Glu Lys Thr Lys Arg Leu Asn
 210 215 220

Glu Leu Lys Leu Ser Val Val Ser Leu Lys Glu Ile Gln Glu Ser Leu
 225 230 235 240

Lys Thr Lys Ile Val Asp Ser Pro Glu Lys Leu Lys Asn Tyr Lys Glu
 245 250 255

Lys Met Lys Asp Thr Val Gln Lys Leu Lys Asn Ala Arg Gln Glu Val
 260 265 270

Val Glu Lys Tyr Glu Ile Tyr Gly Asp Ser Val Asp Cys Leu Pro Ser
 275 280 285

Cys Gln Leu Glu Val Gln Leu Tyr Gln Lys Lys Ile Gln Asp Leu Ser
 290 295 300

Asp Asn Arg Glu Lys Leu Ala Ser Ile Leu Lys Glu Ser Leu Asn Leu
 305 310 315 320

Glu Asp Gln Ile Glu Ser Asp Glu Ser Glu Leu Lys Lys Leu Lys Thr
 325 330 335

Glu Glu Asn Ser Phe Lys Arg Leu Met Ile Val Lys Lys Glu Lys Leu
 340 345 350

Ala Thr Ala Gln Phe Lys Ile Asn Lys Lys His Glu Asp Val Lys Gln
 355 360 365

Tyr Lys Arg Thr Val Ile Glu Asp Cys Asn Lys Val Gln Glu Lys Arg
 370 375 380

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

Ile Lys Leu Gly Ile Gln Gln Leu Lys Asp Ala Ala Glu Arg Glu Lys
 405 410 415

Leu Lys Ser Gln Glu Ile Phe Leu Asn Leu Lys Thr Ala Leu Glu Lys
 420 425 430

Tyr His Asp Gly Ile Glu Lys Ala Ala Glu Asp Ser Tyr Ala Lys Ile
 435 440 445

Asp Glu Lys Thr Ala Glu Leu Lys Arg Lys Met Phe Lys Met Ser Thr
 450 455 460

<210> 48

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> a linker peptide

<400> 48

Asn Lys Arg Lys

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