SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

<120> CDCA1 EPITOPE PEPTIDES AND VACCINES CONTAINING THE SAME

<130> ONC-A0808P

<150> US 61/074,062
<151> 2008-06-19

<150> US 61/197,599
<151> 2008-10-28

<160> 35

<170> PatentIn version 3.4

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

<220>
<223> An artificially synthesized peptide sequence

<400> 1

Leu Tyr Pro Asn Pro Lys Pro Glu Val Leu
1 5 10

<210> 2
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 2

Met Tyr Pro His Leu Met Glu Gly Phe Leu
1 5 10

<210> 3
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 3

Arg Phe Leu Ser Gly Ile Ile Asn Phe Ile
1 5 10

<210> 4
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 4

Lys Thr Glu Glu Asn Ser Phe Lys Arg Leu
1 5 10

<210> 5
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 5

Lys Tyr His Asp Gly Ile Glu Lys Ala Ala
1 5 10

<210> 6
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 6

Lys Gln Leu Ser Asp Gly Ile Gln Glu Leu
1 5 10

<210> 7
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 7

Phe Tyr Met Met Pro Val Asn Ser Glu Val
1 5 10

<210> 8
<211> 10

<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 8

Leu Tyr Gln Lys Lys Ile Gln Asp Leu Ser
1 5 10

<210> 9
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 9

Lys Leu Ala Ser Ile Leu Lys Glu Ser Leu
1 5 10

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

<220>
<223> An artificially synthesized peptide sequence

<400> 10

Lys Ser Ser Ala Asp Lys Met Gln Gln Leu
1 5 10

<210> 11
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 11

Ile Tyr Met Arg Ala Leu Gln Ile Val Tyr
1 5 10

<210> 12
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 12

Asp Gly Ile Gln Glu Leu Gln Gln Ser Leu
1 5 10

<210> 13
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 13

Val Ser Leu Lys Glu Ile Gln Glu Ser Leu
1 5 10

<210> 14
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 14

Ser Phe Pro Arg Tyr Asn Val Ala Glu Ile
1 5 10

<210> 15
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 15

Ile Asn Gln Glu Ile Gln Lys Ile Lys Leu
1 5 10

<210> 16
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 16

Asp Gln Ile Glu Ser Asp Glu Ser Glu Leu
1 5 10

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 17

Asn Leu Val Thr His Leu Asp Ser Phe Leu
1 5 10

<210> 18
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 18

Gln Tyr Lys Arg Thr Val Ile Glu Asp Cys
1 5 10

<210> 19
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 19

Leu Tyr Gln Lys Lys Ile Gln Asp Leu
1 5

<210> 20
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 20

Ile Tyr Gly Asp Ser Val Asp Cys Leu

1 5

<210> 21
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 21

Met Tyr Pro His Leu Met Glu Gly Phe
1 5

<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 22

Arg Tyr Asn Val Ala Glu Ile Val Ile
1 5

<210> 23
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 23

Val Tyr Gly Ile Arg Leu Glu His Phe
1 5

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 24

Ile Phe Leu Asn Leu Lys Thr Ala Leu
1 5

<210> 25
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 25

Arg Phe Leu Ser Gly Ile Ile Asn Phe
1 5

<210> 26
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 26

Gln Tyr Lys Ser Ser Ala Asp Lys Met
1 5

<210> 27
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 27

Lys Ser Gln Glu Ile Phe Leu Asn Leu
1 5

<210> 28
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 28

Asp Phe His Gln Lys Thr Ile Val Leu
1 5

<210> 29
<211> 9
<212> PRT

<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 29

Lys Tyr Glu Ile Tyr Gly Asp Ser Val
1 5

<210> 30
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 30

Lys Tyr His Asp Gly Ile Glu Lys Ala
1 5

<210> 31
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 31

Val Tyr Glu Arg Val Thr Thr Ile Asn
1 5

<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> An artificially synthesized peptide sequence

<400> 32

Gly Ile Gln Glu Leu Gln Gln Ser Leu
1 5

<210> 33
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> An artificially synthesized peptide sequence

<400> 33

Ile Tyr Met Arg Ala Leu Gln Ile Val
1 5

<210> 34
<211> 1980
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (301)..(1695)

<400> 34
gcggaatggg gcgggacttc cagtaggagg cggcaagttt gaaaagtgat gacggttgac 60

gtttgctgat ttttgacttt gcttgtagct gctccccgaa ctcgccgtct tcctgtcggc 120

ggccggcact gtaggtgagc gcgagaggac ggaggaagga agcctgcaga cagacgcctt 180

ctccatccca aggcgcgggc aggtgccggg acgctgggcc tggcggtgtt ttcgtcgtgc 240

tcagcggtgg 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 444
Lys Asn Asp Leu Tyr Pro Asn Pro Lys Pro Glu Val Leu His Met Ile
35 40 45

tac atg aga gcc tta caa ata gta tat gga att cga ctg gaa cat ttt 492
Tyr Met Arg Ala Leu Gln Ile Val Tyr Gly Ile Arg Leu Glu His Phe

```
    50                  55                  60

tac atg atg cca gtg aac tct gaa gtc atg tat cca cat tta atg
gaa      540
Tyr Met Met Pro Val Asn Ser Glu Val Met Tyr Pro His Leu Met
Glu
65                  70                  75                  80

ggc ttc tta cca ttc agc aat tta gtt act cat ctg gac tca ttt
ttg      588
Gly Phe Leu Pro Phe Ser Asn Leu Val Thr His Leu Asp Ser Phe
Leu
                85                  90                  95

cct atc tgc cgg gtg aat gac ttt gag act gct gat att cta tgt
cca      636
Pro Ile Cys Arg Val Asn Asp Phe Glu Thr Ala Asp Ile Leu Cys
Pro
            100                 105                 110

aaa gca aaa cgg aca agt cgg ttt tta agt ggc att atc aac ttt
att      684
Lys Ala Lys Arg Thr Ser Arg Phe Leu Ser Gly Ile Ile Asn Phe
Ile
        115                 120                 125

cac ttc aga gaa gca tgc cgt gaa acg tat atg gaa ttt ctt tgg
caa      732
His Phe Arg Glu Ala Cys Arg Glu Thr Tyr Met Glu Phe Leu Trp
Gln
    130                 135                 140

tat aaa tcc tct gcg gac aaa atg caa cag tta aac gcc gca cac
cag      780
Tyr Lys Ser Ser Ala Asp Lys Met Gln Gln Leu Asn Ala Ala His
Gln
145                 150                 155
160

gag gca tta atg aaa ctg gag aga ctt gat tct gtt cca gtt gaa
gag      828
Glu Ala Leu Met Lys Leu Glu Arg Leu Asp Ser Val Pro Val Glu
Glu
                165                 170                 175

caa gaa gag ttc aag cag ctt tca gat gga att cag gag cta caa
caa      876
Gln Glu Glu Phe Lys Gln Leu Ser Asp Gly Ile Gln Glu Leu Gln
Gln
            180                 185                 190
```

```
tca cta aat cag gat ttt cat caa aaa acg ata gtg ctg caa gag
gga      924
Ser Leu Asn Gln Asp Phe His Gln Lys Thr Ile Val Leu Gln Glu
Gly
        195                 200                 205

aat tcc caa aag aag tca aat att tca gag aaa acc aag cgt ttg
aat      972
Asn Ser Gln Lys Lys Ser Asn Ile Ser Glu Lys Thr Lys Arg Leu
Asn
    210                 215                 220

gaa cta aaa ttg tcg gtg gtt tct ttg aaa gaa ata caa gag agt
ttg     1020
Glu Leu Lys Leu Ser Val Val Ser Leu Lys Glu Ile Gln Glu Ser
Leu
225                 230                 235
240

aaa aca aaa att gtg gat tct cca gag aag tta aag aat tat aaa
gaa     1068
Lys Thr Lys Ile Val Asp Ser Pro Glu Lys Leu Lys Asn Tyr Lys
Glu
                245                 250                 255

aaa atg aaa gat acg gtc cag aag ctt aaa aat gcc aga caa gaa
gtg     1116
Lys Met Lys Asp Thr Val Gln Lys Leu Lys Asn Ala Arg Gln Glu
Val
            260                 265                 270

gtg gag aaa tat gaa atc tat gga gac tca gtt gac tgc ctg cct
tca     1164
Val Glu Lys Tyr Glu Ile Tyr Gly Asp Ser Val Asp Cys Leu Pro
Ser
        275                 280                 285

tgt cag ttg gaa gtg cag tta tat caa aag aaa ata cag gac ctt
tca     1212
Cys Gln Leu Glu Val Gln Leu Tyr Gln Lys Lys Ile Gln Asp Leu
Ser
    290                 295                 300

gat aat agg gaa aaa tta gcc agt atc tta aag gag agc ctg aac
ttg     1260
Asp Asn Arg Glu Lys Leu Ala Ser Ile Leu Lys Glu Ser Leu Asn
Leu
305                 310                 315
320

gag gac caa att gag agt gat gag tca gaa ctg aag aaa ttg aag
act     1308
Glu Asp Gln Ile Glu Ser Asp Glu Ser Glu Leu Lys Lys Leu Lys
```

```
Thr
                325                 330                 335

gaa gaa aat tcg ttc aaa aga ctg atg att gtg aag aag gaa aaa
ctt     1356
Glu Glu Asn Ser Phe Lys Arg Leu Met Ile Val Lys Lys Glu Lys
Leu
            340                 345                 350

gcc aca gca caa ttc aaa ata aat aag aag cat gaa gat gtt aag
caa     1404
Ala Thr Ala Gln Phe Lys Ile Asn Lys Lys His Glu Asp Val Lys
Gln
        355                 360                 365

tac aaa cgc aca gta att gag gat tgc aat aaa gtt caa gaa aaa
aga     1452
Tyr Lys Arg Thr Val Ile Glu Asp Cys Asn Lys Val Gln Glu Lys
Arg
    370                 375                 380

ggt gct gtc tat gaa cga gta acc aca att aat caa gaa atc caa
aaa     1500
Gly Ala Val Tyr Glu Arg Val Thr Thr Ile Asn Gln Glu Ile Gln
Lys
385                 390                 395
400

att aaa ctt gga att caa caa cta aaa gat gct gct gaa agg gag
aaa     1548
Ile Lys Leu Gly Ile Gln Gln Leu Lys Asp Ala Ala Glu Arg Glu
Lys
                405                 410                 415

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 tttgtaaatg gcttgccatc ttttaatttt
1745

ctatttagaa agaaaagttg aagcgaatgg aagtatcaga agtaccaaat
aatgttggct 1805

tcatcagttt ttatacactc tcataagtag ttaataagat gaatttaatg
taggctttta 1865

ttaatttata attaaaataa cttgtgcagc tattcatgtc tctactctgc
cccttgttgt 1925

aaatagtttg agtaaaacaa aactagttac ctttgaaata tatatatttt tttct
1980

<210> 35
<211> 464
<212> PRT
<213> Homo sapiens

<400> 35

Met Glu Thr Leu Ser Phe Pro Arg Tyr Asn Val Ala Glu Ile Val
Ile
1 5 10 15

His Ile Arg Asn Lys Ile Leu Thr Gly Ala Asp Gly Lys Asn Leu
Thr
20 25 30

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