SEQUENCE LISTING

<110> ONCOTHERAPY SCIENCE, INC.

<120> HIG2 AND URLC10 PEPTIDE AND VACCINES COMPRISING THE SAME

<130> ONC-A0815P

<150> US 61/089,972
<151> 2008-08-19

<160> 8

<170> PatentIn version 3.4

<210> 1
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<212> PRT
<213> Artificial

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<223> An artificially synthesized peptide

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Val Leu Asn Leu Tyr Leu Leu Gly Val
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cggctgttcc cccggagggt ccagaggcct ttcagaagga gaaggcagct ctgtttctct 180

gcagaggagt agggtccttt cagcc atg aag cat gtg ttg aac ctc tac ctg 232
Met Lys His Val Leu Asn Leu Tyr Leu
1 5

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tta ggt gtg gta ctg acc cta ctc tcc atc ttc gtt aga gtg atg gag      280
Leu Gly Val Val Leu Thr Leu Leu Ser Ile Phe Val Arg Val Met Glu
10                  15                  20                  25

tcc cta gaa ggc tta cta gag agc cca tcg cct ggg acc tcc tgg acc      328
Ser Leu Glu Gly Leu Leu Glu Ser Pro Ser Pro Gly Thr Ser Trp Thr
                30                  35                  40

acc aga agc caa cta gcc aac aca gag ccc acc aag ggc ctt cca gac      376
Thr Arg Ser Gln Leu Ala Asn Thr Glu Pro Thr Lys Gly Leu Pro Asp
            45                  50                  55

cat cca tcc aga agc atg tga taagacctcc ttccatactg gccatatttt        427
His Pro Ser Arg Ser Met
        60

ggaacactga cctagacatg tccagatggg agtcccattc ctagcagaca agctgagcac   487

cgttgtaacc agagaactat tactaggcct tgaagaacct gtctaactgg atgctcattg   547

cctgggcaag gcctgtttag gccggttgcg gtggctcatg cctgtaatcc tagcactttg   607

ggaggctgag gtgggtggat cacctgaggt caggagttcg agaccagcct cgccaacatg   667

gcgaaacccc atctctacta aaaatacaaa agttagctgg gtgtggtggc agaggcctgt   727

aatcccagtt ccttgggagg ctgaggcggg agaattgctt gaacccgggg acggaggttg   787

cagtgaaccg agatcgcact gctgtaccca gcctgggcca cagtgcaaga ctccatctca   847

aaaaaaaaaa gaaaagaaaa agcctgttta atgcacaggt gtgagtggat tgcttatggc   907

tatgagatag gttgatctcg cccttacccc ggggtctggt gtatgctgtg ctttcctcag   967

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aattatttgg tgttgagcct ctcttccaca agagctcctc catgtttgga tagcagttga  1147

agaggttgtg tgggtgggct gttgggagtg aggatggagt gttcagtgcc catttctcat  1207

tttacatttt aaagtcgttc ctccaacata gtgtgtattg gtctgaaggg ggtggtggga  1267

tgccaaagcc tgctcaagtt atggacattg tggccaccat gtggcttaaa tgatttttc   1327

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Leu Ser Ile Phe Val Arg Val Met Glu Ser Leu Glu Gly Leu Leu Glu
            20                  25                  30
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Ser Pro Ser Pro Gly Thr Ser Trp Thr Thr Arg Ser Gln Leu Ala Asn
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Thr Glu Pro Thr Lys Gly Leu Pro Asp His Pro Ser Arg Ser Met
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acacgcgcct ttcccagggc tcccgcgccc gttcctgcct ggccgccggc cgctccaaca 180

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Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe
145                 150                 155                 160

ctc ctg gaa gag ccc atg ccc ttc ttt tac ctc aag tgt tgt aaa att      769
Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile
                165                 170                 175

cgc tac tgc aat tta gag ggg cca cct atc aac tca tca gtg ttc aaa      817
Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys
            180                 185                 190

gaa tat gct ggg agc atg ggt gag agc tgt ggt ggg ctg tgg ctg gcc      865
Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala
        195                 200                 205

atc ctc ctg ctg ctg gcc tcc att gca gcc ggc ctc agc ctg tct tga      913
Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser
    210                 215                 220

gccacgggac tgccacagac tgagccttcc ggagcatgga ctcgctccag accgttgtca    973

cctgttgcat taaacttgtt ttctgttgat tacctcttgg tttgacttcc cagggtcttg   1033

ggatgggaga gtggggatca ggtgcagttg gctcttaacc ctcaagggtt ctttaactca   1093
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35 40 45

Ala Asp Pro Pro Trp Ala Pro Leu Gly Thr Met Ala Leu Leu Ala Leu
50 55 60

Leu Leu Val Val Ala Leu Pro Arg Val Trp Thr Asp Ala Asn Leu Thr
65 70 75 80

Ala Arg Gln Arg Asp Pro Glu Asp Ser Gln Arg Thr Asp Glu Gly Asp
85 90 95

Asn Arg Val Trp Cys His Val Cys Glu Arg Glu Asn Thr Phe Glu Cys
100 105 110

Gln Asn Pro Arg Arg Cys Lys Trp Thr Glu Pro Tyr Cys Val Ile Ala
115 120 125

Ala Val Lys Ile Phe Pro Arg Phe Phe Met Val Ala Lys Gln Cys Ser
130 135 140

Ala Gly Cys Ala Ala Met Glu Arg Pro Lys Pro Glu Glu Lys Arg Phe
145 150 155 160

Leu Leu Glu Glu Pro Met Pro Phe Phe Tyr Leu Lys Cys Cys Lys Ile
165 170 175

Arg Tyr Cys Asn Leu Glu Gly Pro Pro Ile Asn Ser Ser Val Phe Lys
180 185 190

Glu Tyr Ala Gly Ser Met Gly Glu Ser Cys Gly Gly Leu Trp Leu Ala
195 200 205

Ile Leu Leu Leu Leu Ala Ser Ile Ala Ala Gly Leu Ser Leu Ser
210 215 220

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<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(1098)

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

ctg gcc ctg acc cag acc tgg gcg ggc tct cac tcc atg agg tat ttc 96
Leu Ala Leu Thr Gln Thr Trp Ala Gly Ser His Ser Met Arg Tyr Phe

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            20                  25                  30

tac acc tcc gtg tcc cgg ccc ggc cgc ggg gag ccc cgc ttc atc gca      144
Tyr Thr Ser Val Ser Arg Pro Gly Arg Gly Glu Pro Arg Phe Ile Ala
        35                  40                  45

gtg ggc tac gtg gac gac acg cag ttc gtg cgg ttc gac agc gac gcc      192
Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
    50                  55                  60

gcg agc cag agg atg gag ccg cgg gcg ccg tgg ata gag cag gag ggt      240
Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly
65                  70                  75                  80

ccg gag tat tgg gac ggg gag aca cgg aaa gtg aag gcc cac tca cag      288
Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln
                85                  90                  95

act cac cga gtg gac ctg ggg acc ctg cgc ggc tac tac aac cag agc      336
Thr His Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser
            100                 105                 110

gag gcc ggt tct cac acc gtc cag agg atg tat ggc tgc gac gtg ggg      384
Glu Ala Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly
        115                 120                 125
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        275                 280                 285

ggt ttg ccc aag ccc ctc acc ctg aga tgg gag ccg tct tcc cag ccc      912
Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro
    290                 295                 300

acc atc ccc atc gtg ggc atc att gct ggc ctg gtt ctc ttt gga gct      960
Thr Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Phe Gly Ala
305                 310                 315                 320

gtg atc act gga gct gtg gtc gct gct gtg atg tgg agg agg aag agc     1008
Val Ile Thr Gly Ala Val Val Ala Ala Val Met Trp Arg Arg Lys Ser
                325                 330                 335

tca gat aga aaa gga ggg agc tac tct cag gct gca agc agt gac agt     1056
Ser Asp Arg Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser
            340                 345                 350

gcc cag ggc tct gat gtg tct ctc aca gct tgt aaa gtg tga             1098
Ala Gln Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val
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<213>  Homo sapiens

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

Val Gly Tyr Val Asp Asp Thr Gln Phe Val Arg Phe Asp Ser Asp Ala
    50                  55                  60

Ala Ser Gln Arg Met Glu Pro Arg Ala Pro Trp Ile Glu Gln Glu Gly
65                  70                  75                  80

Pro Glu Tyr Trp Asp Gly Glu Thr Arg Lys Val Lys Ala His Ser Gln
                85                  90                  95

Thr His Arg Val Asp Leu Gly Thr Leu Arg Gly Tyr Tyr Asn Gln Ser
            100                 105                 110

Glu Ala Gly Ser His Thr Val Gln Arg Met Tyr Gly Cys Asp Val Gly
        115                 120                 125

Ser Asp Trp Arg Phe Leu Arg Gly Tyr His Gln Tyr Ala Tyr Asp Gly
    130                 135                 140
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Lys Asp Tyr Ile Ala Leu Lys Glu Asp Leu Arg Ser Trp Thr Ala Ala
145                 150                 155                 160

Asp Met Ala Ala Gln Thr Thr Lys His Lys Trp Glu Ala Ala His Val
                165                 170                 175

Ala Glu Gln Leu Arg Ala Tyr Leu Glu Gly Thr Cys Val Glu Trp Leu
            180                 185                 190

Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg Thr Asp Ala
        195                 200                 205

Pro Lys Thr His Met Thr His His Ala Val Ser Asp His Glu Ala Thr
    210                 215                 220

Leu Arg Cys Trp Ala Leu Ser Phe Tyr Pro Ala Glu Ile Thr Leu Thr
225                 230                 235                 240

Trp Gln Arg Asp Gly Glu Asp Gln Thr Gln Asp Thr Glu Leu Val Glu
                245                 250                 255

Thr Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val
            260                 265                 270

Val Pro Ser Gly Gln Glu Gln Arg Tyr Thr Cys His Val Gln His Glu
        275                 280                 285

Gly Leu Pro Lys Pro Leu Thr Leu Arg Trp Glu Pro Ser Ser Gln Pro
    290                 295                 300

Thr Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Phe Gly Ala
305                 310                 315                 320

Val Ile Thr Gly Ala Val Val Ala Ala Val Met Trp Arg Arg Lys Ser
                325                 330                 335

Ser Asp Arg Lys Gly Gly Ser Tyr Ser Gln Ala Ala Ser Ser Asp Ser
            340                 345                 350

Ala Gln Gly Ser Asp Val Ser Leu Thr Ala Cys Lys Val
        355                 360                 365
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