SEQUENCE LISTING

<110> UTI LIMITED PARTNERSHIP

<120> COMPOSITIONS AND METHODS FOR THE PREVENTION AND TREATMENT OF CANCER

<130> UTI-C-P1356PCT

<140> PCT/EP2011/069931
<141> 2011-11-11

<150> 61/413,330
<151> 2010-11-12

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

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 99

Phe Ile Arg Ala His Thr Pro Tyr Ile
1 5

<210> 100
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 100
Ser Leu Asn Phe Ile Arg Ala His Thr
1 5

<210> 101
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 101
Leu Lys Met Glu Ser Leu Asn Phe Ile
1 5

<210> 102
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 102
Ser His Phe Leu Lys Met Glu Ser Leu
1 5

<210> 103
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<400> 103
Tyr Leu Phe Leu Gly Ile Leu Ser Val
1 5

<210> 104
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polynucleotide"

<220>
<221> CDS
<222> (1)..(1419)

<400> 104
atg gct atc atc tac ctc atc ctc ctg ttc acc gct gtg cgg ggc gat
48
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp
1 5 10 15

gtt gat gaa caa ctg tcc aag tca gtg aaa gat aag gta ttg ctg cct
96
Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp Lys Val Leu Leu Pro
20 25 30

tgc cgt tac aac tct cct cat gaa gat gag tct gaa gac cga atc tac
144
Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser Glu Asp Arg Ile Tyr
35 40 45

tgg caa aaa cat gac aaa gtg gtg ctg tct gtc att gct ggg aaa cta
192
Trp Gln Lys His Asp Lys Val Val Leu Ser Val Ile Ala Gly Lys Leu
50 55 60

aaa gtg tgg ccc gag tat aag aac cgg act tta tat gac aac act acc
240
Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu Tyr Asp Asn Thr Thr
65 70 75 80

tac tct ctt atc atc ctg ggc ctg gtc ctt tca gac cgg ggc aca tac
288
Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser Asp Arg Gly Thr Tyr
85 90 95

agc tgt gtc gtt caa aag aag gaa aga gga acg tat gaa gtt aaa cac
336
Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr Tyr Glu Val Lys His
100 105 110

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ttg gct tta gta aag ttg tcc atc aaa gct gac ttc tct acc ccc aac
384
Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp Phe Ser Thr Pro Asn
        115                 120                 125

ata act gag tct gga aac cca tct gca gac act aaa agg att acc tgc
432
Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys
    130                 135                 140

ttt gct tcc ggg ggt ttc cca aag cct cgc ttc tct tgg ttg gaa aat
480
Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn
145                 150                 155                 160

gga aga gaa tta cct ggc atc aat acg aca att tcc cag gat cct gaa
528
Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu
                165                 170                 175

tct gaa ttg tac acc att agt agc caa cta gat ttc aat acg act cgc
576
Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg
            180                 185                 190

aac cac acc att aag tgt ctc att aaa tat gga gat gct cac gtg tca
624
Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser
        195                 200                 205

gag gac ttc acc tgg gaa aaa ccc cca gaa gac cct cct gat agc aag
672
Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys
    210                 215                 220

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gcg ggg
720
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225                 230                 235                 240

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg
768
Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
                245                 250                 255

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac
816
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg
864
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac
912
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
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    290                 295                 300

cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc
960
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc
1008
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg
1056
Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
            340                 345                 350

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc
1104
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag
1152
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc
1200
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

gtg ttg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg
1248
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
                405                 410                 415

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg
1296
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct
1344
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

ccg ggt aaa ggt agt ggt agt ggt agt gga tct ctg ggt ggt atc ttc
1392
Pro Gly Lys Gly Ser Gly Ser Gly Ser Gly Ser Leu Gly Gly Ile Phe
    450                 455                 460

gag gct atg aag atg gag ctg cgc gat tga
1422
Glu Ala Met Lys Met Glu Leu Arg Asp
465                 470
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<210> 105
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<400> 105
Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp
1 5 10 15

Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp Lys Val Leu Leu Pro
20 25 30

Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser Glu Asp Arg Ile Tyr
35 40 45

Trp Gln Lys His Asp Lys Val Val Leu Ser Val Ile Ala Gly Lys Leu
50 55 60

Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu Tyr Asp Asn Thr Thr
65 70 75 80

Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser Asp Arg Gly Thr Tyr
85 90 95

Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr Tyr Glu Val Lys His
100 105 110

Leu Ala Leu Val Lys Leu Ser Ile Lys Ala Asp Phe Ser Thr Pro Asn
115 120 125

Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys
130 135 140

Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn
145 150 155 160

Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu
165 170 175

Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg
180 185 190

Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser
195 200 205

Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys
210 215 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly
225 230 235 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
260 265 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
275 280 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
290 295 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305 310 315 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
325 330 335

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
340 345 350

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
355 360 365

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
405 410 415

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met

420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly Lys Gly Ser Gly Ser Gly Ser Gly Ser Leu Gly Gly Ile Phe
450 455 460

Glu Ala Met Lys Met Glu Leu Arg Asp
465 470