SEQUENCE LISTING

<110> The United States of America, as represented by the Secretary, Department of Health and Human Services
Childs, Richard W.
Chinnasamy, Dhanalakshmi
Allan, David S.J.

<120> METHODS OF PRODUCING MODIFIED NATURAL KILLER CELLS AND METHODS OF USE

<130> 4239-96570-02

<150> US 62/366,493
<151> 2016-07-25

<160> 7

<170> PatentIn version 3.5

<210> 1
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<212> DNA
<213> Homo sapiens

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<221> CDS
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Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
1               5                   10                  15

ggc tca ggg gac tat gac tcc atg aag gaa ccc tgt ttc cgt gaa gaa         96
Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
            20                  25                  30

aat gct aat ttc aat aaa atc ttc ctg ccc acc atc tac tcc atc atc        144
Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr Ser Ile Ile
        35                  40                  45

ttc tta act ggc att gtg ggc aat gga ttg gtc atc ctg gtc atg ggt        192
Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
    50                  55                  60

tac cag aag aaa ctg aga agc atg acg gac aag tac agg ctg cac ctg        240
Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
65                  70                  75                  80

tca gtg gcc gac ctc ctc ttt gtc atc acg ctt ccc ttc tgg gca gtt        288
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Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val
                85                  90                  95

gat gcc gtg gca aac tgg tac ttt ggg aac ttc cta tgc aag gca gtc        336
Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val
            100                 105                 110

cat gtc atc tac aca gtc aac ctc tac agc agt gtc ctc atc ctg gcc        384
His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala
        115                 120                 125

ttc atc agt ctg gac cgc tac ctg gcc atc gtc cac gcc acc aac agt        432
Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser
    130                 135                 140

cag agg cca agg aag ctg ttg gct gaa aag gtg gtc tat gtt ggc gtc        480
Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val
145                 150                 155                 160

tgg atc cct gcc ctc ctg ctg act att ccc gac ttc atc ttt gcc aac        528
Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn
                165                 170                 175

gtc agt gag gca gat gac aga tat atc tgt gac cgc ttc tac ccc aat        576
Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn
            180                 185                 190

gac ttg tgg gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt        624
Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
        195                 200                 205

atc ctg cct ggt att gtc atc ctg tcc tgc tat tgc att atc atc tcc        672
Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser
    210                 215                 220

aag ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acc        720
Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
225                 230                 235                 240

aca gtc atc ctc atc ctg gct ttc ttc gcc tgt tgg ctg cct tac tac        768
Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
                245                 250                 255

att ggg atc agc atc gac tcc ttc atc ctc ctg gaa atc atc aag caa        816
Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln
            260                 265                 270

ggg tgt gag ttt gag aac act gtg cac aag tgg att tcc atc acc gag        864
Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
        275                 280                 285

gcc cta gct ttc ttc cac tgt tgt ctg aac ccc atc ctc tat gct ttc        912
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Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
    290                 295                 300

ctt gga gcc aaa ttt aaa acc tct gcc cag cac gca ctc acc tct gtg        960
Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His Ala Leu Thr Ser Val
305                 310                 315                 320

agc aga ggg tcc agc ctc aag atc ctc tcc aaa gga aag cga ggt gga       1008
Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
                325                 330                 335

cat tca tct gtt tcc act gag tct gag tct tca agt ttt cac tcc agc       1056
His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
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taa                                                                   1059
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<213> Homo sapiens

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Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
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Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
            20                  25                  30

Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr Ser Ile Ile
        35                  40                  45

Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
    50                  55                  60

Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
65                  70                  75                  80

Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val
                85                  90                  95

Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val
            100                 105                 110
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His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala
        115                 120                 125

Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser
    130                 135                 140

Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val
145                 150                 155                 160

Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn
                165                 170                 175

Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn
            180                 185                 190

Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
        195                 200                 205

Ile Leu Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser
    210                 215                 220

Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
225                 230                 235                 240

Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
                245                 250                 255

Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln
            260                 265                 270

Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
        275                 280                 285

Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
    290                 295                 300

Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His Ala Leu Thr Ser Val
305                 310                 315                 320
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Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
                325                 330                 335


His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
            340                 345                 350


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<213>  Homo sapiens


<220>
<221>  CDS
<222>  (1)..(951)

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atg ccg cgg ggc tgg acc gcg ctt tgc ttg ctg agt ttg ctg cct tct         48
Met Pro Arg Gly Trp Thr Ala Leu Cys Leu Leu Ser Leu Leu Pro Ser
1               5                   10                  15

ggg ttc atg agt ctt gac aac aac ggt act gct acc cca gag tta cct         96
Gly Phe Met Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro
            20                  25                  30

acc cag gga aca ttt tca aat gtt tct aca aat gta tcc tac caa gaa        144
Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu
        35                  40                  45

act aca aca cct agt acc ctt gga agt acc agc ctg cac cct gtg tct        192
Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser
    50                  55                  60

caa cat ggc aat gag gcc aca aca aac atc aca gaa acg aca gtc aaa        240
Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys
65                  70                  75                  80

ttc aca tct acc tct gtg ata acc tca gtt tat gga aac aca aac tct        288
Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser
                85                  90                  95

tct gtc cag tca cag acc tct gta atc agc aca gtg ttc acc acc cca        336
Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro
            100                 105                 110

gcc aac gtt tca act cca gag aca acc ttg aag cct agc ctg tca cct        384
Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro
        115                 120                 125
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gga aat gtt tca gac ctt tca acc act agc act agc ctt gca aca tct        432
Gly Asn Val Ser Asp Leu Ser Thr Thr Ser Thr Ser Leu Ala Thr Ser
    130                 135                 140

ccc act aaa ccc tat aca tca tct tct cct atc cta agt gac atc aag        480
Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys
145                 150                 155                 160

gca gaa atc aaa tgt tca ggc atc aga gaa gtg aaa ttg act cag ggc        528
Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly
                165                 170                 175

atc tgc ctg gag caa aat aag acc tcc agc tgt gcg gag ttt aag aag        576
Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys
            180                 185                 190

gac agg gga gag ggc ctg gcc cga gtg ctg tgt ggg gag gag cag gct        624
Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala
        195                 200                 205

gat gct gat gct ggg gcc cag gta tgc tcc ctg ctc ctt gcc cag tct        672
Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser
    210                 215                 220

gag gtg agg cct cag tgt cta ctg ctg gtc ttg gcc aac aga aca gaa        720
Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu
225                 230                 235                 240

att tcc agc aaa ctc caa ctt atg aaa aag cac caa tct gac ctg aaa        768
Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys
                245                 250                 255

aag ctg ggg atc cta gat ttc act gag caa gat gtt gca agc cac cag        816
Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln
            260                 265                 270

agc tat tcc caa aag acc ctg att gca ctg gtc acc tcg gga gcc ctg        864
Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu
        275                 280                 285

ctg gct gtc ttg ggc atc act ggc tat ttc ctg atg aat cgc cgc agc        912
Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser
    290                 295                 300

tgg agc ccc aca gga gaa agg ctg gaa cta gaa cca tga                    951
Trp Ser Pro Thr Gly Glu Arg Leu Glu Leu Glu Pro
305                 310                 315
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<210> 4
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<213> Homo sapiens

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Gly Phe Met Ser Leu Asp Asn Asn Gly Thr Ala Thr Pro Glu Leu Pro
            20                  25                  30

Thr Gln Gly Thr Phe Ser Asn Val Ser Thr Asn Val Ser Tyr Gln Glu
        35                  40                  45

Thr Thr Thr Pro Ser Thr Leu Gly Ser Thr Ser Leu His Pro Val Ser
    50                  55                  60

Gln His Gly Asn Glu Ala Thr Thr Asn Ile Thr Glu Thr Thr Val Lys
65                  70                  75                  80

Phe Thr Ser Thr Ser Val Ile Thr Ser Val Tyr Gly Asn Thr Asn Ser
                85                  90                  95

Ser Val Gln Ser Gln Thr Ser Val Ile Ser Thr Val Phe Thr Thr Pro
            100                 105                 110

Ala Asn Val Ser Thr Pro Glu Thr Thr Leu Lys Pro Ser Leu Ser Pro
        115                 120                 125

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

Pro Thr Lys Pro Tyr Thr Ser Ser Ser Pro Ile Leu Ser Asp Ile Lys
145                 150                 155                 160

Ala Glu Ile Lys Cys Ser Gly Ile Arg Glu Val Lys Leu Thr Gln Gly
                165                 170                 175

Ile Cys Leu Glu Gln Asn Lys Thr Ser Ser Cys Ala Glu Phe Lys Lys
            180                 185                 190
```

```
Asp Arg Gly Glu Gly Leu Ala Arg Val Leu Cys Gly Glu Glu Gln Ala
        195                 200                 205

Asp Ala Asp Ala Gly Ala Gln Val Cys Ser Leu Leu Leu Ala Gln Ser
    210                 215                 220

Glu Val Arg Pro Gln Cys Leu Leu Leu Val Leu Ala Asn Arg Thr Glu
225                 230                 235                 240

Ile Ser Ser Lys Leu Gln Leu Met Lys Lys His Gln Ser Asp Leu Lys
                245                 250                 255

Lys Leu Gly Ile Leu Asp Phe Thr Glu Gln Asp Val Ala Ser His Gln
            260                 265                 270

Ser Tyr Ser Gln Lys Thr Leu Ile Ala Leu Val Thr Ser Gly Ala Leu
        275                 280                 285

Leu Ala Val Leu Gly Ile Thr Gly Tyr Phe Leu Met Asn Arg Arg Ser
    290                 295                 300

Trp Ser Pro Thr Gly Glu Arg Leu Glu Leu Glu Pro
305                 310                 315
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1               5                   10                  15

ggc atg cgg act gaa gat ctc cca aag gct gtg gtg ttc ctg gag cct         96
Gly Met Arg Thr Glu Asp Leu Pro Lys Ala Val Val Phe Leu Glu Pro
            20                  25                  30

caa tgg tac agg gtg ctc gag aag gac agt gtg act ctg aag tgc cag        144
```

```
Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
        35                  40                  45

gga gcc tac tcc cct gag gac aat tcc aca cag tgg ttt cac aat gag        192
Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
    50                  55                  60

agc ctc atc tca agc cag gcc tcg agc tac ttc att gac gct gcc aca        240
Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65                  70                  75                  80

gtt gac gac agt gga gag tac agg tgc cag aca aac ctc tcc acc ctc        288
Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
                85                  90                  95

agt gac ccg gtg cag cta gaa gtc cat atc ggc tgg ctg ttg ctc cag        336
Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
            100                 105                 110

gcc cct cgg tgg gtg ttc aag gag gaa gac cct att cac ctg agg tgt        384
Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
        115                 120                 125

cac agc tgg aag aac act gct ctg cat aag gtc aca tat tta cag aat        432
His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
    130                 135                 140

ggc aaa ggc agg aag tat ttt cat cat aat tct gac ttc tac att cca        480
Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145                 150                 155                 160

aaa gcc aca ctc aaa gac agc ggc tcc tac ttc tgc agg ggg ctt gtt        528
Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val
                165                 170                 175

ggg agt aaa aat gtg tct tca gag act gtg aac atc acc atc act caa        576
Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
            180                 185                 190

ggt ttg gca gtg tca acc atc tca tca ttc ttt cca cct ggg tac caa        624
Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
        195                 200                 205

gtc tct ttc tgc ttg gtg atg gta ctc ctt ttt gca gtg gac aca gga        672
Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
    210                 215                 220

cta tat ttc tct gtg aag aca aac att cga agc tca aca aga gac tgg        720
Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225                 230                 235                 240

aag gac cat aaa ttt aaa tgg aga aag gac cct caa gac aaa tga            765
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Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
245 250

<210> 6
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Met Trp Gln Leu Leu Leu Pro Thr Ala Leu Leu Leu Leu Val Ser Ala
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20 25 30

Gln Trp Tyr Arg Val Leu Glu Lys Asp Ser Val Thr Leu Lys Cys Gln
35 40 45

Gly Ala Tyr Ser Pro Glu Asp Asn Ser Thr Gln Trp Phe His Asn Glu
50 55 60

Ser Leu Ile Ser Ser Gln Ala Ser Ser Tyr Phe Ile Asp Ala Ala Thr
65 70 75 80

Val Asp Asp Ser Gly Glu Tyr Arg Cys Gln Thr Asn Leu Ser Thr Leu
85 90 95

Ser Asp Pro Val Gln Leu Glu Val His Ile Gly Trp Leu Leu Leu Gln
100 105 110

Ala Pro Arg Trp Val Phe Lys Glu Glu Asp Pro Ile His Leu Arg Cys
115 120 125

His Ser Trp Lys Asn Thr Ala Leu His Lys Val Thr Tyr Leu Gln Asn
130 135 140

Gly Lys Gly Arg Lys Tyr Phe His His Asn Ser Asp Phe Tyr Ile Pro
145 150 155 160

Lys Ala Thr Leu Lys Asp Ser Gly Ser Tyr Phe Cys Arg Gly Leu Val

165 170 175

Gly Ser Lys Asn Val Ser Ser Glu Thr Val Asn Ile Thr Ile Thr Gln
180 185 190

Gly Leu Ala Val Ser Thr Ile Ser Ser Phe Phe Pro Pro Gly Tyr Gln
195 200 205

Val Ser Phe Cys Leu Val Met Val Leu Leu Phe Ala Val Asp Thr Gly
210 215 220

Leu Tyr Phe Ser Val Lys Thr Asn Ile Arg Ser Ser Thr Arg Asp Trp
225 230 235 240

Lys Asp His Lys Phe Lys Trp Arg Lys Asp Pro Gln Asp Lys
245 250

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<213> Artificial Sequence

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gactctgtga ccctgaagtg ccagggcgcc tattctcctg aggataacag cacacagtgg 180

tttcacaatg agagcctgat cagctcccag gcctctagct acttcatcga cgcagcaacc 240

gtggacgatt ccggagagta tcggtgccag accaacctga gcacactgtc cgatccagtg 300

cagctggagg tgcacatcgg atggctgctg ctgcaggcac ctagatgggt gtttaaggag 360

gaggacccca tccacctgcg ctgtcacagc tggaagaata ccgccctgca caaggtgaca 420

tacctgcaga acggcaaggg caggaagtac ttccaccaca attctgactt ttatatcccc 480

aaggccaccc tgaaggattc cggctcttat ttctgccgcg gcctggtggg cagcaagaac 540

gtgtcctctg agaccgtgaa tatcaccatc acacagggcc tggccgtgtc cacaatcagc 600

tccttctttc cccctggcta ccaggtgtct ttctgtctgg tcatggtgct gctgtttgcc 660

gtggacacag gcctgtattt ctccgtgaag accaacatcc ggtctagcac aagagactgg 720

aaggatcaca agttcaagtg gcggaaggac cctcaggata agtga 765