SL

SEQUENCE LISTING

<110> Eli Lilly and Company

<120> BMP-6 Antibodies

<130> X19829

<150> 61/737,859
<151> 2012-12-17

<160> 17

<170> PatentIn version 3.5

<210> 1
<211> 490
<212> PRT
<213> Homo sapiens

<400> 1

```
Pro Pro Pro Leu Arg Pro Pro Leu Pro Ala Ala Ala Ala Ala Ala Ala
1               5                  10                  15

Gly Gly Gln Leu Leu Gly Asp Gly Gly Ser Pro Gly Arg Thr Glu Gln
            20                  25                  30

Pro Pro Pro Ser Pro Gln Ser Ser Ser Gly Phe Leu Tyr Arg Arg Leu
        35                  40                  45

Lys Thr Gln Glu Lys Arg Glu Met Gln Lys Glu Ile Leu Ser Val Leu
    50                  55                  60

Gly Leu Pro His Arg Pro Arg Pro Leu His Gly Leu Gln Gln Pro Gln
65                  70                  75                  80

Pro Pro Ala Leu Arg Gln Gln Glu Glu Gln Gln Gln Gln Gln Gln Leu
                85                  90                  95

Pro Arg Gly Glu Pro Pro Pro Gly Arg Leu Lys Ser Ala Pro Leu Phe
            100                 105                 110

Met Leu Asp Leu Tyr Asn Ala Leu Ser Ala Asp Asn Asp Glu Asp Gly
        115                 120                 125

Ala Ser Glu Gly Glu Arg Gln Gln Ser Trp Pro His Glu Ala Ala Ser
    130                 135                 140

Ser Ser Gln Arg Arg Gln Pro Pro Pro Gly Ala Ala His Pro Leu Asn
145                 150                 155                 160

Arg Lys Ser Leu Leu Ala Pro Gly Ser Gly Ser Gly Gly Ala Ser Pro
                165                 170                 175

Leu Thr Ser Ala Gln Asp Ser Ala Phe Leu Asn Asp Ala Asp Met Val
            180                 185                 190
```

```
Met Ser Phe Val Asn Leu Val Glu Tyr Asp Lys Glu Phe Ser Pro Arg
        195                 200                 205

Gln Arg His His Lys Glu Phe Lys Phe Asn Leu Ser Gln Ile Pro Glu
    210                 215                 220

Gly Glu Val Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp Cys Val
225                 230                 235                 240

Met Gly Ser Phe Lys Asn Gln Thr Phe Leu Ile Ser Ile Tyr Gln Val
                245                 250                 255

Leu Gln Glu His Gln His Arg Asp Ser Asp Leu Phe Leu Leu Asp Thr
            260                 265                 270

Arg Val Val Trp Ala Ser Glu Glu Gly Trp Leu Glu Phe Asp Ile Thr
        275                 280                 285

Ala Thr Ser Asn Leu Trp Val Val Thr Pro Gln His Asn Met Gly Leu
    290                 295                 300

Gln Leu Ser Val Val Thr Arg Asp Gly Val His Val His Pro Arg Ala
305                 310                 315                 320

Ala Gly Leu Val Gly Arg Asp Gly Pro Tyr Asp Lys Gln Pro Phe Met
                325                 330                 335

Val Ala Phe Phe Lys Val Ser Glu Val His Val Arg Thr Thr Arg Ser
            340                 345                 350

Ala Ser Ser Arg Arg Arg Gln Gln Ser Arg Asn Arg Ser Thr Gln Ser
        355                 360                 365

Gln Asp Val Ala Arg Val Ser Ser Ala Ser Asp Tyr Asn Ser Ser Glu
    370                 375                 380

Leu Lys Thr Ala Cys Arg Lys His Glu Leu Tyr Val Ser Phe Gln Asp
385                 390                 395                 400

Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Lys Gly Tyr Ala Ala Asn
                405                 410                 415

Tyr Cys Asp Gly Glu Cys Ser Phe Pro Leu Asn Ala His Met Asn Ala
            420                 425                 430

Thr Asn His Ala Ile Val Gln Thr Leu Val His Leu Met Asn Pro Glu
        435                 440                 445

Tyr Val Pro Lys Pro Cys Cys Ala Pro Thr Lys Leu Asn Ala Ile Ser
    450                 455                 460
```

Val Leu Tyr Phe Asp Asp Asn Ser Asn Val Ile Leu Lys Lys Tyr Arg
465 470 475 480

Asn Met Val Val Arg Ala Cys Gly Cys His
485 490

<210> 2
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 2

Arg Ser Ser Glu Asn Ile Tyr Arg Asn Leu Ala
1 5 10

<210> 3
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 3

Ala Ala Thr Asn Leu Ala Asp
1 5

<210> 4
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 4

Gln Gly Ile Trp Gly Thr Pro Leu Thr
1 5

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

<220>
<223> Synthetic construct

<400> 5

Gly Tyr Thr Phe Thr Ser Tyr Ala Met His
1 5 10

<210> 6
<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 6

Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Asn Phe Lys
1 5 10 15

Gly

<210> 7
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 7

Tyr Ile Asn Pro Tyr Asn Arg Gly Thr Lys Tyr Asn Glu Asn Phe Lys
1 5 10 15

Gly

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 8

Arg Pro Phe Gly Asn Ala Met Asp Ile
1 5

<210> 9
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 9

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Glu Asn Ile Tyr Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

```
Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Ile Trp Gly Thr Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105
```

<210> 10
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 10

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Asn Phe
    50                  55                  60

Lys Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Arg Pro Phe Gly Asn Ala Met Asp Ile Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 11
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 11

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Arg Gly Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Pro Phe Gly Asn Ala Met Asp Ile Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 12
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 12

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Glu Asn Ile Tyr Arg Asn
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gly Ile Trp Gly Thr Pro Leu
85 90 95

SL

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 13
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 13

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Pro Phe Gly Asn Ala Met Asp Ile Trp Gly Gln Gly Thr
100 105 110

```
Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
        115                 120                 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
    130                 135                 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145                 150                 155                 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

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

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380
```

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 14
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 14

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Asn Pro Tyr Asn Arg Gly Thr Lys Tyr Asn Glu Asn Phe
50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Arg Pro Phe Gly Asn Ala Met Asp Ile Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

```
Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
                165                 170                 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
            180                 185                 190

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

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
    210                 215                 220

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225                 230                 235                 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
                245                 250                 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
            260                 265                 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
        275                 280                 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
    290                 295                 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305                 310                 315                 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
                325                 330                 335

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

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
        355                 360                 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
    370                 375                 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385                 390                 395                 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
                405                 410                 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
            420                 425                 430
```

SL
His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
435 440

<210> 15
<211> 642
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 15
gacatccaga tgacccagtc tccatcctcc ctgtctgcat ctgtaggaga cagagtcacc 60

atcacttgcc gatcttccga aaatatttac cgtaatttag catggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcaacaaact tagcagatgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaaggc atttggggta ctccgctcac tttcggcgga 300

gggaccaagg tggagatcaa acgaactgtg gctgcaccat ctgtcttcat cttcccgcca 360

tctgatgagc agttgaaatc tggaactgcc tctgttgtgt gcctgctgaa taacttctat 420

cccagagagg ccaaagtaca gtggaaggtg gataacgccc tccaatcggg taactcccag 480

gagagtgtca cagagcagga cagcaaggac agcacctaca gcctcagcag caccctgacg 540

ctgagcaaag cagactacga gaaacacaaa gtctacgcct gcgaagtcac ccatcagggc 600

ctgagctcgc ccgtcacaaa gagcttcaac aggggagagt gc 642

<210> 16
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 16
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggata tacattcact agctatgcta tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatat attaatcctt ataatgatgg tactaagtac 180

aatgagaact tcaaaggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaaggccc 300

tttggtaacg ctatggacat ttggggccag ggcaccctgg tcaccgtctc ctcagcctcc 360

accaagggcc catcggtctt cccgctagcg ccctgctcca ggagcacctc cgagagcaca 420

gccgccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacgaa gacctacacc 600

tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agagagttga gtccaaatat 660

ggtcccccat gcccaccctg cccagcacct gaggccgccg ggggaccatc agtcttcctg 720

ttccccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggaa 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctaaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gagcctctcc 1320

ctgtctctgg gt 1332

<210> 17
<211> 1332
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic construct

<400> 17
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctgggtcctc ggtgaaggtc 60

tcctgcaagg cttctggata tacattcact agctatgcta tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatat attaatcctt ataatcgtgg tactaagtac 180

aatgagaact tcaaaggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaaggccc 300

tttggtaacg ctatggacat ttggggccag ggcaccctgg tcaccgtctc ctcagcctcc 360

accaagggcc catcggtctt cccgctagcg ccctgctcca ggagcacctc cgagagcaca 420

gccgccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 480

tcaggcgccc tgaccagcgg cgtgcacacc ttcccggctg tcctacagtc ctcaggactc 540

tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcacgaa gacctacacc 600

tgcaacgtag atcacaagcc cagcaacacc aaggtggaca agagagttga gtccaaatat 660

ggtcccccat gcccaccctg cccagcacct gaggccgccg ggggaccatc agtcttcctg 720

ttccccccaa aacccaagga cactctcatg atctcccgga cccctgaggt cacgtgcgtg 780

gtggtggacg tgagccagga agaccccgag gtccagttca actggtacgt ggatggcgtg 840

gaggtgcata atgccaagac aaagccgcgg gaggagcagt tcaacagcac gtaccgtgtg 900

gtcagcgtcc tcaccgtcct gcaccaggac tggctgaacg gcaaggagta caagtgcaag 960

gtctccaaca aaggcctccc gtcctccatc gagaaaacca tctccaaagc caaagggcag 1020

ccccgagagc cacaggtgta caccctgccc ccatcccagg aggagatgac caagaaccag 1080

gtcagcctga cctgcctggt caaaggcttc taccccagcg acatcgccgt ggagtgggaa 1140

agcaatgggc agccggagaa caactacaag accacgcctc ccgtgctgga ctccgacggc 1200

tccttcttcc tctacagcag gctaaccgtg gacaagagca ggtggcagga ggggaatgtc 1260

ttctcatgct ccgtgatgca tgaggctctg cacaaccact acacacagaa gagcctctcc 1320

ctgtctctgg gt 1332