SEQUENCE LISTING

<110> UNIVERSITETET I TROMSØ - NORGES ARKTISKE UNIVERSITET

<120> Marine DNA Polymerases

<130> 59.15.123840/02

<150> GB1604876.1
<151> 2016-03-22

<160> 17

<170> PatentIn version 3.5

<210> 1
<211> 580
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated PB polymerase

<400> 1

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            20                  25                  30

Thr Ser Glu Leu Leu Gly Ile Ala Leu Ser Asp Gly Glu Lys Gly Tyr
        35                  40                  45

Phe Ala Pro Ala Asp Ile Ala Phe Gln Ser Lys Asp Phe Cys Ser Trp
    50                  55                  60

Leu Glu Asn Ala Thr Asn Lys Lys Tyr Leu Ala Asp Ser Lys Ala Thr
65                  70                  75                  80

Gln Ala Val Ser Arg Lys His Asn Val Asn Val His Gly Val Glu Phe
                85                  90                  95

Asp Leu Leu Leu Ala Ala Tyr Ile Val Asn Pro Ala Ile Ser Ser Glu
            100                 105                 110

Asp Val Ala Ala Ile Ala Lys Glu Phe Gly Tyr Phe Asn Leu Leu Thr
        115                 120                 125

Asn Asp Ser Val Tyr Gly Lys Gly Ala Lys Lys Thr Ala Pro Glu Ile
    130                 135                 140

Glu Lys Ile Ala Glu His Ala Val Arg Lys Ala Arg Ala Ile Trp Asp
145                 150                 155                 160

Leu Lys Glu Lys Leu Glu Val Lys Leu Glu Glu Asn Glu Gln Tyr Ala
                165                 170                 175
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Leu Tyr Lys Glu Ile Glu Leu Pro Leu Ala Ser Ile Leu Gly Thr Met
            180                 185                 190

Glu Ser Asp Gly Val Leu Val Asp Lys Gln Ile Leu Val Glu Met Gly
        195                 200                 205

His Glu Leu Asn Ile Lys Leu Arg Ala Ile Glu Gln Asp Ile Tyr Ala
    210                 215                 220

Leu Ala Gly Glu Thr Phe Asn Ile Asn Ser Pro Lys Gln Leu Gly Val
225                 230                 235                 240

Ile Leu Phe Glu Lys Ile Gly Leu Thr Pro Ile Lys Lys Thr Lys Thr
                245                 250                 255

Gly Tyr Ser Thr Ala Ala Asp Val Leu Glu Lys Leu Ala Ser Glu His
            260                 265                 270

Glu Ile Ile Glu Gln Ile Leu Leu Tyr Arg Gln Leu Gly Lys Leu Asn
        275                 280                 285

Ser Thr Tyr Ile Glu Gly Leu Leu Lys Glu Ile His Glu Asp Asp Gly
    290                 295                 300

Lys Ile His Thr Arg Tyr Gln Gln Ala Leu Thr Ser Thr Gly Arg Leu
305                 310                 315                 320

Ser Ser Ile Asn Pro Asn Leu Gln Asn Ile Pro Val Arg Leu Glu Glu
                325                 330                 335

Gly Arg Lys Ile Arg Lys Ala Phe Val Pro Ser Gln Pro Gly Trp Val
            340                 345                 350

Met Phe Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His
        355                 360                 365

Met Ser Glu Asp Glu Asn Leu Val Glu Ala Phe Asn Asn Asp Leu Asp
    370                 375                 380

Ile His Thr Lys Thr Ala Met Asp Val Phe His Val Glu Gln Glu Ala
385                 390                 395                 400

Val Thr Ser Asp Met Arg Arg Ala Ala Lys Ala Val Asn Phe Gly Ile
                405                 410                 415

Val Tyr Gly Ile Ser Asp Tyr Gly Leu Ser Gln Asn Leu Asp Ile Thr
            420                 425                 430

Arg Lys Glu Ala Ala Thr Phe Ile Glu Asn Tyr Leu Asn Ser Phe Pro
        435                 440                 445
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Gly Val Lys Gly Tyr Met Asp Asp Ile Val Gln Asp Ala Lys Gln Thr
    450                 455                 460

Gly Tyr Val Thr Thr Ile Leu Asn Arg Arg Arg Tyr Leu Pro Glu Ile
465                 470                 475                 480

Thr Ser Ser Asn Phe Asn Leu Arg Ser Phe Ala Glu Arg Thr Ala Met
                485                 490                 495

Asn Thr Pro Ile Gln Gly Ser Ala Ala Asp Ile Ile Lys Lys Ala Met
            500                 505                 510

Ile Asp Met Ala Glu Arg Leu Ile Ser Glu Asn Met Gln Thr Lys Met
        515                 520                 525

Leu Leu Gln Val His Asp Glu Leu Ile Phe Glu Ala Pro Pro Glu Glu
    530                 535                 540

Ile Ala Met Leu Glu Lys Ile Val Pro Glu Val Met Glu Asn Ala Ile
545                 550                 555                 560

Lys Leu Ile Val Pro Leu Lys Val Asp Tyr Ala Phe Gly Ser Ser Trp
                565                 570                 575

Tyr Asp Thr Lys
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<210> 2
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<212> DNA
<213> Artificial Sequence

<220>
<223> Truncated PB polymerase

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ttatcagatg gagaaaaggg ttattttgct cctgctgata tagcttttca atcgaaggat      180

ttttgttctt ggttagaaaa tgctacgaat aaaaagtatt tagcagactc caaagcaaca      240

caagcagtga gtagaaaaca taatgtgaat gtacatggag tggaattcga ccttctttta      300

gcagcgtata tagtaaatcc tgctatctct tcagaggatg ttgctgctat tgctaaagaa      360

tttggatatt ttaacttgct gacaaacgat agtgtttatg ggaaaggtgc caaaaaaacc      420

gcacctgaaa tcgagaaaat tgcagaacat gccgtaagaa aagcaagggc tatttgggac      480

ttgaaagaaa agttagaagt aaaactggaa gaaaatgaac aatatgcgtt gtataaagaa      540

atagagctac cgcttgcatc tatccttggt acgatggaat cagatggggt gctggtggat      600

aaacaaattc ttgtagaaat gggtcatgag cttaatatta agttacgagc gattgaacaa      660
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atactatttg aaaaaattgg tcttacccct attaaaaaga caaaaacggg ctattcaact 780

gcagcagatg ttttggaaaa actagcaagt gaacatgaaa taatagagca aattttacta 840

tatcgtcaat taggtaaact caattccaca tatatcgaag gattattaaa agagattcat 900

gaagatgatg ggaagatcca tacccgatat caacaagccc taacttcaac tgggcgtttg 960

agttcgatca atccaaacct tcaaaatata ccagttcgtt tagaagaagg tagaaaaata 1020

cgtaaagcct ttgttccttc acaaccggga tgggtaatgt ttgcggcgga ttactctcaa 1080

attgaattgc gtgttcttgc ccatatgtct gaggatgaaa acctggtaga agcttttaat 1140

aatgatctgg atattcatac taaaacggct atggatgtat tccatgtgga gcaggaagca 1200

gtaacgtccg atatgcgccg tgctgctaag gcagttaact ttgggattgt gtatggtatt 1260

agtgattatg gtttatcaca aaacctagat attactagaa aagaagcggc gacatttatc 1320

gagaattatt taaatagctt cccaggtgta aaaggatata tggatgatat cgttcaagat 1380

gcgaaacaaa caggctacgt tacaacaatt ttgaatagac gaagatattt gcctgaaata 1440

acaagttcta actttaatct ccgcagtttt gcagaacgta ctgctatgaa tacaccaatt 1500

caagggagtg cagccgatat tattaaaaaa gcaatgatcg atatggcgga aagattaata 1560

tcagaaaata tgcagaccaa aatgctacta caagtacatg atgaattaat ttttgaggct 1620

ccaccagagg aaattgcaat gctagaaaaa atagtgccag aggtgatgga aaacgctatt 1680

aaactgattg tacctttgaa agtggattat gcctttggtt catcttggta tgacacgaag 1740

tag 1743

<210> 3
<211> 877
<212> PRT
<213> Psychrobacillus sp.

<400> 3

Met Tyr Leu Ser Thr Glu Lys Ile Leu Leu Leu Asp Gly Asn Ser Leu
1 5 10 15

Ala Tyr Arg Ala Phe Phe Ala Leu Pro Leu Leu Thr Asn Glu His Gly
20 25 30

Ile His Thr Asn Ala Val Tyr Gly Phe Thr Met Met Leu Gln Lys Ile
35 40 45

Met Asp Glu Glu Asn Pro Thr His Met Leu Val Ala Phe Asp Ala Gly
50 55 60

Lys Thr Thr Phe Arg His Ser Thr Phe Gly Asp Tyr Lys Gly Gly Arg
65 70 75 80

Gln Lys Thr Pro Pro Glu Leu Ser Glu Gln Phe Pro Tyr Ile Arg Lys
85 90 95

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Leu Ile Asp Ala Tyr Gly Ile Lys Arg Tyr Glu Leu Glu Met Tyr Glu
            100                 105                 110

Ala Asp Asp Ile Ile Gly Thr Leu Ser Lys Arg Ala Asp Glu Lys Gly
        115                 120                 125

Gln Gln Val Val Ile Val Ser Gly Asp Lys Asp Leu Thr Gln Leu Ala
    130                 135                 140

Thr Asp Lys Thr Thr Val Tyr Ile Thr Arg Lys Gly Ile Thr Asp Ile
145                 150                 155                 160

Glu Lys Tyr Thr Pro Glu His Val Gln Glu Lys Tyr Gly Leu Thr Pro
                165                 170                 175

Leu Gln Ile Ile Asp Met Lys Gly Leu Met Gly Asp Ala Ser Asp Asn
            180                 185                 190

Ile Pro Gly Val Pro Gly Val Gly Glu Lys Thr Ala Ile Lys Leu Leu
        195                 200                 205

Lys Glu His Gly Ser Val Glu Asp Leu Tyr Lys Ala Leu Asp Thr Val
    210                 215                 220

Ser Gly Val Lys Leu Lys Glu Lys Leu Ile Ala Asn Glu Glu Gln Ala
225                 230                 235                 240

Ile Met Ser Lys Ala Leu Ala Thr Ile Glu Thr Ala Ala Pro Ile Gln
                245                 250                 255

Ile Ser Ile Asp Asp Leu Ser Tyr Thr Gly Pro Asn Met Glu Glu Val
            260                 265                 270

Ile Glu Val Trp Lys Glu Leu Ala Phe Lys Thr Leu Leu Glu Lys Ser
        275                 280                 285

Asp Tyr Ile Ser Glu Glu Ser Glu Thr Thr Glu Val Ala Phe Glu Ile
    290                 295                 300

Val Glu Glu Ile Asp Ser Thr Ile Leu Asp Lys Val Met Ser Val His
305                 310                 315                 320

Leu Glu Met Tyr Asp Gly Gln Tyr His Thr Ser Glu Leu Leu Gly Ile
                325                 330                 335

Ala Leu Ser Asp Gly Glu Lys Gly Tyr Phe Ala Pro Ala Asp Ile Ala
            340                 345                 350

Phe Gln Ser Lys Asp Phe Cys Ser Trp Leu Glu Asn Ala Thr Asn Lys
        355                 360                 365
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Lys Tyr Leu Ala Asp Ser Lys Ala Thr Gln Ala Val Ser Arg Lys His
    370                 375                 380

Asn Val Asn Val His Gly Val Glu Phe Asp Leu Leu Leu Ala Ala Tyr
385                 390                 395                 400

Ile Val Asn Pro Ala Ile Ser Ser Glu Asp Val Ala Ala Ile Ala Lys
                405                 410                 415

Glu Phe Gly Tyr Phe Asn Leu Leu Thr Asn Asp Ser Val Tyr Gly Lys
            420                 425                 430

Gly Ala Lys Lys Thr Ala Pro Glu Ile Glu Lys Ile Ala Glu His Ala
        435                 440                 445

Val Arg Lys Ala Arg Ala Ile Trp Asp Leu Lys Glu Lys Leu Glu Val
    450                 455                 460

Lys Leu Glu Glu Asn Glu Gln Tyr Ala Leu Tyr Lys Glu Ile Glu Leu
465                 470                 475                 480

Pro Leu Ala Ser Ile Leu Gly Thr Met Glu Ser Asp Gly Val Leu Val
                485                 490                 495

Asp Lys Gln Ile Leu Val Glu Met Gly His Glu Leu Asn Ile Lys Leu
            500                 505                 510

Arg Ala Ile Glu Gln Asp Ile Tyr Ala Leu Ala Gly Glu Thr Phe Asn
        515                 520                 525

Ile Asn Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Ile Gly
    530                 535                 540

Leu Thr Pro Ile Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Asp
545                 550                 555                 560

Val Leu Glu Lys Leu Ala Ser Glu His Glu Ile Ile Glu Gln Ile Leu
                565                 570                 575

Leu Tyr Arg Gln Leu Gly Lys Leu Asn Ser Thr Tyr Ile Glu Gly Leu
            580                 585                 590

Leu Lys Glu Ile His Glu Asp Asp Gly Lys Ile His Thr Arg Tyr Gln
        595                 600                 605

Gln Ala Leu Thr Ser Thr Gly Arg Leu Ser Ser Ile Asn Pro Asn Leu
    610                 615                 620

Gln Asn Ile Pro Val Arg Leu Glu Glu Gly Arg Lys Ile Arg Lys Ala
625                 630                 635                 640
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Phe Val Pro Ser Gln Pro Gly Trp Val Met Phe Ala Ala Asp Tyr Ser
                645                 650                 655

Gln Ile Glu Leu Arg Val Leu Ala His Met Ser Glu Asp Glu Asn Leu
            660                 665                 670

Val Glu Ala Phe Asn Asn Asp Leu Asp Ile His Thr Lys Thr Ala Met
        675                 680                 685

Asp Val Phe His Val Glu Gln Glu Ala Val Thr Ser Asp Met Arg Arg
    690                 695                 700

Ala Ala Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr
705                 710                 715                 720

Gly Leu Ser Gln Asn Leu Asp Ile Thr Arg Lys Glu Ala Ala Thr Phe
                725                 730                 735

Ile Glu Asn Tyr Leu Asn Ser Phe Pro Gly Val Lys Gly Tyr Met Asp
            740                 745                 750

Asp Ile Val Gln Asp Ala Lys Gln Thr Gly Tyr Val Thr Thr Ile Leu
        755                 760                 765

Asn Arg Arg Arg Tyr Leu Pro Glu Ile Thr Ser Ser Asn Phe Asn Leu
    770                 775                 780

Arg Ser Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser
785                 790                 795                 800

Ala Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Met Ala Glu Arg Leu
                805                 810                 815

Ile Ser Glu Asn Met Gln Thr Lys Met Leu Leu Gln Val His Asp Glu
            820                 825                 830

Leu Ile Phe Glu Ala Pro Pro Glu Glu Ile Ala Met Leu Glu Lys Ile
        835                 840                 845

Val Pro Glu Val Met Glu Asn Ala Ile Lys Leu Ile Val Pro Leu Lys
    850                 855                 860

Val Asp Tyr Ala Phe Gly Ser Ser Trp Tyr Asp Thr Lys
865                 870                 875
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<210> 4
<211> 2634
<212> DNA
<213> Psychrobacillus sp.

<400> 4

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tttacaatga tgctacaaaa aattatggat gaagaaaatc ctactcatat gctcgtggca 180

tttgatgccg ggaaaacgac cttccgtcac tctacttttg gggattataa aggtggaaga 240

caaaaaacac caccagaact atcggaacaa ttcccttata tacgcaagtt aatcgatgct 300

tatggtatta agcgatacga actggaaatg tacgaagcag acgatattat cggtacttta 360

agcaagcgtg cagacgaaaa agggcagcaa gttgtaattg tctcaggtga taaagattta 420

acacaactag ctacagataa aacaactgtg tatatcacaa gaaaaggcat aaccgatatt 480

gaaaaatata cacctgaaca tgtacaagaa aagtatggct taactccatt acagattata 540

gacatgaaag gtttaatggg agatgcttct gataatattc caggagttcc tggtgtcgga 600

gaaaaaacag ctattaagct tttaaaagaa catggttcgg tagaggattt atataaagca 660

cttgatacag ttagtggtgt taaactaaag gaaaaactca tcgccaacga agagcaggca 720

attatgagta aggcattagc tacgattgaa acagctgcac cgatacagat ttctatagac 780

gatctttcat atactggtcc taatatggaa gaagtaattg aagtttggaa ggaactagct 840

tttaaaactc ttcttgagaa atctgactat atttctgagg aatccgaaac tacagaagta 900

gcattcgaga ttgttgaaga aattgactct acaatattag ataaagtaat gtcagtccat 960

ttagaaatgt atgatgggca atatcataca agcgaattat taggtattgc tttatcagat 1020

ggagaaaagg gttattttgc tcctgctgat atagcttttc aatcgaagga tttttgttct 1080

tggttagaaa atgctacgaa taaaaagtat ttagcagact ccaaagcaac acaagcagtg 1140

agtagaaaac ataatgtgaa tgtacatgga gtggaattcg accttctttt agcagcgtat 1200

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tttaacttgc tgacaaacga tagtgtttat gggaaaggtg ccaaaaaaac cgcacctgaa 1320

atcgagaaaa ttgcagaaca tgccgtaaga aaagcaaggg ctatttggga cttgaaagaa 1380

aagttagaag taaaactgga agaaaatgaa caatatgcgt tgtataaaga aatagagcta 1440

ccgcttgcat ctatccttgg tacgatggaa tcagatgggg tgctggtgga taaacaaatt 1500

cttgtagaaa tgggtcatga gcttaatatt aagttacgag cgattgaaca agacatttat 1560

gcgttagctg gtgaaacgtt taatattaat tcacctaaac aattaggtgt aatactattt 1620

gaaaaaattg gtcttacccc tattaaaaag acaaaaacgg gctattcaac tgcagcagat 1680

gttttggaaa aactagcaag tgaacatgaa ataatagagc aaattttact atatcgtcaa 1740

ttaggtaaac tcaattccac atatatcgaa ggattattaa aagagattca tgaagatgat 1800

gggaagatcc atacccgata tcaacaagcc ctaacttcaa ctgggcgttt gagttcgatc 1860

aatccaaacc ttcaaaatat accagttcgt ttagaagaag gtagaaaaat acgtaaagcc 1920

tttgttcctt cacaaccggg atgggtaatg tttgcggcgg attactctca aattgaattg 1980

cgtgttcttg cccatatgtc tgaggatgaa aacctggtag aagcttttaa taatgatctg 2040

gatattcata ctaaaacggc tatggatgta ttccatgtgg agcaggaagc agtaacgtcc 2100

gatatgcgcc gtgctgctaa ggcagttaac tttgggattg tgtatggtat tagtgattat 2160

ggtttatcac aaaacctaga tattactaga aaagaagcgg cgacatttat cgagaattat 2220

ttaaatagct tcccaggtgt aaaaggatat atggatgata tcgttcaaga tgcgaaacaa 2280

acaggctacg ttacaacaat tttgaataga cgaagatatt tgcctgaaat aacaagttct 2340

aactttaatc tccgcagttt tgcagaacgt actgctatga atacaccaat tcaagggagt 2400

gcagccgata ttattaaaaa agcaatgatc gatatggcgg aaagattaat atcagaaaat 2460

atgcagacca aaatgctact acaagtacat gatgaattaa tttttgaggc tccaccagag 2520

gaaattgcaa tgctagaaaa aatagtgcca gaggtgatgg aaaacgctat taaactgatt 2580

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<210> 5
<211> 297
<212> PRT
<213> Artificial Sequence

<220>
<223> Sequence containing a 5'-3' exonuclease functional domain of DNA polymerase I isolated from a Psychrobacillus sp.

<400> 5

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

Ile His Thr Asn Ala Val Tyr Gly Phe Thr Met Met Leu Gln Lys Ile
35 40 45

Met Asp Glu Glu Asn Pro Thr His Met Leu Val Ala Phe Asp Ala Gly
50 55 60

Lys Thr Thr Phe Arg His Ser Thr Phe Gly Asp Tyr Lys Gly Gly Arg
65 70 75 80

Gln Lys Thr Pro Pro Glu Leu Ser Glu Gln Phe Pro Tyr Ile Arg Lys
85 90 95

Leu Ile Asp Ala Tyr Gly Ile Lys Arg Tyr Glu Leu Glu Met Tyr Glu
100 105 110

Ala Asp Asp Ile Ile Gly Thr Leu Ser Lys Arg Ala Asp Glu Lys Gly
115 120 125

Gln Gln Val Val Ile Val Ser Gly Asp Lys Asp Leu Thr Gln Leu Ala
130 135 140

Thr Asp Lys Thr Thr Val Tyr Ile Thr Arg Lys Gly Ile Thr Asp Ile
145 150 155 160

Glu Lys Tyr Thr Pro Glu His Val Gln Glu Lys Tyr Gly Leu Thr Pro
165 170 175

Leu Gln Ile Ile Asp Met Lys Gly Leu Met Gly Asp Ala Ser Asp Asn
180 185 190

Ile Pro Gly Val Pro Gly Val Gly Glu Lys Thr Ala Ile Lys Leu Leu
195 200 205

Lys Glu His Gly Ser Val Glu Asp Leu Tyr Lys Ala Leu Asp Thr Val
210 215 220

Ser Gly Val Lys Leu Lys Glu Lys Leu Ile Ala Asn Glu Glu Gln Ala
225 230 235 240

Ile Met Ser Lys Ala Leu Ala Thr Ile Glu Thr Ala Ala Pro Ile Gln
245 250 255

Ile Ser Ile Asp Asp Leu Ser Tyr Thr Gly Pro Asn Met Glu Glu Val
260 265 270

Ile Glu Val Trp Lys Glu Leu Ala Phe Lys Thr Leu Leu Glu Lys Ser
275 280 285

Asp Tyr Ile Ser Glu Glu Ser Glu Thr
290 295

<210> 6
<211> 605
<212> PRT
<213> Artificial Sequence

<220>
<223> Truncated DNA polymerase of Aliivibrio salmonicida

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20 25 30

Glu Thr Asp Ser Leu Asp Tyr Met Val Ala Asn Leu Ile Gly Leu Ser
35 40 45

Phe Ser Val Glu Glu Gly Glu Ala Ala Tyr Val Pro Val Ala His Asp
50 55 60

Tyr Leu Asp Ala Pro Glu Gln Leu Asp Arg Asp Trp Val Leu Ala Gln
65 70 75 80

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Leu Lys Pro Tyr Leu Glu Asp Glu Thr Lys Ala Lys Val Gly Gln Asn
                85                  90                  95

Leu Lys Tyr Asp Ala Ser Val Leu Ala Arg Tyr Asp Ile Glu Met Lys
            100                 105                 110

Gly Ile Lys Phe Asp Thr Met Leu Glu Ser Tyr Val Tyr Asn Ser Val
        115                 120                 125

Ala Gly Lys His Asn Met Asp Ser Leu Ala Leu Arg Tyr Leu Gln His
    130                 135                 140

Asn Thr Ile Ser Phe Glu Glu Ile Ala Gly Lys Gly Lys Lys Gln Leu
145                 150                 155                 160

Thr Phe Asn Gln Ile Ala Leu Glu Glu Ala Ala Pro Tyr Ala Ala Glu
                165                 170                 175

Asp Ala Asp Ile Thr Leu Arg Leu His Asn Val Leu His Ala Lys Leu
            180                 185                 190

Val Thr Asp Glu Lys Leu Asn Ala Val Phe Thr Asp Ile Glu Leu Pro
        195                 200                 205

Leu Ile Ser Val Leu Ser Arg Met Glu Arg Lys Gly Val Tyr Ile Asp
    210                 215                 220

Asp Met Leu Leu Ser Ala Gln Ser Leu Glu Ile Gly Gln Arg Leu Asp
225                 230                 235                 240

Glu Leu Glu Thr Ala Ser Phe Glu Val Ala Gly Gln Glu Phe Asn Met
                245                 250                 255

Asn Ser Pro Lys Gln Leu Gln Thr Ile Leu Phe Glu Lys Met Glu Leu
            260                 265                 270

Pro Val Ile Lys Lys Thr Pro Ser Gly Ala Ala Ser Thr Asn Glu Glu
        275                 280                 285

Val Leu Gln Glu Leu Ala Leu Glu Tyr Glu Leu Pro Lys Leu Ile Leu
    290                 295                 300

Glu Tyr Arg Gly Leu Ala Lys Leu Lys Ser Thr Tyr Thr Asp Lys Leu
305                 310                 315                 320

Pro Lys Met Ile Asn Pro Ser Thr Gly Arg Val His Thr Ser Tyr His
                325                 330                 335

Gln Ala Val Thr Ala Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu
            340                 345                 350
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Gln Asn Ile Pro Ile Arg Asn Lys Glu Gly Arg Arg Ile Arg Gln Ala
        355                 360                 365

Phe Val Ala Pro His Gly Trp Lys Ile Leu Ala Val Asp Tyr Ser Gln
    370                 375                 380

Ile Glu Leu Arg Ile Met Ala His Leu Ser Gln Asp Arg Ala Leu Leu
385                 390                 395                 400

Glu Ala Phe Ser Ala Gly Lys Asp Ile His Ala Ala Thr Ala Ala Glu
                405                 410                 415

Val Lys Gly Val Ser Ile Glu Glu Val Thr Ser Glu Asp Arg Arg Arg
            420                 425                 430

Ala Lys Ala Ile Asn Phe Gly Leu Ile Tyr Gly Met Ser Ala Phe Gly
        435                 440                 445

Leu Ala Lys Gln Ile Gly Ile Ser Arg Gly Glu Ala Gln Asp Tyr Met
    450                 455                 460

Asn Val Tyr Phe Glu Arg Tyr Pro Gly Val Met Gln Tyr Met Glu Glu
465                 470                 475                 480

Thr Arg Leu Leu Ala Thr Glu Gln Gly Tyr Val Glu Thr Leu Tyr Gly
                485                 490                 495

Arg Arg Leu Tyr Leu Pro Glu Ile Asn Ala Arg Asn Ala Ile Arg Arg
            500                 505                 510

Lys Ala Ala Glu Arg Ala Ala Ile Asn Ala Pro Met Gln Gly Thr Ala
        515                 520                 525

Ala Asp Ile Ile Lys Lys Ala Met Ile Leu Val Asp Asn Trp Ile Glu
    530                 535                 540

Ala Glu Gly Thr Gly Arg Val Asn Leu Leu Met Gln Val His Asp Glu
545                 550                 555                 560

Leu Val Phe Glu Val Lys Glu Asp Glu Leu Glu Ala Ile Thr Lys Gln
                565                 570                 575

Val Thr Ala Leu Met Glu Ala Ala Val Ser Leu Asp Val Pro Leu Ile
            580                 585                 590

Ala Glu Ser Gly Phe Gly Asp Asn Trp Asp Glu Ala His
        595                 600                 605
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<210> 7
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7
caccacagaa gtagcattcg agattgtt 28

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8
ttacttcgtg tcataccaag atgaacc 27

<210> 9
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> molecular beacon template

<220>
<221> misc_feature
<222> (7)..(7)
<223> labeled with the fluorophore Dabcyl

<220>
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<222> (32)..(32)
<223> labeled with the fluorophore FAM

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gtcgtcagaa atttcgcacc ac 82

<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
gtggtgcgaa atttctgac 19

<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Cold primer

<400> 11

tatccaccaa tactaccct 19

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (20)..(20)
<223> labeled with TAMRA fluorophore at 3' end

<400> 12
cgatactttg tccactcaat 20

<210> 13
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Template strand

<220>
<221> misc_feature
<222> (1)..(1)
<223> labeled at 5' end with the Black Hole Quencher 2

<400> 13
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<210> 14
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Template strand

<400> 14
attgagtgga gatagtatcg tagggtagta ttggtggata 40

<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

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<223> labeled at 5' end with the fluorophore FAM

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<220>
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<223> labeled at 5-end with the fluorophore FAM

<400> 17
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