SEQUENCE LISTING

<110> Oxford Nanopore Technologies Limited

<120> Coupling Method

<130> N.112486C

<150> 61/490,860
<151> 2011-05-27

<150> 61/599,246
<151> 2012-02-15

<160> 41

<170> PatentIn version 3.5

<210> 1
<211> 558
<212> DNA
<213> Artificial sequence

<220>
<223> Mycobacterium smegmatis porin A mutant
(D90N/D91N/D93N/D118R/D134R/E139K)

<400> 1
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caatgggata cctttctgaa tggcgttttt ccgctggatc gtaatcgcct gacccgtgaa 120

tggtttcatt ccggtcgcgc aaaatatatc gtcgcaggcc cgggtgctga cgaattcgaa 180

ggcacgctgg aactgggtta tcagattggc tttccgtggt cactgggcgt tggtatcaac 240

ttctcgtaca ccacgccgaa tattctgatc aacaatggta acattaccgc accgccgttt 300

ggcctgaaca gcgtgattac gccgaacctg tttccgggtg ttagcatctc tgcccgtctg 360

ggcaatggtc cgggcattca agaagtggca acctttagtg tgcgcgtttc cggcgctaaa 420

ggcggtgtcg cggtgtctaa cgcccacggt accgttacgg gcgcggccgg cggtgtcctg 480

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ccgtggaata tgaactaa 558

<210> 2
<211> 184
<212> PRT
<213> Artificial sequence

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(D90N/D91N/D93N/D118R/D134R/E139K)

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Thr Val Gln Gln Trp Asp Thr Phe Leu Asn Gly Val Phe Pro Leu Asp
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Arg Asn Arg Leu Thr Arg Glu Trp Phe His Ser Gly Arg Ala Lys Tyr
        35                  40                  45

Ile Val Ala Gly Pro Gly Ala Asp Glu Phe Glu Gly Thr Leu Glu Leu
    50                  55                  60

Gly Tyr Gln Ile Gly Phe Pro Trp Ser Leu Gly Val Gly Ile Asn Phe
65                  70                  75                  80

Ser Tyr Thr Thr Pro Asn Ile Leu Ile Asn Asn Gly Asn Ile Thr Ala
                85                  90                  95

Pro Pro Phe Gly Leu Asn Ser Val Ile Thr Pro Asn Leu Phe Pro Gly
            100                 105                 110

Val Ser Ile Ser Ala Arg Leu Gly Asn Gly Pro Gly Ile Gln Glu Val
        115                 120                 125

Ala Thr Phe Ser Val Arg Val Ser Gly Ala Lys Gly Gly Val Ala Val
    130                 135                 140

Ser Asn Ala His Gly Thr Val Thr Gly Ala Ala Gly Gly Val Leu Leu
145                 150                 155                 160

Arg Pro Phe Ala Arg Leu Ile Ala Ser Thr Gly Asp Ser Val Thr Thr
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Tyr Gly Glu Pro Trp Asn Met Asn
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<210> 3
<211> 882
<212> DNA
<213> Artificial sequence

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<223> alpha-hemolysin mutant (M111R)

<400> 3

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tatagtttta tcgatgataa aaatcacaat aaaaaactgc tagttattag aacaaaaggt      180

accattgctg gtcaatatag agtttatagc gaagaaggtg ctaacaaaag tggtttagcc      240

tggccttcag cctttaaggt acagttgcaa ctacctgata atgaagtagc tcaaatatct      300

gattactatc caagaaattc gattgataca aaagagtata ggagtacttt aacttatgga      360

ttcaacggta atgttactgg tgatgataca ggaaaaattg gcggccttat tggtgcaaat      420

gtttcgattg gtcatacact gaaatatgtt caacctgatt tcaaaacaat tttagagagc      480

ccaactgata aaaaagtagg ctggaaagtg atatttaaca atatggtgaa tcaaaattgg      540

ggaccatacg atcgagattc ttggaacccg gtatatggca atcaactttt catgaaaact      600
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agaaatggtt ctatgaaagc agcagataac ttccttgatc ctaacaaagc aagttctcta 660

ttatcttcag ggttttcacc agacttcgct acagttatta ctatggatag aaaagcatcc 720

aaacaacaaa caaatataga tgtaatatac gaacgagttc gtgatgatta ccaattgcat 780

tggacttcaa caaattggaa aggtaccaat actaaagata aatggacaga tcgttcttca 840

gaaagatata aaatcgattg ggaaaaagaa gaaatgacaa at 882

<210> 4
<211> 293
<212> PRT
<213> Artificial sequence

<220>
<223> alpha-hemolysin mutant (M111R)

<400> 4

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20 25 30

Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
85 90 95

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

Arg Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
115 120 125

Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140

Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160

Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175

Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
180 185 190

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Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
        195                 200                 205

Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
    210                 215                 220

Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225                 230                 235                 240

Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
                245                 250                 255

Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
            260                 265                 270

Lys Trp Thr Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
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Glu Glu Met Thr Asn
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<210> 5
<211> 1830
<212> DNA
<213> bacteriophage phi AR29

<400> 5

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ggtaacagtc tggatgaatt tatggcatgg gtgctgaaag ttcaggcgga tctgtacttc      180

cacaacctga aatttgatgg cgcattcatt atcaactggc tggaacgtaa tggctttaaa      240

tggagcgcgg atggtctgcc gaacacgtat aataccatta tctctcgtat gggccagtgg      300

tatatgattg atatctgcct gggctacaaa ggtaaacgca aaattcatac cgtgatctat      360

gatagcctga aaaaactgcc gtttccggtg aagaaaattg cgaaagattt caaactgacg      420

gttctgaaag gcgatattga ttatcacaaa gaacgtccgg ttggttacaa aatcaccccg      480

gaagaatacg catacatcaa aaacgatatc cagatcatcg cagaagcgct gctgattcag      540

tttaaacagg gcctggatcg catgaccgcg ggcagtgata gcctgaaagg tttcaaagat      600

atcatcacga ccaaaaaatt caaaaaagtg ttcccgacgc tgagcctggg tctggataaa      660

gaagttcgtt atgcctaccg cggcggtttt acctggctga acgatcgttt caaagaaaaa      720

gaaattggcg agggtatggt gtttgatgtt aatagtctgt atccggcaca gatgtacagc      780

cgcctgctgc cgtatggcga accgatcgtg ttcgagggta aatatgtttg ggatgaagat      840

tacccgctgc atattcagca catccgttgt gaatttgaac tgaaagaagg ctatattccg      900

accattcaga tcaaacgtag tcgcttctat aagggtaacg aatacctgaa aagctctggc      960
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gatctgtaca acgttgaata catcagcggc ctgaaattta aagccacgac cggtctgttc 1080

aaagatttca tcgataaatg gacctacatc aaaacgacct ctgaaggcgc gattaaacag 1140

ctggccaaac tgatgctgaa cagcctgtat ggcaaattcg cctctaatcc ggatgtgacc 1200

ggtaaagttc cgtacctgaa agaaaatggc gcactgggtt ttcgcctggg cgaagaagaa 1260

acgaaagatc cggtgtatac cccgatgggt gttttcatta cggcctgggc acgttacacg 1320

accatcaccg cggcccaggc atgctatgat cgcattatct actgtgatac cgattctatt 1380

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gttccgggcg gtgtggttct ggtggatgat acgtttacca ttaaatctgg cggtagtgcg 1740

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tggagccacc cgcagtttga aaaataataa 1830

<210> 6
<211> 608
<212> PRT
<213> bacteriophage phi AR29

<400> 6

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Thr Lys Val Glu Asp Cys Arg Val Trp Ala Tyr Gly Tyr Met Asn Ile
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Glu Asp His Ser Glu Tyr Lys Ile Gly Asn Ser Leu Asp Glu Phe Met
35 40 45

Ala Trp Val Leu Lys Val Gln Ala Asp Leu Tyr Phe His Asn Leu Lys
50 55 60

Phe Asp Gly Ala Phe Ile Ile Asn Trp Leu Glu Arg Asn Gly Phe Lys
65 70 75 80

Trp Ser Ala Asp Gly Leu Pro Asn Thr Tyr Asn Thr Ile Ile Ser Arg
85 90 95

Met Gly Gln Trp Tyr Met Ile Asp Ile Cys Leu Gly Tyr Lys Gly Lys
100 105 110

Arg Lys Ile His Thr Val Ile Tyr Asp Ser Leu Lys Lys Leu Pro Phe
115 120 125

```
Pro Val Lys Lys Ile Ala Lys Asp Phe Lys Leu Thr Val Leu Lys Gly
    130                 135                 140

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

Glu Glu Tyr Ala Tyr Ile Lys Asn Asp Ile Gln Ile Ile Ala Glu Ala
                165                 170                 175

Leu Leu Ile Gln Phe Lys Gln Gly Leu Asp Arg Met Thr Ala Gly Ser
            180                 185                 190

Asp Ser Leu Lys Gly Phe Lys Asp Ile Ile Thr Thr Lys Lys Phe Lys
        195                 200                 205

Lys Val Phe Pro Thr Leu Ser Leu Gly Leu Asp Lys Glu Val Arg Tyr
    210                 215                 220

Ala Tyr Arg Gly Gly Phe Thr Trp Leu Asn Asp Arg Phe Lys Glu Lys
225                 230                 235                 240

Glu Ile Gly Glu Gly Met Val Phe Asp Val Asn Ser Leu Tyr Pro Ala
                245                 250                 255

Gln Met Tyr Ser Arg Leu Leu Pro Tyr Gly Glu Pro Ile Val Phe Glu
            260                 265                 270

Gly Lys Tyr Val Trp Asp Glu Asp Tyr Pro Leu His Ile Gln His Ile
        275                 280                 285

Arg Cys Glu Phe Glu Leu Lys Glu Gly Tyr Ile Pro Thr Ile Gln Ile
    290                 295                 300

Lys Arg Ser Arg Phe Tyr Lys Gly Asn Glu Tyr Leu Lys Ser Ser Gly
305                 310                 315                 320

Gly Glu Ile Ala Asp Leu Trp Leu Ser Asn Val Asp Leu Glu Leu Met
                325                 330                 335

Lys Glu His Tyr Asp Leu Tyr Asn Val Glu Tyr Ile Ser Gly Leu Lys
            340                 345                 350

Phe Lys Ala Thr Thr Gly Leu Phe Lys Asp Phe Ile Asp Lys Trp Thr
        355                 360                 365

Tyr Ile Lys Thr Thr Ser Glu Gly Ala Ile Lys Gln Leu Ala Lys Leu
    370                 375                 380

Met Leu Asn Ser Leu Tyr Gly Lys Phe Ala Ser Asn Pro Asp Val Thr
385                 390                 395                 400
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Gly Lys Val Pro Tyr Leu Lys Glu Asn Gly Ala Leu Gly Phe Arg Leu
                405                 410                 415

Gly Glu Glu Glu Thr Lys Asp Pro Val Tyr Thr Pro Met Gly Val Phe
            420                 425                 430

Ile Thr Ala Trp Ala Arg Tyr Thr Thr Ile Thr Ala Ala Gln Ala Cys
        435                 440                 445

Tyr Asp Arg Ile Ile Tyr Cys Asp Thr Asp Ser Ile His Leu Thr Gly
    450                 455                 460

Thr Glu Ile Pro Asp Val Ile Lys Asp Ile Val Asp Pro Lys Lys Leu
465                 470                 475                 480

Gly Tyr Trp Ala His Glu Ser Thr Phe Lys Arg Ala Lys Tyr Leu Arg
                485                 490                 495

Gln Lys Thr Tyr Ile Gln Asp Ile Tyr Met Lys Glu Val Asp Gly Lys
            500                 505                 510

Leu Val Glu Gly Ser Pro Asp Asp Tyr Thr Asp Ile Lys Phe Ser Val
        515                 520                 525

Lys Cys Ala Gly Met Thr Asp Lys Ile Lys Lys Glu Val Thr Phe Glu
    530                 535                 540

Asn Phe Lys Val Gly Phe Ser Arg Lys Met Lys Pro Lys Pro Val Gln
545                 550                 555                 560

Val Pro Gly Gly Val Val Leu Val Asp Asp Thr Phe Thr Ile Lys Ser
                565                 570                 575

Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly Ser
            580                 585                 590

Gly Gly Gly Ser Gly Gly Ser Ala Trp Ser His Pro Gln Phe Glu Lys
        595                 600                 605
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<210> 7
<211> 1458
<212> DNA
<213> Escherichia coli

<400> 7

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aatgtgattg gcgaaccgga agtgttttat tgcaaaccgg ccgatgatta tctgccgcag      180

ccgggtgcgg tgctgattac cggtattacc ccgcaggaag cgcgcgcgaa aggtgaaaac      240
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gaagcggcgt ttgccgcgcg cattcatagc ctgtttaccg tgccgaaaac ctgcattctg 300

ggctataaca atgtgcgctt cgatgatgaa gttacccgta atatctttta tcgtaacttt 360

tatgatccgt atgcgtggag ctggcagcat gataacagcc gttgggatct gctggatgtg 420

atgcgcgcgt gctatgcgct gcgcccggaa ggcattaatt ggccggaaaa cgatgatggc 480

ctgccgagct ttcgtctgga acatctgacc aaagccaacg gcattgaaca tagcaatgcc 540

catgatgcga tggccgatgt ttatgcgacc attgcgatgg cgaaactggt taaaacccgt 600

cagccgcgcc tgtttgatta tctgtttacc caccgtaaca aacacaaact gatggcgctg 660

attgatgttc cgcagatgaa accgctggtg catgtgagcg gcatgtttgg cgcctggcgc 720

ggcaacacca gctgggtggc cccgctggcc tggcacccgg aaaatcgtaa cgccgtgatt 780

atggttgatc tggccggtga tattagcccg ctgctggaac tggatagcga taccctgcgt 840

gaacgcctgt ataccgccaa aaccgatctg ggcgataatg ccgccgtgcc ggtgaaactg 900

gttcacatta acaaatgccc ggtgctggcc caggcgaaca ccctgcgccc ggaagatgcg 960

gatcgtctgg gtattaatcg ccagcattgt ctggataatc tgaaaatcct gcgtgaaaac 1020

ccgcaggtgc gtgaaaaagt ggtggcgatc ttcgcggaag cggaaccgtt caccccgagc 1080

gataacgtgg atgcgcagct gtataacggc ttctttagcg atgccgatcg cgcggcgatg 1140

aaaatcgttc tggaaaccga accgcgcaat ctgccggcgc tggatattac ctttgttgat 1200

aaacgtattg aaaaactgct gtttaattat cgtgcgcgca attttccggg taccctggat 1260

tatgccgaac agcagcgttg gctggaacat cgtcgtcagg ttttcacccc ggaatttctg 1320

cagggttatg cggatgaact gcagatgctg gttcagcagt atgccgatga taaagaaaaa 1380

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<211> 485
<212> PRT
<213> Escherichia coli

<400> 8

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20 25 30

Ala Ile Arg Thr Asp Ser Glu Phe Asn Val Ile Gly Glu Pro Glu Val
35 40 45

Phe Tyr Cys Lys Pro Ala Asp Asp Tyr Leu Pro Gln Pro Gly Ala Val
50 55 60

Leu Ile Thr Gly Ile Thr Pro Gln Glu Ala Arg Ala Lys Gly Glu Asn
65 70 75 80

```
Glu Ala Ala Phe Ala Ala Arg Ile His Ser Leu Phe Thr Val Pro Lys
                85                  90                  95

Thr Cys Ile Leu Gly Tyr Asn Asn Val Arg Phe Asp Asp Glu Val Thr
            100                 105                 110

Arg Asn Ile Phe Tyr Arg Asn Phe Tyr Asp Pro Tyr Ala Trp Ser Trp
        115                 120                 125

Gln His Asp Asn Ser Arg Trp Asp Leu Leu Asp Val Met Arg Ala Cys
    130                 135                 140

Tyr Ala Leu Arg Pro Glu Gly Ile Asn Trp Pro Glu Asn Asp Asp Gly
145                 150                 155                 160

Leu Pro Ser Phe Arg Leu Glu His Leu Thr Lys Ala Asn Gly Ile Glu
                165                 170                 175

His Ser Asn Ala His Asp Ala Met Ala Asp Val Tyr Ala Thr Ile Ala
            180                 185                 190

Met Ala Lys Leu Val Lys Thr Arg Gln Pro Arg Leu Phe Asp Tyr Leu
        195                 200                 205

Phe Thr His Arg Asn Lys His Lys Leu Met Ala Leu Ile Asp Val Pro
    210                 215                 220

Gln Met Lys Pro Leu Val His Val Ser Gly Met Phe Gly Ala Trp Arg
225                 230                 235                 240

Gly Asn Thr Ser Trp Val Ala Pro Leu Ala Trp His Pro Glu Asn Arg
                245                 250                 255

Asn Ala Val Ile Met Val Asp Leu Ala Gly Asp Ile Ser Pro Leu Leu
            260                 265                 270

Glu Leu Asp Ser Asp Thr Leu Arg Glu Arg Leu Tyr Thr Ala Lys Thr
        275                 280                 285

Asp Leu Gly Asp Asn Ala Ala Val Pro Val Lys Leu Val His Ile Asn
    290                 295                 300

Lys Cys Pro Val Leu Ala Gln Ala Asn Thr Leu Arg Pro Glu Asp Ala
305                 310                 315                 320

Asp Arg Leu Gly Ile Asn Arg Gln His Cys Leu Asp Asn Leu Lys Ile
                325                 330                 335

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

Asn Gly Phe Phe Ser Asp Ala Asp Arg Ala Ala Met Lys Ile Val Leu
    370                 375                 380

Glu Thr Glu Pro Arg Asn Leu Pro Ala Leu Asp Ile Thr Phe Val Asp
385                 390                 395                 400

Lys Arg Ile Glu Lys Leu Leu Phe Asn Tyr Arg Ala Arg Asn Phe Pro
                405                 410                 415

Gly Thr Leu Asp Tyr Ala Glu Gln Gln Arg Trp Leu Glu His Arg Arg
            420                 425                 430

Gln Val Phe Thr Pro Glu Phe Leu Gln Gly Tyr Ala Asp Glu Leu Gln
        435                 440                 445

Met Leu Val Gln Gln Tyr Ala Asp Asp Lys Glu Lys Val Ala Leu Leu
    450                 455                 460

Lys Ala Leu Trp Gln Tyr Ala Glu Glu Ile Val Ser Gly Ser Gly His
465                 470                 475                 480

His His His His His
                485
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<210> 9
<211> 804
<212> DNA
<213> Escherichia coli

<400> 9

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atgtttccgc tggaagaagt ggcgaaactg ggctataacg tgttttatca tggccagaaa      180

ggtcattatg gcgtggccct gctgaccaaa gaaaccccga tcgcggttcg tcgtggtttt      240

ccgggtgatg atgaagaagc gcagcgtcgt attattatgg cggaaattcc gagcctgctg      300

ggcaatgtga ccgttattaa cggctatttt ccgcagggcg aaagccgtga tcatccgatt      360

aaatttccgg ccaaagcgca gttctatcag aacctgcaga actatctgga aaccgaactg      420

aaacgtgata atccggtgct gatcatgggc gatatgaaca ttagcccgac cgatctggat      480

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catgcgaacc cgcagaccgc cgatcgcttt agctggtttg attatcgcag caaaggtttt      660

gatgataacc gtggcctgcg cattgatctg ctgctggcga gccagccgct ggcggaatgc      720
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ccggtgtggg cgacctttcg ccgc 804

<210> 10
<211> 268
<212> PRT
<213> Escherichia coli

<400> 10

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Gln Leu Glu Ala Ile Val Glu Lys His Gln Pro Asp Val Ile Gly Leu
20 25 30

Gln Glu Thr Lys Val His Asp Asp Met Phe Pro Leu Glu Glu Val Ala
35 40 45

Lys Leu Gly Tyr Asn Val Phe Tyr His Gly Gln Lys Gly His Tyr Gly
50 55 60

Val Ala Leu Leu Thr Lys Glu Thr Pro Ile Ala Val Arg Arg Gly Phe
65 70 75 80

Pro Gly Asp Asp Glu Glu Ala Gln Arg Arg Ile Ile Met Ala Glu Ile
85 90 95

Pro Ser Leu Leu Gly Asn Val Thr Val Ile Asn Gly Tyr Phe Pro Gln
100 105 110

Gly Glu Ser Arg Asp His Pro Ile Lys Phe Pro Ala Lys Ala Gln Phe
115 120 125

Tyr Gln Asn Leu Gln Asn Tyr Leu Glu Thr Glu Leu Lys Arg Asp Asn
130 135 140

Pro Val Leu Ile Met Gly Asp Met Asn Ile Ser Pro Thr Asp Leu Asp
145 150 155 160

Ile Gly Ile Gly Glu Glu Asn Arg Lys Arg Trp Leu Arg Thr Gly Lys
165 170 175

Cys Ser Phe Leu Pro Glu Glu Arg Glu Trp Met Asp Arg Leu Met Ser
180 185 190

Trp Gly Leu Val Asp Thr Phe Arg His Ala Asn Pro Gln Thr Ala Asp
195 200 205

Arg Phe Ser Trp Phe Asp Tyr Arg Ser Lys Gly Phe Asp Asp Asn Arg
210 215 220

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

Cys Val Glu Thr Gly Ile Asp Tyr Glu Ile Arg Ser Met Glu Lys Pro
245 250 255

Ser Asp His Ala Pro Val Trp Ala Thr Phe Arg Arg
260 265

<210> 11
<211> 2000
<212> DNA
<213> Thermus thermophilus

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gcagctgcgc tgctggaaga agccctgcgt cagggtaaac gtattcgcgt tcatggcgat 240

tatgacgccg atggcctgac cggtaccgca attctggtcc gtggtctggc ggcactgggt 300

gccgatgtgc atccgtttat tccgcaccgc ctggaagaag gctacggtgt gctgatggaa 360

cgtgttccgg aacacctgga agcgagcgac ctgttcctga cggtggattg cggtatcacc 420

aaccatgccg aactgcgtga actgctggaa aatggcgttg aagtcattgt gaccgatcat 480

cacaccccgg gtaaaacccc gtctccgggc ctggtggttc acccggcgct gacgccggat 540

ctgaaagaaa aaccgaccgg cgctggtgtc gtgtttctgc tgctgtgggc actgcacgaa 600

cgtctgggtc tgccgccgcc gctggaatat gccgacctgg ctgccgttgg taccattgcc 660

gatgttgccc cgctgtgggg ttggaaccgt gcactggtga aagaaggcct ggcacgtatt 720

ccggctagct cttgggttgg tctgcgtctg ctggccgaag cagtcggcta caccggtaaa 780

gcggttgaag tcgccttccg tattgcaccg cgcatcaacg ccgcatcacg cctgggtgaa 840

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ggcgaactgc accgcctgaa tgctcgtcgc cagaccctgg aagaagcgat gctgcgtaaa 960

ctgctgccgc aagcggaccc ggaagccaaa gcaatcgtgc tgctggatcc ggaaggccat 1020

ccgggtgtta tgggcattgt cgcttcacgc atcctggaag cgacgctgcg tccggtcttt 1080

ctggtggcgc agggtaaagg taccgtgcgc agcctggcac cgatttctgc cgttgaagcc 1140

ctgcgtagcg ccgaagacct gctgctgcgt tatggcggtc acaaagaagc cgcaggcttt 1200

gctatggatg aagcgctgtt tccggcattc aaagctcgcg ttgaagccta cgctgcccgt 1260

ttcccggacc cggttcgtga agtcgcactg ctggatctgc tgccggaacc gggtctgctg 1320

ccgcaggtgt ttcgtgaact ggcgctgctg gaaccgtatg gcgaaggtaa tccggaaccg 1380

ctgtttctgc tgtttggtgc accggaagaa gcacgtcgcc tgggtgaagg tcgtcacctg 1440

gcattccgcc tgaaaggtgt gcgtgttctg gcttggaaac agggtgatct ggccctgccg 1500

ccggaagttg aagtggcagg tctgctgtcc gaaaacgcat ggaatggcca tctggcctat 1560

gaagtgcaag cagttgatct gcgtaaaccg gaagcgctgg aaggcggtat tgccccgttt 1620

gcatatccgc tgccgctgct ggaagctctg gcccgtgccc gcctgggcga aggtgtttat 1680

gtcccggaag acaacccgga aggtctggat tacgcacgca aagctggctt ccgtctgctg 1740

ccgccggaag aagcgggtct gtggctgggt ctgccgccgc gcccggtgct gggtcgtcgc 1800

gtggaagttg cactgggccg tgaagcacgt gctcgcctga gtgcaccgcc ggttctgcat 1860

accccggaag ctcgcctgaa agcgctggtg caccgtcgcc tgctgtttgc ctatgaacgt 1920

cgccatccgg gtctgttctc cgaagcgctg ctggcctact gggaagtcaa tcgtgttcag 1980

gaaccggcgg gtagtcctaa 2000

<210> 12
<211> 666
<212> PRT
<213> Thermus thermophilus

<400> 12

Met Arg Asp Arg Val Arg Trp Arg Val Leu Ser Leu Pro Pro Leu Ala
1 5 10 15

Gln Trp Arg Glu Val Met Ala Ala Leu Glu Val Gly Pro Glu Ala Ala
20 25 30

Leu Ala Tyr Trp His Arg Gly Phe Arg Arg Lys Glu Asp Leu Asp Pro
35 40 45

Pro Leu Ala Leu Leu Pro Leu Lys Gly Leu Arg Glu Ala Ala Ala Leu
50 55 60

Leu Glu Glu Ala Leu Arg Gln Gly Lys Arg Ile Arg Val His Gly Asp
65 70 75 80

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

Ala Ala Leu Gly Ala Asp Val His Pro Phe Ile Pro His Arg Leu Glu
100 105 110

Glu Gly Tyr Gly Val Leu Met Glu Arg Val Pro Glu His Leu Glu Ala
115 120 125

Ser Asp Leu Phe Leu Thr Val Asp Cys Gly Ile Thr Asn His Ala Glu
130 135 140

Leu Arg Glu Leu Leu Glu Asn Gly Val Glu Val Ile Val Thr Asp His
145 150 155 160

His Thr Pro Gly Lys Thr Pro Ser Pro Gly Leu Val Val His Pro Ala
165 170 175

```
Leu Thr Pro Asp Leu Lys Glu Lys Pro Thr Gly Ala Gly Val Val Phe
            180                 185                 190

Leu Leu Leu Trp Ala Leu His Glu Arg Leu Gly Leu Pro Pro Pro Leu
        195                 200                 205

Glu Tyr Ala Asp Leu Ala Ala Val Gly Thr Ile Ala Asp Val Ala Pro
    210                 215                 220

Leu Trp Gly Trp Asn Arg Ala Leu Val Lys Glu Gly Leu Ala Arg Ile
225                 230                 235                 240

Pro Ala Ser Ser Trp Val Gly Leu Arg Leu Leu Ala Glu Ala Val Gly
                245                 250                 255

Tyr Thr Gly Lys Ala Val Glu Val Ala Phe Arg Ile Ala Pro Arg Ile
            260                 265                 270

Asn Ala Ala Ser Arg Leu Gly Glu Ala Glu Lys Ala Leu Arg Leu Leu
        275                 280                 285

Leu Thr Asp Asp Ala Ala Glu Ala Gln Ala Leu Val Gly Glu Leu His
    290                 295                 300

Arg Leu Asn Ala Arg Arg Gln Thr Leu Glu Glu Ala Met Leu Arg Lys
305                 310                 315                 320

Leu Leu Pro Gln Ala Asp Pro Glu Ala Lys Ala Ile Val Leu Leu Asp
                325                 330                 335

Pro Glu Gly His Pro Gly Val Met Gly Ile Val Ala Ser Arg Ile Leu
            340                 345                 350

Glu Ala Thr Leu Arg Pro Val Phe Leu Val Ala Gln Gly Lys Gly Thr
        355                 360                 365

Val Arg Ser Leu Ala Pro Ile Ser Ala Val Glu Ala Leu Arg Ser Ala
    370                 375                 380

Glu Asp Leu Leu Leu Arg Tyr Gly Gly His Lys Glu Ala Ala Gly Phe
385                 390                 395                 400

Ala Met Asp Glu Ala Leu Phe Pro Ala Phe Lys Ala Arg Val Glu Ala
                405                 410                 415

Tyr Ala Ala Arg Phe Pro Asp Pro Val Arg Glu Val Ala Leu Leu Asp
            420                 425                 430

Leu Leu Pro Glu Pro Gly Leu Leu Pro Gln Val Phe Arg Glu Leu Ala
        435                 440                 445
```

```
Leu Leu Glu Pro Tyr Gly Glu Gly Asn Pro Glu Pro Leu Phe Leu Leu
    450                 455                 460

Phe Gly Ala Pro Glu Glu Ala Arg Arg Leu Gly Glu Gly Arg His Leu
465                 470                 475                 480

Ala Phe Arg Leu Lys Gly Val Arg Val Leu Ala Trp Lys Gln Gly Asp
                485                 490                 495

Leu Ala Leu Pro Pro Glu Val Glu Val Ala Gly Leu Leu Ser Glu Asn
            500                 505                 510

Ala Trp Asn Gly His Leu Ala Tyr Glu Val Gln Ala Val Asp Leu Arg
        515                 520                 525

Lys Pro Glu Ala Leu Glu Gly Gly Ile Ala Pro Phe Ala Tyr Pro Leu
    530                 535                 540

Pro Leu Leu Glu Ala Leu Ala Arg Ala Arg Leu Gly Glu Gly Val Tyr
545                 550                 555                 560

Val Pro Glu Asp Asn Pro Glu Gly Leu Asp Tyr Ala Arg Lys Ala Gly
                565                 570                 575

Phe Arg Leu Leu Pro Pro Glu Glu Ala Gly Leu Trp Leu Gly Leu Pro
            580                 585                 590

Pro Arg Pro Val Leu Gly Arg Arg Val Glu Val Ala Leu Gly Arg Glu
        595                 600                 605

Ala Arg Ala Arg Leu Ser Ala Pro Pro Val Leu His Thr Pro Glu Ala
    610                 615                 620

Arg Leu Lys Ala Leu Val His Arg Arg Leu Leu Phe Ala Tyr Glu Arg
625                 630                 635                 640

Arg His Pro Gly Leu Phe Ser Glu Ala Leu Leu Ala Tyr Trp Glu Val
                645                 650                 655

Asn Arg Val Gln Glu Pro Ala Gly Ser Pro
            660                 665
```

<210> 13
<211> 681
<212> DNA
<213> Bacteriophage lambda

<400> 13
atgacaccgg acattatcct gcagcgtacc gggatcgatg tgagagctgt cgaacagggg 60

gatgatgcgt ggcacaaatt acggctcggc gtcatcaccg cttcagaagt tcacaacgtg 120

atagcaaaac cccgctccgg aaagaagtgg cctgacatga aaatgtccta cttccacacc 180

ctgcttgctg aggtttgcac cggtgtggct ccggaagtta acgctaaagc actggcctgg 240

ggaaaacagt acgagaacga cgccagaacc ctgtttgaat tcacttccgg cgtgaatgtt 300

actgaatccc cgatcatcta tcgcgacgaa agtatgcgta ccgcctgctc tcccgatggt 360

ttatgcagtg acggcaacgg ccttgaactg aaatgcccgt ttacctcccg ggatttcatg 420

aagttccggc tcggtggttt cgaggccata aagtcagctt acatggccca ggtgcagtac 480

agcatgtggg tgacgcgaaa aaatgcctgg tactttgcca actatgaccc gcgtatgaag 540

cgtgaaggcc tgcattatgt cgtgattgag cgggatgaaa agtacatggc gagttttgac 600

gagatcgtgc cggagttcat cgaaaaaatg gacgaggcac tggctgaaat tggttttgta 660

tttggggagc aatggcgata a 681

<210> 14
<211> 226
<212> PRT
<213> Bacteriophage lambda

<400> 14

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

Val Glu Gln Gly Asp Asp Ala Trp His Lys Leu Arg Leu Gly Val Ile
20 25 30

Thr Ala Ser Glu Val His Asn Val Ile Ala Lys Pro Arg Ser Gly Lys
35 40 45

Lys Trp Pro Asp Met Lys Met Ser Tyr Phe His Thr Leu Leu Ala Glu
50 55 60

Val Cys Thr Gly Val Ala Pro Glu Val Asn Ala Lys Ala Leu Ala Trp
65 70 75 80

Gly Lys Gln Tyr Glu Asn Asp Ala Arg Thr Leu Phe Glu Phe Thr Ser
85 90 95

Gly Val Asn Val Thr Glu Ser Pro Ile Ile Tyr Arg Asp Glu Ser Met
100 105 110

Arg Thr Ala Cys Ser Pro Asp Gly Leu Cys Ser Asp Gly Asn Gly Leu
115 120 125

Glu Leu Lys Cys Pro Phe Thr Ser Arg Asp Phe Met Lys Phe Arg Leu
130 135 140

Gly Gly Phe Glu Ala Ile Lys Ser Ala Tyr Met Ala Gln Val Gln Tyr
145 150 155 160

Ser Met Trp Val Thr Arg Lys Asn Ala Trp Tyr Phe Ala Asn Tyr Asp
165 170 175

Pro Arg Met Lys Arg Glu Gly Leu His Tyr Val Val Ile Glu Arg Asp
180 185 190

Glu Lys Tyr Met Ala Ser Phe Asp Glu Ile Val Pro Glu Phe Ile Glu
195 200 205

Lys Met Asp Glu Ala Leu Ala Glu Ile Gly Phe Val Phe Gly Glu Gln
210 215 220

Trp Arg
225

<210> 15
<211> 184
<212> PRT
<213> Mycobacterium smegmatis

<400> 15

Gly Leu Asp Asn Glu Leu Ser Leu Val Asp Gly Gln Asp Arg Thr Leu
1 5 10 15

Thr Val Gln Gln Trp Asp Thr Phe Leu Asn Gly Val Phe Pro Leu Asp
20 25 30

Arg Asn Arg Leu Thr Arg Glu Trp Phe His Ser Gly Arg Ala Lys Tyr
35 40 45

Ile Val Ala Gly Pro Gly Ala Asp Glu Phe Glu Gly Thr Leu Glu Leu
50 55 60

Gly Tyr Gln Ile Gly Phe Pro Trp Ser Leu Gly Val Gly Ile Asn Phe
65 70 75 80

Ser Tyr Thr Thr Pro Asn Ile Leu Ile Asp Asp Gly Asp Ile Thr Ala
85 90 95

Pro Pro Phe Gly Leu Asn Ser Val Ile Thr Pro Asn Leu Phe Pro Gly
100 105 110

Val Ser Ile Ser Ala Asp Leu Gly Asn Gly Pro Gly Ile Gln Glu Val
115 120 125

Ala Thr Phe Ser Val Asp Val Ser Gly Pro Ala Gly Gly Val Ala Val
130 135 140

Ser Asn Ala His Gly Thr Val Thr Gly Ala Ala Gly Gly Val Leu Leu
145 150 155 160

Arg Pro Phe Ala Arg Leu Ile Ala Ser Thr Gly Asp Ser Val Thr Thr

165 170 175

Tyr Gly Glu Pro Trp Asn Met Asn
180

<210> 16
<211> 184
<212> PRT
<213> Mycobacterium smegmatis

<400> 16

Gly Leu Asp Asn Glu Leu Ser Leu Val Asp Gly Gln Asp Arg Thr Leu
1 5 10 15

Thr Val Gln Gln Trp Asp Thr Phe Leu Asn Gly Val Phe Pro Leu Asp
20 25 30

Arg Asn Arg Leu Thr Arg Glu Trp Phe His Ser Gly Arg Ala Lys Tyr
35 40 45

Ile Val Ala Gly Pro Gly Ala Asp Glu Phe Glu Gly Thr Leu Glu Leu
50 55 60

Gly Tyr Gln Ile Gly Phe Pro Trp Ser Leu Gly Val Gly Ile Asn Phe
65 70 75 80

Ser Tyr Thr Thr Pro Asn Ile Leu Ile Asp Asp Gly Asp Ile Thr Gly
85 90 95

Pro Pro Phe Gly Leu Glu Ser Val Ile Thr Pro Asn Leu Phe Pro Gly
100 105 110

Val Ser Ile Ser Ala Asp Leu Gly Asn Gly Pro Gly Ile Gln Glu Val
115 120 125

Ala Thr Phe Ser Val Asp Val Ser Gly Pro Ala Gly Gly Val Ala Val
130 135 140

Ser Asn Ala His Gly Thr Val Thr Gly Ala Ala Gly Gly Val Leu Leu
145 150 155 160

Arg Pro Phe Ala Arg Leu Ile Ala Ser Thr Gly Asp Ser Val Thr Thr
165 170 175

Tyr Gly Glu Pro Trp Asn Met Asn
180

<210> 17
<211> 183
<212> PRT
<213> Mycobacterium smegmatis

<400> 17

```
Val Asp Asn Gln Leu Ser Val Val Asp Gly Gln Gly Arg Thr Leu Thr
1               5                   10                  15

Val Gln Gln Ala Glu Thr Phe Leu Asn Gly Val Phe Pro Leu Asp Arg
            20                  25                  30

Asn Arg Leu Thr Arg Glu Trp Phe His Ser Gly Arg Ala Thr Tyr His
        35                  40                  45

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

Tyr Gln Val Gly Phe Pro Trp Ser Leu Gly Val Gly Ile Asn Phe Ser
65                  70                  75                  80

Tyr Thr Thr Pro Asn Ile Leu Ile Asp Gly Gly Asp Ile Thr Gln Pro
                85                  90                  95

Pro Phe Gly Leu Asp Thr Ile Ile Thr Pro Asn Leu Phe Pro Gly Val
            100                 105                 110

Ser Ile Ser Ala Asp Leu Gly Asn Gly Pro Gly Ile Gln Glu Val Ala
        115                 120                 125

Thr Phe Ser Val Asp Val Lys Gly Ala Lys Gly Ala Val Ala Val Ser
    130                 135                 140

Asn Ala His Gly Thr Val Thr Gly Ala Ala Gly Gly Val Leu Leu Arg
145                 150                 155                 160

Pro Phe Ala Arg Leu Ile Ala Ser Thr Gly Asp Ser Val Thr Thr Tyr
                165                 170                 175

Gly Glu Pro Trp Asn Met Asn
            180


<210>  18
<211>  70
<212>  DNA
<213>  Artificial sequence

<220>
<223>  Sequence used in the examples

<400>  18
ttttttttt ttttttttt ttttttttt ttttttttt ttttttttt ttttttttt       60

ttttttttt                                                         70


<210>  19
<211>  70
<212>  DNA
<213>  Artificial Sequence
```

<220>
<223> Sequence used in the examples

<400> 19
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60

aaaaaaaaaa 70

<210> 20
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 20
cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc cccccccccc 60

cccccccccc 70

<210> 21
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 21
tgtgttctat gtcttattct tacttcgtta ttcttgtctc tattctgttt atgtttcttg 60

tttgttagca 70

<210> 22
<211> 93
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 22
ttttttttt ttttttttt ttttttttt ttttttttt ttttttttt ttttttttt 60

ttttttttt ggctacgacc tgcatgagaa tgc 93

<210> 23
<211> 79
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 23
ctcacctatc cttccactca ccccccaaaa aacccccccaa aaaacccccc aaaaaagcat 60

tctcatgcag gtcgtagcc 79

<210> 24
<211> 100
<212> DNA

<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 24
aacccccaaa aacccccaaa aacccccaaa aacccccaaa aacccccaaa aacccccaaa 60

aacccccaaa aacccccata gagacaagaa taacgaagta 100

<210> 25
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 25
tacttcgtta ttcttgtctc tat 23

<210> 26
<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 26
ccccccccccc cccccacccc ccccccccccc ccccctattc tgtttatgtt tcttgtttgt 60

tagcc 65

<210> 27
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 27
ggctaacaaa caagaaacat aaacagaata g 31

<210> 28
<211> 65
<212> DNA
<213> Artificial sequence

<220>
<223> Sequence used in the examples

<400> 28
ccccccccccc cccccacccc ccccccccccc ccccctattc tgtttatgtt tcttgtttgt 60

tagcc 65

<210> 29
<211> 81
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<220>
<221> misc_feature
<222> (51)..(54)
<223> n = abasic nucleotide

<400> 29
ttttttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt nnnnggttgt 60

ttctgttggt gctgatattg c   81

<210> 30
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in examples

<400> 30
gttagaccaa accatgaaac caacata   27

<210> 31
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in examples

<400> 31
gaccgcctcc aaacaattta gaca   24

<210> 32
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 32
ggcaatctct ttctgattgt ccag   24

<210> 33
<211> 885
<212> DNA
<213> Artificial sequence

<220>
<223>   sequence for one subunit of alpha-HL-Q

<400> 33
atggcagatt ctgatattaa tattaaaacc ggtactacag atattggaag caatactaca 60

gtaaaaacag gtgatttagt cacttatgat aaagaaaatg gcatgcacaa aaaagtattt 120

tatagtttta tcgatgataa aaatcacaat aaaaaactgc tagttattag aacaaaaggt 180

accattgctg gtcaatatag agtttatagc gaagaaggtg ctaacaaaag tggtttagcc 240

tggccttcag cctttaaggt acagttgcaa ctacctgata atgaagtagc tcaaatatct 300

gattactatc caagaaattc gattgataca aaagagtata tgagtacttt aacttatgga 360

ttcaacggta atgttactgg tgatgataca ggaaaaattg gcggccttat tggtgcacaa 420

gtttcgattg gtcatacact gaaatatgtt caacctgatt tcaaaacaat tttagagagc 480

ccaactgata aaaaagtagg ctggaaagtg atatttaaca atatggtgaa tcaaaattgg 540

ggaccatacg atcgagattc ttggaacccg gtatatggca atcaactttt catgaaaact 600

agaaatggtt ctatgaaagc agcagataac ttccttgatc ctaacaaagc aagttctcta 660

ttatcttcag ggttttcacc agacttcgct acagttatta ctatggatag aaaagcatcc 720

aaacaacaaa caaatataga tgtaatatac gaacgagttc gtgatgatta ccaattgcat 780

tggacttcaa caaattggaa aggtaccaat actaaagata aatggacaga tcgttcttca 840

gaaagatata aaatcgattg ggaaaaagaa gaaatgacaa attaa 885

<210> 34
<211> 293
<212> PRT
<213> Artificial Sequence

<220>
<223> protein sequence for one subunit of alpha-HL-Q

<400> 34

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
85 90 95

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

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

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

```
Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145                 150                 155                 160

Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
                165                 170                 175

Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
            180                 185                 190

Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
        195                 200                 205

Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
    210                 215                 220

Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225                 230                 235                 240

Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
                245                 250                 255

Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
            260                 265                 270

Lys Trp Thr Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
        275                 280                 285

Glu Glu Met Thr Asn
    290


<210>  35
<211>  957
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  polynucleotide sequence of one subunit of
       alpha-HL-E287C-QC-D5FLAG

<400>  35
atggcagatt ctgatattaa tattaaaacc ggtactacag atattggaag caatactaca       60

gtaaaaacag gtgatttagt cacttatgat aaagaaaatg gcatgcacaa aaaagtattt      120

tatagtttta tcgatgataa aaatcacaat aaaaaactgc tagttattag aacaaaaggt      180

accattgctg gtcaatatag agtttatagc gaagaaggtg ctaacaaaag tggtttagcc      240

tggccttcag cctttaaggt acagttgcaa ctacctgata atgaagtagc tcaaatatct      300

gattactatc caagaaattc gattgataca aaagagtata tgagtacttt aacttatgga      360

ttcaacggta atgttactgg tgatgataca ggaaaaattg gcggctgtat tggtgcacaa      420

gtttcgattg gtcatacact gaaatatgtt caacctgatt tcaaaacaat tttagagagc      480

ccaactgata aaaaagtagg ctggaaagtg atatttaaca atatggtgaa tcaaaattgg      540
```

ggaccatacg atcgagattc ttggaacccg gtatatggca atcaactttt catgaaaact 600

agaaatggtt ctatgaaagc agcagataac ttccttgatc ctaacaaagc aagttctcta 660

ttatcttcag ggttttcacc agacttcgct acagttatta ctatggatag aaaagcatcc 720

aaacaacaaa caaatataga tgtaatatac gaacgagttc gtgatgatta ccaattgcat 780

tggacttcaa caaattggaa aggtaccaat actaaagata aatggacaga tcgttcttca 840

gaaagatata aaatcgattg gtgcaaagaa gaaatgacaa atgatgatga tgatgatagc 900

ggcagcggtg attataaaga tgatgatgat aaagcgcacc atcatcatca ccactaa 957

<210> 36
<211> 317
<212> PRT
<213> Artificial Sequence

<220>
<223> amino acid sequence of one subunit of alpha-HL-E287C-QC-D5FLAG

<400> 36

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
1 5 10 15

Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
85 90 95

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
100 105 110

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

Thr Gly Lys Ile Gly Gly Cys Ile Gly Ala Gln Val Ser Ile Gly His
130 135 140

Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160

Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175

```
Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
            180                 185                 190

Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
        195                 200                 205

Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
    210                 215                 220

Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225                 230                 235                 240

Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
                245                 250                 255

Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
            260                 265                 270

Lys Trp Thr Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Cys Lys
        275                 280                 285

Glu Glu Met Thr Asn Asp Asp Asp Asp Asp Ser Gly Ser Gly Asp Tyr
    290                 295                 300

Lys Asp Asp Asp Asp Lys Ala His His His His His His
305                 310                 315
```

<210> 37
<211> 885
<212> DNA
<213> Artificial sequence

<220>
<223> polynucleotide sequence of one subunit of
alpha-hemolysin-E111N/K147N

<400> 37

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atggcagatt ctgatattaa tattaaaacc ggtactacag atattggaag caatactaca       60

gtaaaaacag gtgatttagt cacttatgat aaagaaaatg gcatgcacaa aaaagtattt      120

tatagtttta tcgatgataa aaatcacaat aaaaaactgc tagttattag aacaaaaggt      180

accattgctg gtcaatatag agtttatagc gaagaaggtg ctaacaaaag tggtttagcc      240

tggccttcag cctttaaggt acagttgcaa ctacctgata atgaagtagc tcaaatatct      300

gattactatc caagaaattc gattgataca aaaaactata tgagtacttt aacttatgga      360

ttcaacggta atgttactgg tgatgataca ggaaaaattg gcggccttat tggtgcaaat      420

gtttcgattg gtcatacact gaactatgtt caacctgatt tcaaaacaat tttagagagc      480

ccaactgata aaaaagtagg ctggaaagtg atatttaaca atatggtgaa tcaaaattgg      540

ggaccatacg atcgagattc ttggaacccg gtatatggca atcaactttt catgaaaact      600
```

agaaatggtt ctatgaaagc agcagataac ttccttgatc ctaacaaagc aagttctcta 660

ttatcttcag ggttttcacc agacttcgct acagttatta ctatggatag aaaagcatcc 720

aaacaacaaa caaatataga tgtaatatac gaacgagttc gtgatgatta ccaattgcat 780

tggacttcaa caaattggaa aggtaccaat actaaagata aatggacaga tcgttcttca 840

gaaagatata aaatcgattg ggaaaaagaa gaaatgacaa attaa 885

<210> 38
<211> 293
<212> PRT
<213> artificial sequence

<220>
<223> amino acid sequence of one subunit of alpha-hemolysin-E111N/K147N

<400> 38

Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
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Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
20 25 30

Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
35 40 45

Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
50 55 60

Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
65 70 75 80

Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
85 90 95

Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Asn Tyr
100 105 110

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

Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
130 135 140

Thr Leu Asn Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro
145 150 155 160

Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
165 170 175

Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
180 185 190

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Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
        195                 200                 205

Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
    210                 215                 220

Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
225                 230                 235                 240

Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
                245                 250                 255

Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
            260                 265                 270

Lys Trp Thr Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
        275                 280                 285

Glu Glu Met Thr Asn
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<211> 518
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

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gttggtgctg atattgcgct ccactaaagg gccgattgac ccggtggtac cttggttgtt 120

tctgttggtg ctgatattgc ttttgatgcc gaccctaaat tttttgcctg tttggttcgc 180

tttgagtctt cttcggttcc gactaccctc ccgactgcct atgatgttta tcctttggat 240

ggtcgccatg atggtggtta ttataccgtc aaggactgtg tgactattga cgtccttccc 300

cgtacgccgg gcaataatgt ttatgttggt ttcatggttt ggtctaactt taccgctact 360

aaatgccgcg gattggtttc gctgaatcag gttattaaag agattatttg tctccagcca 420

cttaagtgag gtgatttatg tttggtgcta ttgctggcgg tattgcttct gctcttgctg 480

gtggcgccat gtctaaattg tttggaggcg gtcgagct 518

<210> 40
<211> 530
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the example

<400> 40
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gttggtgctg atattgcgct ccactaaagg gccgattgac gctccactaa agggccgatt 120

gacccggttg tttctgttgg tgctgatatt gcttttgatg ccgaccctaa atttttgcc 180

tgtttggttc gctttgagtc ttcttcggtt ccgactaccc tcccgactgc ctatgatgtt 240

tatcctttgg atggtcgcca tgatggtggt tattataccg tcaaggactg tgtgactatt 300

gacgtccttc cccgtacgcc gggcaataat gtttatgttg gtttcatggt ttggtctaac 360

tttaccgcta ctaaatgccg cggattggtt tcgctgaatc aggttattaa agagattatt 420

tgtctccagc cacttaagtg aggtgattta tgtttggtgc tattgctggc ggtattgctt 480

ctgctcttgc tggtggcgcc atgtctaaat tgtttggagg cggtcgagct 530

<210> 41
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence used in the examples

<400> 41
agcgactaac aaacacaatc tgatggcttt ttttttttt ttttttttt ttttttt 57