

SEQUENCE LISTING

<110> GlaxoSmithKline Biologicals SA

<120> Vaccine

<130> VB62293

<150> 0700760.2

<151> 2007-01-15

<150> 0701262.8

<151> 2007-01-23

<160> 45

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1887

<212> DNA

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - TSGHHHHHH
(plasmid TCMP14)

<400> 1

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<210> 2

<211> 629

<212> PRT

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - TSGHHHHHH
(plasmid TCMP14)

<400> 2

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Ser Asp Lys Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
      20          25          30
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
      35          40          45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
      50          55          60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
      65          70          75          80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
      85          90          95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
      100          105          110
Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser Met
      115          120          125
Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln Ser
      130          135          140
Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu Pro
      145          150          155          160
Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg His
      165          170          175
Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys Leu
      180          185          190
Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr Phe
      195          200          205
Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val Arg
      210          215          220
Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser His
      225          230          235          240
Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr Ser
      245          250          255
Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys Val
      260          265          270
Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu Val
      275          280          285
Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe Ser
      290          295          300
Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu Cys
      305          310          315          320
Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys Met
      325          330          335
Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val Thr
      340          345          350
Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu Gly
      355          360          365
Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala Ser
      370          375          380
Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe Thr
      385          390          395          400
Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp Ser
      405          410          415
Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val Met
      420          425          430
Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu Gly
      435          440          445

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Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser Val
450                      455                      460
Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro Leu
465                      470                      475                      480
Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val Phe
485                      490                      495
Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro Ser
500                      505                      510
Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn Ser
515                      520                      525
Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly Leu
530                      535                      540
Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr Glu
545                      550                      555                      560
Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His Ala
565                      570                      575
Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val Trp
580                      585                      590
Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr Asp
595                      600                      605
Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn Thr Ser Gly His
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His His His His His
625

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<210> 3

<211> 1860

<212> DNA

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - no His tail
(plasmid TCMP14)

<400> 3

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cttgcgtttg cacaacaggc tgattattta gagcaagatt tagcaatgac taaggatggt 180
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caaagttag aaatgacaga aaactttgaa accatggaac gaaggcggtt gtgggggttc 360
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accttaagct tctacgggaa ttccatctcc atatctgcct tgcagagtct cctgcagcac 1620
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gacatccatg gtaccctcca cctggagagg cttgcctatc tgcattgccag gctcagggag 1740
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<210> 4

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - no His tail
(plasmid TCMP14)

<400> 4

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Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
 35          40          45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 50          55          60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 65          70          75          80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85          90          95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
100          105          110
Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser Met
115          120          125
Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln Ser
130          135          140
Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu Pro
145          150          155          160
Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg His
165          170          175
Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys Leu
180          185          190
Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr Phe
195          200          205
Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val Arg
210          215          220
Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser His
225          230          235          240
Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr Ser
245          250          255
Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys Val
260          265          270
Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu Val
275          280          285
Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe Ser
290          295          300
Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu Cys
305          310          315          320
Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys Met
325          330          335
Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val Thr
340          345          350
Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu Gly
355          360          365
Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala Ser
370          375          380
Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe Thr

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Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp Ser
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Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val Met
          420          425          430
Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu Gly
          435          440          445
Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser Val
          450          455          460
Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro Leu
465          470          475          480
Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val Phe
          485          490          495
Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro Ser
          500          505          510
Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn Ser
          515          520          525
Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly Leu
          530          535          540
Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr Glu
545          550          555          560
Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His Ala
          565          570          575
Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val Trp
          580          585          590
Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr Asp
          595          600          605
Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn
          610          615          620

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<210> 5

<211> 1884

<212> DNA

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - LEHHHHHH
(plasmid pET21)

<400> 5

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<210> 6

<211> 628

<212> PRT

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - LEHHHHHH
(plasmid pET21)

<400> 6

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Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
          35          40          45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
          50          55          60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
65          70          75          80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
          85          90          95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
          100          105          110
Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser Met
          115          120          125
Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln Ser
          130          135          140
Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu Pro
145          150          155          160
Arg Glu Leu Phe Pro Leu Phe Met Ala Ala Phe Asp Gly Arg His
          165          170          175
Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys Leu
          180          185          190
Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr Phe
          195          200          205
Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val Arg
          210          215          220
Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser His
225          230          235          240
Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr Ser
          245          250          255
Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys Val
          260          265          270
Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu Val
          275          280          285
Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe Ser
          290          295          300
Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu Cys
305          310          315          320
Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys Met
          325          330          335
Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val Thr
          340          345          350

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Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu Gly
   355                               360                   365
Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala Ser
   370                               375                   380
Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe Thr
   385                               390                   395                   400
Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp Ser
   405                               410                   415
Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val Met
   420                               425                   430
Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu Gly
   435                               440                   445
Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser Val
   450                               455                   460
Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro Leu
   465                               470                   475                   480
Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val Phe
   485                               490                   495
Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro Ser
   500                               505                   510
Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn Ser
   515                               520                   525
Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly Leu
   530                               535                   540
Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr Glu
   545                               550                   555                   560
Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His Ala
   565                               570                   575
Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val Trp
   580                               585                   590
Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr Asp
   595                               600                   605
Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn Leu Glu His His
   610                               615                   620
His His His His
625

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<210> 7

<211> 1860

<212> DNA

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - no His tail
(plasmid pET21)

<400> 7

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cagcccttca ttccagtaga ggtgctcgta gacctgttcc tcaaggaagg tgctgtgat 900
gaattgttct cctacctcat tgagaaagtg aagcgaaaga aaaatgtact acgcctgtgc 960

```

```

tgtaagaagc tgaagatttt tgcaatgccc atgcaggata tcaagatgat cctgaaaatg 1020
gtgcagctgg actctattga agatttggaa gtgacttgta cctggaagct acccaccttg 1080
gcgaaatttt ctccttacct gggccagatg attaactctgc gtagactcct cctctccac 1140
atccatgcat cttcctacat ttccccggag aaggaagagc agtatatcgc ccagttcacc 1200
tctcagttcc tcagtctgca gtgcctgcag gctctctatg tggactcttt atttttcctt 1260
agaggccgcc tggatcagtt gctcaggcac gtgatgaacc ccttggaac cctctcaata 1320
actaactgcc ggctttcgga aggggatgtg atgcatctgt cccagagtcc cagcgtcagt 1380
cagctaagtg tcctgagtct aagtggggtc atgctgaccg atgtaagtcc cgagccccctc 1440
caagctctgc tggagagagc ctctgccacc ctccaggacc tggctcttga tgagtgtggg 1500
atcacggatg atcagctcct tgccctcctg ccttccctga gccactgctc ccagcttaca 1560
accttaagct tctacgggaa ttccatctcc atatctgcct tgcagagtct cctgcagcac 1620
ctcatcgggc tgagcaatct gaccacagtg ctgtatcctg tccccctgga gagttatgag 1680
gacatccatg gtaccctcca cctggagagg cttgcctatc tgcatgccag gctcagggag 1740
ttgctgtgtg agttggggcg gccagcatg gtctggctta gtgccaaccc ctgtcctcac 1800
tgtggggaca gaaccttcta tgaccggag cccatcctgt gccctgttt catgcctaac 1860

```

<210> 8

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - no His tail
(plasmid pET21)

<400> 8

```

Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
1      5      10      15
Ser Asp Lys Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
20     25     30
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
35     40     45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
50     55     60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
65     70     75     80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
85     90     95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
100    105    110
Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser Met
115    120    125
Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln Ser
130    135    140
Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu Pro
145    150    155    160
Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg His
165    170    175
Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys Leu
180    185    190
Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr Phe
195    200    205
Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val Arg
210    215    220
Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser His
225    230    235    240
Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr Ser
245    250    255
Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys Val
260    265    270
Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu Val
275    280    285
Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe Ser

```



```

      290              295              300
Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu Cys
305              310              315              320
Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys Met
      325              330              335
Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val Thr
      340              345              350
Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu Gly
      355              360              365
Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala Ser
      370              375              380
Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe Thr
      385              390              395              400
Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp Ser
      405              410              415
Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val Met
      420              425              430
Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu Gly
      435              440              445
Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser Val
      450              455              460
Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro Leu
      465              470              475              480
Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val Phe
      485              490              495
Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro Ser
      500              505              510
Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn Ser
      515              520              525
Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly Leu
      530              535              540
Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr Glu
      545              550              555              560
Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His Ala
      565              570              575
Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val Trp
      580              585              590
Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr Asp
      595              600              605
Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn
      610              615              620

```

<210> 9

<211> 1878

<212> DNA

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - HHHHHH (plasmid
pET26)

<400> 9

```

atggatccaa gcagccattc atcaaatatg gcgaataccc aaatgaaatc agacaaaatc 60
attattgctc accgtggtgc tagcggttat ttaccagagc atacgttaga atctaaagca 120
cttgcgtttg cacaacaggc tgattattta gagcaagatt tagcaatgac taaggatggt 180
cgtttagtgg ttattcacga tcaacttttta gatggcttga ctgatgttgc gaaaaaattc 240
ccacatcgtc atcgtaaaga tggccgttac tatgtcatcg actttacctt aaaagaaatt 300
caaagttagt aaatgacaga aaactttgaa accatggaac gtcgtcgtct gtggggcagc 360
attcagagcc gttatattag catgagcgtg tggaccagcc cgcgtcgtct ggttgagctg 420
gccggccaga gcctgctgaa agatgaagcg ctggccattg cggcgctgga gctgctgccg 480
cgtgagctgt ttccgccgct gtttatggcg gcgtttgatg gccgtcatag ccagaccctg 540
aaagcgatgg tgcaggcgtg gccgtttacc tgtctgccgc tgggcgtgct gatgaaaggc 600
cagcatctgc atctggaaac ctttaaagcg gtgctggatg gcctggatgt gctgctggcc 660

```

```

caggaagttc gtccgcgtcg ttggaaactg caagtgctgg atctgcgtaa aaacagccat 720
caggattttt ggaccgtgtg gagcggcaat cgtgcgagcc tgtatagctt tccggaaccg 780
gaagcggcgc agccgatgac caaaaaactg aaagtggatg gcctgagcac cgaagcggaa 840
cagccgttta ttccggtgga agtgctggtt gacctgtttc tgaaagaagg cgcctgcgac 900
gagctgttta gctatctgat cgaaaaagtg aaacgcaaaa aaaacgtgct gcgtctgtgc 960
tgcaaaaaac tgaaaatctt cgcgatgccg atgcaggata ttaaaatgat cctgaaaatg 1020
gtgcagctgg atagcattga ggacctggaa gtgacctgca cctggaaact gccgaccctg 1080
gccaaattta gcccgtatct gggccagatg attaacctgc gtcgtctgct gctgtctcat 1140
attcatgcga gcagctatat tagcccggaa aaagaagaac agtatatcgc gcagtttacc 1200
agccagtttc tgagcctgca atgcctgcaa gcgctgtatg tggatagcct gttttttctg 1260
cgtggccgtc tggatcagct gctgcgtcat gtgatgaatc cgctggaaac cctgagcatt 1320
accaactgcc gtctgagcga aggcgatgtg atgcatctga gccagagccc gagcgtagc 1380
cagctgtctg ttctgagcct gagcggcgtg atgctgaccg atgtgagccc ggaaccgctg 1440
caagccctgc tggaacgtgc gagcgcgacc ctgcaagacc tgggtgtttga tgaatgcggc 1500
attaccgatg atcagctgct ggccctgctg ccgagcctga gccattgcag ccagctgacc 1560
accctgagct tttatggcaa cagcattagc attagcgcgc tgcaaagcct gctgcaacat 1620
ctgattggcc tgagcaacct gacctatgtg ctgtatccgg tgccgctgga aagctatgaa 1680
gatattcatg gcaccctgca tctggaacgt ctggcctatc tgcacgcgcg tctgcgtgag 1740
ctgctgtgcg agctgggccc tccgagcatg gtttggtgtg ctgcgaatcc gtgcccgcac 1800
tgcgcgatc gtacctttta tgatccggaa ccgattctgt gccctgtgct tatgccgaac 1860
caccaccacc accaccac 1878

```

<210> 10

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - HHHHHH (plasmid pET26)

<400> 10

```

Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
 1          5          10          15
Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
          20          25          30
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
          35          40          45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
          50          55          60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
65          70          75          80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
          85          90          95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
          100          105          110
Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser Met
          115          120          125
Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln Ser
          130          135          140
Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu Pro
145          150          155          160
Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg His
          165          170          175
Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys Leu
          180          185          190
Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr Phe
          195          200          205
Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val Arg
          210          215          220
Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser His
225          230          235          240
Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr Ser
          245          250          255

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```

Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys Val
      260                      265                      270
Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu Val
      275                      280                      285
Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe Ser
      290                      295                      300
Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu Cys
      305                      310                      315                      320
Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys Met
      325                      330                      335
Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val Thr
      340                      345                      350
Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu Gly
      355                      360                      365
Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala Ser
      370                      375                      380
Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe Thr
      385                      390                      395                      400
Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp Ser
      405                      410                      415
Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val Met
      420                      425                      430
Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu Gly
      435                      440                      445
Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser Val
      450                      455                      460
Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro Leu
      465                      470                      475                      480
Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val Phe
      485                      490                      495
Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro Ser
      500                      505                      510
Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn Ser
      515                      520                      525
Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly Leu
      530                      535                      540
Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr Glu
      545                      550                      555                      560
Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His Ala
      565                      570                      575
Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val Trp
      580                      585                      590
Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr Asp
      595                      600                      605
Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn His His His His
      610                      615                      620
His His
      625

```

<210> 11

<211> 1860

<212> DNA

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - no His tail
(plasmid pET26)

<400> 11

```

atggatccaa gcagccattc atcaaatatg gcgaataccc aaatgaaatc agacaaaatc 60
attattgctc accgtggtgc tagcggttat ttaccagagc atacgttaga atctaaagca 120
cttgcgtttg cacaacaggc tgattattta gagcaagatt tagcaatgac taaggatggt 180
cgtttagtgg ttattcacga tcacttttta gatggcttga ctgatgttgc gaaaaaattc 240

```

```

ccacatcgtc atcgtaaaga tggccggttac tatgtcatcg actttacctt aaaagaaatt 300
caaagtttag aaatgacaga aaactttgaa accatggaac gtcgtcgtct gtggggcagc 360
attcagagcc gttatattag catgagcgtg tggaccagcc cgcgtcgtct ggttgagctg 420
gccggccaga gcttctgtaa agatgaagcg ctggccattg cggcgctgga gctgctgccg 480
cgtgagctgt ttccgccgct gtttatggcg gcgtttgatg gccgtcatag ccagaccctg 540
aaagcgatgg tgcaggcgtg gccgtttacc tgtctgccgc tgggcgtgct gatgaaaggc 600
cagcatctgc atctggaaac ctttaaagcg gtgctggatg gcctggatgt gctgctggcc 660
caggaagttc gtccgcgtcg ttggaaactg caagtgcgtg atctgcgtaa aaacagccat 720
caggattttt ggaccgtgtg gagcggcaat cgtgcgagcc tgtatagctt tccggaaccg 780
gaagcggcgc agccgatgac caaaaaacgt aaagtggatg gcctgagcac cgaagcggaa 840
cagccgttta ttccggtgga agtgctggtt gacctgttcc tgaaagaagg cgctgcgac 900
gagctgttta gctatctgat cgaaaaaagt aaacgcaaaa aaaacgtgct gcgtctgtgc 960
tgcaaaaaac tgaaaatctt cgcatgccc atgcaggata ttaaaatgat cctgaaaatg 1020
gtgcagctgg atagcattga ggacctggaa gtgacctgca cctggaaact gccgaccctg 1080
gccaaattta gcccgatctt gggccagatg attaacctgc gtcgtctgct gctgtctcat 1140
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agccagtttc tgagcctgca atgcctgcaa gcgtgtgatg tggatagcct gttttttctg 1260
cgtggccgctc tggatcagct gctgcgtcat gtgatgaatc cgctggaaac cctgagcatt 1320
accaactgcc gtctgagcga aggcgatgtg atgcatctga gccagagccc gagcgttagc 1380
cagctgtctg ttctgagcct gagcggcgtg atgctgaccg atgtgagccc ggaaccgctg 1440
caagccctgc tggaacgtgc gagcgcgacc ctgcaagacc tgggtgttga tgaatgcggc 1500
attaccgatg atcagctgct ggccctgctg ccgagcctga gccattgcag ccagctgacc 1560
accctgagct tttatggcaa gacgattagc attagcgcgc tgcaaagcct gctgcaacat 1620
ctgattggcc tgagcaacct gacctatgtg ctgtatccgg tgccgctgga aagctatgaa 1680
gatattcatg gcacctgca tctggaacgt ctggcctatc tgcacgcgcg tctgcgtgag 1740
ctgctgtgcg agctgggccc tccgagcatg gtttggtgtg ctgcgaatcc gtgcccgcac 1800
tgccgcgacg gtacctttta tgatccggaa ccgattctgt gcccgctgctt tatgccgaac 1860

```

<210> 12

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> MDP- 20-127 - Protein D - PRAME - no His tail
(plasmid pET26)

<400> 12

```

Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
 1          5          10          15
Ser Asp Lys Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
 20          25          30
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
 35          40          45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 50          55          60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 65          70          75          80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85          90          95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
100          105          110
Glu Arg Arg Arg Leu Trp Gly Ser Ile Gln Ser Arg Tyr Ile Ser Met
115          120          125
Ser Val Trp Thr Ser Pro Arg Arg Leu Val Glu Leu Ala Gly Gln Ser
130          135          140
Leu Leu Lys Asp Glu Ala Leu Ala Ile Ala Ala Leu Glu Leu Leu Pro
145          150          155          160
Arg Glu Leu Phe Pro Pro Leu Phe Met Ala Ala Phe Asp Gly Arg His
165          170          175
Ser Gln Thr Leu Lys Ala Met Val Gln Ala Trp Pro Phe Thr Cys Leu
180          185          190
Pro Leu Gly Val Leu Met Lys Gly Gln His Leu His Leu Glu Thr Phe

```

```

      195              200              205
Lys Ala Val Leu Asp Gly Leu Asp Val Leu Leu Ala Gln Glu Val Arg
  210              215              220
Pro Arg Arg Trp Lys Leu Gln Val Leu Asp Leu Arg Lys Asn Ser His
  225              230              235              240
Gln Asp Phe Trp Thr Val Trp Ser Gly Asn Arg Ala Ser Leu Tyr Ser
      245              250              255
Phe Pro Glu Pro Glu Ala Ala Gln Pro Met Thr Lys Lys Arg Lys Val
      260              265              270
Asp Gly Leu Ser Thr Glu Ala Glu Gln Pro Phe Ile Pro Val Glu Val
      275              280              285
Leu Val Asp Leu Phe Leu Lys Glu Gly Ala Cys Asp Glu Leu Phe Ser
      290              295              300
Tyr Leu Ile Glu Lys Val Lys Arg Lys Lys Asn Val Leu Arg Leu Cys
  305              310              315              320
Cys Lys Lys Leu Lys Ile Phe Ala Met Pro Met Gln Asp Ile Lys Met
      325              330              335
Ile Leu Lys Met Val Gln Leu Asp Ser Ile Glu Asp Leu Glu Val Thr
      340              345              350
Cys Thr Trp Lys Leu Pro Thr Leu Ala Lys Phe Ser Pro Tyr Leu Gly
      355              360              365
Gln Met Ile Asn Leu Arg Arg Leu Leu Leu Ser His Ile His Ala Ser
      370              375              380
Ser Tyr Ile Ser Pro Glu Lys Glu Glu Gln Tyr Ile Ala Gln Phe Thr
  385              390              395              400
Ser Gln Phe Leu Ser Leu Gln Cys Leu Gln Ala Leu Tyr Val Asp Ser
      405              410              415
Leu Phe Phe Leu Arg Gly Arg Leu Asp Gln Leu Leu Arg His Val Met
      420              425              430
Asn Pro Leu Glu Thr Leu Ser Ile Thr Asn Cys Arg Leu Ser Glu Gly
      435              440              445
Asp Val Met His Leu Ser Gln Ser Pro Ser Val Ser Gln Leu Ser Val
      450              455              460
Leu Ser Leu Ser Gly Val Met Leu Thr Asp Val Ser Pro Glu Pro Leu
  465              470              475              480
Gln Ala Leu Leu Glu Arg Ala Ser Ala Thr Leu Gln Asp Leu Val Phe
      485              490              495
Asp Glu Cys Gly Ile Thr Asp Asp Gln Leu Leu Ala Leu Leu Pro Ser
      500              505              510
Leu Ser His Cys Ser Gln Leu Thr Thr Leu Ser Phe Tyr Gly Asn Ser
      515              520              525
Ile Ser Ile Ser Ala Leu Gln Ser Leu Leu Gln His Leu Ile Gly Leu
      530              535              540
Ser Asn Leu Thr His Val Leu Tyr Pro Val Pro Leu Glu Ser Tyr Glu
  545              550              555              560
Asp Ile His Gly Thr Leu His Leu Glu Arg Leu Ala Tyr Leu His Ala
      565              570              575
Arg Leu Arg Glu Leu Leu Cys Glu Leu Gly Arg Pro Ser Met Val Trp
      580              585              590
Leu Ser Ala Asn Pro Cys Pro His Cys Gly Asp Arg Thr Phe Tyr Asp
      595              600              605
Pro Glu Pro Ile Leu Cys Pro Cys Phe Met Pro Asn
      610              615              620

```

```

<210> 13
<211> 9
<212> PRT
<213> Homo sapiens

```

```

<400> 13
Val Leu Asp Gly Leu Asp Val Leu Leu
  1              5

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<210> 14
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 14
 Ser Leu Tyr Ser Phe Pro Glu Pro Glu Ala
 1 5 10

<210> 15
 <211> 10
 <212> PRT
 <213> Homo sapiens

<400> 15
 Ala Leu Tyr Val Asp Ser Leu Phe Phe Leu
 1 5 10

<210> 16
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 16
 Leu Tyr Val Asp Ser Leu Phe Phe Leu
 1 5

<210> 17
 <211> 9
 <212> PRT
 <213> Homo sapiens

<400> 17
 Ser Leu Leu Gln His Leu Ile Gly Leu
 1 5

<210> 18
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sense oligonucleotide CAN008

<400> 18
 atataacata tggatccaag cagccattca tcaaat 36

<210> 19
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> antisense oligonucleotide CAN037

<400> 19
 ccacaaacgc cttcgttcca tggtttcaaa gttttctgtc 40

<210> 20

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

<220>
<223> sense oligonucleotide CAN036

<400> 20
gacagaaaac ttgaaacca tggaacgaag gcgtttgtgg           40

<210> 21
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> antisense oligonucleotide CAN029

<400> 21
agagagacta gtctagttag gcatgaaaca ggggcacag           39

<210> 22
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> antisense oligonucleotide CAN002

<400> 22
ggaggaacta gtgttaggca tgaaacaggg gcacag           36

<210> 23
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> sense oligonucleotide CAN040

<400> 23
agagagcata tgagcagcca ttcacaaat atggcg           36

<210> 24
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> antisense oligonucleotide CAN032

<400> 24
acgtgggcgg ccgcggtttc aaagttttct gtcatttcta a           41

<210> 25
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> sense oligonucleotide CAN033

<400> 25
ttgttggcgg ccgcaatgga acgaaggcgt ttgtggggt           39

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<210> 26
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> antisense oligonucleotide CAN034

 <400> 26
 ggaggactcg aggttaggca tgaaacaggg gcacag 36

 <210> 27
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> antisense oligonucleotide CAN035

 <400> 27
 ggaggactcg agctagttag gcatgaaaca ggggcacag 39

 <210> 28
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sense oligonucleotide CAN106

 <400> 28
 cagaaaactt tgaaaccatg gaacgaaggc g 31

 <210> 29
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> antisense oligonucleotide CAN107

 <400> 29
 cgccttcggtt ccatggtttc aaagttttct g 31

 <210> 30
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sense oligonucleotide CAN104

 <400> 30
 ggagatatac atatggatcc aagcagccat tcatcaaata tgg 43

 <210> 31
 <211> 43
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> antisense oligonucleotide CAN105

<400> 31
 ccatatttga tgaatggctg cttggatcca tatgtatatc tcc 43

 <210> 32
 <211> 40
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 <220>
 <223> sense oligonucleotide CAN123

 <400> 32
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 <210> 33
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 <220>
 <223> antisense oligonucleotide CAN124

 <400> 33
 ccacagacga cgacgttcca tggtttcaaa gttttctgtc 40

 <210> 34
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> sense oligonucleotide CAN199

 <400> 34
 ggaattccat atggatccaa gcagccattc 30

 <210> 35
 <211> 53
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> antisense oligonucleotide CAN19

 <400> 35
 ggagctctcg agtcagtggg ggtgggtggg gtggttcggc ataaagcacg ggc 53

 <210> 36
 <211> 20
 <212> DNA
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 <220>
 <223> immunostimulatory oligonucleotide CpG 1826

 <400> 36
 tccatgacgt tcctgacgtt 20

 <210> 37
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 <212> DNA
 <213> Artificial Sequence

 <220>

<223> immunostimulatory oligonucleotide CpG 1758

<400> 37

tctcccagcg tgcgcat

18

<210> 38

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> immunostimulatory oligonucleotide CpG2006

<400> 38

accgatgacg tcgccggtga cggcaccacg tcgtcgtttt gtcgttttgc cggt

54

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> immunostimulatory oligonucleotide CpG1668

<400> 39

tccatgacgt tcctgatgct

20

<210> 40

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> immunostimulatory oligonucleotide CpG5456

<400> 40

tcgacgtttt cggcgcgcgc cg

22

<210> 41

<211> 127

<212> PRT

<213> Haemophilus influenzae b

<400> 41

Met	Lys	Leu	Lys	Thr	Leu	Ala	Leu	Ser	Leu	Leu	Ala	Ala	Gly	Val	Leu
1				5					10					15	
Ala	Gly	Cys	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
		20						25					30		
Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro
		35				40						45			
Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp
	50					55				60					
Tyr	Leu	Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val
65					70				75					80	
Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe
				85					90					95	
Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr
		100					105					110			
Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	
		115					120					125			

<210> 42

<211> 111

<212> PRT

<213> Artificial Sequence

<220>

<223> 1-Met; 2-Asp; 3-Pro; followed by AA 20 to 127 of
Protein D

<400> 42

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Met Asp Pro Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
 1          5          10          15
Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
          20          25          30
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
          35          40          45
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
          50          55          60
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
65          70          75          80
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
          85          90          95
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr
          100          105          110

```

<210> 43

<211> 450

<212> PRT

<213> Artificial Sequence

<220>

<223> Protein D-MAGE-A3-His

<400> 43

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Met Asp Pro Lys Thr Leu Ala Leu Ser Leu Leu Ala Ala Gly Val Leu
 1          5          10          15
Ala Gly Cys Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys
          20          25          30
Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
          35          40          45
Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp
          50          55          60
Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
65          70          75          80
Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
          85          90          95
Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
          100          105          110
Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
          115          120          125
Asp Leu Glu Gln Arg Ser Gln His Cys Lys Pro Glu Gly Leu Glu
          130          135          140
Ala Arg Gly Glu Ala Leu Gly Leu Val Gly Ala Gln Ala Pro Ala Thr
145          150          155          160
Glu Glu Gln Glu Ala Ala Ser Ser Ser Ser Thr Leu Val Glu Val Thr
          165          170          175
Leu Gly Glu Val Pro Ala Ala Glu Ser Pro Asp Pro Pro Gln Ser Pro
          180          185          190
Gln Gly Ala Ser Ser Leu Pro Thr Thr Met Asn Tyr Pro Leu Trp Ser
          195          200          205
Gln Ser Tyr Glu Asp Ser Ser Asn Gln Glu Glu Glu Gly Pro Ser Thr
          210          215          220
Phe Pro Asp Leu Glu Ser Glu Phe Gln Ala Ala Leu Ser Arg Lys Val
225          230          235          240
Ala Glu Leu Val His Phe Leu Leu Leu Lys Tyr Arg Ala Arg Glu Pro

```

```

                245                250                255
Val Thr Lys Ala Glu Met Leu Gly Ser Val Val Gly Asn Trp Gln Tyr
                260                265                270
Phe Phe Pro Val Ile Phe Ser Lys Ala Ser Ser Ser Leu Gln Leu Val
                275                280                285
Phe Gly Ile Glu Leu Met Glu Val Asp Pro Ile Gly His Leu Tyr Ile
                290                295                300
Phe Ala Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp Asn
305                310                315                320
Gln Ile Met Pro Lys Ala Gly Leu Leu Ile Ile Val Leu Ala Ile Ile
                325                330                335
Ala Arg Glu Gly Asp Cys Ala Pro Glu Glu Lys Ile Trp Glu Glu Leu
                340                345                350
Ser Val Leu Glu Val Phe Glu Gly Arg Glu Asp Ser Ile Leu Gly Asp
                355                360                365
Pro Lys Lys Leu Leu Thr Gln His Phe Val Gln Glu Asn Tyr Leu Glu
                370                375                380
Tyr Arg Gln Val Pro Gly Ser Asp Pro Ala Cys Tyr Glu Phe Leu Trp
385                390                395                400
Gly Pro Arg Ala Leu Val Glu Thr Ser Tyr Val Lys Val Leu His His
                405                410                415
Met Val Lys Ile Ser Gly Gly Pro His Ile Ser Tyr Pro Pro Leu His
                420                425                430
Glu Trp Val Leu Arg Glu Gly Glu Glu Gly Gly His His His His His
                435                440                445
His His
                450

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<210> 44

<211> 109

<212> PRT

<213> Artificial Sequence

<220>

<223> the aa from protein D from Haemophilus influenzae
for use in a pD1/3-PRAME-His sequence

<400> 44

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Met Ser Ser His Ser Ser Asn Met Ala Asn Thr Gln Met Lys Ser Asp
 1                5                10                15
Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro Glu His
                20                25                30
Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Gln Ala Asp Tyr Leu
                35                40                45
Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val Ile His
                50                55                60
Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe Pro His
65                70                75                80
Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr Leu Lys
                85                90                95
Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr
                100                105

```

<210> 45

<211> 127

<212> PRT

<213> Artificial Sequence

<220>

<223> the aa from protein D from Haemophilus influenzae
for use in a pD1/3-MAGE-His sequence

<400> 45

Met	Asp	Pro	Lys	Thr	Leu	Ala	Leu	Ser	Leu	Leu	Ala	Ala	Gly	Val	Leu
1				5					10					15	
Ala	Gly	Cys	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
			20					25					30		
Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro
		35					40					45			
Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp
		50				55					60				
Tyr	Leu	Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val
65					70					75					80
Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe
				85					90					95	
Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr
			100					105					110		
Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	
		115					120					125			