Fig. 1a

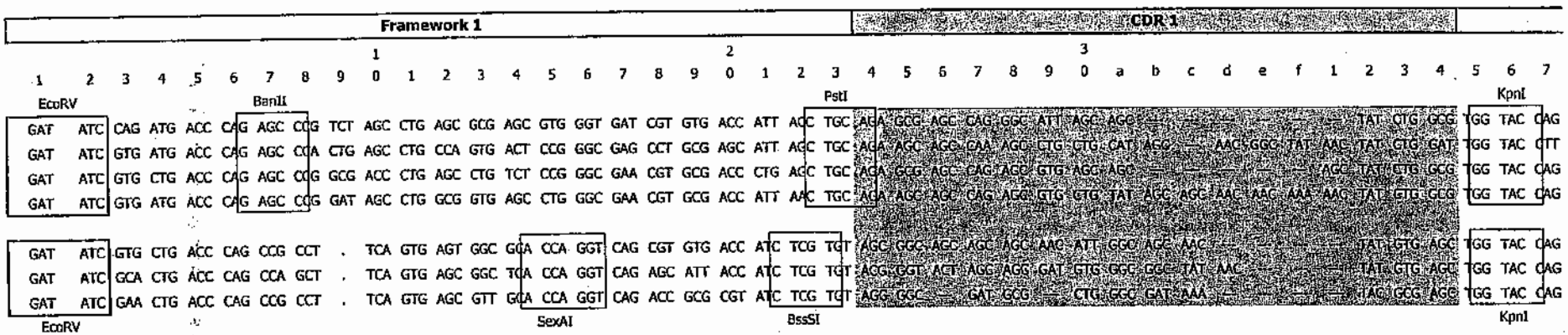
Sequence Summary of HuCAL-Fab1 Library
VL
Framework 1
CDR 1
Framework 2
CDR 2
Position
VLκ1
VLκ2
VLκ3
VLκ4
VLλ1
VLλ2
VLλ3
VH
Framework 1
CDR 1
Framework 2
CDR 2
VH1A
VH1B
VH2
VH3
VH4
VH5
VH6

Fig. 1a cont.

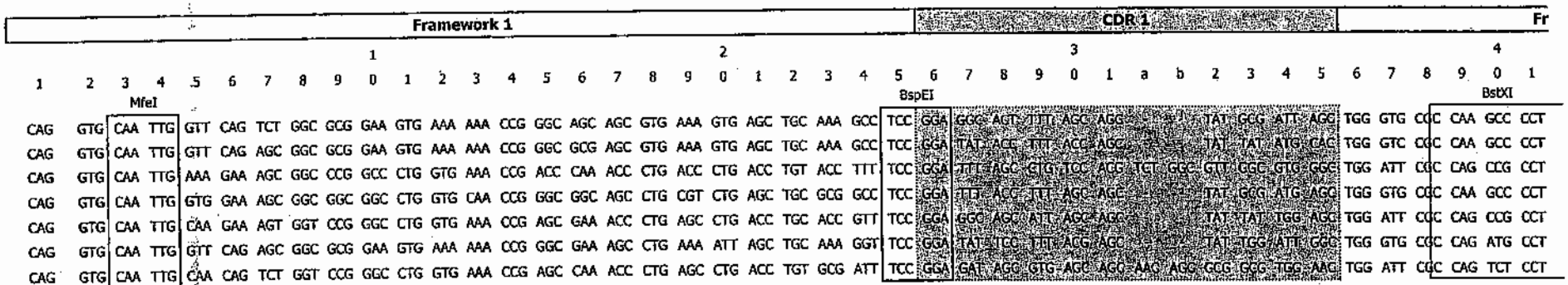
Framework 3
CDR 3
Framework 4
BamHI
BbsI
MscI
BsiWI
HpaI
MscI
BamHI
BbsI
Framework 3
CDR 3
Framework 4
BstEII
NspV
EagI
BssHII
StyI
BlpI

Sequence Summary of HuCAL-Fab1 Library

VL

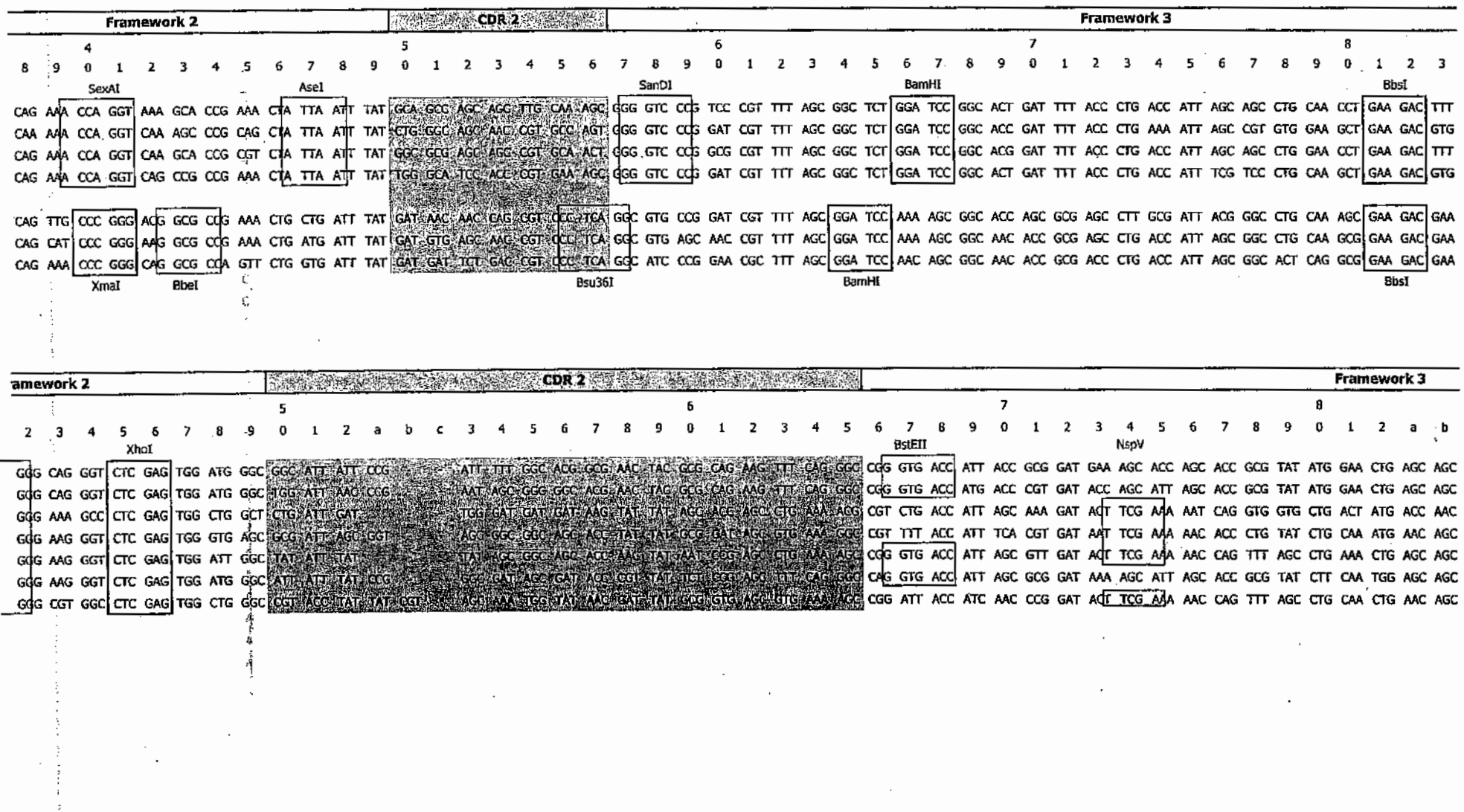


VH



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Fig. 1b cont.

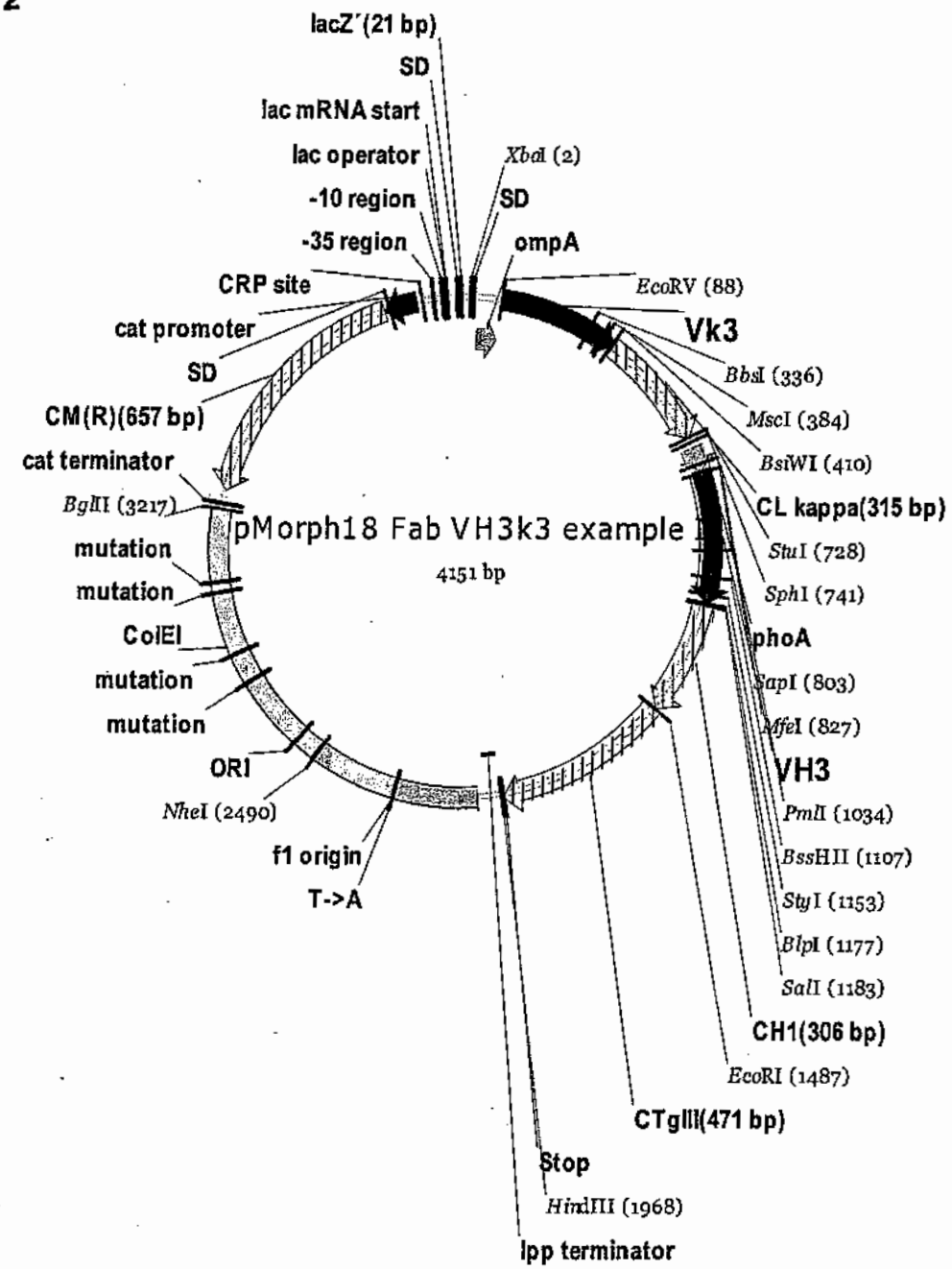


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Fig. 1b cont.

Fig. 2




```
lacZ´        SD                    ompA
--          ----        ---------------------------------
 XbaI
------
                                M  K  K   T  A  I  A   I  A  V ·
1   TCTAGATAAC GAGGGCAAAA AATGAAAAAG ACAGCTATCG CGATTGCAGT
    AGATCTATTG CTCCCGTTTT TTACTTTTTC TGTCGATAGC GCTAACGTCA
                                                 Vk3
                                                 ----------------
                  ompA
    ---------------------------------------
                                          EcoRV
                                          -------
    · A  L  A   G  F  A  T   V  A  Q   A  D  I   V  L  T  Q ·
51  GGCACTGGCT GGTTTCGCTA CCGTAGCGCA GGCCGATATC GTGCTGACCC
```

Fig. 2 cont.

```
        CCGTGACCGA CCAAAGCGAT GGCATCGCGT CCGGCTATAG CACGACTGGG
                                  Vk3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        · S P A T L S L S P G E R A T L S
  101   AGAGCCCGGC GACCCTGAGC CTGTCTCCGG GCGAACGTGC GACCCTGAGC
        TCTCGGGCCG CTGGGACTCG GACAGAGGCC CGCTTGCACG CTGGGACTCG
                                  Vk3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         C R A S Q S V S S S Y L A W Y Q Q ·
  151   TGCAGAGCGA GCCAGAGCGT GAGCAGCAGC TATCTGGCGT GGTACCAGCA
        ACGTCTCGCT CGGTCTCGCA CTCGTCGTCG ATAGACCGCA CCATGGTCGT
                                  Vk3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        · K P G Q A P R L L I Y G A S S R A ·
  201   GAAACCAGGT CAAGCACCGC GTCTATTAAT TTATGGCGCG AGCAGCCGTG
        CTTTGGTCCA GTTCGTGGCG CAGATAATTA AATACCGCGC TCGTCGGCAC
                                  Vk3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        · T G V P A R F S G S G S G T D F
  251   CAACTGGGGT CCCGGCGCGT TTTAGCGGCT CTGGATCCGG CACGGATTTT
        GTTGACCCCA GGGCCGCGCA AAATCGCCGA GACCTAGGCC GTGCCTAAAA
                                  Vk3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                     BbsI
                                     ~~~~~~~
         T L T I S S L E P E D F A V Y Y C ·
  301   ACCCTGACCA TTAGCAGCCT GGAACCTGAA GACTTTGCGG TGTATTATTG
        TGGGACTGGT AATCGTCGGA CCTTGGACTT CTGAAACGCC ACATAATAAC
                                  Vk3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                           MscI
                                           ~~~~~~
        · Q Q H Y T T P P T F G Q G T K V E ·
  351   CCAGCAGCAT TATACCACCC CGCCGACCTT TGGCCAGGGT ACGAAAGTTG
        GGTCGTCGTA ATATGGTGGG GCGGCTGGAA ACCGGTCCCA TGCTTTCAAC
                                  CL kappa
                     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        ·    Vk3
        ~~~~~~~~~~~~~~~
              BsiWI
              ~~~~~~~
        · I K R T V A A P S V F I F P P S
  401   AAATTAAACG TACGGTGGCT GCTCCGAGCG TGTTTATTTT TCCGCCGAGC
        TTTAATTTGC ATGCCACCGA CGAGGCTCGC ACAAATAAAA AGGCGGCTCG
                                  CL kappa
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         D E Q L K S G T A S V V C L L N N ·
  451   GATGAACAAC TGAAAAGCGG CACGGCGAGC GTGGTGTGCC TGCTGAACAA
        CTACTTGTTG ACTTTTCGCC GTGCCGCTCG CACCACACGG ACGACTTGTT
                                  CL kappa
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        · F Y P R E A K V Q W K V D N A L Q ·
  501   CTTTTATCCG CGTGAAGCGA AAGTTCAGTG GAAAGTAGAC AACGCGCTGC
        GAAAATAGGC GCACTTCGCT TTCAAGTCAC CTTTCATCTG TTGCGCGACG
                                  CL kappa
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        · S G N S Q E S V T E Q D S K D S
  551   AAAGCGGCAA CAGCCAGGAA AGCGTGACCG AACAGGATAG CAAAGATAGC
        TTTCGCCGTT GTCGGTCCTT TCGCACTGGC TTGTCCTATC GTTTCTATCG
                                  CL kappa
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

Fig. 2 cont.

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```
      T  Y  S  L  S  S  T  L  T  L  S  K  A  D  Y  E  K ·
601   ACCTATTCTC TGAGCAGCAC CCTGACCCTG AGCAAAGCGG ATTATGAAAA
      TGGATAAGAG ACTCGTCGTG GGACTGGGAC TCGTTTCGCC TAATACTTTT
                          CL kappa
      ------------------------------------------------------
      · H  K  V  Y  A  C  E  V  T  H  Q  G  L  S  S  P  V ·
651   ACATAAAGTG TATGCGTGCG AAGTGACCCA TCAAGGTCTG AGCAGCCCGG
      TGTATTTCAC ATACGCACGC TTCACTGGGT AGTTCCAGAC TCGTCGGGCC
               CL kappa
      ---------------------------------
                                  StuI        SphI
                                  -------     -------
      ·  T  K  S  F  N  R  G  E  A
701   TGACTAAATC TTTTAATCGT GGCGAGGCCT GATAAGCATG CGTAGGAGAA
      ACTGATTTAG AAAATTAGCA CCGCTCCGGA CTATTCGTAC GCATCCTCTT
                                phoA
            ------------------------------------------------
                                                       SapI
                                                       ------
            M  K  Q  S  T  I  A  L  A  L  L  P  L  L  F ·
751   AATAAAATGA AACAAAGCAC TATTGCACTG GCACTCTTAC CGTTGCTCTT
      TTATTTTACT TTGTTTCGTG ATAACGTGAC CGTGAGAATG GCAACGAGAA
                                      VH3
                          ------------------------------------
            phoA
      ---------------------
      SapI                        MfeI
      ~                           -------
      · T  P  V  T  K  A  Q  V  Q  L  V  E  S  G  G  G  L ·
801   CACCCCTGTT ACCAAAGCCG AAGTGCAATT GGTGGAAAGC GGCGGCGGCC
      GTGGGGACAA TGGTTTCGGC TTCACGTTAA CCACCTTTCG CCGCCGCCGG
                                VH3
      ------------------------------------------------------
      · V  Q  P  G  G  S  L  R  L  S  C  A  A  S  G  F
851   TGGTGCAACC GGGCGGCAGC CTGCGTCTGA GCTGCGCGGC CTCCGGATTT
      ACCACGTTGG CCCGCCGTCG GACGCAGACT CGACGCGCCG GAGGCCTAAA
                                VH3
      ------------------------------------------------------
       T  F  S  S  Y  A  M  S  W  V  R  Q  A  P  G  K  G ·
901   ACCTTTAGCA GCTATGCGAT GAGCTGGGTG CGCCAAGCCC CTGGGAAGGG
      TGGAAATCGT CGATACGCTA CTCGACCCAC GCGGTTCGGG GACCCTTCCC
                                VH3
      ------------------------------------------------------
      · L  E  W  V  S  A  I  S  G  S  G  G  S  T  Y  Y  A ·
951   TCTCGAGTGG GTGAGCGCGA TTAGCGGTAG CGGCGGCAGC ACCTATTATG
      AGAGCTCACC CACTCGCGCT AATCGCCATC GCCGCCGTCG TGGATAATAC
                                VH3
      ------------------------------------------------------
                                            PmlI
                                            ------
      ·  D  S  V  K  G  R  F  T  I  S  R  D  N  S  K  N
1001  CGGATAGCGT GAAAGGCCGT TTTACCATTT CACGTGATAA TTCGAAAAAC
      GCCTATCGCA CTTTCCGGCA AAATGGTAAA GTGCACTATT AAGCTTTTTG
                                VH3
      ------------------------------------------------------
       T  L  Y  L  Q  M  N  S  L  R  A  E  D  T  A  V  Y ·
1051  ACCCTGTATC TGCAAATGAA CAGCCTGCGT GCGGAAGATA CGGCCGTGTA
      TGGGACATAG ACGTTTACTT GTCGGACGCA CGCCTTCTAT GCCGGCACAT
                                VH3
      ------------------------------------------------------
          BssHII
```

Fig. 2 cont.

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```
                 -------
      · Y  C  A   R  W  G  G   D  G  F   Y  A  M   D  Y  W  G ·
1101  TTATTGCGCG CGTTGGGGCG GCGATGGCTT TTATGCGATG GATTATTGGG
      AATAACGCGC GCAACCCCGC CGCTACCGAA AATACGCTAC CTAATAACCC
                                                 CH1
                                        ------------------------
                    VH3
      ---------------------------------
                                                  SalI
                                                  ------
        StyI                          BlpI
        ------                        --------
      ·  Q  G  T   L  V  T   V  S  S  A   S  T  K   G  P  S
1151  GCCAAGGCAC CCTGGTGACG GTTAGCTCAG CGTCGACCAA AGGTCCAAGC
      CGGTTCCGTG GGACCACTGC CAATCGAGTC GCAGCTGGTT TCCAGGTTCG
                               CH1
      ------------------------------------------------------
       V  F  P  L   A  P  S   S  K  S   T  S  G  G   T  A  A ·
1201  GTGTTTCCGC TGGCTCCGAG CAGCAAAAGC ACCAGCGGCG GCACGGCTGC
      CACAAAGGCG ACCGAGGCTC GTCGTTTTCG TGGTCGCCGC CGTGCCGACG
                               CH1
      ------------------------------------------------------
      · L  G  C   L  V  K  D   Y  F  P   E  P  V   T  V  S  W ·
1251  CCTGGGCTGC CTGGTTAAAG ATTATTTCCC GGAACCAGTC ACCGTGAGCT
      GGACCCGACG GACCAATTTC TAATAAAGGG CCTTGGTCAG TGGCACTCGA
                               CH1
      ------------------------------------------------------
      ·  N  S  G   A  L  T   S  G  V  H   T  F  P   A  V  L
1301  GGAACAGCGG GGCGCTGACC AGCGGCGTGC ATACCTTTCC GGCGGTGCTG
      CCTTGTCGCC CCGCGACTGG TCGCCGCACG TATGGAAAGG CCGCCACGAC
                               CH1
      ------------------------------------------------------
       Q  S  S  G   L  Y  S   L  S  S   V  V  T  V   P  S  S ·
1351  CAAAGCAGCG GCCTGTATAG CCTGAGCAGC GTTGTGACCG TGCCGAGCAG
      GTTTCGTCGC CGGACATATC GGACTCGTCG CAACACTGGC ACGGCTCGTC
                               CH1
      ------------------------------------------------------
      · S  L  G   T  Q  T  Y   I  C  N   V  N  H   K  P  S  N ·
1401  CAGCTTAGGC ACTCAGACCT ATATTTGCAA CGTGAACCAT AAACCGAGCA
      GTCGAATCCG TGAGTCTGGA TATAAACGTT GCACTTGGTA TTTGGCTCGT
                    CH1                              CTgIII
      ---------------------------------------      ----------
                                              EcoRI
                                              -------
      ·  T  K  V   D  K  K   V  E  P  K   S  E  F   G  G  G
1451  ACACCAAAGT GGATAAAAAA GTGGAACCGA AAAGCGAATT CGGGGGAGGG
      TGTGGTTTCA CCTATTTTTT CACCTTGGCT TTTCGCTTAA GCCCCCTCCC
                               CTgIII
      ------------------------------------------------------
       S  G  S  G   D  F  D   Y  E  K   M  A  N  A   N  K  G ·
1501  AGCGGGAGCG GTGATTTTGA TTATGAAAAG ATGGCAAACG CTAATAAGGG
      TCGCCCTCGC CACTAAAACT AATACTTTTC TACCGTTTGC GATTATTCCC
                               CTgIII
      ------------------------------------------------------
      · A  M  T  E  N  A  D  E  N  A  L  Q  S  D  A  K  G ·
1551  GGCTATGACC GAAAATGCCG ATGAAAACGC GCTACAGTCT GACGCTAAAG
      CCGATACTGG CTTTTACGGC TACTTTTGCG CGATGTCAGA CTGCGATTTC
                               CTgIII
      ------------------------------------------------------
      ·  K  L  D   S  V  A   T  D  Y  G   A  A  I   D  G  F
1601  GCAAACTTGA TTCTGTCGCT ACTGATTACG GTGCTGCTAT CGATGGTTTC
```

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```
        CGTTTGAACT AAGACAGCGA TGACTAATGC CACGACGATA GCTACCAAAG
                                CTgIII
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         I  G  D  V   S  G  L   A  N  G   N  G  A  T   G  D  F
1651    ATTGGTGACG TTTCCGGCCT TGCTAATGGT AATGGTGCTA CTGGTGATTT
        TAACCACTGC AAAGGCCGGA ACGATTACCA TTACCACGAT GACCACTAAA
                                CTgIII
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         A  G  S   N  S  Q  M   A  Q  V   G  D  G   D  N  S  P
1701    TGCTGGCTCT AATTCCCAAA TGGCTCAAGT CGGTGACGGT GATAATTCAC
        ACGACCGAGA TTAAGGGTTT ACCGAGTTCA GCCACTGCCA CTATTAAGTG
                                CTgIII
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         L  M  N   N  F  R   Q  Y  L   P  S  L   P  Q  S  V
1751    CTTTAATGAA TAATTTCCGT CAATATTTAC CTTCCCTCCC TCAATCGGTT
        GAAATTACTT ATTAAAGGCA GTTATAAATG GAAGGGAGGG AGTTAGCCAA
                                CTgIII
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         E  C  R  P   F  V  F   G  A  G   K  P  Y  E   F  S  I
1801    GAATGTCGCC CTTTTGTCTT TGGCGCTGGT AAACCATATG AATTTTCTAT
        CTTACAGCGG GAAAACAGAA ACCGCGACCA TTTGGTATAC TTAAAAGATA
                                CTgIII
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         D  C  D   K  I  N  L   F  R  G   V  F  A   F  L  L  Y
1851    TGATTGTGAC AAAATAAACT TATTCCGTGG TGTCTTTGCG TTTCTTTTAT
        ACTAACACTG TTTTATTTGA ATAAGGCACC ACAGAAACGC AAAGAAAATA
                                CTgIII
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         V  A  T   F  M  Y   V  F  S  T   F  A  N   I  L  R
1901    ATGTTGCCAC CTTTATGTAT GTATTTTCTA CGTTTGCTAA CATACTGCGT
        TACAACGGTG GAAATACATA CATAAAAGAT GCAAACGATT GTATGACGCA
           CTgIII
        ~~~~~~~~~~~~
                    Stop              lpp terminator
                    ~~~               ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                        HindIII
                        ~~~~~~~
         N  K  E  S
1951    AATAAGGAGT CTTGATAAGC TTGACCTGTG AAGTGAAAAA TGGCGCAGAT
        TTATTCCTCA GAACTATTCG AACTGGACAC TTCACTTTTT ACCGCGTCTA
        lpp terminator
        ~~~~~~~~~
2001    TGTGCGACAT TTTTTTTGTC TGCCGTTTAA TGAAATTGTA AACGTTAATA
        ACACGCTGTA AAAAAAACAG ACGGCAAATT ACTTTAACAT TTGCAATTAT
                                                 ~~~~~~~~~~~~~~~~
                                                        f1 origin
2051    TTTTGTTAAA ATTCGCGTTA AATTTTTGTT AAATCAGCTC ATTTTTTAAC
        AAAACAATTT TAAGCGCAAT TTAAAAACAA TTTAGTCGAG TAAAAAATTG
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                f1 origin
2101    CAATAGGCCG AAATCGGCAA AATCCCTTAT AAATCAAAAG AATAGACCGA
        GTTATCCGGC TTTAGCCGTT TTAGGGAATA TTTAGTTTTC TTATCTGGCT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                f1 origin
2151    GATAGGGTTG AGTGTTGTTC CAGTTTGGAA CAAGAGTCCA CTATTAAAGA
        CTATCCCAAC TCACAACAAG GTCAAACCTT GTTCTCAGGT GATAATTTCT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                f1 origin
2201    ACGTGGACTC CAACGTCAAA GGGCGAAAAA CCGTCTATCA GGGCGATGGC
        TGCACCTGAG GTTGCAGTTT CCCGCTTTTT GGCAGATAGT CCCGCTACCG
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

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Fig. 2 cont.

```
                                f1 origin
                 T->A
                  ~
2251    CCACTACGAG AACCATCACC CTAATCAAGT TTTTTGGGGT CGAGGTGCCG
        GGTGATGCTC TTGGTAGTGG GATTAGTTCA AAAAACCCCA GCTCCACGGC
        ----------------------------------------------------------
                                f1 origin
2301    TAAAGCACTA AATCGGAACC CTAAAGGGAG CCCCCGATTT AGAGCTTGAC
        ATTTCGTGAT TTAGCCTTGG GATTTCCCTC GGGGGCTAAA TCTCGAACTG
        ----------------------------------------------------------
                                f1 origin
2351    GGGGAAAGCC GGCGAACGTG GCGAGAAAGG AAGGGAAGAA AGCGAAAGGA
        CCCCTTTCGG CCGCTTGCAC CGCTCTTTCC TTCCCTTCTT TCGCTTTCCT
        ----------------------------------------------------------
                                f1 origin
2401    GCGGGCGCTA GGGCGCTGGC AAGTGTAGCG GTCACGCTGC GCGTAACCAC
        CGCCCGCGAT CCCGCGACCG TTCACATCGC CAGTGCGACG CGCATTGGTG
        ----------------------------------------------------------
                                f1 origin
                                                      NheI
                                                      ~~~~~~~
2451    CACACCCGCC GCGCTTAATG CGCCGCTACA GGGCGCGTGC TAGCCATGTG
        GTGTGGGCGG CGCGAATTAC GCGGCGATGT CCCGCGCACG ATCGGTACAC
        ------------------------------------------      ~~
                        f1 origin                        ColEI
2501    AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAAGGCC GCGTTGCTGG
        TCGTTTTCCG GTCGTTTTCC GGTCCTTGGC ATTTTTCCGG CGCAACGACC
        ----------------------------------------------------------
                                ColEI
           ORI
            ~
2551    CGTTTTTCCA TAGGCTCCGC CCCCCTGACG AGCATCACAA AAATCGACGC
        GCAAAAAGGT ATCCGAGGCG GGGGGACTGC TCGTAGTGTT TTTAGCTGCG
        ----------------------------------------------------------
                                ColEI
2601    TCAAGTCAGA GGTGGCGAAA CCCGACAGGA CTATAAAGAT ACCAGGCGTT
        AGTTCAGTCT CCACCGCTTT GGGCTGTCCT GATATTTCTA TGGTCCGCAA
        ----------------------------------------------------------
                                ColEI
2651    TCCCCCTGGA AGCTCCCTCG TGCGCTCTCC TGTTCCGACC CTGCCGCTTA
        AGGGGGACCT TCGAGGGAGC ACGCGAGAGG ACAAGGCTGG GACGGCGAAT
        ----------------------------------------------------------
                                ColEI
                                                              mutation
                                                              ~
2701    CCGGATACCT GTCCGCCTTT CTCCCTTCGG GAAGCGTGGC GCTTTCTCAT
        GGCCTATGGA CAGGCGGAAA GAGGGAAGCC CTTCGCACCG CGAAAGAGTA
        ----------------------------------------------------------
                                ColEI
        mutation
        ~
2751    AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTC GCTCCAAGCT
        TCGAGTGCGA CATCCATAGA GTCAAGCCAC ATCCAGCAAG CGAGGTTCGA
        ----------------------------------------------------------
                                ColEI
                                        mutation
                                        ~
2801    GGGCTGTGTG CACGAACCCC CCGTTCAGTC CGACCGCTGC GCCTTATCCG
        CCCGACACAC GTGCTTGGGG GGCAAGTCAG GCTGGCGACG CGGAATAGGC
        ----------------------------------------------------------
                                ColEI
```

Fig. 2 cont.

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```
2851   GTAACTATCG TCTTGAGTCC AACCCGGTAA GACACGACTT ATCGCCACTG
       CATTGATAGC AGAACTCAGG TTGGGCCATT CTGTGCTGAA TAGCGGTGAC
       ----------------------------------------------------
                            ColEI
2901   GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG TAGGCGGTGC
       CGTCGTCGGT GACCATTGTC CTAATCGTCT CGCTCCATAC ATCCGCCACG
       ----------------------------------------------------
                            ColEI
                                                      mutation
                                                      -
2951   TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGGCTACACT AGAAGAACAG
       ATGTCTCAAG AACTTCACCA CCGGATTGAT GCCGATGTGA TCTTCTTGTC
       ----------------------------------------------------
                            ColEI
                               mutation
                               -
3001   TATTTGGTAT CTGCGCTCTG CTGTAGCCAG TTACCTTCGG AAAAAGAGTT
       ATAAACCATA GACGCGAGAC GACATCGGTC AATGGAAGCC TTTTTCTCAA
       ----------------------------------------------------
                            ColEI
3051   GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT
       CCATCGAGAA CTAGGCCGTT TGTTTGGTGG CGACCATCGC CACCAAAAAA
       ----------------------------------------------------
                            ColEI
3101   TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC
       ACAAACGTTC GTCGTCTAAT GCGCGTCTTT TTTTCCTAGA GTTCTTCTAG
       ----------------------------------------------------
                            ColEI
3151   CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGAACGA AAACTCACGT
       GAAACTAGAA AAGATGCCCC AGACTGCGAG TCACCTTGCT TTTGAGTGCA
       ----------------------------------------------------
                            ColEI
                                                cat terminator
                                               ~~~~~~~~~~~~~~~~~~~
                     BglII
                     -------
3201   TAAGGGATTT TGGTCAGATC TAGCACCAGG CGTTTAAGGG CACCAATAAC
       ATTCCCTAAA ACCAGTCTAG ATCGTGGTCC GCAAATTCCC GTGGTTATTG
       ~~~~~~~~~~~~~~~~
            ColEI
       cat terminator
       ~~~~~~~~~
3251   TGCCTTAAAA AAATTACGCC CCGCCCTGCC ACTCATCGCA GTACTGTTGT
       ACGGAATTTT TTTAATGCGG GGCGGGACGG TGAGTAGCGT CATGACAACA
                      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                          CM(R)
3301   AATTCATTAA GCATTCTGCC GACATGGAAG CCATCACAAA CGGCATGATG
       TTAAGTAATT CGTAAGACGG CTGTACCTTC GGTAGTGTTT GCCGTACTAC
       ----------------------------------------------------
                            CM(R)
3351   AACCTGAATC GCCAGCGGCA TCAGCACCTT GTCGCCTTGC GTATAATATT
       TTGGACTTAG CGGTCGCCGT AGTCGTGGAA CAGCGGAACG CATATTATAA
       ----------------------------------------------------
                            CM(R)
3401   TGCCCATAGT GAAAACGGGG GCGAAGAAGT TGTCCATATT GGCTACGTTT
       ACGGGTATCA CTTTTGCCCC CGCTTCTTCA ACAGGTATAA CCGATGCAAA
       ----------------------------------------------------
                            CM(R)
3451   AAATCAAAAC TGGTGAAACT CACCCAGGGA TTGGCTGAGA CGAAAAACAT
       TTTAGTTTTG ACCACTTTGA GTGGGTCCCT AACCGACTCT GCTTTTTGTA
       ----------------------------------------------------
```

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Fig. 2 cont.

```
                              CM(R)
3501   ATTCTCAATA AACCCTTTAG GGAAATAGGC CAGGTTTTCA CCGTAACACG
       TAAGAGTTAT TTGGGAAATC CCTTTATCCG GTCCAAAAGT GGCATTGTGC
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              CM(R)
3551   CCACATCTTG CGAATATATG TGTAGAAACT GCCGGAAATC GTCGTGGTAT
       GGTGTAGAAC GCTTATATAC ACATCTTTGA CGGCCTTTAG CAGCACCATA
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              CM(R)
3601   TCACTCCAGA GCGATGAAAA CGTTTCAGTT TGCTCATGGA AAACGGTGTA
       AGTGAGGTCT CGCTACTTTT GCAAAGTCAA ACGAGTACCT TTTGCCACAT
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              CM(R)
3651   ACAAGGGTGA ACACTATCCC ATATCACCAG CTCACCGTCT TTCATTGCCA
       TGTTCCCACT TGTGATAGGG TATAGTGGTC GAGTGGCAGA AAGTAACGGT
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              CM(R)
3701   TACGGAACTC CGGGTGAGCA TTCATCAGGC GGGCAAGAAT GTGAATAAAG
       ATGCCTTGAG GCCCACTCGT AAGTAGTCCG CCCGTTCTTA CACTTATTTC
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              CM(R)
3751   GCCGGATAAA ACTTGTGCTT ATTTTTCTTT ACGGTCTTTA AAAAGGCCGT
       CGGCCTATTT TGAACACGAA TAAAAAGAAA TGCCAGAAAT TTTTCCGGCA
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              CM(R)
3801   AATATCCAGC TGAACGGTCT GGTTATAGGT ACATTGAGCA ACTGACTGAA
       TTATAGGTCG ACTTGCCAGA CCAATATCCA TGTAACTCGT TGACTGACTT
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              CM(R)
3851   ATGCCTCAAA ATGTTCTTTA CGATGCCATT GGGATATATC AACGGTGGTA
       TACGGAGTTT TACAAGAAAT GCTACGGTAA CCCTATATAG TTGCCACCAT
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              CM(R)
3901   TATCCAGTGA TTTTTTTCTC CATTTTAGCT TCCTTAGCTC CTGAAAATCT
       ATAGGTCACT AAAAAAAGAG GTAAAATCGA AGGAATCGAG GACTTTTAGA
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~                ~~~~~
                CM(R)                              SD
                                        ~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                                cat promoter
3951   CGATAACTCA AAAAATACGC CCGGTAGTGA TCTTATTTCA TTATGGTGAA
       GCTATTGAGT TTTTTATGCG GGCCATCACT AGAATAAAGT AATACCACTT
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                           cat promoter
                                              CRP site
                                          ~~~~~~~~~~~~~~~~
4001   AGTTGGAACC TCACCCGACG TCTAATGTGA GTTAGCTCAC TCATTAGGCA
       TCAACCTTGG AGTGGGCTGC AGATTACACT CAATCGAGTG AGTAATCCGT
       ~~~~~~~~~~~~~~
       cat promoter
                                                          lac mRNA
       start
                                                          ~
                                                        lac operator
                                                        ~~~~~~~
                -35 region                    -10 region
                ~~~~~~~                       ~~~~~~
4051   CCCCAGGCTT TACACTTTAT GCTTCCGGCT CGTATGTTGT GTGGAATTGT
       GGGGTCCGAA ATGTGAAATA CGAAGGCCGA GCATACAACA CACCTTAACA
        lac operator              SD                  lacZ´
       ~~~~~~~~~~~~~~~~       ~~~~~          ~~~~~~~~~~~~~~~~~~~
4101   GAGCGGATAA CAATTTCACA CAGGAAACAG CTATGACCAT GATTACGAAT
```

Fig. 2 cont.

```
        CTCGCCTATT GTTAAAGTGT GTCCTTTGTC GATACTGGTA CTAATGCTTA
        lacZ´
        ~
4151    T
        A
```

Fig. 3

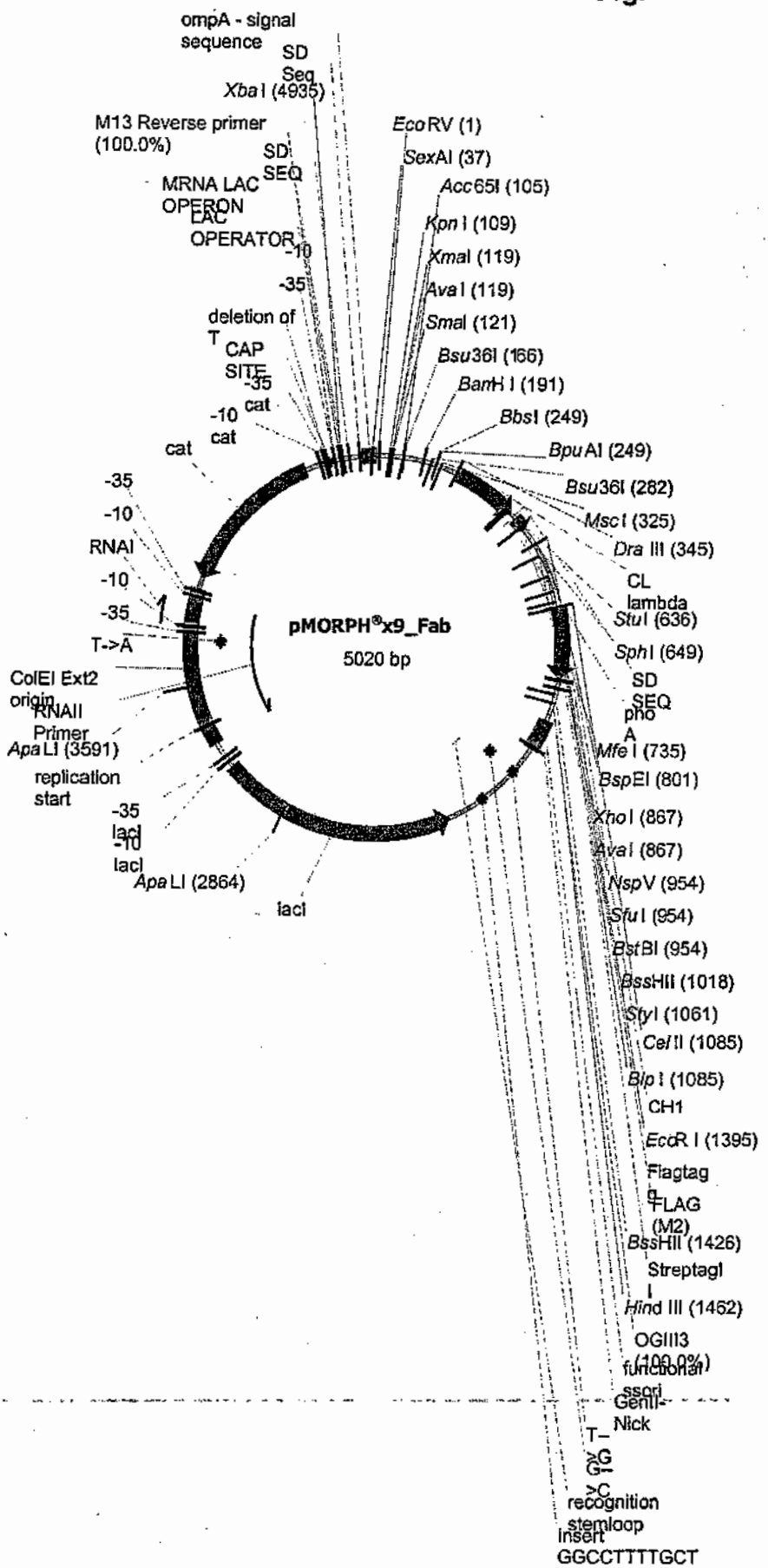

pMORPH®x9_Fab
5020 bp
ompA - signal sequence
SD Seq
XbaI (4935)
M13 Reverse primer (100.0%)
SD SEQ
MRNA LAC OPERON
LAC OPERATOR
-10
-35
deletion of T
CAP SITE
-35
cat
-10
cat
cat
-35
-10
RNAI
-10
-35
T->A
ColEI Ext2 origin
RNAII Primer
ApaLI (3591)
replication start
-35
lacI
-10
lacI
ApaLI (2864)
lacI
EcoRV (1)
SexAI (37)
Acc65I (105)
KpnI (109)
XmaI (119)
AvaI (119)
SmaI (121)
Bsu36I (166)
BamH I (191)
BbsI (249)
BpuAI (249)
Bsu36I (282)
MscI (325)
Dra III (345)
CL lambda
StuI (636)
SphI (649)
SD SEQ pho A
MfeI (735)
BspEI (801)
XhoI (867)
AvaI (867)
NspV (954)
SfuI (954)
BstBI (954)
BssHII (1018)
StyI (1061)
CelII (1085)
BlpI (1085)
CH1
EcoR I (1395)
Flagtag
FLAG (M2)
BssHII (1426)
Streptagl
Hind III (1462)
OGIII3 (100.0%)
functional ssori
GenII-Nick
T_
>G
G_
>C
recognition stemloop
insert
GGCCTTTTGCT

Fig. 3 cont.

```
      EcoRV                                                SexAI
      ~~~                                                  ~~~~~~~~
    1 ATCGTGCTGA CCCAGCCGCC TTCAGTGAGT GGCGCACCAG GTCAGCGTGT
      TAGCACGACT GGGTCGGCGG AAGTCACTCA CCGCGTGGTC CAGTCGCACA

   51 GACCATCTCG TGTAGCGGCA GCAGCAGCAA CATTGGCAGC AACTATGTGA
      CTGGTAGAGC ACATCGCCGT CGTCGTCGTT GTAACCGTCG TTGATACACT

                         XmaI
                         ~~~~~~~
          KpnI           SmaI
          ~~~~~~         ~~~~~~~
         Acc65I          AvaI
         ~~~~~~          ~~~~~~~
  101 GCTGGTACCA GCAGTTGCCC GGGACGGCGC CGAAACTGCT GATTTATGAT
      CGACCATGGT CGTCAACGGG CCCTGCCGCG GCTTTGACGA CTAAATACTA

                    Bsu36I                              BamHI
                    ~~~~~~~                             ~~~~~~~
  151 AACAACCAGC GTCCCTCAGG CGTGCCGGAT CGTTTTAGCG GATCCAAAAG
      TTGTTGGTCG CAGGGAGTCC GCACGGCCTA GCAAAATCGC CTAGGTTTTC

                                                        BpuAI
                                                        ~~~~~~
                                                        BbsI
                                                        ~~~~~~
  201 CGGCACCAGC GCGAGCCTTG CGATTACGGG CCTGCAAAGC GAAGACGAAG
      GCCGTGGTCG CGCTCGGAAC GCTAATGCCC GGACGTTTCG CTTCTGCTTC

                                        Bsu36I
                                        ~~~~~~~~
  251 CGGATTATTA TTGCCAGAGC TATGACATGC CTCAGGCTGT GTTTGGCGGC
      GCCTAATAAT AACGGTCTCG ATACTGTACG GAGTCCGACA CAAACCGCCG

                                 MscI                DraIII
                                 ~~~~~~              ~~~~~~~~~~
  301 GGCACGAAGT TTAACCGTTC TTGGCCAGCC GAAAGCCGCA CCGAGTGTGA
      CCGTGCTTCA AATTGGCAAG AACCGGTCGG CTTTCGGCGT GGCTCACACT

  351 CGCTGTTTCC GCCGAGCAGC GAAGAATTGC AGGCGAACAA AGCGACCCTG
      GCGACAAAGG CGGCTCGTCG CTTCTTAACG TCCGCTTGTT TCGCTGGGAC

  401 GTGTGCCTGA TTAGCGACTT TTATCCGGGA GCCGTGACAG TGGCCTGGAA
      CACACGGACT AATCGCTGAA AATAGGCCCT CGGCACTGTC ACCGGACCTT

  451 GGCAGATAGC AGCCCCGTCA AGGCGGGAGT GGAGACCACC ACACCCTCCA
      CCGTCTATCG TCGGGGCAGT TCCGCCCTCA CCTCTGGTGG TGTGGGAGGT

  501 AACAAAGCAA CAACAAGTAC GCGGCCAGCA GCTATCTGAG CCTGACGCCT
      TTGTTTCGTT GTTGTTCATG CGCCGGTCGT CGATAGACTC GGACTGCGGA

  551 GAGCAGTGGA AGTCCCACAG AAGCTACAGC TGCCAGGTCA CGCATGAGGG
      CTCGTCACCT TCAGGGTGTC TTCGATGTCG ACGGTCCAGT GCGTACTCCC
```

Fig. 3 cont.

```
                                                    StuI        SphI
                                                    ~~~~~~      ~~~~~~
 601  GAGCACCGTG GAAAAAACCG TTGCGCCGAC TGAGGCCTGA TAAGCATGCG
      CTCGTGGCAC CTTTTTTGGC AACGCGGCTG ACTCCGGACT ATTCGTACGC

 651  TAGGAGAAAA TAAAATGAAA CAAAGCACTA TTGCACTGGC ACTCTTACCG
      ATCCTCTTTT ATTTTACTTT GTTTCGTGAT AACGTGACCG TGAGAATGGC

                                                   MfeI
                                                   ~~~~~~
 701  TTGCTCTTCA CCCCTGTTAC CAAAGCCCAG GTGCAATTGA AAGAAAGCGG
      AACGAGAAGT GGGGACAATG GTTTCGGGTC CACGTTAACT TTCTTTCGCC

                                                          BspEI
                                                          ~
 751  CCCGGCCCTG GTGAAACCGA CCCAAACCCT GACCCTGACC TGTACCTTTT
      GGGCCGGGAC CACTTTGGCT GGGTTTGGGA CTGGGACTGG ACATGGAAAA

      BspEI
      ~~~~~
 801  CCGGATTTAG CCTGTCCACG TCTGGCGTTG GCGTGGGCTG GATTCGCCAG
      GGCCTAAATC GGACAGGTGC AGACCGCAAC CGCACCCGAC CTAAGCGGTC

                        XhoI
                        ~~~~~~~
                        AvaI
                        ~~~~~~~
 851  CCGCCTGGGA AAGCCCTCGA GTGGCTGGCT CTGATTGATT GGGATGATGA
      GGCGGACCCT TTCGGGAGCT CACCGACCGA GACTAACTAA CCCTACTACT

 901  TAAGTATTAT AGCACCAGCC TGAAAACGCG TCTGACCATT AGCAAAGATA
      ATTCATAATA TCGTGGTCGG ACTTTTGCGC AGACTGGTAA TCGTTTCTAT

       BstBI
       ~~~~~~
       SfuI
       ~~~~~~
       NspV
       ~~~~~~
 951  CTTCGAAAAA TCAGGTGGTG CTGACTATGA CCAACATGGA CCCGGTGGAT
      GAAGCTTTTT AGTCCACCAC GACTGATACT GGTTGTACCT GGGCCACCTA

                        BssHII
                        ~~~~~~~
1001  ACGGCCACCT ATTATTGCGC GCGTTCTCCT CGTTATCGTG GTGCTTTTGA
      TGCCGGTGGA TAATAACGCG CGCAAGAGGA GCAATAGCAC CACGAAAACT

                                                   BlpI
                                                   ~~~~~~~
                    StyI                           CelII
                    ~~~~~~~                        ~~~~~~~
1051  TTATTGGGGC CAAGGCACCC TGGTGACGGT TAGCTCAGCG TCGACCAAAG
      AATAACCCCG GTTCCGTGGG ACCACTGCCA ATCGAGTCGC AGCTGGTTTC
```

Fig. 3 cont.

```
1101  GTCCAAGCGT GTTTCCGCTG GCTCCGAGCA GCAAAAGCAC CAGCGGCGGC
      CAGGTTCGCA CAAAGGCGAC CGAGGCTCGT CGTTTTCGTG GTCGCCGCCG

1151  ACGGCTGCCC TGGGCTGCCT GGTTAAAGAT TATTTCCCGG AACCAGTCAC
      TGCCGACGGG ACCCGACGGA CCAATTTCTA ATAAAGGGCC TTGGTCAGTG

1201  CGTGAGCTGG AACAGCGGGG CGCTGACCAG CGGCGTGCAT ACCTTTCCGG
      GCACTCGACC TTGTCGCCCC GCGACTGGTC GCCGCACGTA TGGAAAGGCC

1251  CGGTGCTGCA AAGCAGCGGC CTGTATAGCC TGAGCAGCGT TGTGACCGTG
      GCCACGACGT TTCGTCGCCG GACATATCGG ACTCGTCGCA ACACTGGCAC

1301  CCGAGCAGCA GCTTAGGCAC TCAGACCTAT ATTTGCAACG TGAACCATAA
      GGCTCGTCGT CGAATCCGTG AGTCTGGATA TAAACGTTGC ACTTGGTATT

                                                      EcoRI
                                                      ~~~~~~
1351  ACCGAGCAAC ACCAAAGTGG ATAAAAAAGT GGAACCGAAA AGCGAATTCG
      TGGCTCGTTG TGGTTTCACC TATTTTTTCA CCTTGGCTTT TCGCTTAAGC

                                  BssHII
                                  ~~~~~~
1401  ACTATAAAGA TGACGATGAC AAAGGCGCGC CGTGGAGCCA CCCGCAGTTT
      TGATATTTCT ACTGCTACTG TTTCCGCGCG GCACCTCGGT GGGCGTCAAA

                HindIII
                ~~~~~~
1451  GAAAAATGAT AAGCTTGACC TGTGAAGTGA AAAATGGCGC AGATTGTGCG
      CTTTTTACTA TTCGAACTGG ACACTTCACT TTTTACCGCG TCTAACACGC
                         OGIII3  100.0%
                       ====================

1501  ACATTTTTTT TGTCTGCCGT TTAATTAAAG GGGGGGGGGG GCCGGCCTGG
      TGTAAAAAAA ACAGACGGCA AATTAATTTC CCCCCCCCCC CGGCCGGACC

1551  GGGGGGGTGT ACATGAAATT GTAAACGTTA ATATTTTGTT AAAATTCGCG
      CCCCCCCACA TGTACTTTAA CATTTGCAAT TATAAAACAA TTTTAAGCGC

1601  TTAAATTTTT GTTAAATCAG CTCATTTTTT AACCAATAGG CCGAAATCGG
      AATTTAAAAA CAATTTAGTC GAGTAAAAAA TTGGTTATCC GGCTTTAGCC

1651  CAAAATCCCT TATAAATCAA AAGAATAGAC CGAGATAGGG TTGAGTGTTG
      GTTTTAGGGA ATATTTAGTT TTCTTATCTG GCTCTATCCC AACTCACAAC

1701  TTCCAGTTTG GAACAAGAGT CCACTATTAA AGAACGTGGA CTCCAACGTC
      AAGGTCAAAC CTTGTTCTCA GGTGATAATT TCTTGCACCT GAGGTTGCAG

1751  AAAGGGCGAA AAACCGTCTA TCAGGGCGAT GGCCCACTAC GAGAACCATC
      TTTCCCGCTT TTTGGCAGAT AGTCCCGCTA CCGGGTGATG CTCTTGGTAG

1801  ACCCTAATCA AGTTTTTTGG GGTCGAGGTG CCGTAAAGCA CTAAATCGGA
      TGGGATTAGT TCAAAAAACC CCAGCTCCAC GGCATTTCGT GATTTAGCCT
```

Fig. 3 cont.

```
1851  ACCCTAAAGG GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC
      TGGGATTTCC CTCGGGGGCT AAATCTCGAA CTGCCCCTTT CGGCCGCTTG

1901  GTGGCGAGAA AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT
      CACCGCTCTT TCCTTCCCTT CTTTCGCTTT CCTCGCCCGC GATCCCGCGA

1951  GGCAAGTGTA GCGGTCACGC TGCGCGTAAC CACCACACCC GCCGCGCTTA
      CCGTTCACAT CGCCAGTGCG ACGCGCATTG GTGGTGTGGG CGGCGCGAAT

2001  ATGCGCCGCT ACAGGGCGCG TGCTAGACTA GTGTTTAAAC CGGACCGGGG
      TACGCGGCGA TGTCCCGCGC ACGATCTGAT CACAAATTTG GCCTGGCCCC

2051  GGGGGCTTAA GTGGGCTGCA AAACAAAACG GCCTCCTGTC AGGAAGCCGC
      CCCCCGAATT CACCCGACGT TTTGTTTTGC CGGAGGACAG TCCTTCGGCG

2101  TTTTATCGGG TAGCCTCACT GCCCGCTTTC CAGTCGGGAA ACCTGTCGTG
      AAAATAGCCC ATCGGAGTGA CGGGCGAAAG GTCAGCCCTT TGGACAGCAC

2151  CCAGCTGCAT CAGTGAATCG GCCAACGCGC GGGGAGAGGC GGTTTGCGTA
      GGTCGACGTA GTCACTTAGC CGGTTGCGCG CCCCTCTCCG CCAAACGCAT

2201  TTGGGAGCCA GGGTGGTTTT TCTTTTCACC AGTGAGACGG GCAACAGCTG
      AACCCTCGGT CCCACCAAAA AGAAAAGTGG TCACTCTGCC CGTTGTCGAC

2251  ATTGCCCTTC ACCGCCTGGC CCTGAGAGAG TTGCAGCAAG CGGTCCACGC
      TAACGGGAAG TGGCGGACCG GGACTCTCTC AACGTCGTTC GCCAGGTGCG

2301  TGGTTTGCCC CAGCAGGCGA AAATCCTGTT TGATGGTGGT CAGCGGCGGG
      ACCAAACGGG GTCGTCCGCT TTTAGGACAA ACTACCACCA GTCGCCGCCC

2351  ATATAACATG AGCTGTCCTC GGTATCGTCG TATCCCACTA CCGAGATGTC
      TATATTGTAC TCGACAGGAG CCATAGCAGC ATAGGGTGAT GGCTCTACAG

2401  CGCACCAACG CGCAGCCCGG ACTCGGTAAT GGCACGCATT GCGCCCAGCG
      GCGTGGTTGC GCGTCGGGCC TGAGCCATTA CCGTGCGTAA CGCGGGTCGC

2451  CCATCTGATC GTTGGCAACC AGCATCGCAG TGGGAACGAT GCCCTCATTC
      GGTAGACTAG CAACCGTTGG TCGTAGCGTC ACCCTTGCTA CGGGAGTAAG

2501  AGCATTTGCA TGGTTTGTTG AAAACCGGAC ATGGCACTCC AGTCGCCTTC
      TCGTAAACGT ACCAAACAAC TTTTGGCCTG TACCGTGAGG TCAGCGGAAG

2551  CCGTTCCGCT ATCGGCTGAA TTTGATTGCG AGTGAGATAT TTATGCCAGC
      GGCAAGGCGA TAGCCGACTT AAACTAACGC TCACTCTATA AATACGGTCG

2601  CAGCCAGACG CAGACGCGCC GAGACAGAAC TTAATGGGCC AGCTAACAGC
      GTCGGTCTGC GTCTGCGCGG CTCTGTCTTG AATTACCCGG TCGATTGTCG

2651  GCGATTTGCT GGTGGCCCAA TGCGACCAGA TGCTCCACGC CCAGTCGCGT
      CGCTAAACGA CCACCGGGTT ACGCTGGTCT ACGAGGTGCG GGTCAGCGCA

2701  ACCGTCCTCA TGGGAGAAAA TAATACTGTT GATGGGTGTC TGGTCAGAGA
      TGGCAGGAGT ACCCTCTTTT ATTATGACAA CTACCCACAG ACCAGTCTCT
```

Fig. 3 cont.

```
2751  CATCAAGAAA TAACGCCGGA ACATTAGTGC AGGCAGCTTC CACAGCAATA
      GTAGTTCTTT ATTGCGGCCT TGTAATCACG TCCGTCGAAG GTGTCGTTAT

2801  GCATCCTGGT CATCCAGCGG ATAGTTAATA ATCAGCCCAC TGACACGTTG
      CGTAGGACCA GTAGGTCGCC TATCAATTAT TAGTCGGGTG ACTGTGCAAC

                    ApaLI
                    ~~~~~~
2851  CGCGAGAAGA TTGTGCACCG CCGCTTTACA GGCTTCGACG CCGCTTCGTT
      GCGCTCTTCT AACACGTGGC GGCGAAATGT CCGAAGCTGC GGCGAAGCAA

2901  CTACCATCGA CACGACCACG CTGGCACCCA GTTGATCGGC GCGAGATTTA
      GATGGTAGCT GTGCTGGTGC GACCGTGGGT CAACTAGCCG CGCTCTAAAT

2951  ATCGCCGCGA CAATTTGCGA CGGCGCGTGC AGGGCCAGAC TGGAGGTGGC
      TAGCGGCGCT GTTAAACGCT GCCGCGCACG TCCCGGTCTG ACCTCCACCG

3001  AACGCCAATC AGCAACGACT GTTTGCCCGC CAGTTGTTGT GCCACGCGGT
      TTGCGGTTAG TCGTTGCTGA CAAACGGGCG GTCAACAACA CGGTGCGCCA

3051  TAGGAATGTA ATTCAGCTCC GCCATCGCCG CTTCCACTTT TTCCCGCGTT
      ATCCTTACAT TAAGTCGAGG CGGTAGCGGC GAAGGTGAAA AAGGGCGCAA

3101  TTCGCAGAAA CGTGGCTGGC CTGGTTCACC ACGCGGGAAA CGGTCTGATA
      AAGCGTCTTT GCACCGACCG GACCAAGTGG TGCGCCCTTT GCCAGACTAT

3151  AGAGACACCG GCATACTCTG CGACATCGTA TAACGTTACT GGTTTCACAT
      TCTCTGTGGC CGTATGAGAC GCTGTAGCAT ATTGCAATGA CCAAAGTGTA

3201  TCACCACCCT GAATTGACTC TCTTCCGGGC GCTATCATGC CATACCGCGA
      AGTGGTGGGA CTTAACTGAG AGAAGGCCCG CGATAGTACG GTATGGCGCT

3251  AAGGTTTTGC GCCATTCGAT GCTAGCCATG TGAGCAAAAG GCCAGCAAAA
      TTCCAAAACG CGGTAAGCTA CGATCGGTAC ACTCGTTTTC CGGTCGTTTT

3301  GGCCAGGAAC CGTAAAAAGG CCGCGTTGCT GGCGTTTTTC CATAGGCTCC
      CCGGTCCTTG GCATTTTTCC GGCGCAACGA CCGCAAAAAG GTATCCGAGG

3351  GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA GAGGTGGCGA
      CGGGGGGACT GCTCGTAGTG TTTTTAGCTG CGAGTTCAGT CTCCACCGCT

3401  AACCCGACAG GACTATAAAG ATACCAGGCG TTTCCCCCTG GAAGCTCCCT
      TTGGGCTGTC CTGATATTTC TATGGTCCGC AAAGGGGGAC CTTCGAGGGA

3451  CGTGCGCTCT CCTGTTCCGA CCCTGCCGCT TACCGGATAC CTGTCCGCCT
      GCACGCGAGA GGACAAGGCT GGGACGGCGA ATGGCCTATG GACAGGCGGA

3501  TTCTCCCTTC GGGAAGCGTG GCGCTTTCTC ATAGCTCACG CTGTAGGTAT
      AAGAGGGAAG CCCTTCGCAC CGCGAAAGAG TATCGAGTGC GACATCCATA

                                                    ApaLI
                                                    ~~~~~~~
3551  CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG TGCACGAACC
      GAGTCAAGCC ACATCCAGCA AGCGAGGTTC GACCCGACAC ACGTGCTTGG
```

Fig. 3 cont.

```
3601  CCCCGTTCAG CCCGACCGCT GCGCCTTATC CGGTAACTAT CGTCTTGAGT
      GGGGCAAGTC GGGCTGGCGA CGCGGAATAG GCCATTGATA GCAGAACTCA

3651  CCAACCCGGT AAGACACGAC TTATCGCCAC TGGCAGCAGC CACTGGTAAC
      GGTTGGGCCA TTCTGTGCTG AATAGCGGTG ACCGTCGTCG GTGACCATTG

3701  AGGATTAGCA GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG
      TCCTAATCGT CTCGCTCCAT ACATCCGCCA CGATGTCTCA AGAACTTCAC

3751  GTGGCCTAAC TACGGCTACA CTAGAAGAAC AGTATTTGGT ATCTGCGCTC
      CACCGGATTG ATGCCGATGT GATCTTCTTG TCATAAACCA TAGACGCGAG

3801  TGCTGTAGCC AGTTACCTTC GGAAAAAGAG TTGGTAGCTC TTGATCCGGC
      ACGACATCGG TCAATGGAAG CCTTTTTCTC AACCATCGAG AACTAGGCCG

3851  AAACAAACCA CCGCTGGTAG CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT
      TTTGTTTGGT GGCGACCATC GCCACCAAAA AAACAAACGT TCGTCGTCTA

3901  TACGCGCAGA AAAAAAGGAT CTCAAGAAGA TCCTTTGATC TTTTCTACGG
      ATGCGCGTCT TTTTTTCCTA GAGTTCTTCT AGGAAACTAG AAAAGATGCC

3951  GGTCTGACGC TCAGTGGAAC GAAAACTCAC GTTAAGGGAT TTTGGTCAGA
      CCAGACTGCG AGTCACCTTG CTTTTGAGTG CAATTCCCTA AAACCAGTCT

4001  TCTAGCACCA GGCGTTTAAG GGCACCAATA ACTGCCTTAA AAAAATTACG
      AGATCGTGGT CCGCAAATTC CCGTGGTTAT TGACGGAATT TTTTTAATGC

4051  CCCCGCCCTG CCACTCATCG CAGTACTGTT GTAATTCATT AAGCATTCTG
      GGGGCGGGAC GGTGAGTAGC GTCATGACAA CATTAAGTAA TTCGTAAGAC

4101  CCGACATGGA AGCCATCACA AACGGCATGA TGAACCTGAA TCGCCAGCGG
      GGCTGTACCT TCGGTAGTGT TTGCCGTACT ACTTGGACTT AGCGGTCGCC

4151  CATCAGCACC TTGTCGCCTT GCGTATAATA TTTGCCCATA GTGAAAACGG
      GTAGTCGTGG AACAGCGGAA CGCATATTAT AAACGGGTAT CACTTTTGCC

4201  GGGCGAAGAA GTTGTCCATA TTGGCTACGT TTAAATCAAA ACTGGTGAAA
      CCCGCTTCTT CAACAGGTAT AACCGATGCA AATTTAGTTT TGACCACTTT

4251  CTCACCCAGG GATTGGCTGA GACGAAAAAC ATATTCTCAA TAAACCCTTT
      GAGTGGGTCC CTAACCGACT CTGCTTTTTG TATAAGAGTT ATTTGGGAAA

4301  AGGGAAATAG GCCAGGTTTT CACCGTAACA CGCCACATCT TGCGAATATA
      TCCCTTTATC CGGTCCAAAA GTGGCATTGT GCGGTGTAGA ACGCTTATAT

4351  TGTGTAGAAA CTGCCGGAAA TCGTCGTGGT ATTCACTCCA GAGCGATGAA
      ACACATCTTT GACGGCCTTT AGCAGCACCA TAAGTGAGGT CTCGCTACTT

4401  AACGTTTCAG TTTGCTCATG GAAAACGGTG TAACAAGGGT GAACACTATC
      TTGCAAAGTC AAACGAGTAC CTTTTGCCAC ATTGTTCCCA CTTGTGATAG

4451  CCATATCACC AGCTCACCGT CTTTCATTGC CATACGGAAC TCCGGGTGAG
      GGTATAGTGG TCGAGTGGCA GAAAGTAACG GTATGCCTTG AGGCCCACTC
```

Fig. 3 cont.

```
4501  CATTCATCAG GCGGGCAAGA ATGTGAATAA AGGCCGGATA AAACTTGTGC
      GTAAGTAGTC CGCCCGTTCT TACACTTATT TCCGGCCTAT TTTGAACACG

4551  TTATTTTTCT TTACGGTCTT TAAAAAGGCC GTAATATCCA GCTGAACGGT
      AATAAAAAGA AATGCCAGAA ATTTTTCCGG CATTATAGGT CGACTTGCCA

4601  CTGGTTATAG GTACATTGAG CAACTGACTG AAATGCCTCA AAATGTTCTT
      GACCAATATC CATGTAACTC GTTGACTGAC TTTACGGAGT TTTACAAGAA

4651  TACGATGCCA TTGGGATATA TCAACGGTGG TATATCCAGT GATTTTTTTC
      ATGCTACGGT AACCCTATAT AGTTGCCACC ATATAGGTCA CTAAAAAAAG

4701  TCCATTTTAG CTTCCTTAGC TCCTGAAAAT CTCGATAACT CAAAAAATAC
      AGGTAAAATC GAAGGAATCG AGGACTTTTA GAGCTATTGA GTTTTTTATG

4751  GCCCGGTAGT GATCTTATTT CATTATGGTG AAAGTTGGAA CCTCACCCGA
      CGGGCCATCA CTAGAATAAA GTAATACCAC TTTCAACCTT GGAGTGGGCT

4801  CGTCTAATGT GAGTTAGCTC ACTCATTAGG CACCCCAGGC TTTACACTTT
      GCAGATTACA CTCAATCGAG TGAGTAATCC GTGGGGTCCG AAATGTGAAA

4851  ATGCTTCCGG CTCGTATGTT GTGTGGAATT GTGAGCGGAT AACAATTTCA
      TACGAAGGCC GAGCATACAA CACACCTTAA CACTCGCCTA TTGTTAAAGT

      M13 Reverse  primer 100.0%          XbaI
        ==================              ~~~~~~
4901  CACAGGAAAC AGCTATGACC ATGATTACGA ATTTCTAGAT AACGAGGGCA
      GTGTCCTTTG TCGATACTGG TACTAATGCT TAAAGATCTA TTGCTCCCGT

4951  AAAAATGAAA AAGACAGCTA TCGCGATTGC AGTGGCACTG GCTGGTTTCG
      TTTTTACTTT TTCTGTCGAT AGCGCTAACG TCACCGTGAC CGACCAAAGC

                      EcoRV
                       ~~~
5001  CTACCGTAGC GCAGGCCGAT
      GATGGCATCG CGTCCGGCTA
```

Fig. 4a

Sequence of MS-Roche#3, #7 and #8
VL
Framework 1
CDR 1
Framework 2
CDR 2
EcoRV
BanII
PstI
KpnI
SexAI
AseI
MS-Roche #3
MS-Roche #7
MS-Roche #8
VH
Framework 1
CDR 1
Framework 2
CDR 2
MfeI
BspEI
BstXI
XhoI
MS-Roche #3
MS-Roche #7
MS-Roche #8

Fig. 4a cont.

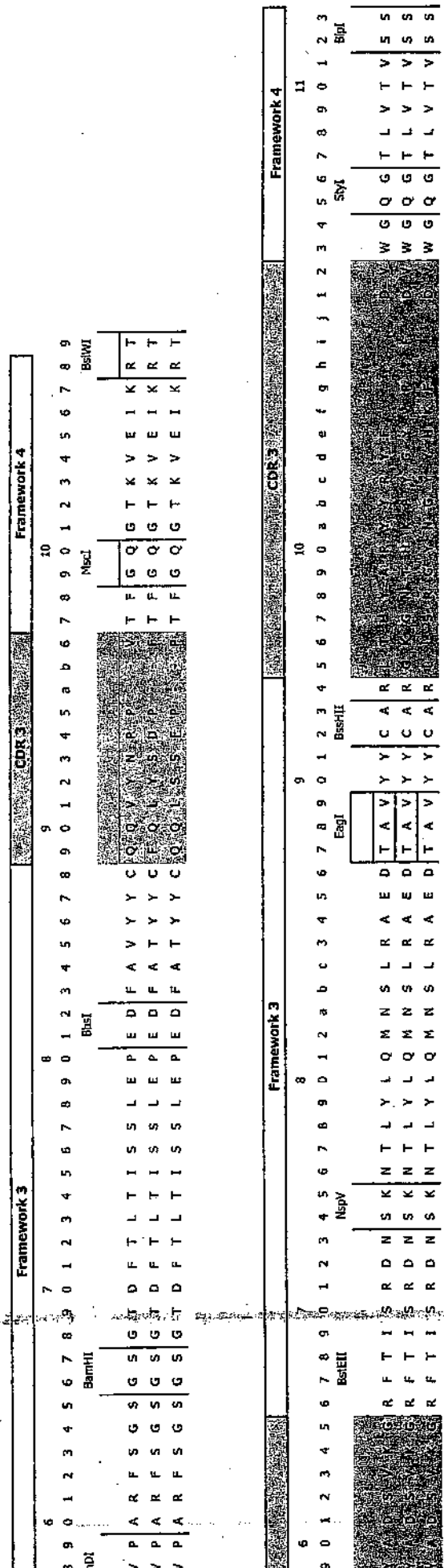

Framework 3
CDR 3
Framework 4
BamHI
BlnI
NspV
BstEII
MscI
BstWI
EagI
BssHII
SfyI
BlpI

Fig. 4b

Sequence of MS-Roche#3, #7 and #8

Fig. 4b cont.

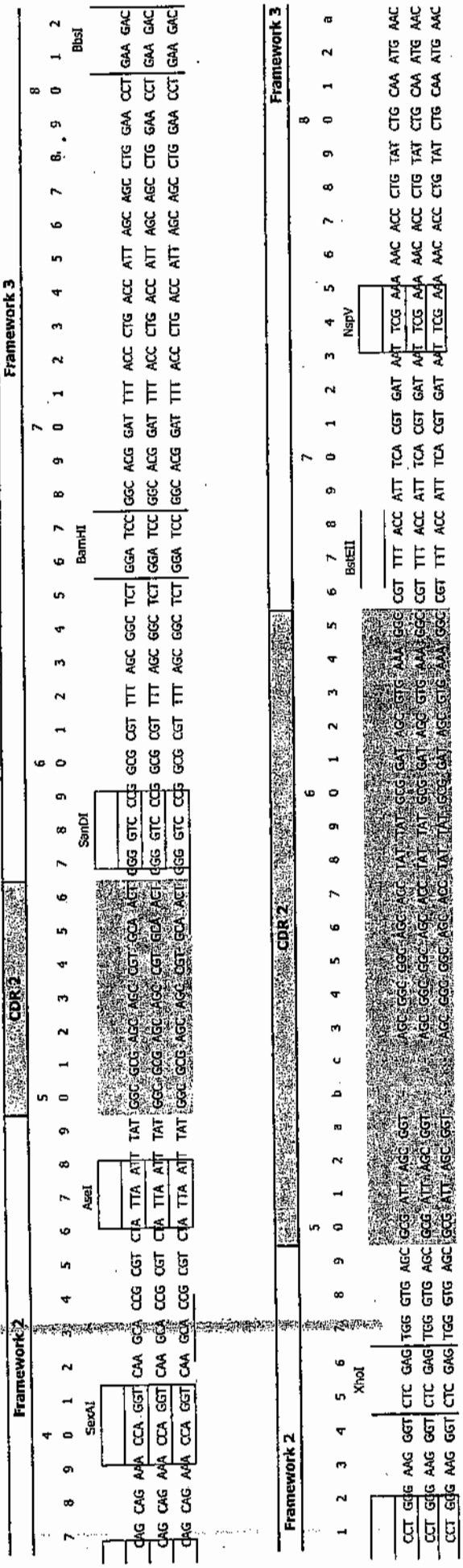

Framework 2
CDR 2
Framework 3
SexAI
AgeI
SanDI
BamHI
BbsI
XhoI
NspV
BstEII

Fig. 4b cont.

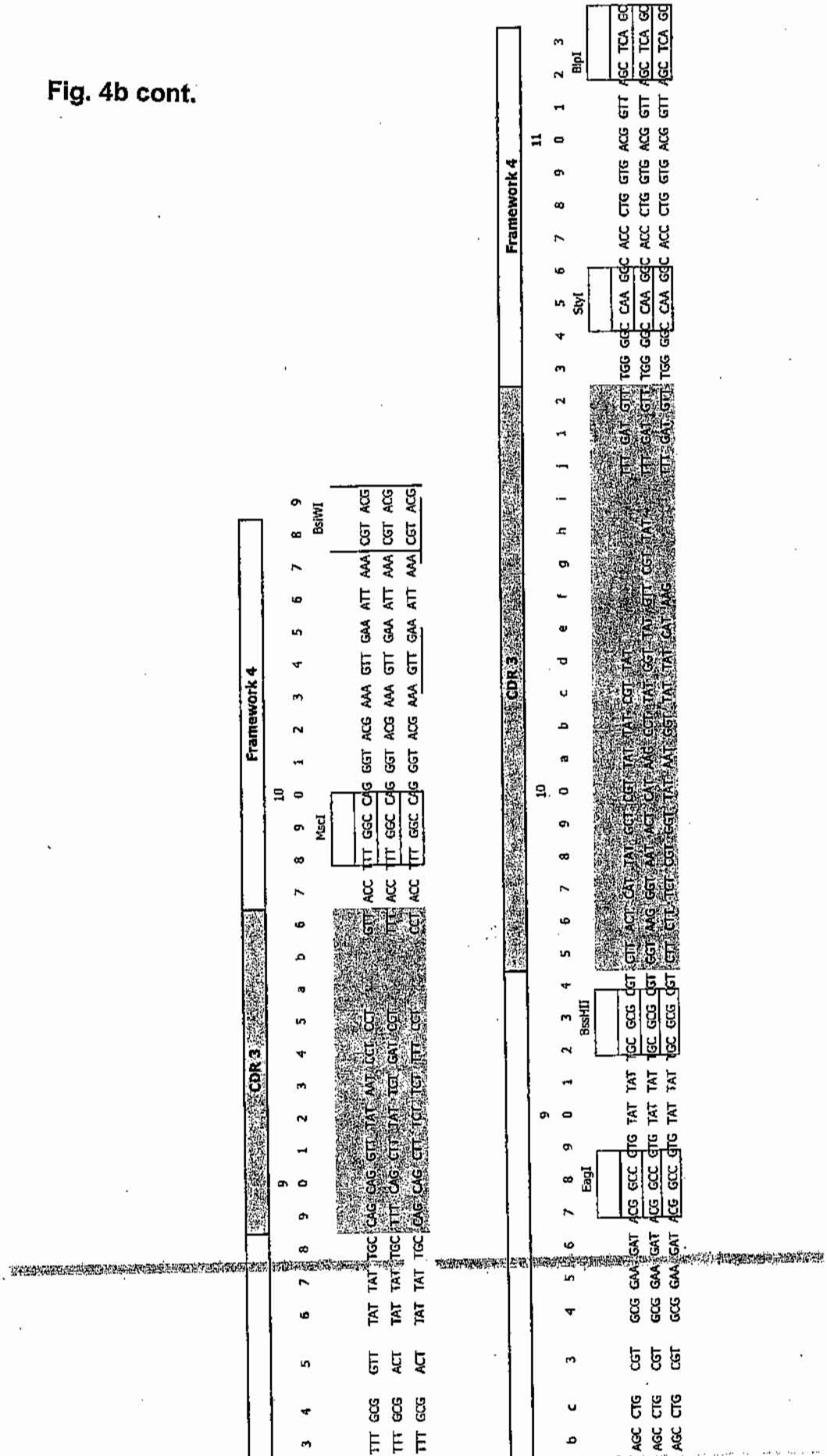

CDR3
Framework 4
MscI
BsiWI
BssHII
EagI
CDR3
Framework 4
StyI
BlpI

Fig. 5



Fig. 6

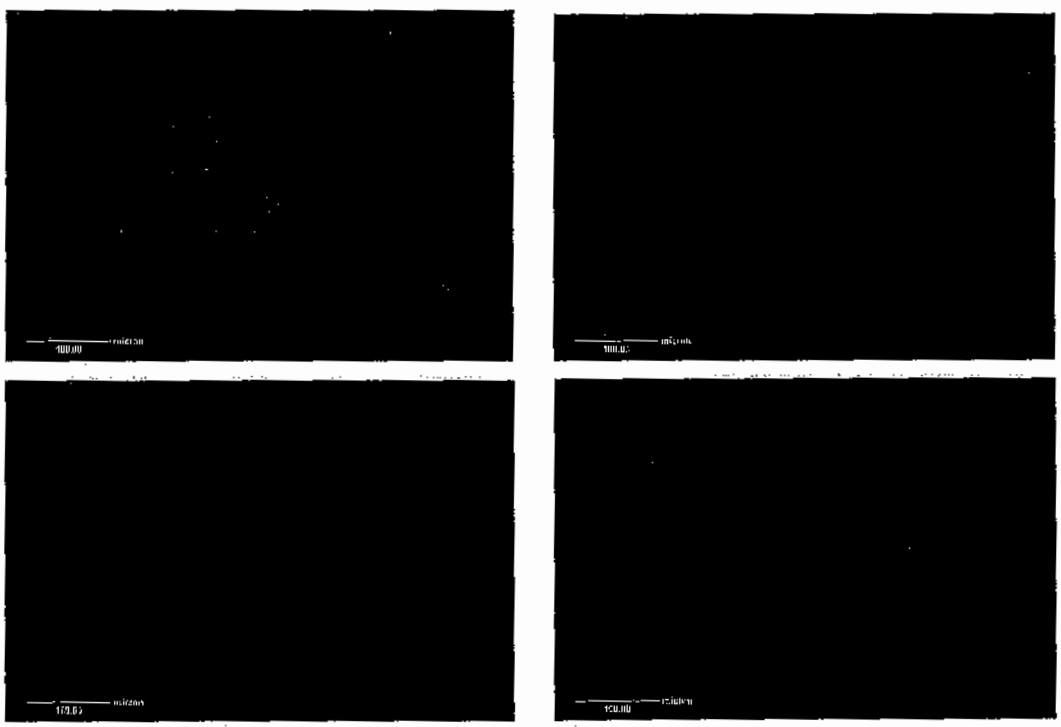


Fig. 7

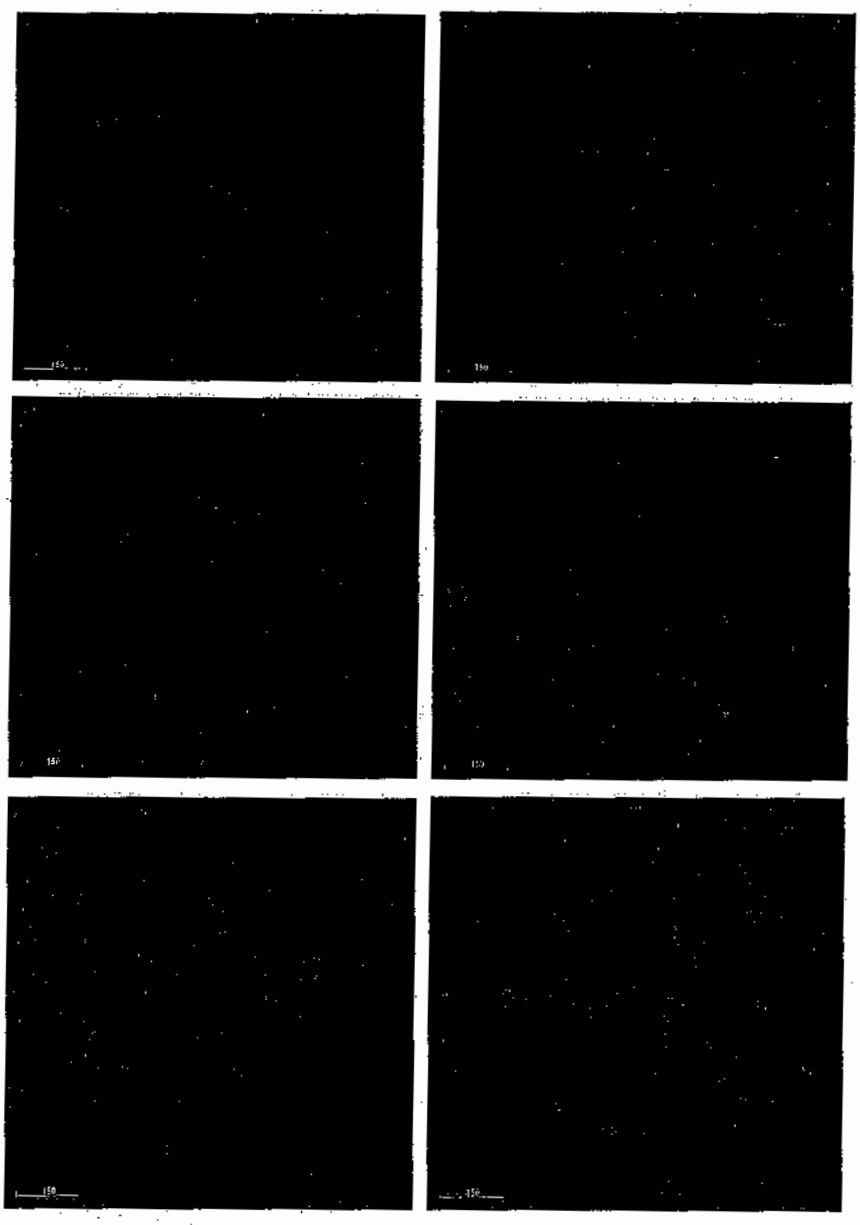
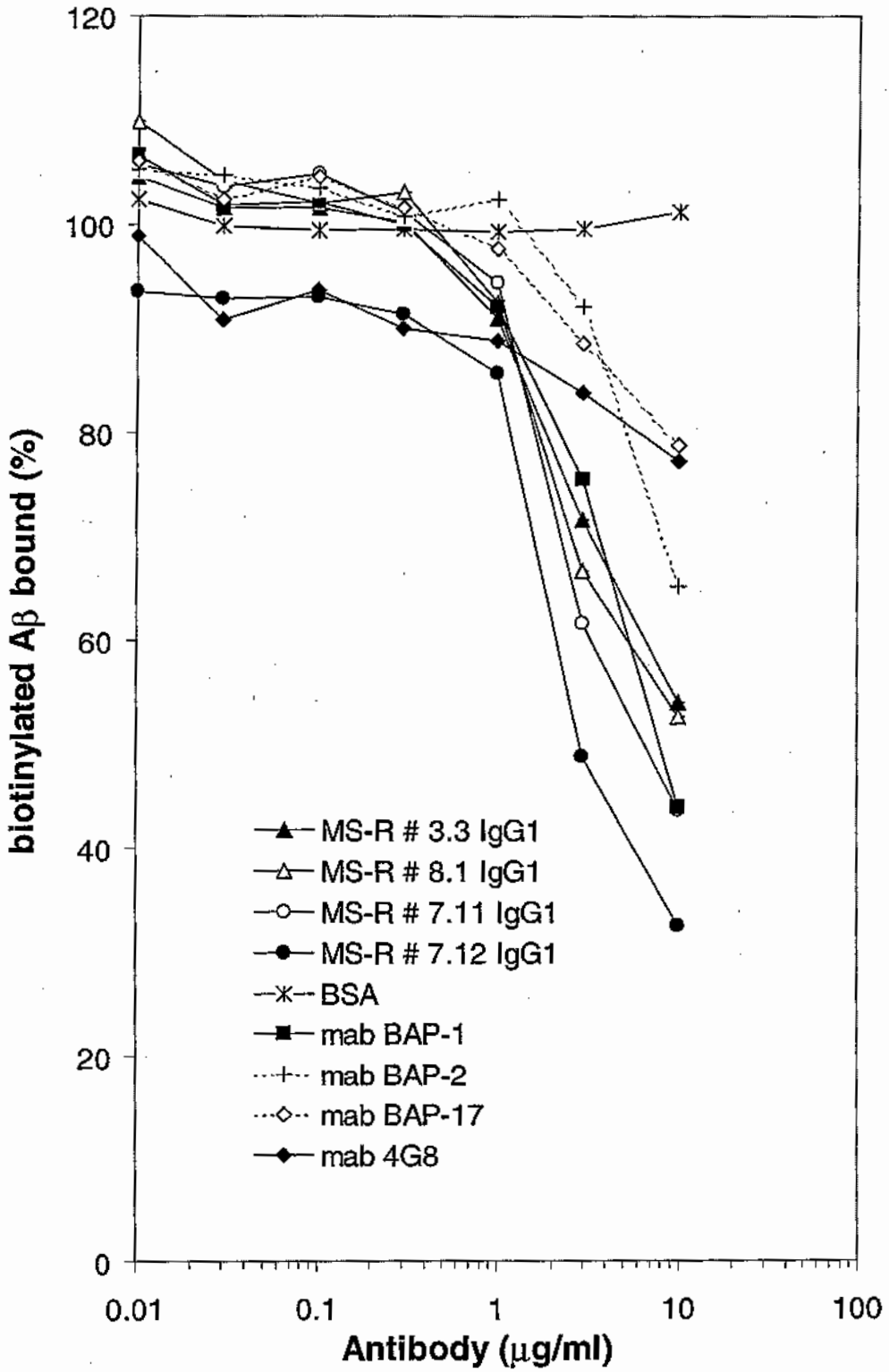


Fig. 8


120
100
80
60
40
20
0
biotinylated Aβ bound (%)
0.01
0.1
1
10
100
Antibody (μg/ml)
MS-R # 3.3 IgG1
MS-R # 8.1 IgG1
MS-R # 7.11 IgG1
MS-R # 7.12 IgG1
BSA
mab BAP-1
mab BAP-2
mab BAP-17
mab 4G8

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Fig. 9A

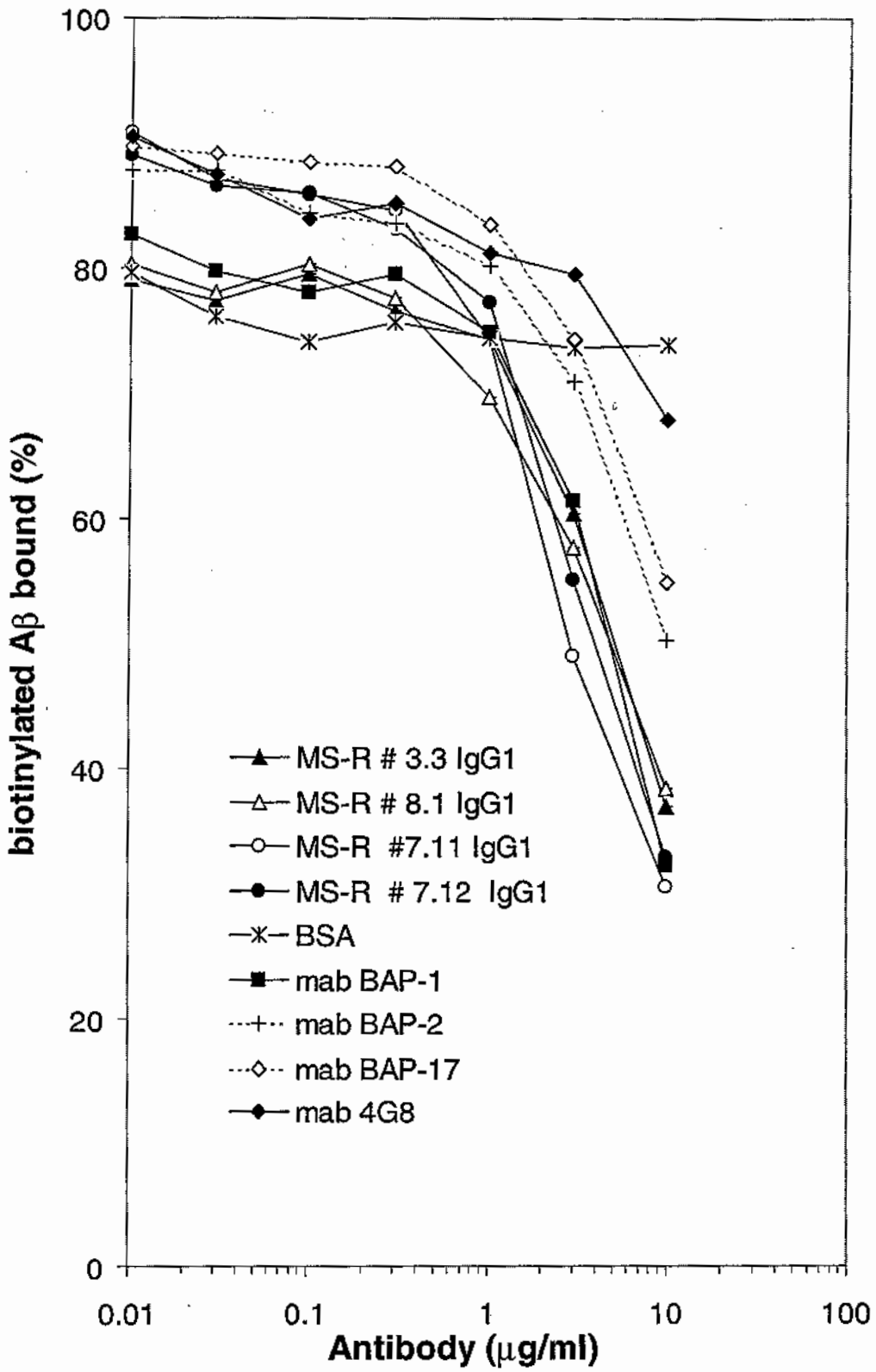


Fig. 9B

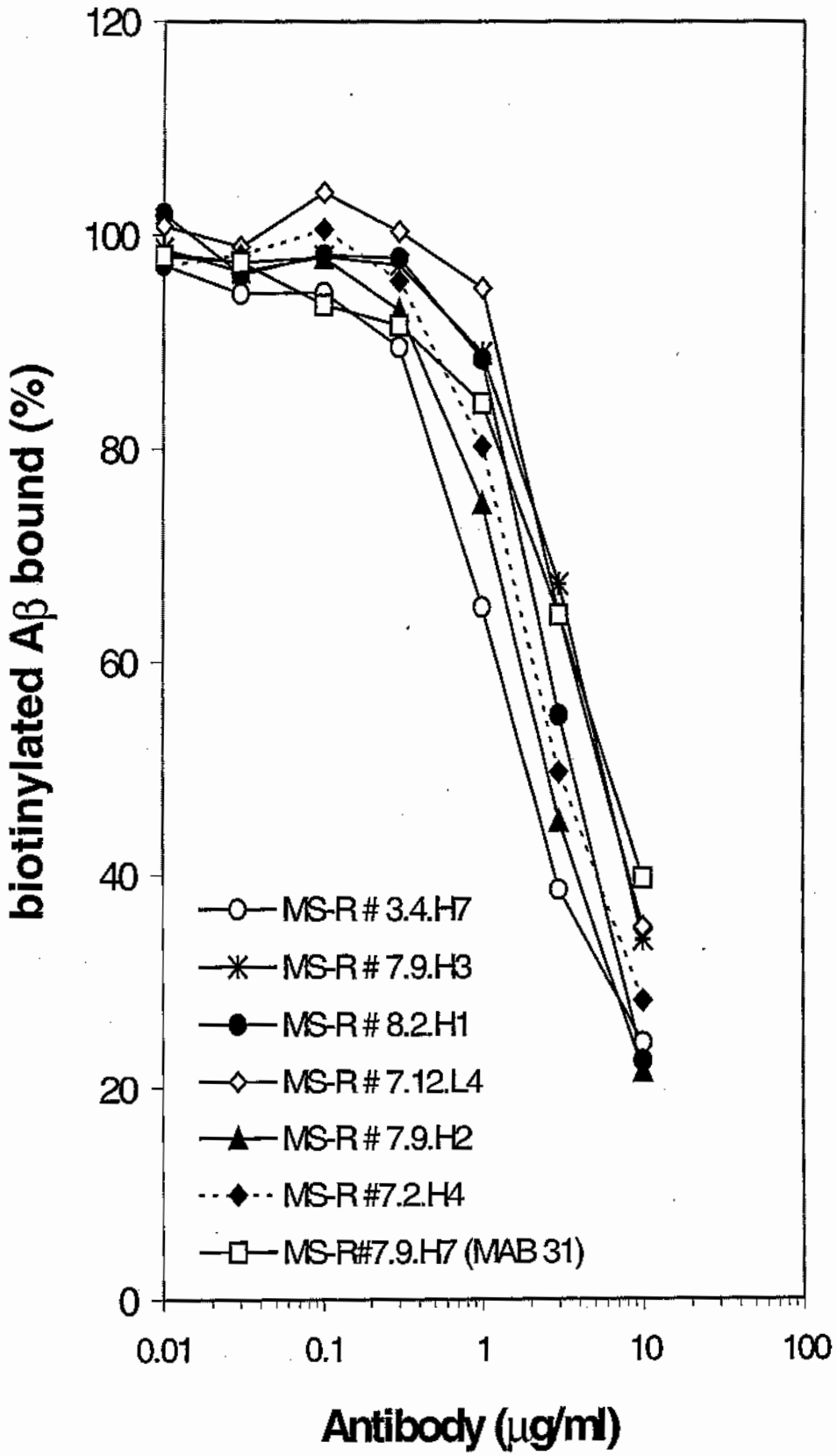

120
100
80
60
40
20
0
biotinylated Aβ bound (%)
0.01
0.1
1
10
100
Antibody (µg/ml)
MS-R # 3.4.H7
MS-R # 7.9.H3
MS-R # 8.2.H1
MS-R # 7.12.L4
MS-R # 7.9.H2
MS-R #7.2.H4
MS-R#7.9.H7 (MAB 31)

Fig. 9C

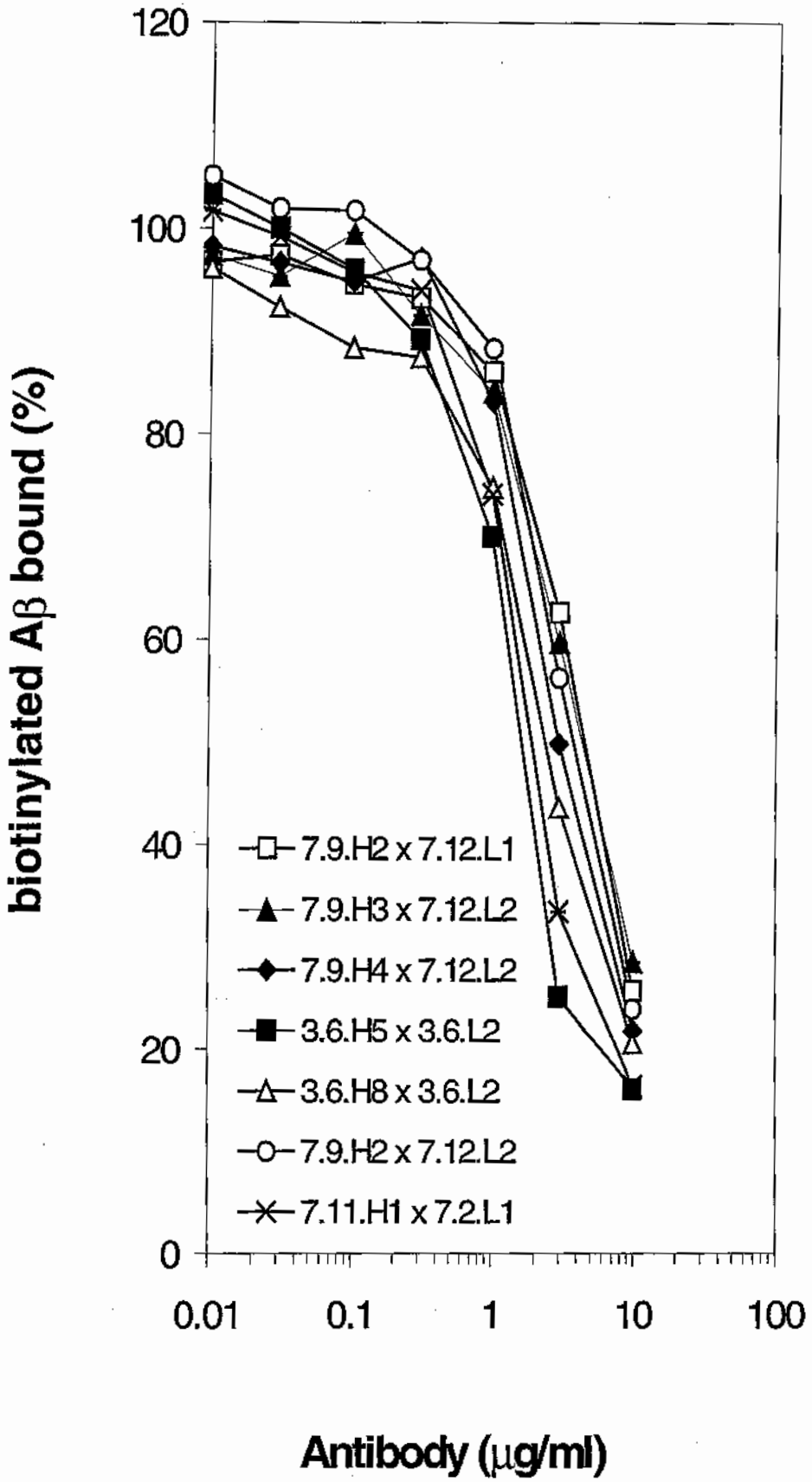

120
100
80
60
40
20
0
0.01
0.1
1
10
100
biotinylated Aβ bound (%)
Antibody (μg/ml)
7.9.H2 x 7.12.L1
7.9.H3 x 7.12.L2
7.9.H4 x 7.12.L2
3.6.H5 x 3.6.L2
3.6.H8 x 3.6.L2
7.9.H2 x 7.12.L2
7.11.H1 x 7.2.L1

Fig. 9D

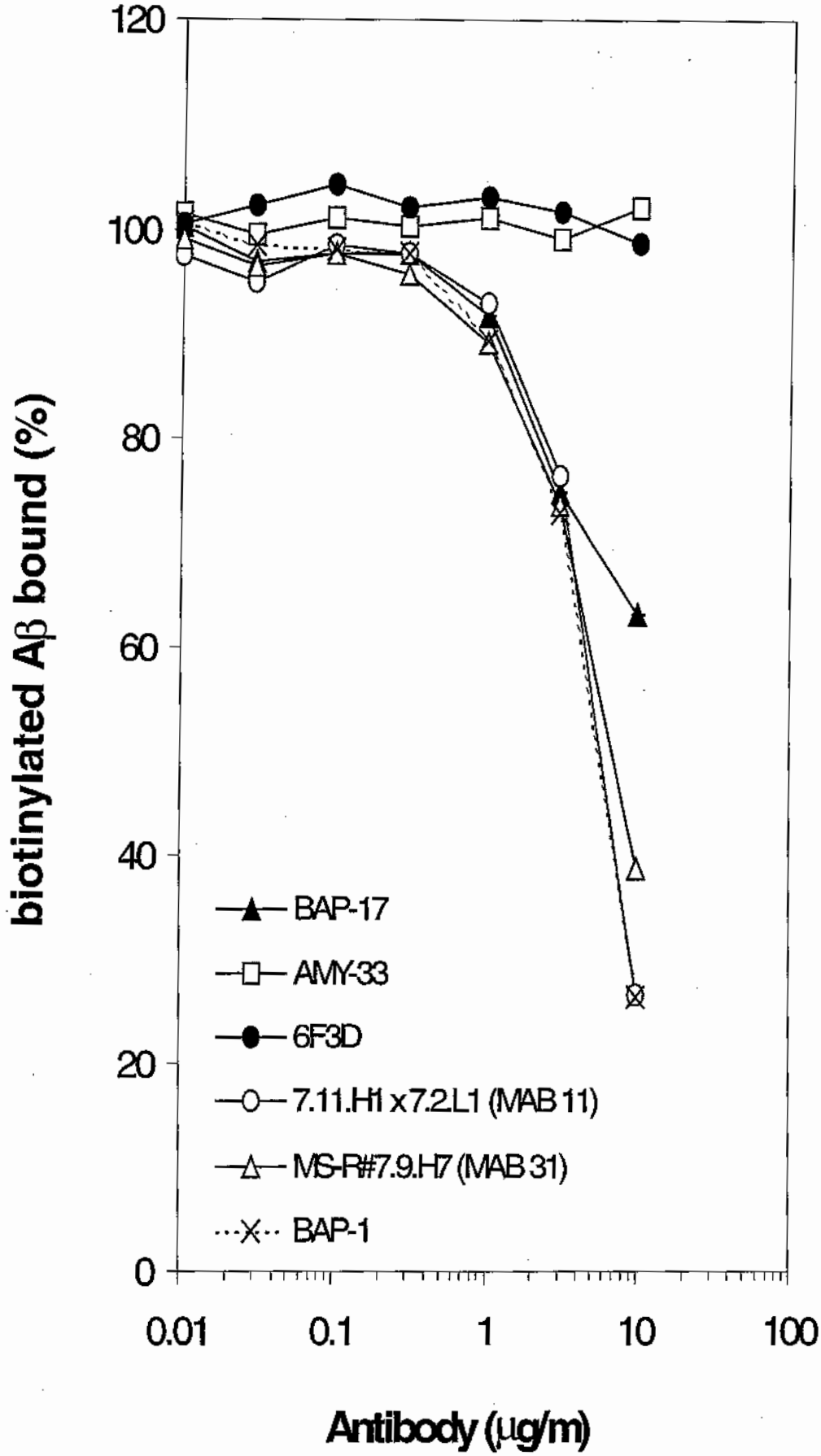

120
100
80
60
40
20
0
biotinylated Aβ bound (%)
0.01
0.1
1
10
100
Antibody (µg/m)
BAP-17
AMY-33
6F3D
7.11.H1 x 7.2.L1 (MAB 11)
MS-R#7.9.H7 (MAB 31)
BAP-1

Fig. 10

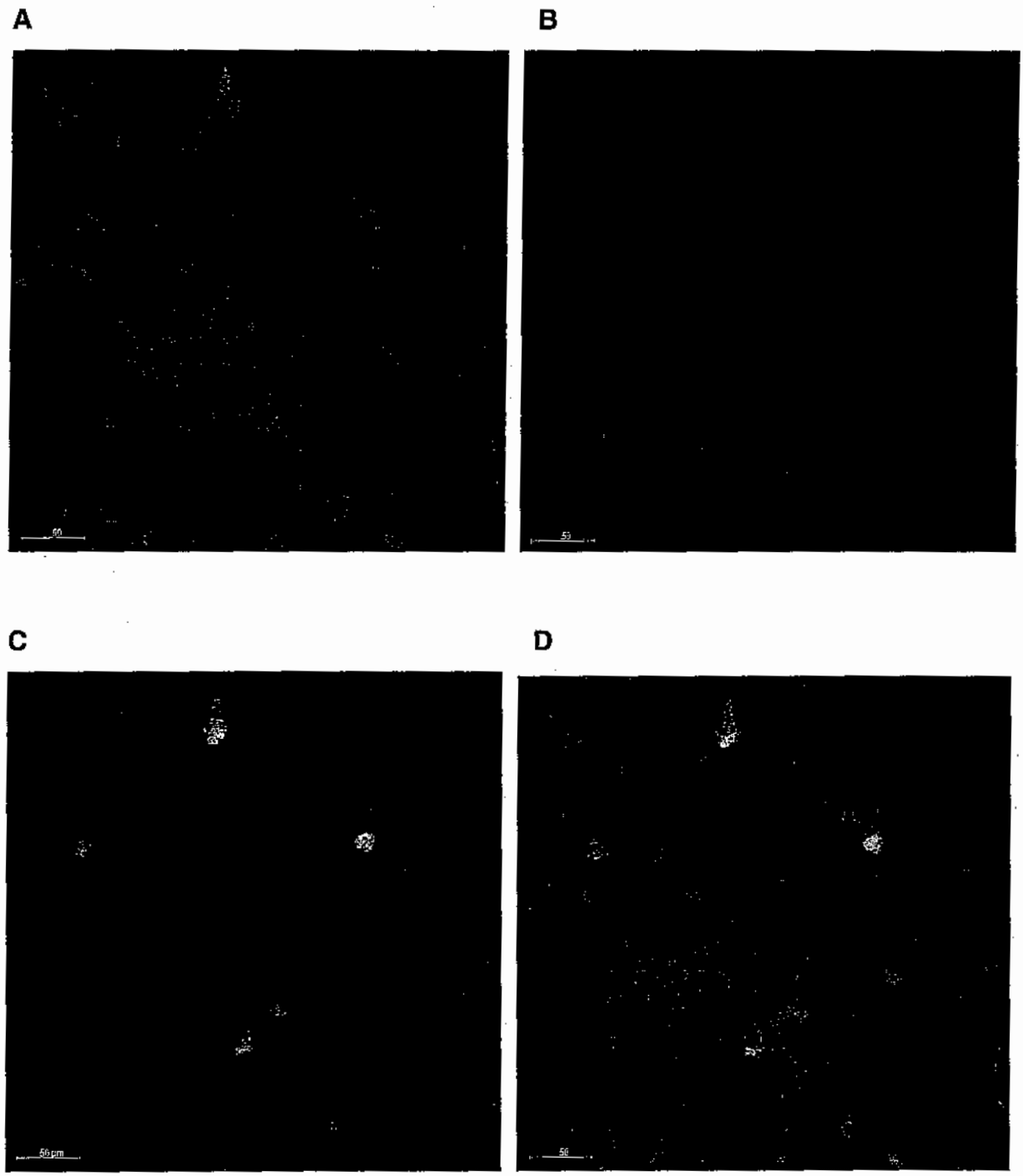


Fig. 11

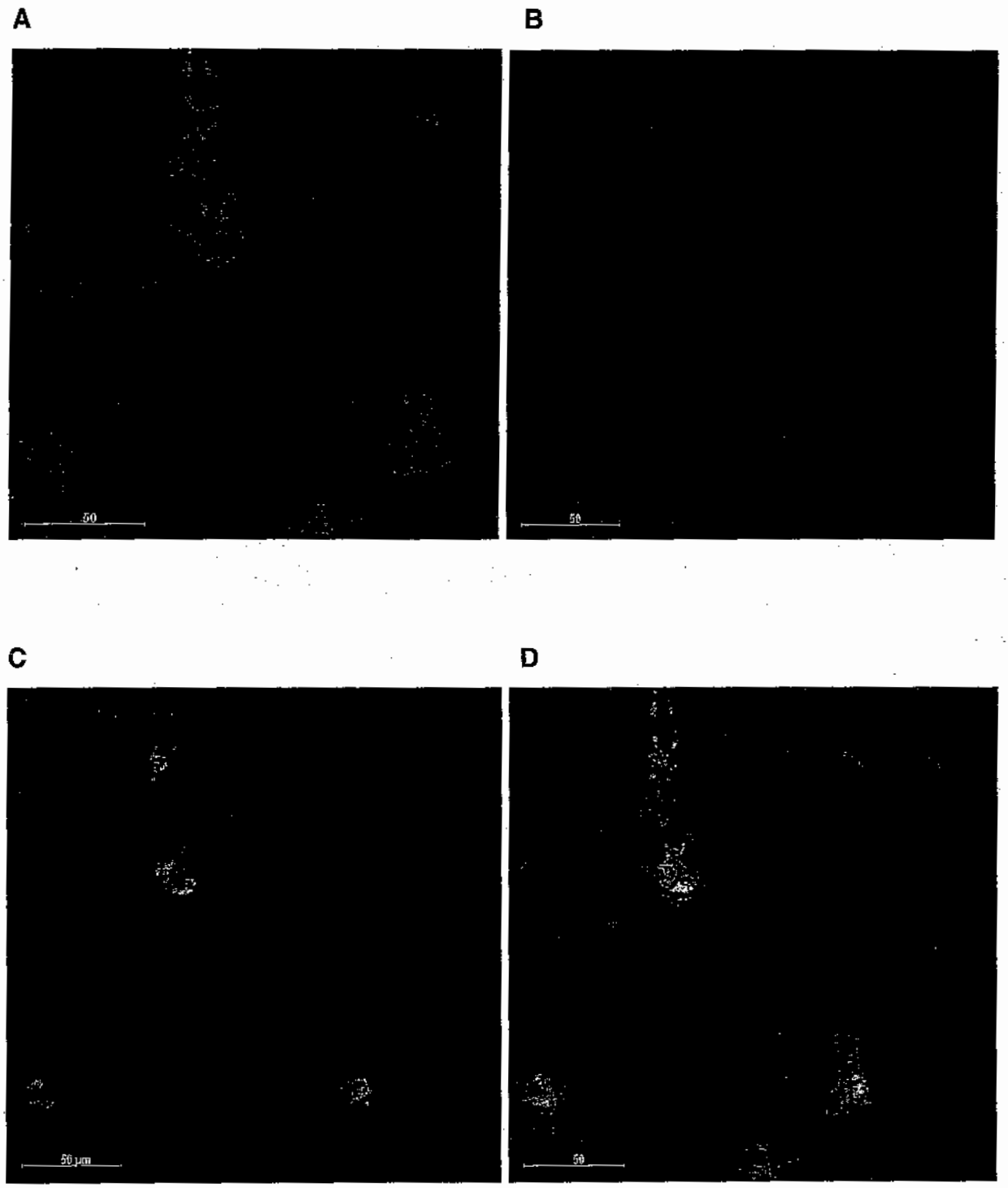


Fig. 12

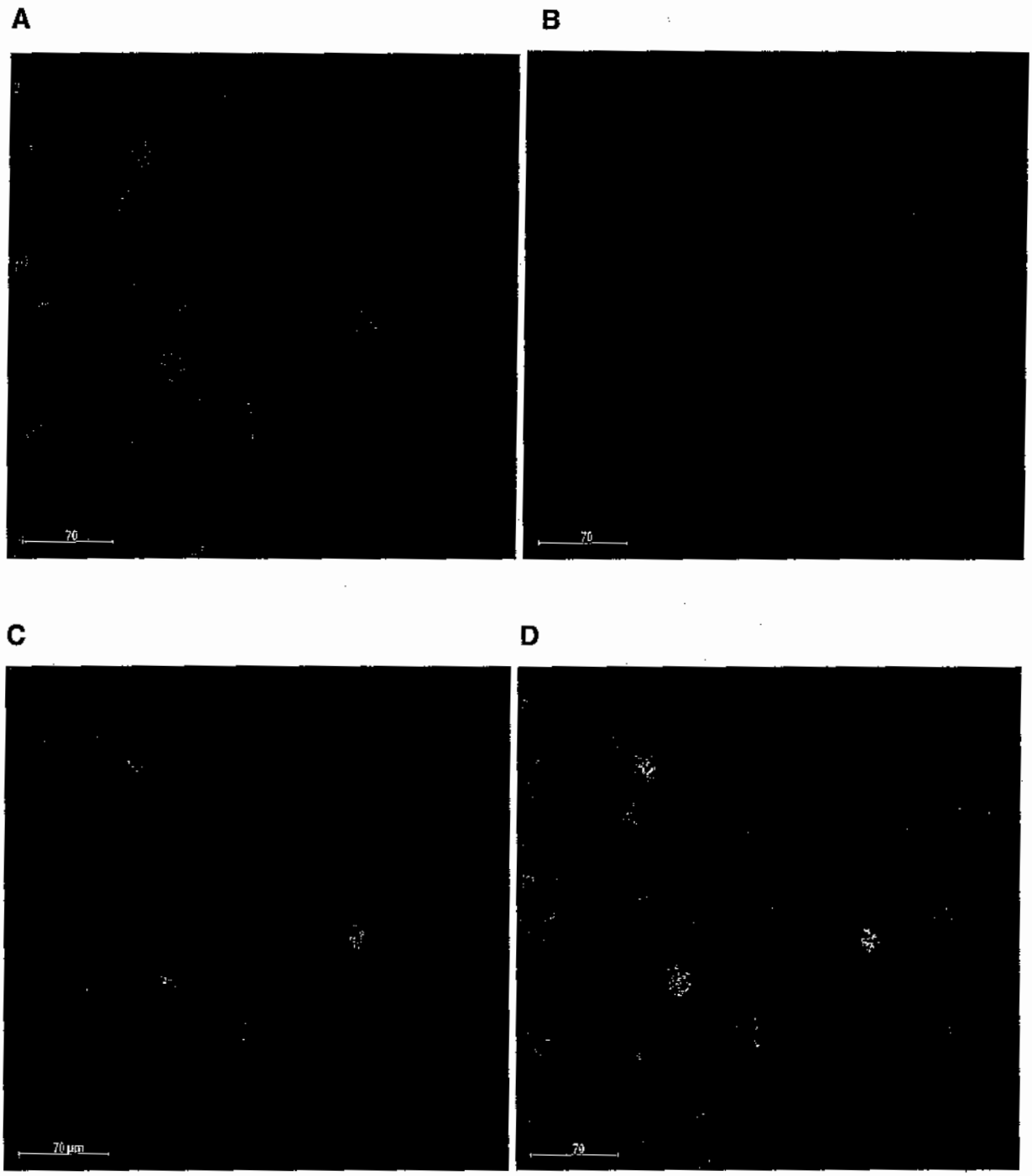


Fig. 13

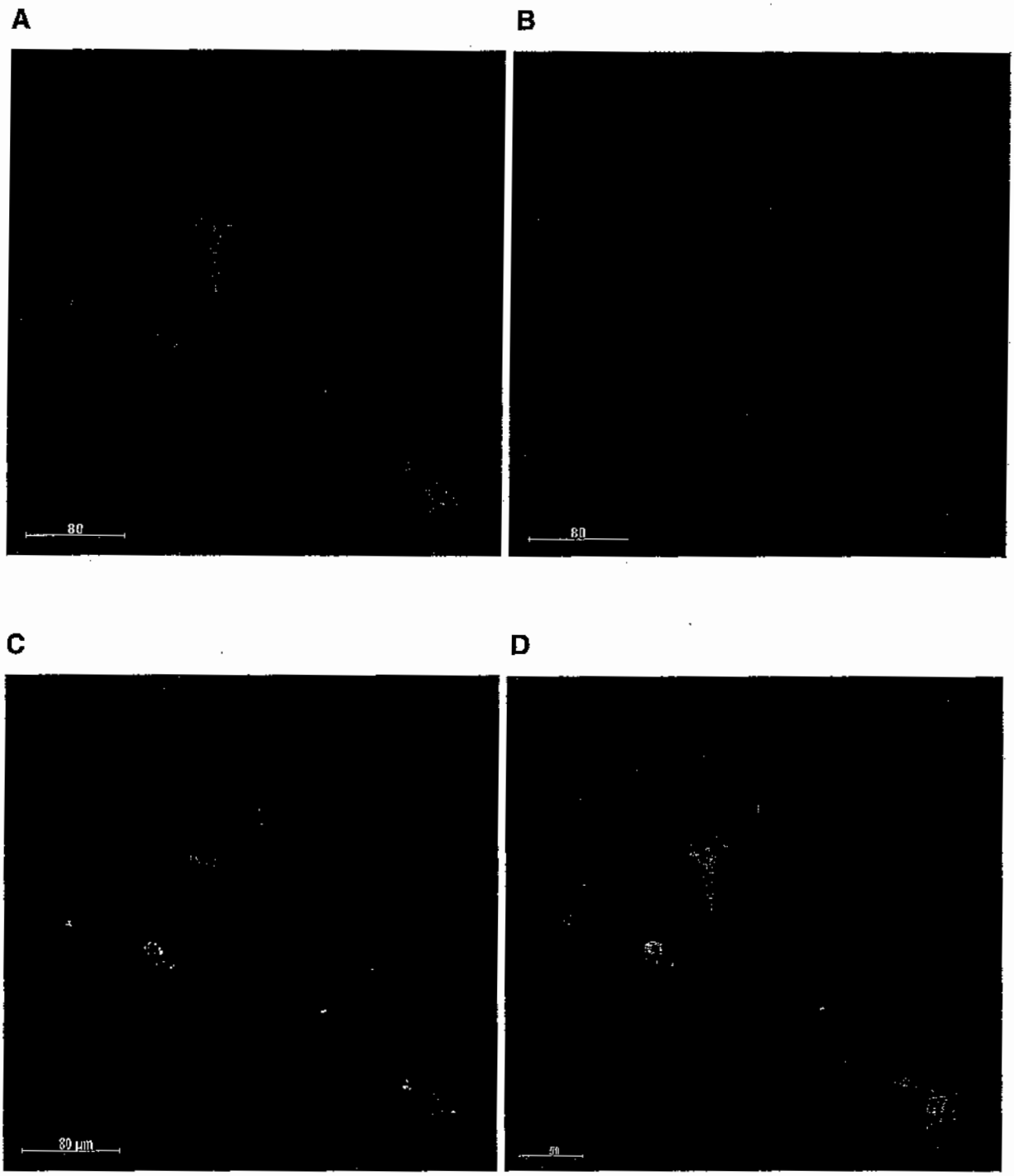


Fig. 14

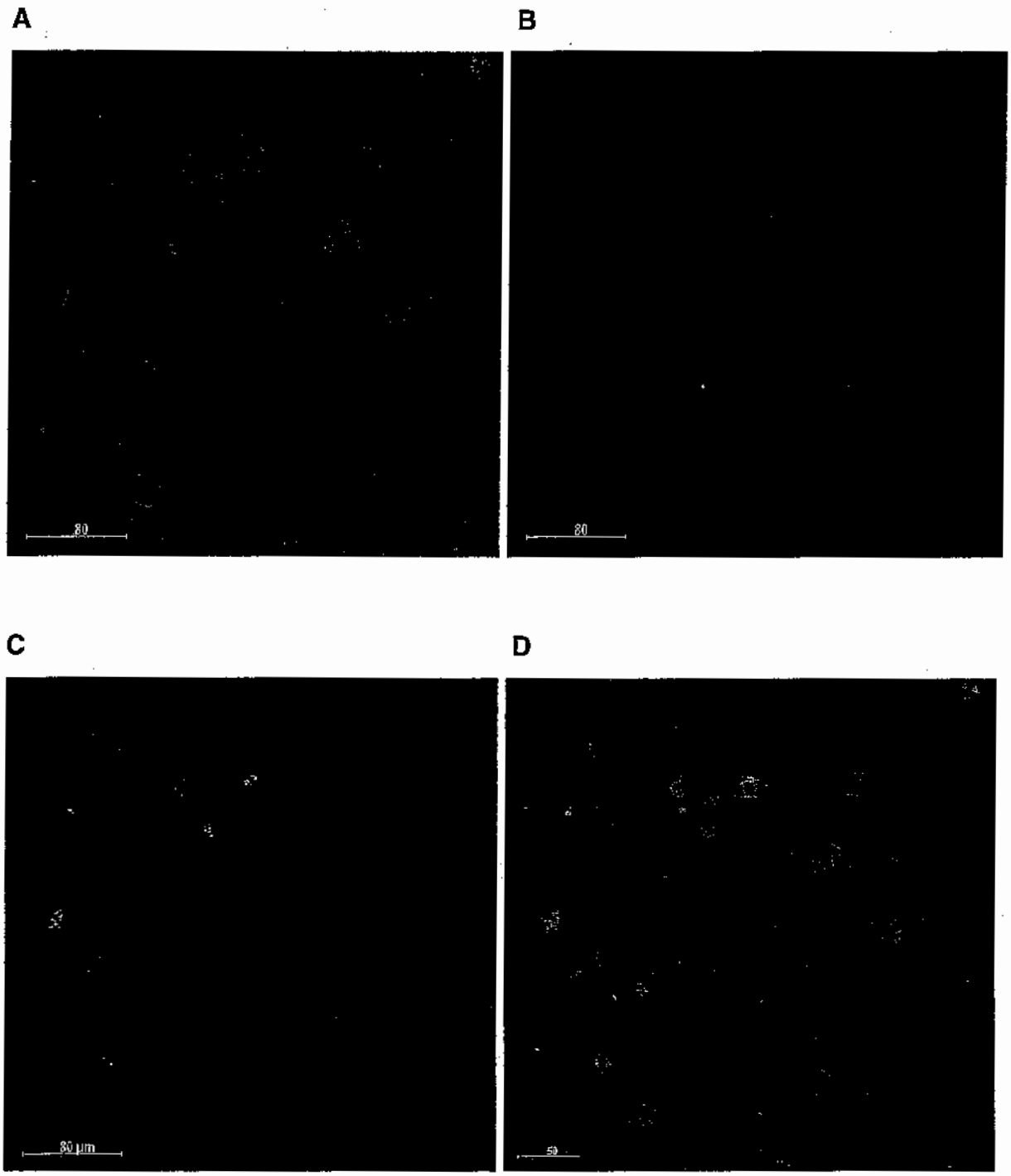


Fig. 15 - 1

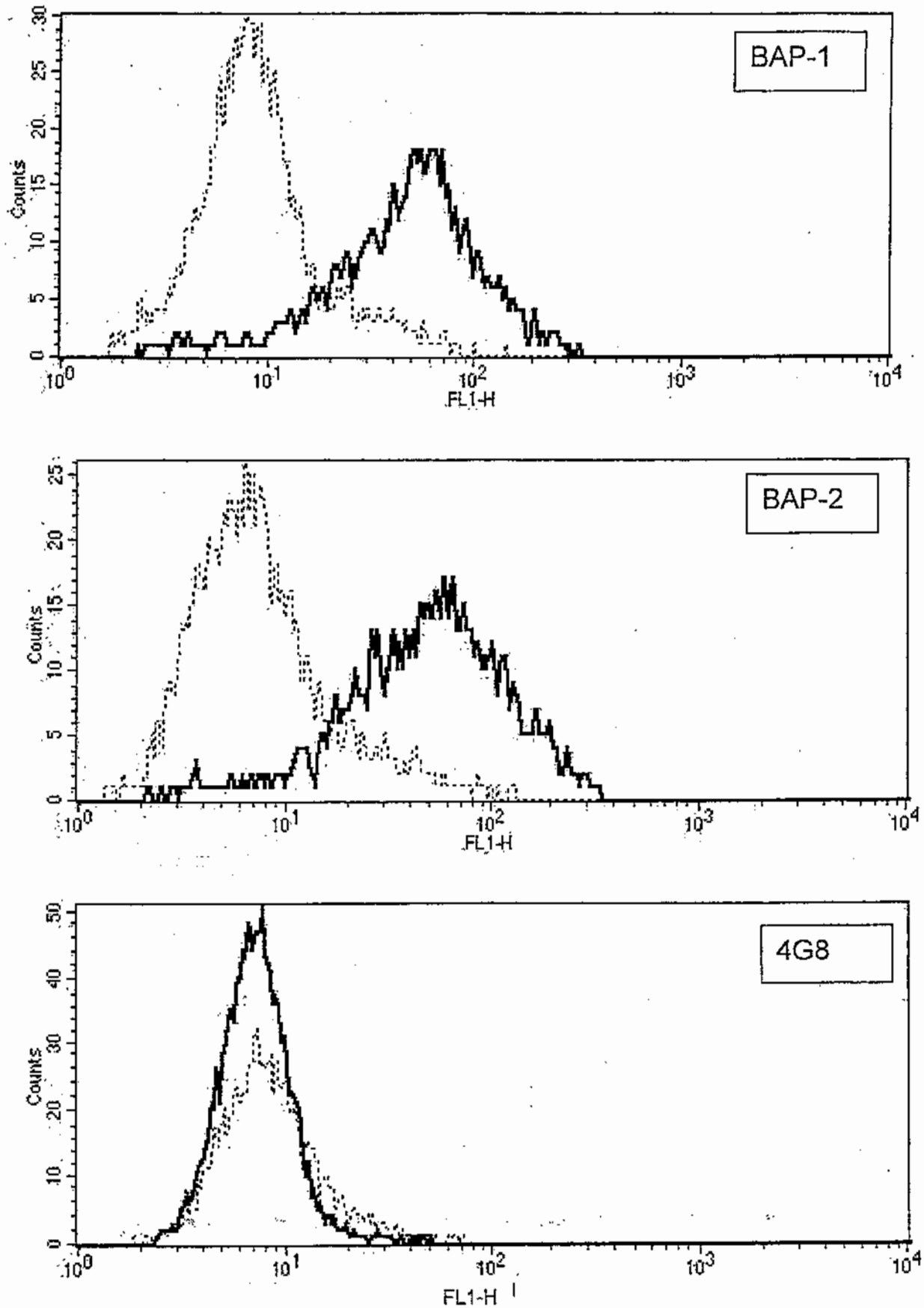
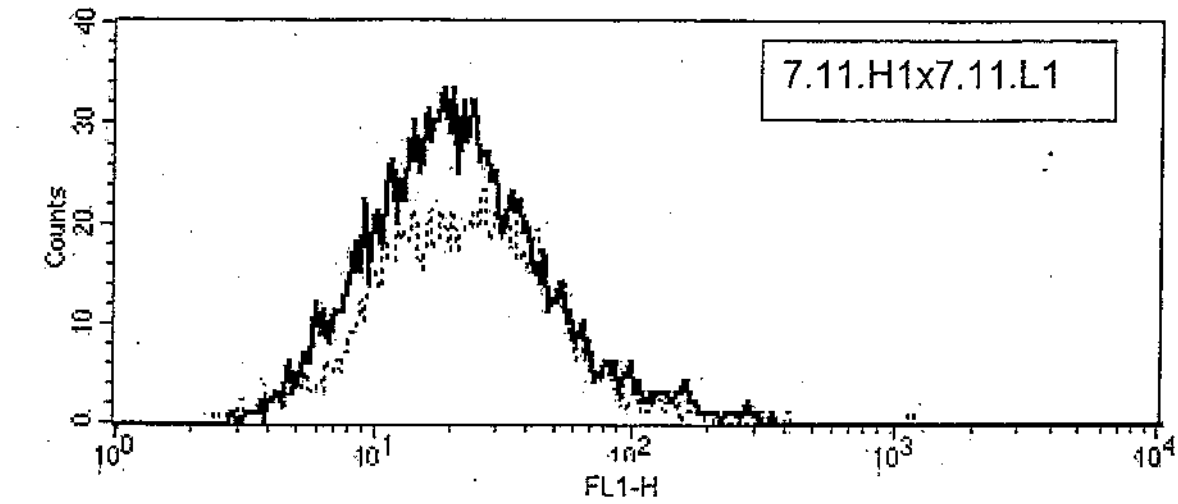
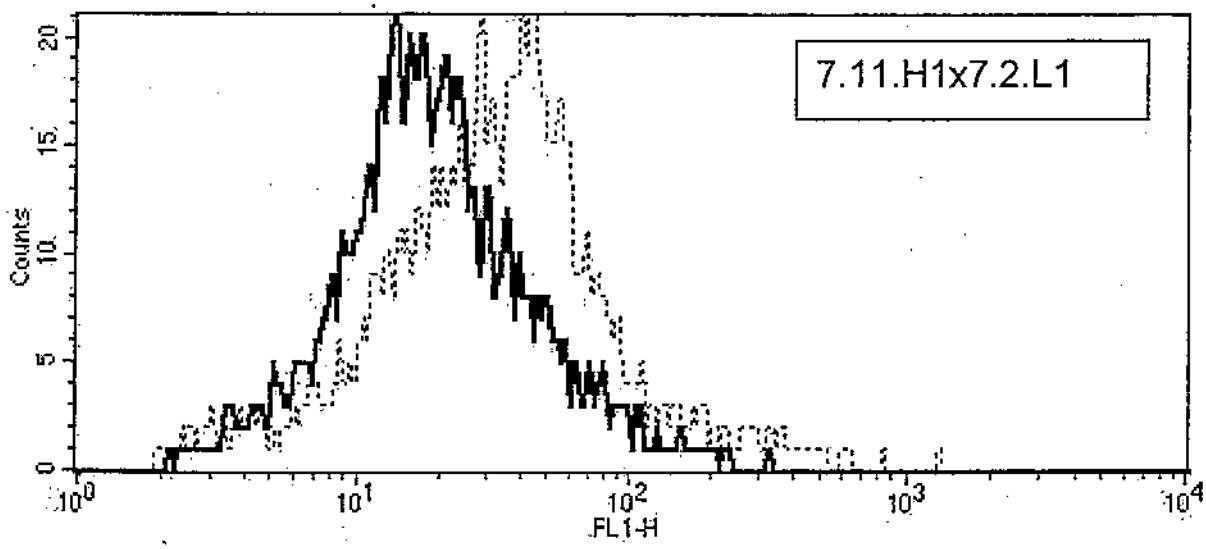


Fig. 15 - 2


7.11.H1x7.11.L1
Counts
FL1-H


7.11.H1x7.2.L1
Counts
FL1-H

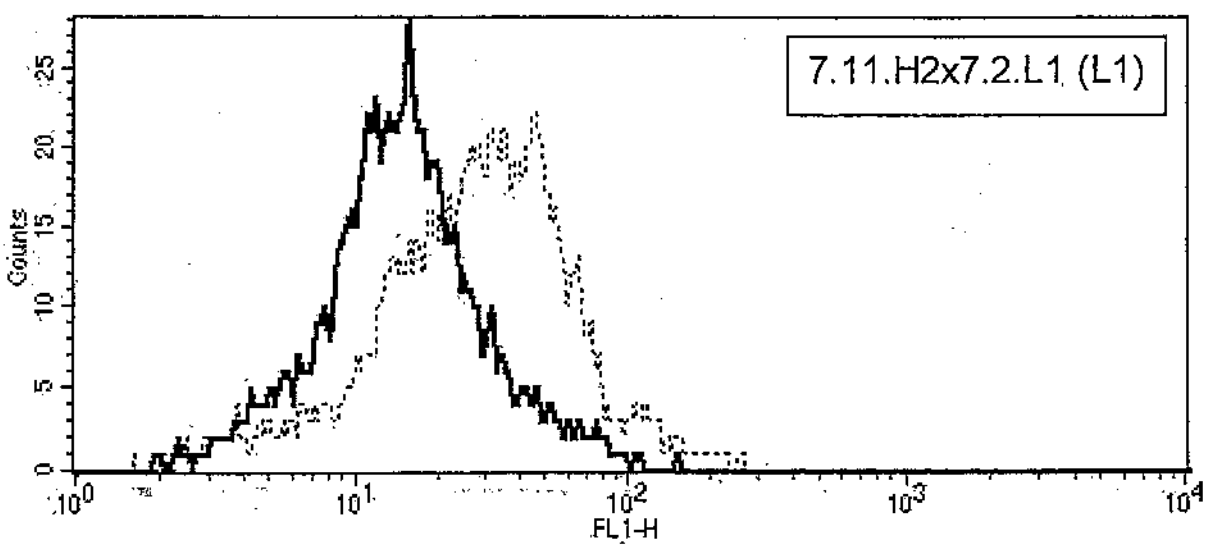
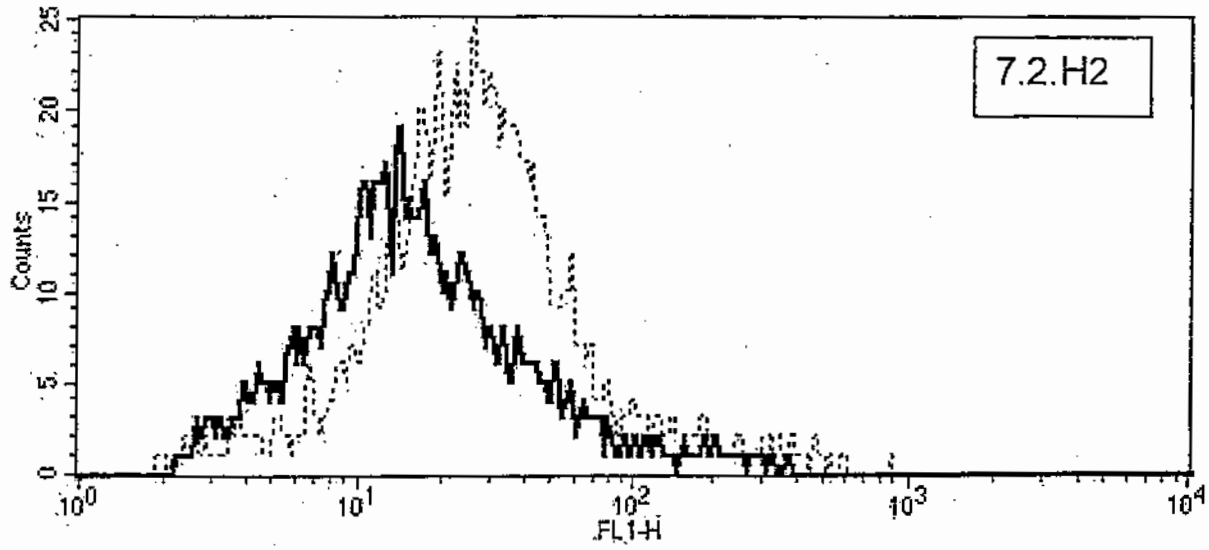
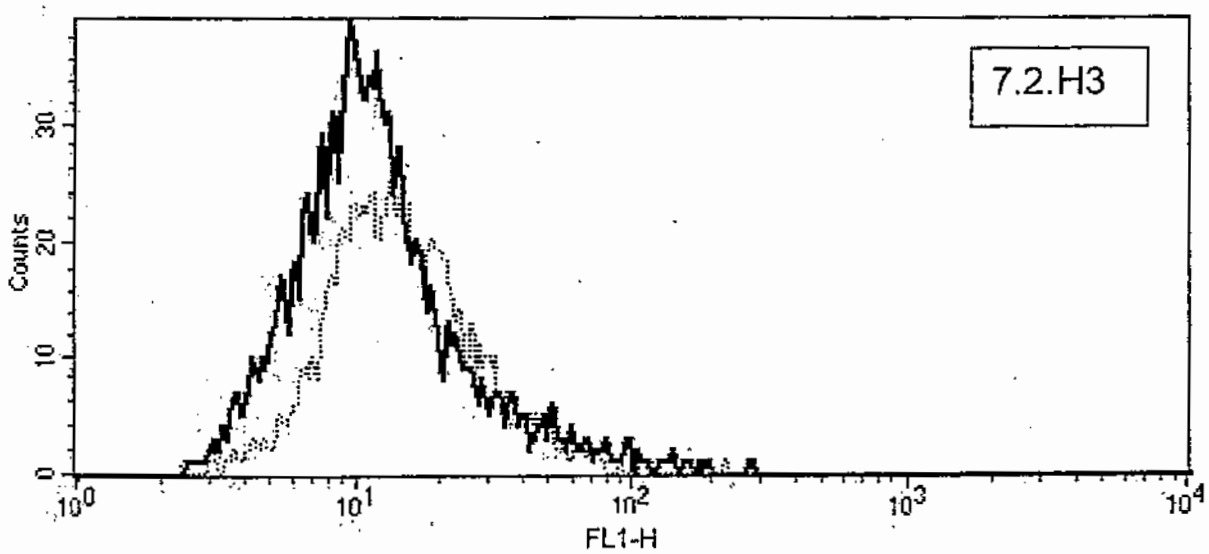

7.11.H2x7.2.L1 (L1)
Counts
FL1-H

Fig. 15 - 3





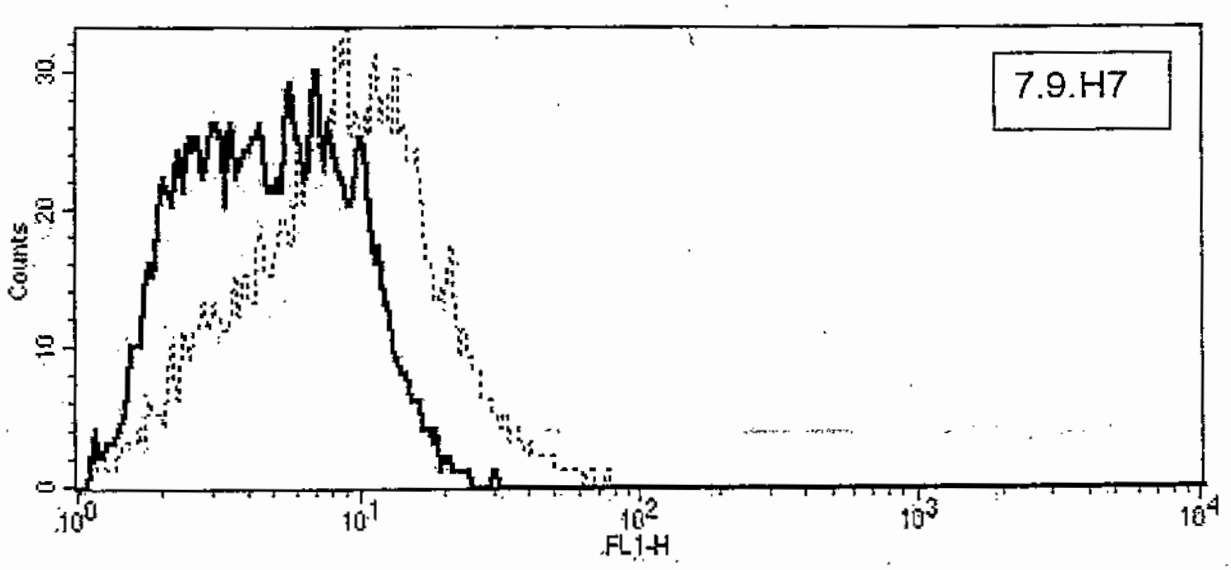
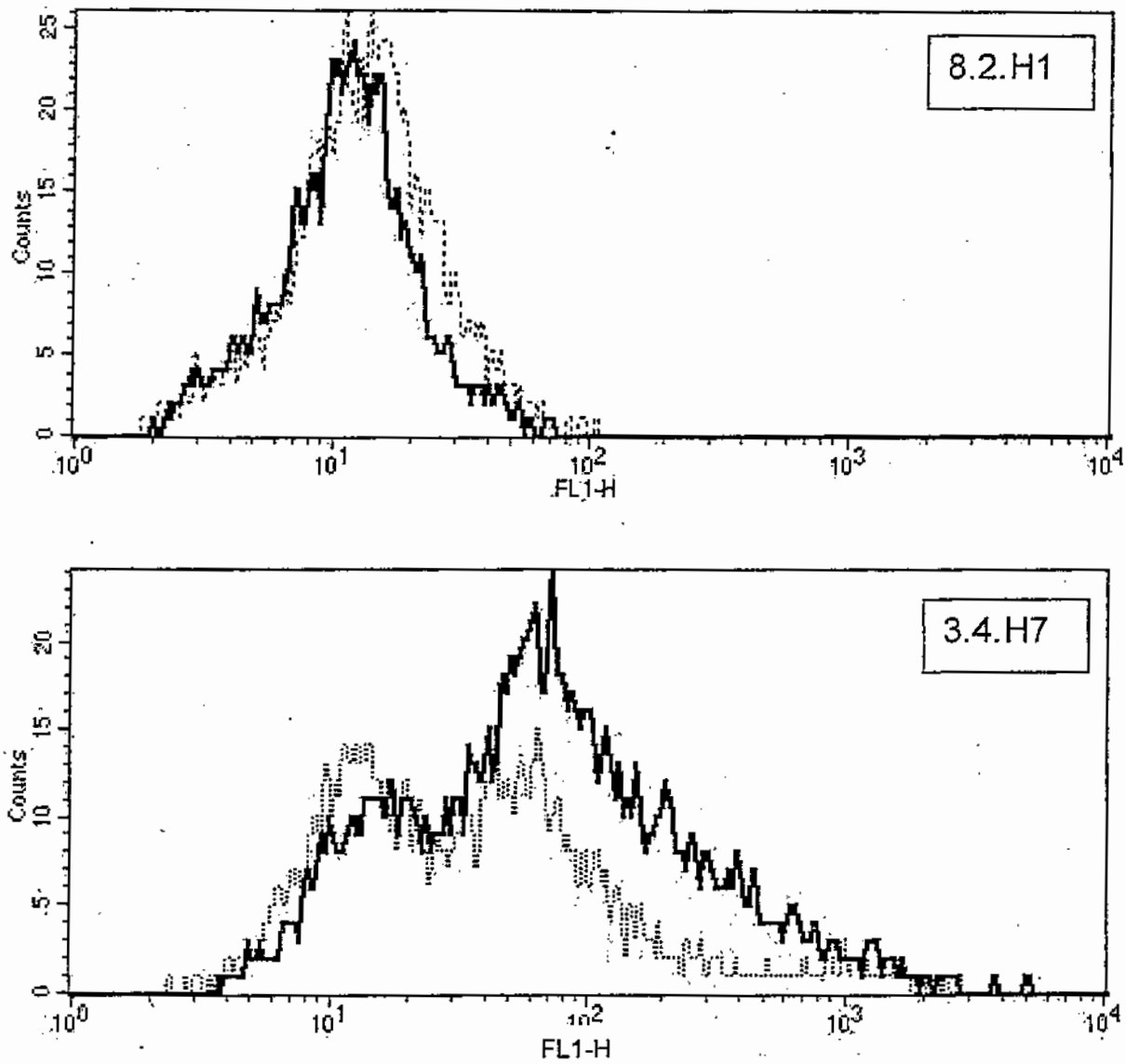


Fig. 15 - 4



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MorphoSys AG

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<130> F 2842 PCT

<140> EP 02003844.4
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<220>
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1 5

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<211> 14
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<213> artificial sequence

<220>
<223> synthetic construct; second region of beta-A4 peptide

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<211> 368
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH-region of MS-Roche#3

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cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat 180

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ctgcaaatga acagcctgcg tgcggaagat acggccgtgt attattgcgc gcgtcttact 300

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agctcagc 368

<210> 4
<211> 122
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH-region of MS-Roche#3

<400> 4

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Arg Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 5
<211> 379
<212> DNA
<213> artificial sequence

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<400> 5
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cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat 180

gcggatagcg tgaaaggccg tttaccattt cacgtgataa ttcgaaaaac accctgtatc 240

tgcaaatgaa cagcctgcgt gcggaagata cggccgtgta ttattgcgcg cgtggtaagg 300

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tggtgacggt tagctcagc 379

<210> 6
<211> 126
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH-region of MS-Roche#7

<400> 6

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Arg Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr
100 105 110

Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 7
<211> 374
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH-region of MS-Roche#8

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cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat 180

gcggatagcg tgaaaggccg ttttaccatt tcacgtgata attcgaaaaa caccctgtat 240

ctgcaaatga acagcctgcg tgcggaagat acggccgtgt attattgcgc gcgtcttctt 300

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acggttagct cagc 374

<210> 8
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH-region of MS-Roche#8

<400> 8

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Arg Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 9
<211> 330
<212> DNA
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<220>
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ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcggttta ttattgccag caggtttata atcctcctgt tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 10
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL-region of MS-Roche#3

<400> 10

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Val Tyr Asn Pro Pro
85 90 95

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

<210> 11
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL-region of MS-Roche#7

<400> 11
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgcttt cagctttatt ctgatccttt tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 12
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL-region of MS-Roche#7

<400> 12

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu

65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Leu Tyr Ser Asp Pro
85 90 95

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

<210> 13
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<220>
<223> synthetic construct; VL-region of MS-Roche#8

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ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

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cagggtacga aagttgaaat taaacgtacg 330

<210> 14
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL-region of MS-Roche#8

<400> 14

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Ser Ser Phe Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 15
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; CDR3 of VL-region of MS-Roche#3

<400> 15
cagcaggttt ataatcctcc tgtt 24

<210> 16
<211> 8
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<213> artificial sequence

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<400> 16

Gln Gln Val Tyr Asn Pro Pro Val
1 5

<210> 17
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<212> DNA
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<220>
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<400> 17
tttcagcttt attctgatcc tttt 24

<210> 18
<211> 8
<212> PRT
<213> artificial sequence

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<400> 18

Phe Gln Leu Tyr Ser Asp Pro Phe
1 5

<210> 19
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; CDR3 of VL-region of MS-Roche#8

<400> 19
cagcagcttt cttcttttcc tcct 24

<210> 20
<211> 8
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<220>
<223> synthetic construct; CDR3 of VL-region of MS-Roche#8

<400> 20

Gln Gln Leu Ser Ser Phe Pro Pro
1 5

<210> 21
<211> 39
<212> DNA
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<220>
<223> synthetic construct; CDR3 of VH-region of MS-Roche#3

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cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 22
<211> 13
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Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 23
<211> 51

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<210> 24
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<213> artificial sequence

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<400> 24

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 25
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<400> 25
cttctttctc gtggttataa tggttattat cataagtttg atgtt 45

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<211> 15
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<400> 26

Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp Val
1 5 10 15

<210> 27
<211> 42
<212> PRT
<213> artificial sequence

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<220>
<223> synthetic construct; beta-A4 peptide

<400> 27

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1 5 10 15

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

Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40

<210> 28
<211> 17
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL-primer for

<400> 28
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<210> 29
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<212> DNA
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<220>
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<220>
<223> synthetic construct; control primer for

<400> 30
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<210> 31
<211> 19
<212> DNA
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<220>

<223> synthetic construct; control primer back

<400> 31
taccgttgct cttcacccc 19

<210> 32
<211> 360
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<220>
<223> synthetic construct; VH MS-Roche#3.6H5 x 3.6L2

<400> 32
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctatttct gagtctggta agactaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 33
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#3.6H5 x 3.6L2

<400> 33

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Ser Glu Ser Gly Lys Thr Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg

85 90 95

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 34
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#3.6H8 x 3.6L2

<400> 34
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctatttct gagtattcta agtttaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 35
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#3.6H8 x 3.6L2

<400> 35

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Ser Glu Tyr Ser Lys Phe Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 36
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.4H2 x 7.2L1

<400> 36
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat tataatggtg ctcgtattta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 37
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.4H2 x 7.2L1

<400> 37

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala

35 40 45

Ile Asn Tyr Asn Gly Ala Arg Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 38
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.9H2 x 7.12L2

<400> 38
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat gctgatggta atcgtaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 39
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.9H2 x 7.12L2

<400> 39

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Ala Asp Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 40
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.9H4 x 7.12L2

<400> 40
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat gctgttggta tgaagaagtt ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 41
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.9H4 x 7.12L2

<400> 41

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Ala Val Gly Met Lys Lys Phe Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 42
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.11H1 x 7.11L1

<400> 42
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cggtattaat gctgctggtt ttcgtactta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 43
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.11H1 x 7.1lL1

<400> 43

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly
35 40 45

Ile Asn Ala Ala Gly Phe Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 44
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.11H1 x 7.2L1

<400> 44
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cggtattaat gctgctggtt ttcgtactta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 45
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH MS-Roche#7.11H1 x 7.2L1

<400> 45

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Gly
35 40 45

Ile Asn Ala Ala Gly Phe Arg Thr Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 46
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#3.6H5 x 3.6L2

<400> 46
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtttctttct cgttattatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcggttta ttattgccag cagacttata attatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 47
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#3.6H5 x 3.6L2

<400> 47

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Phe Leu Ser Arg Tyr
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Tyr Asn Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 48
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#3.6H8 x 3.6L2

<400> 48
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtttctttct cgttattatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcggttta ttattgccag cagacttata attatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 49
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#3.6H8 x 3.6L2

<400> 49

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Phe Leu Ser Arg Tyr
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Tyr Asn Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 50
<211> 330
<212> DNA
<213> artificial sequence

<220>

<223> synthetic construct; VL MS-Roche#7.4H2 x 7.2L1

<400> 50
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtatgttgat cgtacttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 51
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.4H2 x 7.2L1

<400> 51

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 52
<211> 330
<212> DNA
<213> artificial sequence

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<220>
<223> synthetic construct; VL MS-Roche#7.9H2 x 7.12L2

<400> 52
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gcgtttttt tataagtatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttct ggttcttcta accgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa taccttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 53
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.9H2 x 7.12L2

<400> 53

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Phe Phe Tyr Lys
20 25 30

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

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
85 90 95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 54
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.9H4 x 7.12L2

<400> 54
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gcgtttttt tataagtatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttct ggttcttcta accgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 55
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.9H4 x 7.12L2

<400> 55

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Phe Phe Tyr Lys
20 25 30

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

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
85 90 95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 56
<211> 330
<212> DNA

<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.11H1 x 7.11L1

<400> 56
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gcgtattctt cgtatttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag caggtttatt ctcctcctca tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 57
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.11H1 x 7.11L1

<400> 57

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Ile Leu Arg Ile
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Val Tyr Ser Pro Pro
85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 58
<211> 330

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<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.11H1 x 7.2L1

<400> 58
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtatgttgat cgtacttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 59
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.11H1 x 7.2L1

<400> 59

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 60

<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#3.6H5 x 3.6L2

<400> 60
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 61
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#3.6H5 x 3.6L2

<400> 61

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 62
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#3.6H8 x 3.6L2

<400> 62
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 63
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#3.6H8 x 3.6L2

<400> 63

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 64
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.4H2x7.2L1

<400> 64
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 65
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.4H2x7.2L1

<400> 65

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 66
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.9H2x7.12L2

<400> 66
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 67
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.9H2x7.12L2

<400> 67

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 68
<211> 51
<212> DNA
<213> artificial sequence

<220>
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<400> 68
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<210> 69
<211> 17
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<220>
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<400> 69

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 70
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.11H1x7.11L1

<400> 70
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 71
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> HCDR3 MS-Roche#7.11H1x7.11L1

<400> 71

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 72
<211> 51
<212> DNA
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<220>

<223> HCDR3 MS-Roche#7.11H1x7.2L1

<400> 72
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<210> 73
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<220>
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<400> 73

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 74
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> LCDR3 MS-Roche#3.6H5 x 3.6L2

<400> 74
cagcagactt ataattatcc tcct 24

<210> 75
<211> 8
<212> PRT
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<220>
<223> LCDR3 MS-Roche#3.6H5 x 3.6L2

<400> 75

Gln Gln Thr Tyr Asn Tyr Pro Pro
1 5

<210> 76
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> LCDR3 MS-Roche#3.6H8 x 3.6L2

<400> 76

cagcagactt ataattatcc tcct 24

<210> 77
<211> 8
<212> PRT
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<220>
<223> LCDR3 MS-Roche#3.6H8 x 3.6L2

<400> 77

Gln Gln Thr Tyr Asn Tyr Pro Pro
1 5

<210> 78
<211> 24
<212> DNA
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<220>
<223> LCDR3 MS-Roche#7.4H2x7.2L1

<400> 78
cagcagattt attcttttcc tcat 24

<210> 79
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<220>
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<400> 79

Gln Gln Ile Tyr Ser Phe Pro His
1 5

<210> 80
<211> 24
<212> DNA
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<220>
<223> LCDR3 MS-Roche#7.9H2x7.12L2

<400> 80
cttcagcttt ataatattcc taat 24

<210> 81
<211> 8
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<220>
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<400> 81

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 82
<211> 24
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<220>
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<400> 82
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<210> 83
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<220>
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<400> 83

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 84
<211> 24
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<220>
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<400> 84
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<210> 85
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<220>
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<400> 85

Gln Gln Val Tyr Ser Pro Pro His

1 5

<210> 86
<211> 24
<212> DNA
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<220>
<223> LCDR3 MS-Roche#7.11H1x7.2L1

<400> 86
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<210> 87
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<220>
<223> LCDR3 MS-Roche#7.11H1x7.2L1

<400> 87

Gln Gln Ile Tyr Ser Phe Pro His
1 5

<210> 88
<211> 378
<212> DNA
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<220>
<223> synthetic construct; VH MS-Roche#7.9H7

<400> 88
caggtgcaat tggtggaaag cggcggcggc ctggtgcaac cgggcggcag cctgcgtctg 60

agctgcgcgg cctccggatt tacctttagc agctatgcga tgagctgggt gcgccaagcc 120

cctgggaagg gtctcgagtg ggtgagcgct attaatgctt ctggtactcg tacttattat 180

gctgattctg ttaagggtcg ttttaccatt tcacgtgata attcgaaaaa caccctgtat 240

ctgcaaatga acagcctgcg tgcggaagat acggccgtgt attattgcgc gcgtggtaag 300

ggtaatactc ataagcctta tggttatgtt cgttattttg atgtttgggg ccaaggcacc 360

ctggtgacgg ttagctca 378

<210> 89
<211> 126
<212> PRT
<213> artificial sequence

<220>

<223> synthetic construct; VH MS-Roche#7.9H7

<400> 89

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

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

Ser Ala Ile Asn Ala Ser Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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

Ala Arg Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr
100 105 110

Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 90
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.9H7

<400> 90
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgcctt cagatttata atatgcctat tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 91

<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL MS-Roche#7.9H7

<400> 91

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Ile Tyr Asn Met Pro
85 90 95

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

<210> 92
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; HCDR3 MS-Roche#7.9H7

<400> 92
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 93
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR3 MS-Roche#7.9H7

<400> 93

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 94
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 MS-Roche#7.9H7

<400> 94
cttcagattt ataatatgcc tatt 24

<210> 95
<211> 8
<212> PRT
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<220>
<223> synthetic construct; LCDR3 MS-Roche#7.9H7

<400> 95

Leu Gln Ile Tyr Asn Met Pro Ile
1 5

<210> 96
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3

<400> 96

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 97
<211> 7
<212> PRT
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<220>
<223> synthetic construct; LCDR2 of MS-Roche#3

<400> 97

Gly Ala Ser Ser Arg Ala Thr

1 5

<210> 98
<211> 8
<212> PRT
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<220>
<223> synthetic construct; LCDR3 of MS-Roche#3

<400> 98

Gln Gln Val Tyr Asn Pro Pro Val
1 5

<210> 99
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR1 of MS-Roche#3

<400> 99

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

<210> 100
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3

<400> 100

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 101
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR3 of MS-Roche#3

<400> 101

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 102
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.1

<400> 102

Gln Gln Val Tyr Ser Val Pro Pro
1 5

<210> 103
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.2

<400> 103

Gln Gln Ile Tyr Ser Tyr Pro Pro
1 5

<210> 104
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.3

<400> 104

His Gln Met Ser Ser Tyr Pro Pro
1 5

<210> 105
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.4

<400> 105

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 106
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.5

<400> 106

Gln Gln Ile Tyr Asp Tyr Pro Pro
1 5

<210> 107
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#3.6

<400> 107

Gln Gln Thr Tyr Asn Tyr Pro Pro
1 5

<210> 108
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.2H1

<400> 108

Ala Ile Ser Glu His Gly Leu Asn Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 109
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.2H2

<400> 109

Ala Ile Ser Gln Arg Gly Gln Phe Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 110
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.3H1

<400> 110

Val Ile Ser Glu Lys Ser Arg Phe Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 111
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.3H2

<400> 111

Val Ile Ser Gln Glu Ser Gln Tyr Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 112
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.3H3

<400> 112

Ala Ile Ser Gln Asn Gly Phe His Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 113
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H1

<400> 113

Ala Ile Ser Glu Thr Ser Ile Arg Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 114
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H2

<400> 114

Val Ile Asp Met Val Gly His Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 115
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H3

<400> 115

Val Ile Ser Gln Thr Gly Arg Lys Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 116
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H4

<400> 116

Ala Ile Ser Glu Thr Gly Met His Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 117
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H5

<400> 117

Val Ile Ser Gln Val Gly Ala His Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 118
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H6

<400> 118

Ala Ile Ser Glu Ser Gly Trp Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 119
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H7

<400> 119

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

Gly

<210> 120
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H8

<400> 120

Ala Ile Ser Glu His Gly Arg Phe Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 121
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H9

<400> 121

Ala Ile Ser Glu Ser Ser Lys Asn Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 122
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H10

<400> 122

Ala Ile Ser Glu Ser Gly Arg Gly Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 123
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H11

<400> 123

Ala Ile Ser Glu Phe Gly Lys Asn Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 124
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H12

<400> 124

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

Gly

<210> 125
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H13

<400> 125

Ala Ile Ser Glu Gln Gly Arg Asn Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 126
<211> 17
<212> PRT
<213> artificial sequence

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<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H14

<400> 126

Ala Ile Ser Glu Ser Gly Gln Tyr Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 127
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H16

<400> 127

Ala Ile Ser Glu Ser Gly Val Asn Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 128
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H17

<400> 128

Ala Ile Ser Glu Phe Gly Gln Phe Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 129
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.4H18

<400> 129

Ala Ile Ser Gln Gln Ser Asn Phe Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 130
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.4L7

<400> 130

Arg Ala Ser Gln Arg Leu Gly Arg Leu Tyr Leu Ala
1 5 10

<210> 131
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.4L8

<400> 131

Arg Ala Ser Gln Trp Ile Thr Lys Ser Tyr Leu Ala
1 5 10

<210> 132
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.4L9

<400> 132

Arg Ala Ser Arg Arg Ile His Val Tyr Tyr Leu Ala
1 5 10

<210> 133
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.4L11

<400> 133

Arg Ala Ser Gln Leu Val Gly Arg Ala Tyr Leu Ala
1 5 10

<210> 134
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H1

<400> 134

Val Ile Ser Glu Ser Gly Gln Tyr Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 135
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H2

<400> 135

Val Ile Ser Glu Arg Gly Ile Asn Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 136
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H3

<400> 136

Val Ile Ser Glu Thr Gly Lys Phe Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 137
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H4

<400> 137

Ala Ile Ser Glu Arg Gly Arg His Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 138
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H5

<400> 138

Ala Ile Ser Glu Ser Gly Lys Thr Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 139
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H6

<400> 139

Ala Ile Ser Glu His Gly Thr Asn Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 140
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#3.6H8

<400> 140

Ala Ile Ser Glu Tyr Ser Lys Phe Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 141
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.6L1

<400> 141

Arg Ala Ser Gln Phe Ile Gln Arg Phe Tyr Leu Ala
1 5 10

<210> 142
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#3.6L2

<400> 142

Arg Ala Ser Gln Phe Leu Ser Arg Tyr Tyr Leu Ala
1 5 10

<210> 143
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7

<400> 143

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 144
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR2 of MS-Roche#7

<400> 144

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 145
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7

<400> 145

Phe Gln Leu Tyr Ser Asp Pro Phe
1 5

<210> 146
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR1 of MS-Roche#7

<400> 146

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

<210> 147
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7

<400> 147

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 148
<211> 17
<212> PRT

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<213> artificial sequence

<220>
<223> synthetic construct; HCDR3 of MS-Roche#7

<400> 148

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 149
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.1

<400> 149

His Gln Leu Tyr Ser Ser Pro Tyr
1 5

<210> 150
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3of MS-Roche#7.2

<400> 150

Gln Gln Ile Tyr Ser Phe Pro His
1 5

<210> 151
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.3

<400> 151

His Gln Val Tyr Ser His Pro Phe
1 5

<210> 152
<211> 8

<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.4

<400> 152

Gln Gln Ile Tyr Asn Phe Pro His
1 5

<210> 153
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.5

<400> 153

His Gln Val Tyr Ser Ser Pro Phe
1 5

<210> 154
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.6

<400> 154

His Gln Leu Tyr Ser Pro Pro Tyr
1 5

<210> 155
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.7

<400> 155

His Gln Val Tyr Ser Ala Pro Phe
1 5

<210> 156
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.8

<400> 156

His Gln Val Tyr Ser Phe Pro Ile
1 5

<210> 157
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.9

<400> 157

Leu Gln Ile Tyr Asn Met Pro Ile
1 5

<210> 158
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.10

<400> 158

Gln Gln Val Tyr Asn Pro Pro His
1 5

<210> 159
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.11

<400> 159

Gln Gln Val Tyr Ser Pro Pro His
1 5

<210> 160
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12

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<400> 160

Arg Ala Ser Gln Tyr Val Ser Ser Pro Tyr Leu Ala
1 5 10

<210> 161
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR2 of MS-Roche#7.12

<400> 161

Gly Ser Ser Asn Arg Ala Thr
1 5

<210> 162
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.12

<400> 162

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 163
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR1 of MS-Roche#7.12

<400> 163

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

<210> 164
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.12

<400> 164

Asn Ile Ser Gly Ser Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val Lys

1 5 10 15

Gly

<210> 165
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR3 of MS-Roche#7.12

<400> 165

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 166
<211> 8
<212> PRT
<213> artificial sequence

<220>
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<400> 166

His Gln Val Tyr Ser Pro Pro Phe
1 5

<210> 167
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H1

<400> 167

Ala Ile Asn Ala Asn Gly Leu Lys Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 168
<211> 17

<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H2

<400> 168

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

Gly

<210> 169
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H3

<400> 169

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

Gly

<210> 170
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H4

<400> 170

Ala Ile Asn Ser Lys Gly Ser Arg Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 171
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H5

<400> 171

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

Gly

<210> 172
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H6

<400> 172

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

Gly

<210> 173
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H7

<400> 173

Ala Ile Asn Ser Arg Gly Ser Asp Thr His Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 174
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.2H8

<400> 174

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

Gly

<210> 175
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.2L1

<400> 175

Arg Ala Ser Gln Tyr Val Asp Arg Thr Tyr Leu Ala
1 5 10

<210> 176
<211> 12
<212> PRT
<213> artificial sequence

<220>
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<400> 176

Arg Ala Ser Gln Tyr Ile Ser Phe Arg Tyr Leu Ala
1 5 10

<210> 177
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.2L4

<400> 177

Arg Ala Ser Gln Phe Ile Arg Arg Ser Tyr Leu Ala
1 5 10

<210> 178
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.3H1

<400> 178

His Gln Val Tyr Ser His Pro Phe

1 5

<210> 179
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.3H1

<400> 179

Ala Ile Ser Ala Ile Ser Asn Lys Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 180
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.3L1

<400> 180

Arg Ala Ser Gln Tyr Leu His Tyr Gly Tyr Leu Ala
1 5 10

<210> 181
<211> 17
<212> PRT
<213> artificial sequence

<220>
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<400> 181

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

Gly

<210> 182
<211> 17
<212> PRT
<213> artificial sequence

<220>

<223> synthetic construct; HCDR2 of MS-Roche#7.4H2

<400> 182

Ala Ile Asn Tyr Asn Gly Ala Arg Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 183
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.9H1

<400> 183

Leu Gln Ile Tyr Asn Met Pro Ile
1 5

<210> 184
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H1

<400> 184

Ala Ile Asn Ala Asn Gly Gln Arg Lys Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 185
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H2

<400> 185

Ala Ile Asn Ala Asp Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 186
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H3

<400> 186

Ala Ile Asn Tyr Gln Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 187
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H4

<400> 187

Ala Ile Asn Ala Val Gly Met Lys Lys Phe Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 188
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H5

<400> 188

Ala Ile Asn His Ala Gly Asn Lys Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 189
<211> 12

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<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.9L1

<400> 189

Arg Ala Ser Gln Arg Leu Ser Pro Arg Tyr Leu Ala
1 5 10

<210> 190
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.9L2

<400> 190

Arg Ala Ser Gln Tyr Leu His Lys Arg Tyr Leu Ala
1 5 10

<210> 191
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H6

<400> 191

Ala Ile Asn Ala Ser Gly Arg Leu Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 192
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H7

<400> 192

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

Gly

<210> 193
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H8

<400> 193

Ala Ile Asn Ala Ser Gly Ser Lys Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 194
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.9H9

<400> 194

Ala Ile Asn Gly Lys Gly Asn Lys Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 195
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H1

<400> 195

Gly Ile Asn Ala Ala Gly Phe Arg Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 196
<211> 17

<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H2

<400> 196

Ala Ile Asn Ala Asn Gly Tyr Lys Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 197
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H3

<400> 197

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

Gly

<210> 198
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H4

<400> 198

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

Gly

<210> 199
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.11H5

<400> 199

Ala Ile Asn Ala His Gly Gln Arg Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 200
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.11L1

<400> 200

Arg Ala Ser Gln Arg Ile Leu Arg Ile Tyr Leu Ala
1 5 10

<210> 201
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12H1

<400> 201

Arg Ala Ser Gln Tyr Val Phe Arg Arg Tyr Leu Ala
1 5 10

<210> 202
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#7.12H1

<400> 202

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 203
<211> 10
<212> PRT
<213> artificial sequence

<220>

<223> synthetic construct; HCDR1 of MS-Roche#7.12H1

<400> 203

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

<210> 204
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.12H1

<400> 204

Asn Ile Asn Gly Asn Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 205
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#7.12L1

<400> 205

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

Gly

<210> 206
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L2

<400> 206

Arg Ala Ser Gln Arg Phe Phe Tyr Lys Tyr Leu Ala
1 5 10

<210> 207

<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L3

<400> 207

Arg Ala Ser Gln Phe Val Arg Arg Gly Phe Leu Ala
1 5 10

<210> 208
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L4

<400> 208

Arg Ala Ser Gln Arg Leu Lys Arg Ser Tyr Leu Ala
1 5 10

<210> 209
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L6

<400> 209

Arg Ala Ser Gln Tyr Leu Trp Tyr Arg Tyr Leu Ala
1 5 10

<210> 210
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#7.12L7

<400> 210

Arg Ala Ser Gln Trp Ile Arg Lys Thr Tyr Leu Ala
1 5 10

<210> 211
<211> 12
<212> PRT
<213> artificial sequence

21 AUG 2006

<220>
<223> synthetic construct; LCDR1 of MS-Roche#8

<400> 211

Arg Ala Ser Gln Ser Val Ser Ser Ser Tyr Leu Ala
1 5 10

<210> 212
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR2 of MS-Roche#8

<400> 212

Gly Ala Ser Ser Arg Ala Thr
1 5

<210> 213
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#8

<400> 213

Gln Gln Leu Ser Ser Phe Pro Pro
1 5

<210> 214
<211> 10
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR1 of MS-Roche#8

<400> 214

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

<210> 215
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#8

<400> 215

Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 216
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR3 of MS-Roche#8

<400> 216

Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp Val
1 5 10 15

<210> 217
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#8.1

<400> 217

Gln Gln Leu Ser Asn Tyr Pro Pro
1 5

<210> 218
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#8.2

<400> 218

Gln Gln Leu Ser Ser Tyr Pro Pro
1 5

<210> 219
<211> 17
<212> PRT
<213> artificial sequence

<220>

21 AUG 2006

<223> synthetic construct; HCDR2 of MS-Roche#8.1H1

<400> 219

Ala Ile Ser Arg Ser Gly Ser Asn Ile Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 220
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR3 of MS-Roche#8.2H1

<400> 220

Gln Gln Leu Ser Ser Tyr Pro Pro
1 5

<210> 221
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#8.2H1

<400> 221

Ala Ile Ser Ile Thr Gly Arg Arg Lys Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 222
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#8.2H2

<400> 222

Ala Ile Ser Arg Thr Gly Ser Lys Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 223
<211> 16
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; HCDR2 of MS-Roche#8.2H4

<400> 223

Ala Thr Ser Val Lys Gly Lys Thr Tyr Tyr Ala Asp Ser Val Lys Gly
1 5 10 15

<210> 224
<211> 12
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; LCDR1 of MS-Roche#8.2L1

<400> 224

Arg Ala Ser Gln Arg Val Ser Gly Arg Tyr Leu Ala
1 5 10

<210> 225
<211> 109
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa1

<220>
<221> MISC_FEATURE
<222> (96)..(96)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> MISC_FEATURE
<222> (93)..(93)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Gly, His, Leu, Asn or Ser

<220>
<221> MISC_FEATURE
<222> (92)..(92)
<223> Xaa = any amino acid of a mixture of Asp, Gly, Asn, Ser or Tyr

21 AUG 2006

<220>
<221> MISC_FEATURE
<222> (91)..(91)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His , Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp or Tyr

<220>
<221> MISC_FEATURE
<222> (89)..(89)
<223> Xaa = any amino acid of a mixture of Phe, His, Ile, Leu, Met or Gln,

<220>
<221> MISC_FEATURE
<222> (85)..(85)
<223> Xaa = can be Thr or Val

<220>
<221> MISC_FEATURE
<222> (94)..(94)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His , Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> MISC_FEATURE
<222> (95)..(95)
<223> Xaa = any amino acid of a mixture of Leu, Pro or Ser

<400> 225

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Tyr
20 25 30

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

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

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

Glu Asp Phe Ala Xaa Tyr Tyr Cys Xaa Gln Xaa Xaa Xaa Xaa Xaa Xaa
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 226
<211> 114
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa2

<220>
<221> misc_feature
<222> (101)..(101)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> misc_feature
<222> (94)..(94)
<223> Xaa = any amino acid of a mixture of Phe, His, Ile, Leu, Met or Gln,

<220>
<221> misc_feature
<222> (96)..(96)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp or Tyr

<220>
<221> misc_feature
<222> (97)..(97)
<223> Xaa = any amino acid of a mixture of Asp, Gly, Asn, Ser or Tyr

<220>
<221> misc_feature
<222> (98)..(98)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Gly, His, Leu, Asn or Ser

<220>
<221> misc_feature
<222> (99)..(99)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> misc_feature

<222> (100)..(100)
<223> Xaa = any amino acid of a mixture of Leu, Pro or Ser

<400> 226

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

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Xaa Gln Xaa
85 90 95

Xaa Xaa Xaa Xaa Xaa Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr

<210> 227
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa3

<220>
<221> misc_feature
<222> (97)..(97)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> misc_feature
<222> (90)..(90)
<223> Xaa = any amino acid of a mixture of Phe, His, Ile, Leu, Met or Gln,

<220>
<221> misc_feature
<222> (86)..(86)
<223> Xaa = Thr or Val

<220>
<221> misc_feature
<222> (92)..(92)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His
, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp or Tyr

<220>
<221> misc_feature
<222> (93)..(93)
<223> Xaa = any amino acid of a mixture of Asp, Gly, Asn, Ser or Tyr

<220>
<221> misc_feature
<222> (94)..(94)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Gly, His, Leu, Asn
or Ser

<220>
<221> misc_feature
<222> (95)..(95)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His
, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or
Tyr

<220>
<221> misc_feature
<222> (96)..(96)
<223> Xaa = any amino acid of a mixture of Leu, Pro or Ser

<400> 227

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Xaa Tyr Tyr Cys Xaa Gln Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 228
<211> 115
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa4

<220>
<221> MISC_FEATURE
<222> (102)..(102)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> MISC_FEATURE
<222> (95)..(95)
<223> Xaa = any amino acid of a mixture of Phe, His, Ile, Leu, Met or Gln,

<220>
<221> MISC_FEATURE
<222> (97)..(97)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Gln, Arg, Ser, Thr, Val, Trp or Tyr

<220>
<221> MISC_FEATURE
<222> (98)..(98)
<223> Xaa = any amino acid of a mixture of Asp, Gly, Asn, Ser or Tyr

<220>
<221> MISC_FEATURE
<222> (99)..(99)
<223> Xaa = any amino acid of a mixture of Ala, Asp, Gly, His, Leu, Asn or Ser

<220>
<221> MISC_FEATURE
<222> (100)..(100)

<223> Xaa = any amino acid of a mixture of Ala, Asp, Glu, Phe, Gly, His , Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, or Tyr

<220>
<221> MISC_FEATURE
<222> (101)..(101)
<223> Xaa = any amino acid of a mixture of Leu, Pro or Ser

<400> 228

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

Glu Arg Ala Thr Ile Asn Cys Arg Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Xaa Gln
85 90 95

Xaa Xaa Xaa Xaa Xaa Xaa Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr
115

<210> 229
<211> 111
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL lambda1

<220>
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<222> (99)..(99)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (97)..(98)
<223> Xaa = any amino acid except a Cys or a deletion

<220>
<221> MISC_FEATURE
<222> (94)..(96)
<223> Xaa = any amino acid except a Cys

<220>
<221> MISC_FEATURE
<222> (92)..(92)
<223> Xaa = any amino acid of Cys, Phe, His, Arg, Trp or Tyr

<400> 229

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

Arg Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn
20 25 30

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu
35 40 45

Ile Tyr Asp Asn Asn Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser
50 55 60

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Thr Gly Leu Gln
65 70 75 80

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Xaa Asp Xaa Xaa Xaa
85 90 95

Xaa Xaa Xaa Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105 110

<210> 230
<211> 112
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VL lambda2

<220>
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<222> (100)..(100)

<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (93)..(93)
<223> Xaa = any amino acid of Cys, Phe, His, Arg, Trp or Tyr

<220>
<221> MISC_FEATURE
<222> (95)..(97)
<223> Xaa = any amino acid except a Cys

<220>
<221> MISC_FEATURE
<222> (98)..(99)
<223> Xaa = any amino acid except a Cys or a deletion

<400> 230

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

Ser Ile Thr Ile Ser Cys Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr
            20                  25                  30

Asn Tyr Val Ser Trp Tyr Gln Gln His Pro Gly Lys Ala Pro Lys Leu
        35                  40                  45

Met Ile Tyr Asp Val Ser Asn Arg Pro Ser Gly Val Ser Asn Arg Phe
    50                  55                  60

Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu Thr Ile Ser Gly Leu
65                  70                  75                  80

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Xaa Asp Xaa Xaa
                85                  90                  95

Xaa Xaa Xaa Xaa Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
            100                 105                 110
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<210> 231
<211> 109
<212> PRT
<213> artificial sequence

<220>
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<220>
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<222> (97)..(97)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (90)..(90)
<223> Xaa = any amino acid of Cys, Phe, His, Arg, Trp or Tyr

<220>
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<222> (92)..(94)
<223> Xaa = any amino acid except a Cys

<220>
<221> MISC_FEATURE
<222> (95)..(96)
<223> Xaa = any amino acid except a Cys or a deletion

<400> 231

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

Thr Ala Arg Ile Ser Cys Ser Gly Asp Ala Leu Gly Asp Lys Tyr Ala
20 25 30

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

Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
50 55 60

Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr Gln Ala Glu
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Gln Ser Xaa Asp Xaa Xaa Xaa Xaa Xaa
85 90 95

Xaa Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
100 105

<210> 232
<211> 127
<212> PRT
<213> artificial sequence

21 AUG 2006

<220>
<223> synthetic construct; VH1A

<220>
<221> MISC_FEATURE
<222> (99)..(112)
<223> Xaa = any amino acid or a deletion

<220>
<221> MISC_FEATURE
<222> (116)..(116)
<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<220>
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<222> (114)..(114)
<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly, Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<220>
<221> MISC_FEATURE
<222> (113)..(113)
<223> Xaa = any amino acid

<400> 232

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

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

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

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

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

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

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

21 AUG 2006

Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 233
<211> 127
<212> PRT
<213> artificial sequence

<220>
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<223> Xaa = any amino acid

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<222> (114)..(114)
<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly, Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<220>
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<222> (116)..(116)
<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<400> 233

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

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

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

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Ile Ser Thr Ala Tyr
65 70 75 80

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

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 234
<211> 128
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH2

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<221> MISC_FEATURE
<222> (100)..(113)
<223> Xaa = any amino acid or a deletion

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<222> (114)..(114)
<223> Xaa = any amino acid

<220>
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<222> (117)..(117)
<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<220>
<221> MISC_FEATURE
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<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly, Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<400> 234

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

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Gly Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

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Trp Leu Ala Leu Ile Asp Trp Asp Asp Asp Lys Tyr Tyr Ser Thr Ser
    50                  55                  60

Leu Lys Thr Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
65                  70                  75                  80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
                85                  90                  95

Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100                 105                 110

Xaa Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125
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<210> 235
<211> 127
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH3

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<221> MISC_FEATURE
<222> (99)..(112)
<223> Xaa = any amino acid or a deletion

<220>
<221> MISC_FEATURE
<222> (113)..(113)
<223> Xaa = any amino acid

<220>
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<222> (116)..(116)
<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<220>
<221> MISC_FEATURE
<222> (114)..(114)
<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly, Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<400> 235

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

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
            20                  25                  30

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

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
    50                  55                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

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

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
            100                 105                 110

Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120                 125


<210>  236
<211>  126
<212>  PRT
<213>  artificial sequence

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<223>  synthetic construct; VH4

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<221>  MISC_FEATURE
<222>  (112)..(112)
<223>  Xaa = any amino acid


<220>
<221>  MISC_FEATURE
<222>  (113)..(113)
<223>  Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly,
       Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr


<220>
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<221> MISC_FEATURE
<222> (115)..(115)
<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<400> 236

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

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Tyr
20 25 30

Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35 40 45

Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys
50 55 60

Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu
65 70 75 80

Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala
85 90 95

Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 237
<211> 127
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH5

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<222> (99)..(112)
<223> Xaa = any amino acid or a deletion

<220>
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<222> (113)..(113)
<223> Xaa = any amino acid

<220>
<221> MISC_FEATURE
<222> (116)..(116)
<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<220>
<221> MISC_FEATURE
<222> (114)..(114)
<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly, Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<400> 237

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

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

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

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120 125

<210> 238
<211> 130
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; VH6

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<222> (102)..(115)
<223> Xaa = any amino acid or a deletion

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<223> Xaa = any amino acid

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<222> (119)..(119)
<223> Xaa = any amino acid out of a mixture of Phe, His, Ile, Leu, Asn, Pro, Ser, Val, Trp or Tyr

<220>
<221> MISC_FEATURE
<222> (117)..(117)
<223> Xaa = any amino acid out of a mixture of Ala, Asp, Glu, Phe, Gly, Ile, Leu, Met, Pro, Gln, Ser, Thr, Val or Tyr

<400> 238

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

Thr Leu Ser Leu Thr Cys Ala Ile Ser Gly Asp Ser Val Ser Ser Asn
20 25 30

Ser Ala Ala Trp Asn Trp Ile Arg Gln Ser Pro Gly Arg Gly Leu Glu
35 40 45

Trp Leu Gly Arg Thr Tyr Tyr Arg Ser Lys Trp Tyr Asn Asp Tyr Ala
50 55 60

Val Ser Val Lys Ser Arg Ile Thr Ile Asn Pro Asp Thr Ser Lys Asn
65 70 75 80

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

Tyr Tyr Cys Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Xaa Xaa Xaa Xaa Asp Xaa Trp Gly Gln Gly Thr Leu Val Thr Val
115 120 125

Ser Ser

130

<210> 239
<211> 327
<212> DNA
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<220>
<223> synthetic construct; VL kappa1

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<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
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<222> (271)..(273)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
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<222> (265)..(267)
<223> nnn = TTT, CAT, CTT, ATG or CAG

<220>
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<222> (253)..(256)
<223> nnn = can be ACT or GTT

<220>
<221> misc_feature
<222> (283)..(285)
<223> nnn = CTT, CCT or TCT

<220>
<221> misc_feature
<222> (280)..(282)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
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<222> (277)..(279)
<223> nnn = GCT, GAT, GGT, CAT, CTT, AAT or TCT

<220>
<221> misc_feature
<222> (274)..(276)

<223> nnn = GAT, GGT, AAT, TCT or TAT

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attacctgca gagcgagcca gggcattagc agctatctgg cgtggtacca gcagaaacca 120

ggtaaagcac cgaaactatt aatttatgca gccagcagct tgcaaagcgg ggtcccgtcc 180

cgttttagcg gctctggatc cggcactgat tttaccctga ccattagcag cctgcaacct 240

gaagactttg cgnnntatta ttgcnnncag nnnnnnnnnn nnnnnnnnac ctttggccag 300

ggtacgaaag ttgaaattaa acgtacg 327

<210> 240
<211> 328
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa2

<220>
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<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
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<222> (280)..(280)
<223> n = TTT, CAT, CTT, ATG or CAG

<220>
<221> misc_feature
<222> (284)..(284)
<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
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<222> (285)..(285)
<223> n = GAT, GGT, AAT, TCT or TAT

<220>
<221> misc_feature
<222> (286)..(289)
<223> n = GCT, GAT, GGT, CAT, CTT, AAT or TCT

<220>
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<222> (287)..(287)
<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, C
AG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
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<223> n = CTT, CCT or TCT

<400> 240
gatatcgtga tgacccagag cccactgagc ctgccagtga ctccgggcga gcctgcgagc 60

attagctgca gaagcagcca aagcctgctg catagcaacg gctataacta tctggattgg 120

taccttcaaa aaccaggtca aagcccgcag ctattaattt atctgggcag caaccgtgcc 180

agtggggtcc cggatcgttt tagcggctct ggatccggca ccgattttac cctgaaaatt 240

agccgtgtgg aagctgaaga cgtgggcgtg tattattgcn cagnnnnnna cctttggcca 300

gggtacgaaa gttgaaatta aacgtacg 328

<210> 241
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa3

<220>
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CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (256)..(258)
<223> nnn = can be ACT or GTT

<220>
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<222> (265)..(276)
<223> nnn = TTT, CAT, CTT, ATG or CAG

<220>
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<222> (274)..(276)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CAG,
CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (277)..(279)
<223> nnn = GAT, GGT, AAT, TCT or TAT

<220>
<221> misc_feature
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<223> nnn = GCT, GAT, GGT, CAT, CTT, AAT or TCT

<220>
<221> misc_feature
<222> (283)..(285)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (286)..(288)
<223> nnn = CTT, CCT or TCT

<400> 241
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gagcgtgagc agcagctatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgnnnta ttattgcnnn cagnnnnnnn nnnnnnnnnn naccttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 242
<211> 345
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL kappa4

<220>
<221> misc_feature
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<220>
<221> misc_feature
<222> (283)..(285)
<223> nnn = TTT, CAT, CTT, ATG or CAG

<220>
<221> misc_feature
<222> (289)..(291)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (292)..(294)
<223> nnn = GAT, GGT, AAT, TCT or TAT

<220>
<221> misc_feature
<222> (295)..(297)
<223> nnn = GCT, GAT, GGT, CAT, CTT, AAT or TCT

<220>
<221> misc_feature
<222> (298)..(300)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (301)..(303)
<223> nnn = CTT, CCT or TCT

<400> 242
gatatcgtga tgacccagag cccggatagc ctggcggtga gcctgggcga acgtgcgacc 60

attaactgca gaagcagcca gagcgtgctg tatagcagca acaacaaaaa ctatctggcg 120

tggtaccagc agaaaccagg tcagccgccg aaactattaa tttattgggc atccacccgt 180

gaaagcgggg tcccggatcg ttttagcggc tctggatccg gcactgattt taccctgacc 240

atttcgtccc tgcaagctga agacgtggcg gtgtattatt gcnnncagnn nnnnnnnnnn 300

nnnnnnacct ttggccaggg tacgaaagtt gaaattaaac gtacg 345

<210> 243
<211> 322
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL lambda1

<220>
<221> misc_feature
<222> (274)..(274)
<223> n = TGT, TTT, CAT, CGT, TGG or TAT

<220>
<221> misc_feature
<222> (278)..(280)
<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, C
AG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (281)..(282)
<223> n = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, C
AG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

<220>
<221> misc_feature
<222> (283)..(283)
<223> n = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, C
CT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<400> 243
gatatcgtgc tgacccagcc gccttcagtg agtggcgcac caggtcagcg tgtgaccatc 60

tcgtgtagcg gcagcagcag caacattggc agcaactatg tgagctggta ccagcagttg 120

cccgggacgg cgccgaaact gctgatttat gataacaacc agcgtccctc aggcgtgccg 180

gatcgtttta gcggatccaa aagcggcacc agcgcgagcc ttgcgattac gggcctgcaa 240

agcgaagacg aagcggatta ttattgccag tctngatnnn nnngtgtttg gcggcggcac 300

gaagttaacc gttcttggcc ag 322

<210> 244
<211> 336
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL lambda2

<220>
<221> misc_feature
<222> (274)..(276)
<223> nnn = TGT, TTT, CAT, CGT, TGG or TAT

<220>
<221> misc_feature
<222> (290)..(295)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,
CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

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<221> misc_feature
<222> (296)..(298)
<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
<221> misc_feature
<222> (280)..(289)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

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tcgtgtacgg gtactagcag cgatgtgggc ggctataact atgtgagctg gtaccagcag 120

catcccggga aggcgccgaa actgatgatt tatgatgtga gcaaccgtcc ctcaggcgtg 180

agcaaccgtt ttagcggatc caaaagcggc aacaccgcga gcctgaccat tagcggcctg 240

caagcggaag acgaagcgga ttattattgc cagnnngatn nnnnnnnnnn nnnnnngtg 300

tttggcggcg gcacgaagtt aaccgttctt ggccag 336

<210> 245
<211> 327
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VL lambda3

<220>
<221> misc_feature
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<223> nnn = TGT, TTT, CAT, CGT, TGG or TAT

<220>
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<222> (286)..(288)
<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

<220>
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<222> (280)..(285)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

<220>
<221> misc_feature
<222> (271)..(279)
<223> nnn = GCT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT,

CAG, CGT, TCT, ACT, GTT, TGG or TAT

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caggcgccag ttctggtgat ttatgatgat tctgaccgtc cctcaggcat cccggaacgc 180

tttagcggat ccaacagcgg caacaccgcg accctgacca ttagcggcac tcaggcggaa 240

gacgaagcgg attattattg ccagnnngat nnnnnnnnnn nnnnnnnngt gtttggcggc 300

ggcacgaagt taaccgttct tggccag 327

<210> 246
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<212> DNA
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<223> synthetic construct; VH1A

<220>
<221> misc_feature
<222> (345)..(347)
<223> nnn = TTT, CAT, ATT, CTT, AAT, CCT, TCT, GTT, TGG or TAT

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<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

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agctgcaaag cctccggagg cacttttagc agctatgcga ttagctgggt gcgccaagcc 120

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gcgcagaagt ttcagggccg ggtgaccatt accgcggatg aaagcaccag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtnnnnnn 300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn ngatnnntgg ggccaaggca 360

ccctggtgac ggttagctca gc 382

<210> 247
<211> 383
<212> DNA
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<220>
<223> synthetic construct; VH1B

<220>
<221> misc_feature
<222> (346)..(348)
<223> nnn = TTT, CAT, ATT, CTT, AAT, CCT, TCT, GTT, TGG or TAT

<220>
<221> misc_feature
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<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

<220>
<221> misc_feature
<222> (337)..(339)
<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

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<221> misc_feature
<222> (340)..(342)
<223> nnn = GCT, GAT, GAG, TTT, GGT, ATT, CTT, ATG, CCT, CAG, TCT, ACT, GTT or TAT

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cctgggcagg gtctcgagtg gatgggctgg attaacccga atagcggcgg cacgaactac 180

gcgcagaagt ttcagggccg ggtgaccatg acccgtgata ccagcattag caccgcgtat 240

atggaactga gcagcctgcg tagcgaagat acggccgtgt attattgcgc gcgtnnnnnn 300

nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nngatnnntg gggccaaggc 360

accctggtga cggttagctc agc 383

<210> 248
<211> 386
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct; VH2

<220>
<221> misc_feature
<222> (349)..(351)
<223> nnn = TTT, CAT, ATT, CTT, AAT, CCT, TCT, GTT, TGG or TAT

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<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

<220>
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<222> (340)..(342)
<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, CCT, CAG, CGT, TCT, ACT, GTT, TGG or TAT

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<222> (343)..(345)
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acctgtacct tttccggatt tagcctgtcc acgtctggcg ttggcgtggg ctggattcgc 120

cagccgcctg ggaaagccct cgagtggctg gctctgattg attgggatga tgataagtat 180

tatagcacca gcctgaaaac gcgtctgacc attagcaaag atacttcgaa aaatcaggtg 240

gtgctgacta tgaccaacat ggacccggtg gatacggcca cctattattg cgcgcgtnnn 300

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ggcaccctgg tgacggttag ctcagc 386

<210> 249
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<222> (314)..(314)
<223> n = TTT, CAT, ATT, CTT, AAT, CCT, TCT, GTT, TGG or TAT

<220>
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cctgggaagg gtctcgagtg ggtgagcgcg attagcggta gcggcggcag cacctattat 180

gcggatagcg tgaaaggccg ttttaccatt tcacgtgata attcgaaaaa caccctgtat 240

ctgcaaatga acagcctgcg tgcggaagat acggccgtgt attattgcgc gcgtnnnnnn 300

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<210> 250
<211> 346
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<223> n = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, C
CT, CAG, CGT, TCT, ACT, GTT, TGG or TAT or a deletion

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<220>
<221> misc_feature
<222> (307)..(307)
<223> n = GCT, GAT, GAG, TTT, GGT, ATT, CTT, ATG, CCT, CAG, TCT, ACT, G
TT or TAT

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acctgcaccg tttccggagg cagcattagc agctattatt ggagctggat tcgccagccg 120

cctgggaagg gtctcgagtg gattggctat atttattata gcggcagcac caactataat 180

ccgagcctga aaagccgggt gaccattagc gttgatactt cgaaaaacca gtttagcctg 240

aaactgagca gcgtgacggc ggcggatacg gccgtgtatt attgcgcgcg tnnnnnnnnn 300

nnnnnnngat ntggggccaa ggcaccctgg tgacggttag ctcagc 346

<210> 251
<211> 349
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<222> (314)..(314)
<223> n = TTT, CAT, ATT, CTT, AAT, CCT, TCT, GTT, TGG or TAT

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<223> n = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT, C
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TT or TAT

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cttcaatgga gcagcctgaa agcgagcgat acggccatgt attattgcgc gcgtnnnnnn 300

nnnnnnnnnn gatntggggc caaggcaccc tggtgacggt tagctcagc 349

<210> 252
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<223> nnn = TTT, CAT, ATT, CTT, AAT, CCT, TCT, GTT, TGG or TAT

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<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT,
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<220>
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<222> (346)..(348)
<223> nnn = GCT, TGT, GAT, GAG, TTT, GGT, CAT, ATT, AAG, CTT, ATG, AAT,
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<220>
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GTT or TAT

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cagtttagcc tgcaactgaa cagcgtgacc ccggaagata cggccgtgta ttattgcgcg 300

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<210> 253
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Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val
65                  70                  75                  80

Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
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Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
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His Tyr Thr Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
        115                 120                 125

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
    130                 135                 140

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145                 150                 155                 160

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
                165                 170                 175

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

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
        195                 200                 205

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

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Ala Met Lys Gln Ser
225                 230                 235                 240

Thr Ile Ala Leu Ala Leu Leu Pro Leu Leu Phe Thr Pro Val Thr Lys
                245                 250                 255
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Ala Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
            260                 265                 270

Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
        275                 280                 285

Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
    290                 295                 300

Val Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser
305                 310                 315                 320

Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
                325                 330                 335

Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
            340                 345                 350

Cys Ala Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly
        355                 360                 365

Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
    370                 375                 380

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
385                 390                 395                 400

Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
                405                 410                 415

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
            420                 425                 430

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
        435                 440                 445

Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His
    450                 455                 460

Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Glu
465                 470                 475                 480

Phe Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala
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485 490 495

Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu
500 505 510

Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly
515 520 525

Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly
530 535 540

Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln
545 550 555 560

Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr
565 570 575

Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly
580 585 590

Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu
595 600 605

Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr
610 615 620

Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
625 630 635

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cgttttagcg gatccaaaag cggcaccagc gcgagccttg cgattacggg cctgcaaagc 240

gaagacgaag cggattatta ttgccagagc tatgacatgc ctcaggctgt gtttggcggc 300

ggcacgaagt ttaaccgttc ttggccagcc gaaagccgca ccgagtgtga cgctgtttcc 360

gccgagcagc gaagaattgc aggcgaacaa agcgaccctg gtgtgcctga ttagcgactt 420

ttatccggga gccgtgacag tggcctggaa ggcagatagc agccccgtca aggcgggagt 480

ggagaccacc acaccctcca aacaaagcaa caacaagtac gcggccagca gctatctgag 540

cctgacgcct gagcagtgga agtcccacag aagctacagc tgccaggtca cgcatgaggg 600

gagcaccgtg gaaaaaaccg ttgcgccgac tgaggcctga taagcatgcg taggagaaaa 660

taaaatgaaa caaagcacta ttgcactggc actcttaccg ttgctcttca cccctgttac 720

caaagcccag gtgcaattga aagaaagcgg cccggccctg gtgaaaccga cccaaaccct 780

gaccctgacc tgtacctttt ccggatttag cctgtccacg tctggcgttg gcgtgggctg 840

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gaaagcgaaa ggagcgggcg ctagggcgct ggcaagtgta gcggtcacgc tgcgcgtaac 1980

caccacaccc gccgcgctta atgcgccgct acagggcgcg tgctagacta gtgtttaaac 2040

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taccggatac ctgtccgcct ttctcccttc gggaagcgtg gcgctttctc atagctcacg 3540

ctgtaggtat ctcagttcgg tgtaggtcgt tcgctccaag ctgggctgtg tgcacgaacc 3600

ccccgttcag cccgaccgct gcgccttatc cggtaactat cgtcttgagt ccaacccggt 3660

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<400> 256

Ala Glu Phe Arg His Asp Cys
1 5

<210> 257
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<220>
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<400> 257

Glu Phe Arg His Asp Ser Cys
1 5

<210> 258
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<400> 258

Phe Arg His Asp Ser Gly Cys
1 5

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<400> 259

Arg His Asp Ser Gly Tyr Cys
1 5

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<400> 260

His Asp Ser Gly Tyr Glu Cys
1 5

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<400> 261

Asp Ser Gly Tyr Glu Val Cys
1 5

<210> 262
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<220>
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<400> 262

Ser Gly Tyr Glu Val His Cys
1 5

<210> 263
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<220>
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<400> 263

Tyr Glu Val His His Gln Cys
1 5

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<400> 264

Glu Val His His Gln Lys Cys
1 5

<210> 265
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<220>
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<400> 265

Val His His Gln Lys Leu Cys

1 5

<210> 266
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<220>
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<400> 266

His His Gln Lys Leu Val Cys
1 5

<210> 267
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<220>
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<400> 267

His Gln Lys Leu Val Phe Cys
1 5

<210> 268
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<220>
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<400> 268

Gln Lys Leu Val Phe Phe Cys
1 5

<210> 269
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<400> 269

Lys Leu Val Phe Phe Ala Cys
1 5

<210> 270
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<220>
<223> synthetic construct

<400> 270

Leu Val Phe Phe Ala Glu Cys
1 5

<210> 271
<211> 7
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<220>
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<400> 271

Val Phe Phe Ala Glu Asp Cys
1 5

<210> 272
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<400> 272

Phe Phe Ala Glu Asp Val Cys
1 5

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Phe Ala Glu Asp Val Gly Cys
1 5

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<220>
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<400> 274

Ala Glu Asp Val Gly Ser Cys
1 5

<210> 275
<211> 7
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<220>
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<400> 275

Glu Asp Val Gly Ser Asn Cys
1 5

<210> 276
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<220>
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<400> 276

Asp Val Gly Ser Asn Lys Cys
1 5

<210> 277
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<400> 277

Val Gly Ser Asn Lys Gly Cys
1 5

<210> 278
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<223> synthetic construct

<400> 278

Gly Ser Asn Lys Gly Ala Cys
1 5

<210> 279
<211> 7
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<220>
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<400> 279

Cys Ser Asn Lys Gly Ala Ile
1 5

<210> 280
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<213> artificial sequence

<220>
<223> synthetic construct

<400> 280

Cys Asn Lys Gly Ala Ile Ile
1 5

<210> 281
<211> 7
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<220>
<223> synthetic construct

<400> 281

Cys Lys Gly Ala Ile Ile Gly
1 5

<210> 282
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<213> artificial sequence

<220>
<223> synthetic construct

<400> 282

Cys Gly Leu Met Val Gly Gly
1 5

<210> 283
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 283

Cys Met Val Gly Gly Val Val
1 5

<210> 284
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 284

Cys Gly Gly Val Val Ile Ala
1 5

<210> 285
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; peptide 1 A beta

<400> 285

Ala Glu Phe Arg His Asp
1 5

<210> 286
<211> 7
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; peptide 2 A beta

<400> 286

Glu Phe Arg His Asp Ser Gly
1 5

<210> 287
<211> 5
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; peptide 3 A beta

<400> 287

Glu Phe Arg His Asp
1 5

<210> 288
<211> 4
<212> PRT
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<220>
<223> synthetic construct; peptide 4 A beta

<400> 288

His Asp Ser Gly
1

<210> 289
<211> 5
<212> PRT
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<220>
<223> synthetic construct; peptide 5 A beta

<400> 289

His His Gln Lys Leu
1 5

<210> 290
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; peptide 6 A beta

<400> 290

Leu Val Phe Phe Ala Glu
1 5

<210> 291

<211> 6
<212> PRT
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<220>
<223> synthetic construct; peptide 7 A beta

<400> 291

Val Phe Phe Ala Glu Asp
1 5

<210> 292
<211> 4
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; peptide 8 A beta

<400> 292

Val Phe Phe Ala
1

<210> 293
<211> 6
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct; peptide 9 A beta

<400> 293

Phe Phe Ala Glu Asp Val
1 5

<210> 294
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 294
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gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgttatttct gagaagtctc gttttattta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 295
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 295

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
35 40 45

Ile Ser Glu Lys Ser Arg Phe Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 296
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 296
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gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agccccctggg 120

aagggtctcg agtgggtgag cgctatttct gagacttcta ttcgtaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 297
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 297

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Ser Glu Thr Ser Ile Arg Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 298
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 298
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gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgttatttct cagactggtc gtaagattta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 299
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 299

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
35 40 45

Ile Ser Gln Thr Gly Arg Lys Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 300
<211> 360
<212> DNA

<213> artificial sequence

<220>
<223> synthetic construct

<400> 300
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gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgttatttct cagactggtc gtaagattta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 301
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 301

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
35 40 45

Ile Ser Gln Thr Gly Arg Lys Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 302
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 302
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgttatttct gagactggta agaatattta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 303
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 303

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
35 40 45

Ile Ser Glu Thr Gly Lys Asn Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln

100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 304
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 304
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgttatttct gagactggta agaatattta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 305
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 305

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Val
35 40 45

Ile Ser Glu Thr Gly Lys Asn Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 306
<211> 360
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 306
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctatttct gagtctggta agactaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tactcattat 300

gctcgttatt atcgttattt tgatgtttgg ggccaaggca ccctggtgac ggttagctca 360

<210> 307
<211> 120
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 307

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Ser Glu Ser Gly Lys Thr Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 308
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 308
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat ggtactggta tgaagaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 309
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 309

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Gly Thr Gly Met Lys Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 310
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 310
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agccccctggg 120

aagggtctcg agtgggtgag cgctattaat tataatggtg ctcgtattta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 311
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 311

Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu

1 5 10 15

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Tyr Asn Gly Ala Arg Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 312
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 312
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat gctgatggta atcgtaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 313
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 313

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Ala Asp Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 314
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 314
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat gctgatggta atcgtaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 315
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 315

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Ala Asp Gly Asn Arg Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 316
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 316
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat gctaatggtt ataagaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 317
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 317

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Ala Asn Gly Tyr Lys Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 318
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 318
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat gctaatggtt ataagaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 319
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 319

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Ala Asn Gly Tyr Lys Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 320
<211> 372
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 320
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctattaat gctaatggtt ataagaagta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtgg taagggtaat 300

actcataagc cttatggtta tgttcgttat tttgatgttt ggggccaagg caccctggtg 360

acggttagct ca 372

<210> 321
<211> 124
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 321

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Asn Ala Asn Gly Tyr Lys Lys Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp

100 105 110

Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 322
<211> 366
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 322
caattggtgg aaagcggcgg cggcctggtg caaccgggcg gcagcctgcg tctgagctgc 60

gcggcctccg gatttacctt tagcagctat gcgatgagct gggtgcgcca agcccctggg 120

aagggtctcg agtgggtgag cgctatttct cgttctggtt ctaatattta ttatgctgat 180

tctgttaagg gtcgttttac catttcacgt gataattcga aaaacaccct gtatctgcaa 240

atgaacagcc tgcgtgcgga agatacggcc gtgtattatt gcgcgcgtct tctttctcgt 300

ggttataatg gttattatca taagtttgat gtttggggcc aaggcaccct ggtgacggtt 360

agctca 366

<210> 323
<211> 122
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 323

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

Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met
20 25 30

Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser Ala
35 40 45

Ile Ser Arg Ser Gly Ser Asn Ile Tyr Tyr Ala Asp Ser Val Lys Gly
50 55 60

Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln
65 70 75 80

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

Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 324
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 324
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagccg gcgtattcat gtttattatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 325
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 325

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Arg Ile His Val Tyr
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser

50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 326
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 326
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagccg gcgtattcat gtttattatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 327
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 327

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Arg Ile His Val Tyr
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 328
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 328
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gcgtcttggt cgtctttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 329
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 329

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Leu Gly Arg Leu
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 330
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 330
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagccg gcgtattcat gtttattatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 331
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 331

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Arg Ile His Val Tyr
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 332
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 332
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagccg gcgtattcat gtttattatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 333
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 333

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Arg Arg Ile His Val Tyr
20 25 30

Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu

35 40 45

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 334
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 334
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gcgtcttggt cgtctttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagacttatg attatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 335
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 335

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Leu Gly Arg Leu
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 336
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 336
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtttattcag cgtttttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcggttta ttattgccag cagacttata ttatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 337
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 337

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Phe Ile Gln Arg Phe
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Thr Tyr Asn Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 338
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 338
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtatgttgat cgtacttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 339
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 339

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
85 90 95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 340
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 340
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gcgtttttt tataagtatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttct ggttcttcta accgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa taccttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 341
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 341

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Phe Phe Tyr Lys

20 25 30

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

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
85 90 95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 342
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 342
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtatgttgat cgtacttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 343
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 343

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

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
            20                  25                  30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
                85                  90                  95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110
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<210> 344
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 344

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gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc     60

ctgagctgca gagcgagcca gtatgttttt cgtcgttatc tggcgtggta ccagcagaaa    120

ccaggtcaag caccgcgtct attaatttct ggttcttcta accgtgcaac tggggtcccg    180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa    240

cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa taccttggc     300

cagggtacga aagttgaaat taaacgtacg                                     330
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<210> 345
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 345

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Phe Arg Arg
20 25 30

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

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
85 90 95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 346
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 346
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gtatgttgat cgtacttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagatttatt cttttcctca tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 347
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 347

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

```
Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Asp Arg Thr
            20                  25                  30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ile Tyr Ser Phe Pro
                85                  90                  95

His Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110
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<210> 348
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 348
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gcgtctttct cctcgttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgcctt cagatttata atatgcctat tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 349
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 349

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Leu Ser Pro Arg
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Ile Tyr Asn Met Pro
85 90 95

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

<210> 350
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 350
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ctgagctgca gagcgagcca gtatgttttt cgtcgttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttct ggttcttcta accgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcggttta ttattgcctt cagctttata atattcctaa tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 351
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 351

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Tyr Val Phe Arg Arg
            20                  25                  30

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

Ile Ser Gly Ser Ser Asn Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Leu Gln Leu Tyr Asn Ile Pro
                85                  90                  95

Asn Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
            100                 105                 110
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<210> 352
<211> 330
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 352
gatatcgtgc tgacccagag cccggcgacc ctgagcctgt ctccgggcga acgtgcgacc 60

ctgagctgca gagcgagcca gcgtgtttct ggtcgttatc tggcgtggta ccagcagaaa 120

ccaggtcaag caccgcgtct attaatttat ggcgcgagca gccgtgcaac tggggtcccg 180

gcgcgtttta gcggctctgg atccggcacg gattttaccc tgaccattag cagcctggaa 240

cctgaagact ttgcgactta ttattgccag cagctttctt cttatcctcc tacctttggc 300

cagggtacga aagttgaaat taaacgtacg 330

<210> 353
<211> 110
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 353

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Arg Val Ser Gly Arg
20 25 30

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

Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Val Pro Ala Arg Phe Ser
50 55 60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu
65 70 75 80

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Leu Ser Ser Tyr Pro
85 90 95

Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105 110

<210> 354
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 354
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 355
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 355

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 356
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 356
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 357
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 357

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 358
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 358
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 359
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 359

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 360
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 360
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 361
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 361

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 362
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 362
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 363
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 363

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 364
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 364
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 365
<211> 13
<212> PRT
<213> artificial sequence

<220>

<223> synthetic construct

<400> 365

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 366
<211> 39
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 366
cttactcatt atgctcgtta ttatcgttat tttgatgtt 39

<210> 367
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 367

Leu Thr His Tyr Ala Arg Tyr Tyr Arg Tyr Phe Asp Val
1 5 10

<210> 368
<211> 51
<212> DNA
<213> artificial sequence

<220>
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<400> 368
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 369
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 369

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 370
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 370
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 371
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 371

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 372
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 372
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 373
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 373

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 374
<211> 51
<212> DNA
<213> artificial sequence

<220>
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<400> 374
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 375
<211> 17
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<213> artificial sequence

<220>
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<400> 375

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 376
<211> 51
<212> DNA
<213> artificial sequence

<220>
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<400> 376
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 377
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 377

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp

1 5 10 15

Val

<210> 378
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 378
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 379
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 379

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 380
<211> 51
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 380
ggtaagggta atactcataa gccttatggt tatgttcgtt attttgatgt t 51

<210> 381
<211> 17
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 381

Gly Lys Gly Asn Thr His Lys Pro Tyr Gly Tyr Val Arg Tyr Phe Asp
1 5 10 15

Val

<210> 382
<211> 45
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 382
cttctttctc gtggttataa tggttattat cataagtttg atgtt 45

<210> 383
<211> 15
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 383

Leu Leu Ser Arg Gly Tyr Asn Gly Tyr Tyr His Lys Phe Asp Val
1 5 10 15

<210> 384
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 384
cagcagactt atgattatcc tcct 24

<210> 385
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 385

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 386
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 386
cagcagactt atgattatcc tcct 24

<210> 387
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 387

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 388
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 388
cagcagactt atgattatcc tcct 24

<210> 389
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 389

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 390
<211> 24
<212> DNA
<213> artificial sequence

<220>

<223> synthetic construct

<400> 390
cagcagactt atgattatcc tcct 24

<210> 391
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 391

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 392
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 392
cagcagactt atgattatcc tcct 24

<210> 393
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 393

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 394
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 394
cagcagactt atgattatcc tcct 24

<210> 395

<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 395

Gln Gln Thr Tyr Asp Tyr Pro Pro
1 5

<210> 396
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 396
cagcagactt ataattatcc tcct 24

<210> 397
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 397

Gln Gln Thr Tyr Asn Tyr Pro Pro
1 5

<210> 398
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 398
cagcagattt attcttttcc tcat 24

<210> 399
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 399

Gln Gln Ile Tyr Ser Phe Pro His
1 5

<210> 400
<211> 24
<212> DNA
<213> artificial sequence

<220>
<223> synthetic construct

<400> 400
cttcagcttt ataatattcc taat 24

<210> 401
<211> 8
<212> PRT
<213> artificial sequence

<220>
<223> synthetic construct

<400> 401

Leu Gln Leu Tyr Asn Ile Pro Asn
1 5

<210> 402
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Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala
35 40 45

Thr Val Ile Val
50