





pDRAW32 - pMAHD - 1020 bp. - [Sequence]

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AGTC

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      EciI
      BtgZI
1  CGCGGGGAAAA AGTGAAGCG GCGATGGCGG AGCTGAATTA CATTCCCAAC
   M A E L N Y I P N      Frame 3

51  CGCGTGGCAC AACAACTGGC GGGCAAACAG TCGTTGCTGA TTGGCGTTGC
   R V A Q Q L A G K Q S L L I G V A      Frame 3

      BpmI      BsgI      BceAI
101  CACCTCCAGT CTGGCCCTGC ACGCGCCGTC GCAAATTGTC GCGGCGATTA
     T S S L A L H A P S Q I V A A I K      Frame 3

      BmrI BanI      TaqI
151  AATCTCGCGC CGATCAACTG GGTGCCAGCG TGGTGGTGTG GATGGTAGAA
     S R A D Q L G A S V V V S M V E      Frame 3

      Bsp1286I
      BsiHKAI
      BaeGI
      TaqI
      BsaHI      PciI
201  CGAAGCGGCG TCGAAGCCTG TAAAGCGGCG GTGCACAATC TTCTCGCGCA
     R S G V E A C K A A V H N L L A Q      Frame 3

      MluI      FokI      FokI
      AflIII      BclI      BtsCI      BtsCI      BsrDI
251  ACGGCTCAGT GGGGTGATCA TTAACATATCC GCTGGATGAC CAGGATGCCA
     R V S G L I I N Y P L D D Q D A I      Frame 3

      BsgI      Hpy188III
301  TTGCTGTGGA AGCTGCCTGC ACTAATGTTC CGGCGTTATT TCTTGATGTC
     A V E A A C T N V P A L F L D V      Frame 3

      Hpy188I      BbsI      RsaI
      TspDTI      CviQI
351  TCTGACGAGA CAGCCATCAA CAGTATATAT TTCTCCCATG AACACGGTAC

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New DNA entry Analysis complete 12:00

pDRAW32 - pMAHD - 1020 bp. - [Restriction analysis]

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pMAHD, 1020 bp. (LINEAR)
 Restriction analysis 07/09/2014
 pDRAW32 revision 1.1.126
 UNLICENSED
 Rebase containing 277 enzymes.
 69 enzymes match enzyme selection criteria.

AflIII (A'CryG_T)
 Cuts 1 time.
 Cuts at position 251.
 Fragment sizes 251, 769.

AgsI (TT_s'AA)
 Cuts 1 time.
 Cuts at position 579.
 Fragment sizes 579, 441.

ApaI (G_GGCC'C) [Bsp120I,PspOMI]
 [dcm methylated]
 Cuts 1 time.
 Cuts at position 462.
 Fragment sizes 462, 558.

ApaLI (G'TGCA_C) [Alw44I,VneI]
 Cuts 1 time.
 Cuts at position 231.
 Fragment sizes 231, 789.

ApoI (r'AATT_y) [AcsI,XapI]
 Cuts 1 time.
 Cuts at position 526.

New DNA entry Analysis complete 12:00

