GENEART
THE GENE OF YOUR CHOICE

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                                                              SacII
                                                               NotI
            KpnI  NheI  attB1-5'                                EagI
       GGGCGAATTGGGTACCGCTAGCACAAGTTTGTACAAAAAAGCAGGCTCCGCGGCCGCCCC
  1    ---------+---------+---------+---------+---------+---------+
       CCCGCTTAACCCATGGCGATCGTGTTCAAACATGTTTTTTCGTCCGAGGCGCCGGCGGGG


            NcoI                                    HinfI
       CTTGCCACCATGGCATCAGTTTTCTTTTCGTACACGCATATAGACGAGTCGCTGCGCGAC
  61   ---------+---------+---------+---------+---------+---------+
       GAACGGTGGTACCGTAGTCAAAAGAAAAGCATGTGCGTATATCTGCTCAGCGACGCGCTG
            M__A__S__V__F__F__S__Y__T__H__I__D__E__S__L__R__D__


       CAGCTCGAAATCCACCTCTCGCTTATGAAGCGCGAGGGCCTCATTACCGCATGGCATGAC
  121  ---------+---------+---------+---------+---------+---------+
       GTCGAGCTTTAGGTGGAGAGCGAATACTTCGCGCTCCCGGAGTAATGGCGTACCGTACTG
       Q__L__E__I__H__L__S__L__M__K__R__E__G__L__I__T__A__W__H__D__


                       ClaI         ClaI
       CGGCGCATCGTCGCAGGCTCCGACATCGATGACAGCATCGATGAGCACCTTGAGAGCGCA
  181  ---------+---------+---------+---------+---------+---------+
       GCCGCGTAGCAGCGTCCGAGGCTGTAGCTACTGTCGTAGCTACTCGTGGAACTCTCGCGT
       R__R__I__V__A__G__S__D__I__D__D__S__I__D__E__H__L__E__S__A__


                                                  ScaI
       GACATCATCTTGCTGCTAGTGAGCGCGAACTTCATCGCATCCGAGTACTGCTTCGCGACC
  241  ---------+---------+---------+---------+---------+---------+
       CTGTAGTAGAACGACGATCACTCGCGCTTGAAGTAGCGTAGGCTCATGACGAAGCGCTGG
       D__I__I__L__L__L__V__S__A__N__F__I__A__S__E__Y__C__F__A__T__


       GAGATGAAGCGTGCAATGGAGCGTCATAAGGCTGGTGAGGTGCGCGTCATCCCCGTCATC
  301  ---------+---------+---------+---------+---------+---------+
       CTCTACTTCGCACGTTACCTCGCAGTATTCCGACCACTCCACGCGCAGTAGGGGCAGTAG
       E__M__K__R__A__M__E__R__H__K__A__G__E__V__R__V__I__P__V__I__


                       HaeII
            BssHII      HaeII
       CTGCGCGCTTGTGACTGGCACAGCGCCCCGTTCGGAAAACTGAACGCAGTTCCGACCGAT
  361  ---------+---------+---------+---------+---------+---------+
       GACGCGCGAACACTGACCGTGTCGCGGGGCAAGCCTTTTGACTTGCGTCAAGGCTGGCTA
       L__R__A__C__D__W__H__S__A__P__F__G__K__L__N__A__V__P__T__D__


         EagI BstEII                                         HinfI
       GGCCGGCCGGTGACCTCTTGGCCCAACCAAGATGAGGCGTTTGCCGACATCACGAAGTCG
  421  ---------+---------+---------+---------+---------+---------+
       CCGGCCGGCCACTGGAGAACCGGGTTGGTTCTACTCCGCAAACGGCTGTAGTGCTTCAGC
       G__R__P__V__T__S__W__P__N__Q__D__E__A__F__A__D__I__T__K__S__
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                                                          NarI
                                                          KasI
                                                          HaeII
                                                          HaeII
     ATTCGCGCTGCTGTGAGTGCGACCGCGTCGTCATCGGCGCGAGCGCGGGTTGCGGCGCCG
481  ---------+---------+---------+---------+---------+---------+
     TAAGCGCGACGACACTCACGCTGGCGCAGCAGTAGCCGCGCTCGCGCCCAACGCCGCGGC
      I_R_A_A_V_S_A_T_A_S_S_S_A_R_A_R_V_A_A_P_

     BssHII                                            SacII
     GCGCGCGAGGCAGGGGCGGCCCGCGCAGTGGCAGTGCCCGCCGCGAGTACGCAATTGCCG
541  ---------+---------+---------+---------+---------+---------+
     CGCGCGCTCCGTCCCCGCCGGGCGCGTCACCGTCACGGGCGGCGCTCATGCGTTAACGGC
      A_R_E_A_G_A_A_R_A_V_A_V_P_A_A_S_T_Q_L_P_

     CGGTCTAGCAACATGCGCGTCAAACATCAGTTCTCGGACTTGGACAGAGATACGTTTGTT
601  ---------+---------+---------+---------+---------+---------+
     GCCAGATCGTTGTACGCGCAGTTTGTAGTCAAGAGCCTGAACCTGTCTCTATGCAAACAA
      R_S_S_N_M_R_V_K_H_Q_F_S_D_L_D_R_D_T_F_V_

                                          PflMI
          BsmBI                           BstNI
     TCGGAGACGTTTGACTTTATCGCCCGTTTCTTCGATGGCTCGCTCCAGGAGCTGGAAAAG
661  ---------+---------+---------+---------+---------+---------+
     AGCCTCTGCAAACTGAAATAGCGGGCAAAGAAGCTACCGAGCGAGGTCCTCGACCTTTTC
      S_E_T_F_D_F_I_A_R_F_F_D_G_S_L_Q_E_L_E_K_

                               HinfI
          BstNI                ClaI  BssHII
     CGGCACGGCCAGTTCCAGGGTCGATTTACCCGAATCGATGCGCGCCGCTTCACTGCGAGC
721  ---------+---------+---------+---------+---------+---------+
     GCCGTGCCGGTCAAGGTCCCAGCTAAATGGGCTTAGCTACGCGCGGCGAAGTGACGCTCG
      R_H_G_Q_F_Q_G_R_F_T_R_I_D_A_R_R_F_T_A_S_

                                                          NarI
                                                          KasI
                                                          HaeII
                               BsmBI                      HaeII
     ATCTACAAGGACGGCAAGAGTATCTCGCAGTGCAGCGTCTCCCACGGCGGCGCCTTCGGT
781  ---------+---------+---------+---------+---------+---------+
     TAGATGTTCCTGCCGTTCTCATAGAGCGTCACGTCGCAGAGGGTGCCGCCGCGGAAGCCA
      I_Y_K_D_G_K_S_I_S_Q_C_S_V_S_H_G_G_A_F_G_

     GGGAGCAGCAACCGCGAGATTACGTACTCCAGTCAGATTTCAACGCATACCAACAGCTTC
841  ---------+---------+---------+---------+---------+---------+
     CCCTCGTCGTTGGCGCTCTAATGCATGAGGTCAGTCTAAAGTTGCGTATGGTTGTCGAAG
      G_S_S_N_R_E_I_T_Y_S_S_Q_I_S_T_H_T_N_S_F_

         HaeII
         HaeII                         HinfI
     AACGAGGCGCTTACCATCGCGGAAGATAGCCAGACTCTGTACCTAAAGCCGATGATGAAC
901  ---------+---------+---------+---------+---------+---------+
     TTGCTCCGCGAATGGTAGCGCCTTCTATCGGTCTGAGACATGGATTTCGGCTACTACTTG
      N_E_A_L_T_I_A_E_D_S_Q_T_L_Y_L_K_P_M_M_N_

         BstNI
     ATGGCCAGGGGAGTGTCCGAAAAGCTGTCTGACACCGGAGCCGCTGAGTATCTGTGGTCA
961  ---------+---------+---------+---------+---------+---------+
     TACCGGTCCCCTCACAGGCTTTTCGACAGACTGTGGCCTCGGCGACTCATAGACACCAGT
      M_A_R_G_V_S_E_K_L_S_D_T_G_A_A_E_Y_L_W_S_
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                        BssHII
                        AscI       attB2-3'
            ATGTTGATGGAACCCGTCCAGCGCAAGGGTGGGCGCGCCGACCCAGCTTTCTTGTACAAA
     1021   ---------+---------+---------+---------+---------+---------+
            TACAACTACCTTGGGCAGGTCGCGTTCCCACCCGCGCGGCTGGGTCGAAAGAACATGTTT
             M__L__M__E__P__V__Q__R__K__G__G__R__A__D__P__A__F__L__Y__K__


                        SacII
                XbaI ApaI       BstBI                                 BsaI
            GTGGTTGATCTAGAGGGCCCGCGGTTCGAAGGTAAGCCTATCCCTAACCCTCTCCTCGGT
     1081   ---------+---------+---------+---------+---------+---------+
            CACCAACTAGATCTCCCGGGCGCCAAGCTTCCATTCGGATAGGGATTGGGAGAGGAGCCA
             V__V__D__L__E__G__P__R__F__E__G__K__P__I__P__N__P__L__L__G__


                HinfI                BamHI SacI
            CTCGATTCTACGTGATAATGAGGATCCGAGCTCCAGCTTTTGTTCCC
     1141   ---------+---------+---------+---------+-------
            GAGCTAAGATGCACTATTACTCCTAGGCTCGAGGTCGAAAACAAGGG
             L__D__S__T__*__*__*__
```

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