

CAGAAAGCGGTGCAGATAGCGTTATTGCAATTGGTGGTGGTAGCGCACTGGATACCGCAA
 301 -----+-----+-----+-----+-----+-----+
 GTCTTTGCCACGTCTATCGCAATAACGTTAACCACCACCATCGCGTGACCTATGGCGTT
 _E_S_G_A_D_S_V_I_A_I_G_G_S_A_L_D_T_A_K

AAATTGCAAATCTGCTGGCAACCTATGGTGGTCGTGTTTCGTGATTATGTTGCACCGCCTT
 361 -----+-----+-----+-----+-----+-----+
 TTTAACGTTTAGACGACCGTTGGATACCACCAGCACAAGCACTAATACAACGTGGCGGAA
 _I_A_N_L_L_A_T_Y_G_G_R_V_R_D_Y_V_A_P_P_Y

AgeI

ATGGTGAAGGTAAACCGGTTCCGGGTCCGGTTAAACCGATGGTTGCAGTTCCGACCACCG
 421 -----+-----+-----+-----+-----+-----+
 TACCACTTCCATTTGGCCAAGGCCAGGCCAATTTGGCTACCAACGTCAAGGCTGGTGGC
 _G_E_G_K_P_V_P_G_P_V_K_P_M_V_A_V_P_T_T_A

AgeI

CAGGCACCGGTAGCGAAGTTACCAGCGTTGCAGTTGTTACCCTGAAAGATGTTGGTGTTA
 481 -----+-----+-----+-----+-----+-----+
 GTCCGTGGCCATCGCTTCAATGGTCGCAACGTCAACAATGGGACTTTCTACAACCACAAT
 _G_T_G_S_E_V_T_S_V_A_V_V_T_L_K_D_V_G_V_K

AAGTTGGTATCAGCAGCGATTTTCTGCGTCCGAGCCTGGCACTGCTGGACCCGGAAGTGA
 541 -----+-----+-----+-----+-----+-----+
 TTCAACCATAGTCGTCGCTAAAAGACGCAGGCTCGGACCGTGACGACCTGGGCCTTGACT
 _V_G_I_S_S_D_F_L_R_P_S_L_A_L_L_D_P_E_L_T

AgeI

CCATGACCGTTCCGCCTAAAGTTACCGCAGATACCGGTATGGATGCACTGACCCATGCAG
 601 -----+-----+-----+-----+-----+-----+
 GGTA CTGGCAAGGCGGATTTCAATGGCGTCTATGGCCATACCTACGTGACTGGGTACGTC
 _M_T_V_P_P_K_V_T_A_D_T_G_M_D_A_L_T_H_A_V

TTGAAAGCTATATCGCAAAACCGTATTGGGCACGTGAACGTCCGGAAGATCCGGCAAAAC
 661 -----+-----+-----+-----+-----+-----+
 AACTTTTCGATATAGCGTTTTGGCATAACCCGTGCACTTGCAGGCCTTCTAGGCCGTTTTG
 _E_S_Y_I_A_K_P_Y_W_A_R_E_R_P_E_D_P_A_K_R

GTCCGGTTTATGTTGGTAGCTTTACCGTTACCGATGCACTGGCCGAACGTGCAATTGAAC
 721 -----+-----+-----+-----+-----+-----+
 CAGGCCAAATACAACCATCGAAATGGCAATGGCTACGTGACCGGCTTGACGTAACTTG
P V Y V G S F T V T D A L A E R A I E L

TGATTGGTAAATATCTGCGTCGTGCAGTTTATCAGGGTCGTACCGATCTGGAAGCACGTA
 781 -----+-----+-----+-----+-----+-----+
 ACTAACCATTATAGACGCAGCACGTCAAATAGTCCCAGCATGGCTAGACCTTCGTGCAT
I G K Y L R R A V Y Q G R T D L E A R S

BspMI

GCGGTATGCTGATTGCAAGCTATCTGGCAGGTCTGGCATTGTTGTAATGCCGGTGTTGGTC
 841 -----+-----+-----+-----+-----+-----+
 CGCCATACGACTAACGTTTCGATAGACCGTCCAGACCGTAAACCATTACGGCCACAACCAG
G M L I A S Y L A G L A F G N A G V G L

TGGCACATGCAGCAAGCTATCCGCTGGGTGGTCGTTATAAAGTTACACATGGTGAAGCAG
 901 -----+-----+-----+-----+-----+-----+
 ACCGTGTACGTCGTTTCGATAGGCGACCCACCAGCAATATTTCAATGTGTACCACTTCGTC
A H A A S Y P L G G R Y K V T H G E A V

PstI

TTGGTATTCTGCTGCCTGCAGTTCTGGAATTTAATGCACCGGCAAATTATGAAAAAGCCA
 961 -----+-----+-----+-----+-----+-----+
 AACCATAAGACGACGGACGTCAAGACCTTAAATTACGTGGCCGTTTAATACTTTTTCGGT
G I L L P A V L E F N A P A N Y E K A K

AgeI

AACGTGTTGGCGAACTGCTGACCGGTGAAAAATGTCCGGAACGTGATCCTGCAAAATGTG
 1021 -----+-----+-----+-----+-----+-----+
 TTGCACAACCGCTTGACGACTGGCCACTTTTTACAGGCCTTGCACTAGGACGTTTTACAC
R V G E L L T G E K C P E R D P A K C A

PstI *EcoRV*

1081 CAGAATGGGCAGCAAATGCAATTCGTGAACTGCAGCGTGATATCAAATTTACACGGGTC
 -----+-----+-----+-----+-----+-----+
 GTCTTACCCGTCGTTTACGTTAAGCACTTGACGTCGCACTATAGTTTAAATGTGGCCCAG
 _E_W_A_A_N_A_I_R_E_L_Q_R_D_I_K_F_T_P_G_L

TGGAAGCAGTGGGTGTTAAAGAAGAGGATCTGATGGAAATGGCAAAAGAAACCCTGAATC
 1141 -----+-----+-----+-----+-----+-----+
 ACCTTCGTCACCCACAATTTCTTCTCCTAGACTACCTTTACCGTTTTCTTTGGGACTTAG
 _E_A_V_G_V_K_E_E_D_L_M_E_M_A_K_E_T_L_N_Q

BstEII

1201 AGAAACGTCTGCTGGCCACCAATCCGCGTCCGGTTACCGAAGAAGATGTTTATTGGGTTT
 -----+-----+-----+-----+-----+-----+
 TCTTTGCAGACGACCGGTGGTTAGGCGCAGGCCAATGGCTTCTTCTACAAATAACCCAAA
 _K_R_L_L_A_T_N_P_R_P_V_T_E_E_D_V_Y_W_V_Y

EcoRI *HindIII*

SphI *NcoI* *BstBI*

1261 ATAAACGTAGCATGCGCAACTATTAACCATGGAATTCGAAGCTTGATCCGGCTGCTAACA
 -----+-----+-----+-----+-----+-----+
 TATTTGCATCGTACGCGTTGATAATTGGTACCTTAAGCTTCGAAGTAGGCCGACGATTGT
 _K_R_S_M_R_N_Y_*_

AAGCCCG
 1321 -----
 TTCGGGC