

BglIII

PvuII

TTGTTGATGCACTGACCCAGAAAAGAAGATCTGGCATTTCAGCTGAATGATAGCGCACCGA
301 -----+-----+-----+-----+-----+-----+
AACAACTACGTGACTGGGTCTTTCTTCTAGACCGTAAAGTCGACTTACTATCGCGTGGCT
_V_D_A_L_T_Q_K_E_D_L_A_F_Q_L_N_D_S_A_P_K

PstI

AAGTTGTTCTGGCAGATGAAGAAGTTCTGCAGCGCGAAAGCGAAACCCTGAAAGGTTATG
361 -----+-----+-----+-----+-----+-----+
TTCAACAAGACCGTCTACTTCTTCAAGACGTCGCGCTTTCGCTTTGGGACTTTCCAATAC
_V_V_L_A_D_E_E_V_L_Q_R_E_S_E_T_L_K_G_Y_A

BglIII

CAGTTCTGACCGAAAAAGATCTGAGCAGCGCAAGCGGTGAACATGAAGTTGTTGTTGGTT
421 -----+-----+-----+-----+-----+-----+
GTCAAGACTGGCTTTTTCTAGACTCGTCGCTTCGCCACTTGTACTTCAACAACAACCAA
_V_L_T_E_K_D_L_S_S_A_S_G_E_H_E_V_V_V_G_Y

BspMI

BspMI

BspMI

ATGAAGATGATGCCCCGTGTTTTCTATTATGCAGGTATTGCAGGTCGTACCATGCAGGTTA
481 -----+-----+-----+-----+-----+-----+
TACTTCTACTACGGGCACAAAAGATAATACGTCCATAACGTCCAGCATGGTACGTCCAAT
_E_D_D_A_R_V_F_Y_Y_A_G_I_A_G_R_T_M_Q_V_I

AgeI

TTCATAGCCATCGTAGCTTTACCGGTGCAATTATGCCGCTGGTTCAGGCCGAAGGTATTA
541 -----+-----+-----+-----+-----+-----+
AAGTATCGGTAGCATCGAAATGGCCACGTTAATACGGCGACCAAGTCCGGCTTCCATAAT
_H_S_H_R_S_F_T_G_A_I_M_P_L_V_Q_A_E_G_I_N

BstEII

PflMI

ATGCAAAATGATGTTAGCCTGGTTACCGTTCGCTGACCCATGTTCTGGGTCTGGATGCAG
601 -----+-----+-----+-----+-----+-----+
TACGTTTACTACAATCGGACCAATGGCAAGGCGACTGGGTACAAGACCCAGACCTACGTC
_A_N_D_V_S_L_V_T_V_P_L_T_H_V_L_G_L_D_A_A

CACTGCTGAGCGCACTGGTTAGCGGTGCAACCGCACTGCTGCTGAAAAAGTTCAATATGG
661 -----+-----+-----+-----+-----+-----+
GTGACGACTCGCGTGACCAATCGCCACGTTGGCGTGACGACGACTTTTTCAAGTTATACC
_L_L_S_A_L_V_S_G_A_T_A_L_L_L_K_K_F_N_M_D

ATAAAATCAAAGAGATGGTTGCACGTCGTAGCCCCGACCTATCTGGTTGCAGTTCCGCTGG
 721 -----+-----+-----+-----+-----+-----+
 TATTTTAGTTTCTCTACCAACGTGCAGCATCGGGCTGGATAGACCAACGTCAAGGCGACC
K I K E M V A R R S P T Y L V A V P L V

TTTTTCAGACCCTGATGAAAGAAGATGAAGAATTTGTTAAAAGCCTGGGTCAGAGCCTGC
 781 -----+-----+-----+-----+-----+-----+
 AAAAAAGTCTGGGACTACTTTCTTCTACTTCTTAAACAATTTTCGGACCCAGTCTCGGACG
F Q T L M K E D E E F V K S L G Q S L R

BclI

GTTGGGCAATGAGCGGTGGTGCATATCTGCCTCCGGATGATCAGCGTCGTTGGGAAGAAC
 841 -----+-----+-----+-----+-----+-----+
 CAACCCGTTACTCGCCACCACGTATAGACGGAGGCCTACTAGTCGCAGCAACCCTTCTTG
W A M S G G A Y L P P D D Q R R W E E L

PstI

AgeI

BspMI

TGACCGGTAAACCGCTGCTGCAGGTTTATGGTATGACCGAAGCACCGCAGATTTTTGCAA
 901 -----+-----+-----+-----+-----+-----+
 ACTGGCCATTTGGCGACGACGTCCAAATACCATACTGGCTTCGTGGCGTCTAAAAACGTT
T G K P L L Q V Y G M T E A P Q I F A T

CCACACCCGAAAAACATAAAATTGGTAGCCTGGGTTTTCCGCTGCCTGGTGTGAAGCAC
 961 -----+-----+-----+-----+-----+-----+
 GGTGTGGGCTTTTTGTATTTTAACCATCGGACCCAAAAGGCGACGGACCACAACCTTCGTG
T P E K H K I G S L G F P L P G V E A L

AgeI

TGCTGGTTAATCCGGAAACCCTGGAACCGGTTGAAGATCAGGGTGAACTGCTGGTTCGTG
 1021 -----+-----+-----+-----+-----+-----+
 ACGACCAATTAGGCCTTTGGGACCTTGGCCAACTTCTAGTCCCACTTGACGACCAAGCAC
L V N P E T L E P V E D Q G E L L V R G

BspMI

BamHI

GTCCGCAAGTTATGAAATGTTATCCGGATCCTGAAGAAAACAGCAAAGCCTTTGTTGAAG
 1081 -----+-----+-----+-----+-----+-----+
 CAGGCGTCCAATACTTTACAATAGGCCTAGGACTTCTTTTGTCTTTTCGGAAACAACCTC
P Q V M K C Y P D P E E N S K A F V E V

AgeI

1141 TGAATGGTAAAGTTTGGATGCGCACCGGTGATATTCTGGCAAAAGATGAAGAAGGCTTCT
-----+-----+-----+-----+-----+-----+
ACTTACCATTTCAAACCTACGCGTGGCCACTATAAGACCGTTTTCTACTTCTTCCGAAGA
_N_G_K_V_W_M_R_T_G_D_I_L_A_K_D_E_E_G_F_Y

1201 ATTATTTCCGTGGTGTTCGTAAACGTATGCTGAAATACAAAGGCTATCCGATCTTTCCGA
-----+-----+-----+-----+-----+-----+
TAATAAAGGCACCACAAGCATTTGCATACGACTTTATGTTTCCGATAGGCTAGAAAGGCT
_Y_F_R_G_V_R_K_R_M_L_K_Y_K_G_Y_P_I_F_P_K

1261 AAGACCTGGAAGTCTGCTGAAACATCCGTGTGTTGCCGAAGCCGAAGTTGTTGGTG
-----+-----+-----+-----+-----+-----+
TTCTGGACCTTGACTAAGACGACTTTGTAGGCACACAACGGCTTCGGCTTCAACAACCAC
_D_L_E_L_I_L_L_K_H_P_C_V_A_E_A_E_V_V_G_E

1321 AACCGGCAGGCGAAGTTGGTCAGATTCCGGTTGCAAAAGTTAAACTGAAAGAAGGTTGTA
-----+-----+-----+-----+-----+-----+
TTGGCCGTCCGCTTCAACCAGTCTAAGGCCAACGTTTTCAATTTGACTTTCTTCCAACAT
_P_A_G_E_V_G_Q_I_P_V_A_K_V_K_L_K_E_G_C_K

1381 AAGCCACACCGGAAGAAATCATGGATTTTGTGAATAAACGTGTGGCAGCCTACAAAAAAG
-----+-----+-----+-----+-----+-----+
TTCGGTGTGGCCTTCTTTAGTACCTAAAACACTTATTTGCACACCGTCGGATGTTTTTTC
_A_T_P_E_E_I_M_D_F_V_N_K_R_V_A_A_Y_K_K_V

EcoRI HindIII

NcoI BstBI

1441 TGC GCAAAGTTATTATCCTGGAATAACCATGGAATTCGAAGCTTGATCCGGCTGCTAACA
-----+-----+-----+-----+-----+-----+
ACGCGTTTCAATAATAGGACCTTATTGGTACCTTAAGCTTCGAAGTACGCGGACGATTGT
_R_K_V_I_I_L_E_*_

1501 AAGCCCG

TTCGGGC