

GAAAAGCAAAGGCTTTCACCCGGACATGATTAAAACCCATGAAGATGTTGTTAAAATCCC
 301 -----+-----+-----+-----+-----+-----+
 CTTTTCGTTTCCGAAAAGTGGGCCTGTACTAATTTTGGGTACTTCTACAACAATTTTAGGG
K S K G F H P D M I K T H E D V V K I P

BglIII *PstI*

GGTGCTGACCAAAAAAGATCTGCGTGCCGATCTGCAGAAAAATCCGCCTTATGGCACCAT
 361 -----+-----+-----+-----+-----+-----+
 CCACGACTGGTTTTTTCTAGACGCACGGCTAGACGTCTTTTATAGGCGGAATACCGTG GTA
V L T K K D L R A D L Q K N P P Y G T I

AgeI

TATGGTTCCGGAAGTGGCCAAATATATCCATTTTGTGTTGGTGCAACCAGCGGTAGCACC GG
 421 -----+-----+-----+-----+-----+-----+
 ATACCAAGGCCTTGACCGGTTTATATAGGTAAAACAACCACGTTGGTCGCCATCGTGGCC
M V P E L A K Y I H F V G A T S G S T G

TATGCCGACCTTTCAGGGTTGGGGTCGTGTTGAACTGGATTATTTTGAAGAACAGCAGGC
 481 -----+-----+-----+-----+-----+-----+
 ATACGGCTGGAAAAGTCCCAACCCCAGCACAACTTGACCTAATAAACTTCTTGTCGTCCG
M P T F Q G W G R V E L D Y F E E Q Q A

ACGTTATCTGTGGACCTTTGCCGGTGTTAAACCGGGTGTTGTTTATGCCAATTATCTGAA
 541 -----+-----+-----+-----+-----+-----+
 TGCAATAGACACCTGGAAACGGCCACAATTTGGCCCACAACAAATACGGTTAATAGACTT
R Y L W T F A G V K P G V V Y A N Y L N

TATGAGCGGCTTTTATAGCTGGGGTCCGCCTCTGGTTGAAACCGCAATGTGGCGTTGTGG
 601 -----+-----+-----+-----+-----+-----+
 ATACTCGCCGAAAATATCGACCCCAGGCGGAGACCAACTTTGGCGTTACACCGCAACACC
M S G F Y S W G P P L V E T A M W R C G

NdeI

TGCAACCGCAATTGCCGGTGGTGGTGAAACCTTTTTTACCTGGAAAGATCGTCATATGCT
 661 -----+-----+-----+-----+-----+-----+
 ACGTTGGCGTTAACGGCCACCACCACTTTGGAAAAAATGGACCTTTCTAGCAGTATACGA
A T A I A G G G E T F F T W K D R H M L

Pf1MI

GATTATGAAACTGTGGAAAGTTGATGTTTTTGCAACCACCCCGTGGCTGCATCGTTGGAT
721 -----+-----+-----+-----+-----+-----+
CTAATACTTTGACACCTTTCAACTACAAAAACGTTGGTGGGGCACCGACGTAGCAACCTA
I M K L W K V D V F A T T P W L H R W I

BstEII

TGGTGAACAGGCAAAACTGGAAGGTTGGGTACCCCGTTTAAAGTTCTGCTGCTGCATGG
781 -----+-----+-----+-----+-----+-----+
ACCACTTGTCCGTTTTGACCTTCCAACCCAATGGGGCAAATTTCAAGACGACGACGTACC
G E Q A K L E G W V T P F K V L L L H G

TGGTGCAGCAGCCGAAAAAACCAAAGAAAACTGATGGAAGTTCACCCGAATGTCGAAAA
841 -----+-----+-----+-----+-----+-----+
ACCACGTCGTCGGCTTTTTTGGTTTTCTTTTTGACTACCTTCAAGTGGGCTTACAGCTTTT
G A A A E K T K E K L M E V H P N V E K

NdeI

AGTTATTAGCGTTTGGGGCACCACCGATGGTCATATGGCAATTGAACCGCCTGATGCACC
901 -----+-----+-----+-----+-----+-----+
TCAATAATCGCAAACCCCGTGGTGGCTACCAGTATACCGTTAACTTGGCGGACTACGTGG
V I S V W G T T D G H M A I E P P D A P

GGGTACACTGGTTTTTTTGGGAAGATACCCAGATTTTCGATATTGTTGTTCCGGGTAGCTA
961 -----+-----+-----+-----+-----+-----+
CCCATGTGACCAAAAAACCCCTTCTATGGGTCTAAAAGCTATAACAACAAGGCCCATCGAT
G T L V F W E D T Q I F D I V V P G S Y

BspMI

TGAAGAACGTCCGGAAGGTGAACCGGCAGGTCAGGGTGAACGTGGTGAACCTGATTGCAAC
1021 -----+-----+-----+-----+-----+-----+
ACTTCTTGACAGGCCTTCCACTTGGCCGTCCAGTCCCACTTGCAACCACTTGACTAACGTTG
E E R P E G E P A G Q G E R G E L I A T

1081 CCTGCTGACCCACTATACCATGCCGCTGATTCGTTATAGCCTGGGTGATTATGTGAAAAA
 -----+-----+-----+-----+-----+-----+
 GGACGACTGGGTGATATGGTACGGCGACTAAGCAATATCGGACCCACTAATACACTTTTT
 _L_L_T_H_Y_T_M_P_L_I_R_Y_S_L_G_D_Y_V_K_N_

1141 CGAATTTATCTGTGATCCGACACCGGAACTGGGTATTACCCATTGTCGTTTTGCAGAACT
 -----+-----+-----+-----+-----+-----+
 GCTTAAATAGACACTAGGCTGTGGCCTTGACCCATAATGGGTAACAGCAAAACGTCTTGA
 _E_F_I_C_D_P_T_P_E_L_G_I_T_H_C_R_F_A_E_L_

PvuI

1201 GATTCCGGGTCGTGTGGAATGGATGTTTAAAGTTAAAGGCAAACCTGCTGTTTCCGATCGT
 -----+-----+-----+-----+-----+-----+
 CTAAGGCCCCAGCACACCTTACCTACAAATTTCAATTTCCGTTTGACGACAAAGGCTAGCA
 _I_P_G_R_V_E_W_M_F_K_V_K_G_K_L_L_F_P_I_V_

AgeI

1261 TGTTGAAAATGCAGTTAGCCAGATTCCGGATACCACCGGTGCATATAATATTGTGGTGTA
 -----+-----+-----+-----+-----+-----+
 ACAACTTTTACGTCAATCGGTCTAAGGCCTATGGTGGCCACGTATATTATAACACCACAT
 _V_E_N_A_V_S_Q_I_P_D_T_T_G_A_Y_N_I_V_V_Y_

1321 TGATGATAATATGGATAAACTGAAAATCAAAGTGGAAACCCGCAAACCGATTCCGCCTCC
 -----+-----+-----+-----+-----+-----+
 ACTACTATTATACCTATTTGACTTTTAGTTTCACCTTTGGGCGTTTGGCTAAGGCGGAGG
 _D_D_N_M_D_K_L_K_I_K_V_E_T_R_K_P_I_P_P_P_

1381 GCCTGAATATGATAAAGAAGCACGCGAAATTATTGCACGTGAACTGGGTCTGAGTCCGGA
 -----+-----+-----+-----+-----+-----+
 CGGACTTATACTATTTCTTCGTGCGCTTTAATAACGTGCACTTGACCCAGACTCAGGCCT
 _P_E_Y_D_K_E_A_R_E_I_I_A_R_E_L_G_L_S_P_E_

PstI

BspMI

1441 AGATGTTGAAATTGAATGGATTCGTCCGGGTGAATCAGTTTGGAAAGGTTATAAACTGCA
-----+-----+-----+-----+-----+-----+
TCTACAACCTTTAACTTACCTAAGCAGGCCCACTTAGTCAAACCTTTCCAATATTTGACGT
_D_V_E_I_E_W_I_R_P_G_E_S_V_W_K_G_Y_K_L_Q_

NcoI

1501 GGTCTTTCTGGATGAACGCAAAAAATGACCATGGCTGGGCCTCATGGGCCTTCCTTTCAC
-----+-----+-----+-----+-----+-----+
CCAGAAAGACCTACTTGCGTTTTTTTACTGGTACCGACCCGGAGTACCCGGAAGGAAAGTG
_V_F_L_D_E_R_K_K_*_

1561 TGCCCGCTTTCCAG
-----+-----
ACGGGCGAAAGGTC