



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) **Bsu36I (291)**
Psp1406I (203) **PvuII (239)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCGCCCTACCTGAGGCC
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCACGTTTCGATGCCTTCATCTGCTATTGCCCCAG
601 CGACATCCAGTTTGTGCAGGAGATGATCCGGCAACTGGAACAGACAACTATCGACTGAAGTTGTGTGTCTGACCCGATGCTCCTGCCGTCACCTGT
130 ▶ D I Q F V Q E M I R Q L E Q T N Y R L K L C V S D R D V L P G T C
PstI (772)

BsaBI (846) **XmnI (873)** **Bsu36I (891)**
801 CCAAAATTTGCACTCAGCCTCTCCAGGTGCCATCAGAAGCGACTGATCCCCATCAAGTACAAGGCAATGAAGAAAGAGTCCCCAGCATCTGAGGTT
80 ▶ T K F A L S L S P G A H Q K R L I P I K Y K A M K K E F P S I L R F
StuI (962) **BbsI (980)** **EcoO109I (993)**
901 CATCACTGTCTGCGACTACCAACCCCTGCACAAATCTTGGTTCTGGACTCGCCTTGCCAAAGCCTTGCCCTGCCTGAAGACTGTTCTGAGGCCCT
113 ▶ I T V C D Y T N P C T K S W F W T R L A K A L S L P •

MscI (1057)
NheI (1051)
1001 GGGTGTGTGTATCTGTCTGCCTGTCCATGTACTTCTGCCCTGCCTCTCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCA

HpaI (1189)
1101 CAACTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

MfeI (1200) **EcoRI (1285)**
1201 CAATTGCATTCATTTTATGTTTCAGGTTAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACA
1301 GCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTA

SapI (1467)
1401 GCTGTTTGACGCTCACCTCTTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTAAATGCACTGA

SspI (1524) **SwaI (1538)** **EcoO109I (1599)**
1501 CCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAA
1601 GGCCCTTCATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTT
1701 CCTGGTGTACTTGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATG
139 ▶ R T Y K L P I L E E I T T K V L K G N M E I L V F C D P A Y D S I

BstXI (1828)
1801 AGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCT
105 ▶ L E R C M G C P S V V R I S R D V E D S Y P H R V A V I T D F D K Q
StuI (1963)
1901 GCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCCAGT
72 ▶ G N S V A S G I A I A E A C V T V R G I Y A E I H V A S I I E G T
2001 CTTGGTCTGATGGCCGCCCCGACATGGTGTCTGCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAG
39 ▶ K T R I A A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q S

BbsI (2109) **AseI (2171)**
XmnI (2105)
2101 ATGTTGAAGGTTCTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGT
5 ▶ I N F T K M
2201 CTCACGTTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTAC

SpeI (2326)
2301 GACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCC

2401 **SnaBI (2454)**
ACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTAC

2501 **NdeI (2559)**
TGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACC

2601 **NdeI (2559)**
GTAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGG

2701 **PstI (2738)** **PacI (2745)** **SdaI (2737)** **BspLU11I (2755)**
TCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG

2801 **BspLU11I (2755)**
CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG

2901 **BspLU11I (2755)**
ATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG

3001 **ApaLI (3069)**
GCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCT

3101 **ApaLI (3069)**
GCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA

3201 **ApaLI (3069)**
TGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC

3301 **ApaLI (3069)**
GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGAT

3401 **PacI (3485)** **SwaI (3494)**
CTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA

3501 **EagI (3505)** **NotI (3504)**
ATCAGCGCGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGA

3601 **EagI (3505)** **NotI (3504)**
AACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA