



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82) EcoNI (96)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

HindIII (245) **Bsu36I (291)**
Psp1406I (203) **PvuII (239)** 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC EcoNI (287)

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **SphI (560)**
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCAGCATGCACAAGGAGGAACATGAGGTGGCTGTGCTGGGGGC 1▶ M H K E E H E V A V L G A

BsaBI (633) **Tth111I (664)**
601 ACCCCCCAGCACCATCCTTCCAAGTCCACCGTATCAACATCCACAGCGAGACCTCCGTGCCGACCATGTCGTCTGGTCCCTGTTCAACACCTCTTC 13▶ P P S T I L P R S T V I N I H S E T S V P D H V V W S L F N T L F

StuI (788)
701 TTGAAGTGGTGTCTGGGCTTCATAGCATTGCGCTACTCCGTGAAGTCTAGGGACAGGAAGATGGTTGGCGACGTGACCGGGGCCAGGCCATGCGCT Bsp120I (782)

47▶ L N W C C L G F I A F A Y S V K S R D R K M V G D V T G A Q A Y A

Bsp120I (824) **BspHI (845)**
801 CCACCGCCAAGTGCCTGAACATCTGGGCGCTGATTCTGGGCATCCTCATGACCATGGATTATCCTGTTACTGGTATTCGGCTCTGTGACAGTCTACCA 80▶ S T A K C L N I W A L I L G I L M T I G F I L L L V F G S V T V Y H

MscI (948)
901 TATTATGTTACAGATAATACAGGAAAAACGGGGTTACTAGTAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAA 113▶ I M L Q I I Q E K R G Y •

SpeI (935) **NheI (942)**

1001 TGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCAT HpaI (1080) MfeI (1091)

EcoRI (1176)
1101 TCATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAATACAGCATAGCAA

1201 AACTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGC

SapI (1358)
1301 AGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTCTTTCATTTCTTTATGTTTTAATGCAGTACCTCCACA

SspI (1415) **SwaI (1429)**
1401 TTCCCTTTTATGATAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCA

1501 TAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTTCTGGTGTGA 141▶ • N R T Y

SacI (1690)
1601 CTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTG 136▶ 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 L E R

BstXI (1719)
1701 CACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGC 102▶ 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 G N S

StuI (1854)
1801 TCACAGCAGACCAATGGCAATGGCTTACAGCACAGACAGTACCTGCCAATGTAGCCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCT 69▶ 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 K T R

XmnI (1996)
1901 GATGGCCGCCCCGACATGGTCTTGTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAG 36▶ 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 I N F

BbsI (2000) **AseI (2062)**
2001 GTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTT 24▶ T K M

SacI (2119)
2101 ATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTG

SpeI (2217)
2201 GAAAGTCCCCTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATT

SnaBI (2345)
2301 GATGTAAGTCCAAACCGCATCATCATGGTAATAGCGTAGTAATAACGTAAGTACTGCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAA

2401 TGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTAAGTGGCCAAAGTGGGCAGTTTACCGTAAATACT
2501 CCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTTCGTTGGGCGGTACGCCAGG

PacI (2636)
PstI (2629) SdaI (2628) BspLU11I (2646)

2601 CGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC
2701 TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGC
2801 GTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGCGCCTTTCT

ApaLI (2960)

2901 CATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCGACCGCTGCGCCTTAT
3001 CCGGTAACATATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGG
3101 TGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGA
3201 GTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAG

EagI (3396)
PacI (3376) SmaI (3385) NotI (3395)

3301 ATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGC
3401 CGCAATAAAATATCTTTATTTTCATTACATCTGTGTGGTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACA
3501 AACTAGCAAAATAGGCTGTCCCCAGTGCAGGTGCCAGAACATTTCTCTATCGAA