



PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BspLU11I (560)

501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCAACATGTCCTGTTCATCACTCCCTCTCCTTCTCCTGAG
1▶ M S L F P S L P L L L S

BstAPI (661)

601 TATGGTGGCAGCGTCTTACTCAGAACTGTGACCTGTGAGGATGCCAAAAGACTGCCTGCAGTATTGCCTGTAGCTCTCCAGGCATCAACGGCTTC
13▶ M V A A S Y S E T V T C E D A Q K T C P A V I A C S S P G I N G F

Bsp120I (771)

701 CCAGGCAAAGATGGGCGTGTGGCACCAGGGAGAAAAGGGGAACCAGGCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGCCTCCAG
47▶ P G K D G R D G T K G E K G E P G Q G L R G L Q G P P G K L G P P

BstEII (818)
BspEI (861)

801 GAAATCCAGGGCTTCTGGGTCACCAGGACCAAGGGCAAAAGGAGACCCTGGAAAAGTCCGGATGGTATAGTAGCCTGGCTGCCTCAGAAAGAAA
80▶ G N P G P S G S P G P K G Q K G D P G K S P D G D S S L A A S E R K

XmnI (966)

901 AGCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTCTTCTGACCAATGGTGAATAATG
113▶ A L Q T E M A R I K K W L T F S L G K Q V G N K F F L T N G E I M

SfiI (1038)

1001 ACCTTTGAAAAGTGAAGGCCTTGTGTGCAAGTTCAGGCTCTGTGGCCACCCCGAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGG
147▶ T F E K V K A L C V K F Q A S V A T P R N A A E N G A I Q N L I K

BbsI (1128)

1101 AGGAAGCCTTCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCTACACAACTGGAACGAGGGTGAACC
180▶ E E A F L G I T D E K T E G Q F V D L T G N R L T Y T N W N E G E P

XcmI (1271)

1201 CAACAATGCTGGTCTGTGAAGATTGTGATTGCTACTGAAAAATGGCCAGTGAAGTACGCTCCCTGCTCCACCTCCATCTGGCCGTCTGTGAGTTC
213▶ N N A G S D E D C V L L L K N G Q W N D V P C S T S H L A V C E F

NheI (1316)

1301 CCTATCTGAAGGGTCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGT
247▶ P I •

HpaI (1454) **MfeI (1465)**

1401 GAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTATTTTATGTTTCAGGTTTCAGGGGG

EcoRI (1550)

1501 AGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAATAACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCT
 1601 ACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTCATGGAGTTTA

SapI (1732)
SspI (1789)

1701 AGATATAGTGATTTTTCCCAAGGTTTGAAGTCTCTTCAATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAATATTCAGAA

Swal (1803)

1801 ATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGA
 1901 CTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTTCTCAATGG
141▶ • N R T Y K L P I L E E I T

SacI (2064) **BstXI (2093)**

2001 TGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCCT
127▶ T K V L K G N M E I L V F C D P A Y D S I L E R C M G C P S V V R

2101 GATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCCTGCTCACAGCAGACCCAATGGCAATGGCT
94▶ 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 V A S G I A I A

2201 TCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTGGTCCCTGATGGCCGCCCGACATGGTGCTTGT
60▶ 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 I A A G V H H K N

BbsI (2374) **XmnI (2370)**

2301 TGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTG
27▶ D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M

AseI (2436) **SacI (2493)**

2401 AGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACATAAACGAGCTCT

2501 GCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTTACTAGTCAA **SpeI (2591)**
2601 AACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCA
SnaBI (2719)
2701 TGGTAATAGCGATGACTAATACGTAGATGTAAGTACGCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATT
NdeI (2824)
2801 GACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTC
2901 CCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAA
PacI (3010)
SdaI (3002) **BspLU11I (3020)**
3001 CGCCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGAAAGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCC
3101 CCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGC
3201 GCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTTCTCCCTTCGGGAAGCGTGGCGCTTTTCTCATAGCTCACGCTGTAGGTATCTCAG
ApaLI (3334)
3301 TTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAC
3401 CCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC
3501 CTAACACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACA
3601 AACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCT
EagI (3770)
3701 GACGCTCAGTGGAACGAAAACACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC **PacI (3750)** **SwaI (3759)** **NotI (3769)** AGCGCCGCAATAAAATATCTTTATTTTCATT
3801 ACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGT
3901 GCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA