



PvuI (7)
SgfI (6)
MfeI (82)

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) SphI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTGAGTGTGCTGCTCAGGCTGCTCTTGGCTCTCAACTTATCCCTTC

1▶ M L R L L L A L N L F P S

BsiWI (653)

601 AATTCAAGTAACAGGAAACAAGATTTTGGTGAAGCAGTCGCCATGCTTGAGCGTACGACAATGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTC

13▶ I Q V T G N K I L V K Q S P M L V A Y D N A V N L S C K Y S Y N L

701 TTCTCAAGGGAGTTCCGGGCATCCCTTCACAAAGGACTGGATAGTGTGTGGAAGTCTGTGTTGTATATGGGAATTACTCCCAGCAGCTTCAGGTTTACT

47▶ F S R E F R A S L H K G L D S A V E V C V V Y G N Y S Q Q L Q V Y

HpaI (871)

801 CAAAAACGGGTTCAACTGTGATGGGAAATTGGGCAATGAATCAGTGACATTCTACCTCCAGAATTTGTATGTTAACCAGATATTTACTTCTGCAA

80▶ S K T G F N C D G K L G N E S V T F Y L Q N L Y V N Q T D I Y F C K

SapI (939)

901 AATTGAAGTTATGTATCCTCCTTACCTAGACAATGAGAAGAGCAATGGAACCATTATCCATGTGAAAGGGAAACACCTTTGTCCAAGTCCCCTATTT

113▶ I E V M Y P P P Y L D N E K S N G T I I H V K G K H L C P S P L F

1001 CCCGGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTGGTGGAGTCTGGCTTGTATAGCTTGTAGTAAACAGTGGCCTTTATTTTCTGGGTGA

147▶ P G P S K P F W V L V V V G G V L A C Y S L L V T V A F I I F W V

Bsp120I (1159)

XmaI (1156)

1101 GGAGTAAGAGGAGCAGGCTCCTGCACAGTGACTACATGAACATGACTCCCCGCGCCCGGGCCACCCGCAAGCATTACCAGCCCTATGCCCCACCAG

180▶ R S K R S R L L H S D Y M N M T P R R P G P T R K H Y Q P Y A P P R

NheI (1244)

XcmI (1238) MscI (1250)

1201 CGACTTCGAGCCTATCGCTCCTGACACGGACGCCTATCCAGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGT

213▶ D F A A Y R S •

HpaI (1382) MfeI (1393)

1301 AATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAACAAACAATTGC

EcoRI (1478)

1401 ATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGC

1501 AAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTT

SapI (1660)

1601 GCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCATTTCTTATGTTTTAAATGCACTGACCTCCA

SspI (1717) SmaI (1731)
EcoO109I (1792)

1701 CATTCCCTTTTATAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTT

1801 CATAATATCCCCAGTTTAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTG

141▶ • N R T

SacI (1992)

1901 TACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTC

136▶ 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 L E R

BstXI (2021)

2001 TGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTT

103▶ 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

StuI (2156)

2101 GCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTC

70▶ 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 K T

XmnI (2298)

2201 CTGATGGCCGCCCGACATGGTGCTTGTGTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGA

36▶ 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 I N F

BspHI (2306)
BbsI (2302) 3' T K M ←
 2301 AGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGC

Sacl (2421)
 2401 IIATCTGACGGTTCAC^{TAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTT}

SpeI (2519)
 2501 TGGAAAGTCCCCTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCTGAGTCAAACCGCTATCCACGCCCA

SnaBI (2647)
 2601 TTGATGTA^{CTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTA}CTGGGCAT

NdeI (2752)
 2701 AATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATA
 2801 CTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGCGGTGACGCCA

PacI (2938)
PstI (2931)
SdaI (2930)
BspLU11I (2948)
 2901 GCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTT
 3001 GCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA^{AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA}GATACCAG
 3101 GCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTT

ApaLI (3262)
 3201 CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTT
 3301 ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC
 3401 GGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAA
 3501 GAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGA

PacI (3678) SwaI (3687) **EagI (3698)**
NotI (3697)
 3601 AGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCG

3701 GCGCAATAAAAATATCTTTATTTTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAACAAAA
 3801 CAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA