



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)
AgeI (552) **NcoI (560)** **DraIII (583)**

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGTCCTTGAGGTGAGTGACCACCAAGTGCTAAATGA

SapI (632)
1▶ M V L E V S D H Q V L N D

601 CGCCGAGGTTGCCGCCCTCTGGAGAACTTCAGCTCTTCTATGACTATGGAGAAAACGAGAGTGACTCGTGTGTACTCTCCCGCCCTGCCACAGGAC

13▶ A E V A A L L E N F S S S Y D Y G E N E S D S C C T S P P C P Q D

701 TTCAGCCTGAACCTCGACCGGCTTCTGCGACGCCCTCTACAGCCTCTCTTCTGCTGGGCTGCTGGGCAACGGCGGGTGGCAGCCGTGCTGTGA

47▶ F S L N F D R A F L P A L Y S L L F L L G L L G N G A V A A V L L

NgoMIV (800) **BsrBI (880)**

801 GCCGGCGGACAGCCCTGAGCAGCACCGACACCTTCTGCTCCACCTAGCTGTAGCAGACAGCTGCTGGTGTGACTGCGCCTCTGGGCGTGGACGC

80▶ S R R T A L S S T D T F L L H L A V A D T L L V L T L P L W A V D A

901 TGCCGTCCAGTGGGTCTTTGGCTCTGGCCTCTGCAAAGTGGCAGGTGCCCTCTTCAACATCAACTTCTACGCAGGAGCCCTCCTGCTGGCCTGCATCAGC

113▶ A V Q W V F G S G L C K V A G A L F N I N F Y A G A L L L A C I S

Bsp120I (1048)

1001 TTTGACCGCTACCTGAACATAGTTCATGCCACCCAGCTCTACCGCGGGGCCCGCGTGCCTCACCTGCCTGGCTGTCTGGGGCTCTGCC

147▶ F D R Y L N I V H A T Q L Y R R G P P A R V T L T C L A V W G L C

1101 TGCTTTTCGCCCTCCAGACTTCATCTTCTGTGCGCCACCACGACGAGCGCCTCAACGCCACCCACTGCCAATACTCCACAGGTGGGCGCAC

180▶ L L F A L P D F I F L S A H H D E R L N A T H C Q Y N F P Q V G R T

PvuII (1216)
PstI (1213)

1201 GGCTCTGCGGGTCTGCAGCTGGTGGCTGGCTTCTGCTGCCCTGCTGGTATGGCTACTGCTATGCCACATCCTGGCCGTGCTGCTGGTTTCCAGG

213▶ A L R V L Q L V A G F L L P L L V M A Y C Y A H I L A V L L V S R

BstXI (1319) **DraIII (1375)**

1301 GGCCAGCGCGCCTGCGGGCCATGCGGCTGGTGGTGGTGGTGGTGGTGGCCTTGGCCCTGCTGGACCCCTATCACCTGGTGGTGGTGGGACATCC

247▶ G Q R R L R A M R L V V V V V A F A L C W T P Y H L V V L V D I

Bsu36I (1469)
MscI (1454) **BstEII (1464)**

1401 TCATGGACCTGGGCGCTTTGGCCGCAACTGTGGCCGAGAAAGCAGGGTAGACGTGGCCAAGTCGGTCACCTCAGGCCTGGGCTACATGACTGCTGCCT

280▶ L M D L G A L A R N C G R E S R V D V A K S V T S G L G Y M H C C L

BsrBI (1540)

1501 CAACCCGCTGCTCTATGCCTTTGTAGGGTCAAGTTCGGGAGCGGATGTGGATGCTGCTCTTGCCTGGGCTGCCCAACAGAGAGGGTCCAGAGG

313▶ N P L L Y A F V G V K F R E R M W M L L L R L G C P N Q R G L Q R

BbsI (1608)

1601 CAGCCATCGTCTCCCGCGGGATTATCCTGGTCTGAGACCTCAGAGGCCTCTACTCGGGCTGTGAGGCCGAATCCGGGCTCCCTTTCCGCCACA

347▶ Q P S S S R R D S S W S E T S E A S Y S G L •

MscI (1714)
NheI (1708)

1701 GTCTGACTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTG

HpaI (1846) **MfeI (1857)**

1801 TGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAACAAGTTAACAACAACAATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGTGG

EcoRI (1942)

1901 GAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAAT

2001 CCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAG

SapI (2124) **SspI (2181)** **SwaI (2195)**

2101 TGTATTTTCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTGTAGTAAATATTCAGAAATAATTTA

2201 AATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTTGGACTTAGGGA

2301 ACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTG
141 • N R T Y K L P I L E E I T T K
SacI (2456) BstXI (2485)

2401 ACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACACATGCCACAGGGCTGACCACCCTGATGGATC
124 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 I S R
2501 TGCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACA
91 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 E A C
2601 GACAGTGACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCCGACATGGTGTCTGTGCTCTCA
58 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 D E
BbsI (2766)
XmnI (2762)

2701 TAGAGCATGGTATCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCGTAT
24 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 (2828) SacI (2885)

2801 TATACTATGCCGATATACTATGCCGATGATTAATTGTCAA AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCTACTAAACGAGCTCTGCTTATAT
SpeI (2983)

2901 AGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACT
3001 CCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATA
SnaBI (3111)

3101 GCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAA
NdeI (3216)

3201 TAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGG
PstI (3395)
SdaI (3394)

3301 CGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCA
PacI (3402) BspLU11I (3412)

3401 GGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCCCGCTTGTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGA
3501 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGGCTCTCCT
3601 GTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGT
ApaLI (3726)

3701 AGGTCGTTGCTCCAAGTGGGCTGTGTGCAGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGTAAGTATCGTCTTGAGTCCAACCCGGTAAG
3801 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTAC
3901 GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCG
4001 CTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCA
EagI (4162)

4101 GTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGT
PacI (4142) SmaI (4151) NotI (4161)

4201 GTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGC
4301 AGGTGCCAGAACATTTCTATCGAA