



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) **NcoI (560)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGGGCGGCTGGTTCTGCTGTGGGAGCTGCCGTCTT

1 ▶ M G R L V L L W G A A V F

BsaBI (654)

601 TCTGCTGGGAGGCTGGATGGCTTTGGGCAAGGAGGAGCAGCAGAAGGAGTACAGATTCAGATCATCTACTTCAATTTAGAAAACCGTGCAGGTGACATGG

13▶ L L G G W M A L G Q G G A A E G V Q I Q I I Y F N L E T V Q V T W

ApaLI (771)

701 AATGCCAGCAAATACTCCAGGACCAACCTGACTTTCCACTACAGATTCACCGTGATGAGGCCTATGACCAGTGACCAACTACCTTCTCCAGGAAGGTC

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

801 ACATTCGGGGTGCCTCTAGACGCAGAGCAGGACGACATTCTCTATTTCTCCATCAGGAATGGGACGCACCCCGTTTTCCCGCAAGTCGCTGGAT

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

BbrPI (931)

901 GGTATTACCTGAAACCCAGTCCCCGAAGCACGTGAGATTTTCGTGGCATCAGGATGCAGTGACGGTGACGTGTTCTGACCTGCTCCTACGGGGATCTC

113▶ V Y Y L K P S S P K H V R F S W H Q D A V T V T C S D L S Y G D L

DraIII (1032)

1001 CTCTATGAGGTTTCAGTACCGGAGCCCTTCGACACCGAGTGGCAGTCCAAACAGGAAAATACCTGCAACGTCACCATAGAAGGCTTGATGCCGAGAAGT

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

1101 GTTACTCTTTCTGGGTCAGGGTGAAGGCTATGGAGGATGTATATGGCCAGACACATACCCAAAGCAGCTGGTCAGAGGTGACATGCTGGCAGAGAGGCCGA

180▶ C Y S F W V R V K A M E D V Y G P D T Y P S D W S E V T C W Q R G E

1201 GATTCCGGGATGCCTGTGCAGAGACCAACGCCTCCAAACAAAGCTGTCCAAATTTATTTAATTTCCAGCCTGGCCATCCTTCTGATGGTGTCTCTC

213▶ I R D A C A E T P T P P K P K L S K F I L I S S L A I L L M V S L

XmaI (1378)

1301 CTCCTTGTCTTTATGGAAATTATGGAGAGTGAGGAAGTTTCTCATTCCCAGCGTGCCAGACCCGAAATCCATCTTCCCGGGCTCTTTGAGATACCC

247▶ L L L S L W K L W R V R K F L I P S V P D P K S I F P G L F E I H

Bsu36I (1483)

1401 AAGGAACTTCCAGGAGTGGATCACAGACACCCAGAACGTGGCCACCTCCACAAGATGGCAGGTGCAGAGCAAGAAAGTGGCCCTGAGGAGCCCCTGGT

280▶ Q G N F Q E W I T D T Q N V A H L H K M A G A E Q E S G P E E P L V

BamHI (1576)

1501 GTTCCAGTTGGCCAAAGCTGAAGCCGAGTCTCCAGGATGCTGGACCCACAGACCGAGGAGAAAGAGGCCTCTGGGGATCCCTCCAGCTTCCCACCAG

313▶ V Q L A K T E A E S P R M L D P Q T E E K E A S G G S L Q L P H Q

BsrBI (1656)

1601 CCCCTCAAGGIGGTGATGTGGTCACAATCGGGGGCTTACCTTTGTGATGAATGACCGCTCTACGTGGCGTTGTGATGGACACACCACTGTCAAAGTC

347▶ P L Q G G D V V T I G G F T F V M N D R S Y V A L •

NheI (1708)

1701 AACGTCAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTG

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

1801 TGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGG

EcoRI (1942)

1901 GAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTAAATAACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAAT

2001 CCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTATGAGGTTTAAAGATATAG

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

2101 TGTATTTTCCAAGGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTA

EcoO109I (2256)

2201 AATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGA

2301 ACAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTG

141 ▶ • N R T Y K L P I L E E I T T K

2401 ACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATC
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 TGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACA
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 GACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTGTCTCA
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

SacI (2456)

BbsI (2766)
XmnI (2762)

2701 TAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTAT
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 TATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATAT

SpeI (2983)

2901 AGACCTCCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACT
3001 CCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATA

SnaBI (3111)

3101 GCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGTCTGACTGGGCATAATGCCAGGCGGGCCATTTACCGTATTGACGTCAA

NdeI (3216)

3201 TAGGGGGCGTACTTGGCATATGATACACTTGATGTAAGTGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGG

PstI (3395)
SdaI (3394)

3301 CGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCA

PacI (3402) BspLU11I (3412)

3401 GGTTAAITTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGA
3501 GCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAAGTCCCTCGTGCGCTCTCCT
3601 GTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGT

ApaLI (3726)

3701 AAGTCTGTTGCTCCAAGTGGGTGTGTGCAGAACCCCGTTCAGCCGACCGTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG
3801 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTAC
3901 GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCCG
4001 CTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGTCTGACGCTCA

EagI (4162)
PacI (4142) SmaI (4151) NotI (4161)

4101 GTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGT
4201 GTGTTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGC
4301 AGGTGCCAGAACATTTCTATCGAA