



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

1 GGATCTGCGATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGGTTCGCGCCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTCGTCTATCTTCTCATCGAGGGTCTTGTGCGGCA

AgeI (552) **BspLU11I (560)**

1▶ M S S S S S S R V L L R Q

BstAPI (600) **SacII (659)**

601 GCAGCTAATGCGGGCCAGGCGCAGGAGCAGGAGGCGTGAGCGTCGGGAACAGGCCGCGCGCTCCCTTCCCCAGTCTGCACCTGCCTCTCCTGCC

13▶ Q L M R A Q A Q E Q E R R E R R E Q A A A A P F P S P A P A S P A

701 ATCTCTGTGGTTGGCGTCTGCTGGGGCCACACATTGAGCCGTCCACCCCTGCTCAGGTGCCAGGGAGGTGCTCAAGGTGCAGACCCATCTGGAGA

47▶ I S V V G V S A G G H T L S R P P P A Q V P R E V L K V Q T H L E

BssHII (826)

AscI (825)

801 ACCCAACGCGCTACCACCTGCAGCAGGCGCGCCGGCAGGAGGAAACAGTACTGTCCACCACACTCGGGCCCAAGCTGGTTCAGGCCCTCACCCC

80▶ N P T R Y H L Q Q A R R Q Q V K Q Y L S T T L G P K L A S Q A L T P

Bsu36I (937) **XcmI (977)** **NcoI (986)**

901 ACCGCCGGGGCCGCAAGTGCCAGCCACTGCCTGCCCTGAGGCTGCCACACTACCGCCCCACAGGCAGTGCGCCAACAGCCCCATGGCGCTGCTC

113▶ P P G P A S A Q P L P A P E A A H T T G P T G S A P N S P M A L L

1001 ACCATCGGGTCCAGCTCAGAGAAGGAGATTGATGATGTCATTGATGAGATCATCAGCCTGGAGTCCAGTTACAATGATGAAATGCTCAGTATCTGCCCG

147▶ T I G S S S E K E I D D V I D E I I S L E S S Y N D E M L S Y L P

BsrGI (1160)

1101 GAGGCACCACAGGACTGCAGCTCCCCAGCAGCTGCCTGTGTGAGGAATCTGCTTGTGTACAGTAGTCAAGGCGTGCCACACCAGCCATCACTGT

180▶ G G T T G L Q L P S T L P V S G N L L D V Y S S Q G V A T P A I T V

BstAPI (1202) **BglII (1241)**

1201 CAGCAACTCTGCCAGCTGAGCTGCCCAACATCAAACGGGAGATCTCTGAGACCGAGGCAAAGGCCCTTTTGAAGGAACGGCAGAAGAAAGACAATCAC

213▶ S N S C P A E L P N I K R E I S E T E A K A L L K E R Q K K D N H

1301 AACCTAATTGAGCGTCGACGGGATTCAACATTAACGACAGGATCAAGGAAGTGGGACTCTCATCCCTAAGTCCAGTGACCCGGAGATGCCTGGAACA

247▶ N L I E R R R F N I N D R I K E L G T L I P K S S D P E M R W N

StuI (1415) **Eco47III (1457)**

1401 AGGGCACCATCCTGAAGGCTCTGTGGATTATCCGCAAGCTGCAGAAGGAGCAGCAGCGTCCAAAGACCTGGAGAGCCGGCAGCGATCCCTGGAGCA

280▶ K G T I L K A S V D Y I R K L Q K E Q Q R S K D L E S R Q R S L E Q

EcoRI (1523) **NcoI (1554)**

1501 GGCCAACCGCAGCCTGCAGCTCCGAATTCAGGAAGTGAAGTGCAGGCCAGATCCATGGCCTGCCAGTCCCTCCCCTCCAGGGCTGCTTTCCTTGGCC

313▶ A N R S L Q L R I Q E L E L Q A Q I H G L P V P P T P G L L S L A

Psp1406I (1671)

1601 ACGACTTCGGCTTCTGACAGCCTCAAGCCAGAGCAGCTGGACATTGAGGAGGAGGGCAGGCCAGGCGCAGCAACGTTCCATGTAGGGGGGGACCTGCC

347▶ T T S A S D S L K P E Q L D I E E E G R P G A A T F H V G G G P A

XcmI (1763)

1701 AGAATGCTCCCCATCAGCAGCCCTGCACCGCCTCAGATGCCCTTCTGGACCTGCATTTCCAGCGACCACCTGGGGACCTGGGAGACCCCTTCCA

380▶ Q N A P H Q Q P P A P P S D A L L D L H F P S D H L G D L G D P F H

1801 CCTGGGGCTGGAGGACATTCTGATGGAGGAGGAGGGGGTGGTGGGAGGACTGTCCGGGGTGCCTGTCCCCTGCGGGCTGCCCTCCGATCCCTGT

413▶ L G L E D I L M E E E E G V V G G L S G G A L S P L R A A S D P L

NheI (1978)

1901 CTCTTTCAGTGTCCCCTGCTGTCTCCAAGGCCAGCAGCCGCGCAGCAGCTTTCAGCATGGAAGAGGAGTCCCTGATCAGCTAGCTGGCCAGACATGATAA

447▶ L S S V S P A V S K A S S R R S S F S M E E E S •

2001 GATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAGGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTA

HpaI (2116) **MfeI (2127)**

2101 AAGCTGCAATAAACAAGTTAAACAACAACATTCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGGGAGGTTTTTAAAGCAAGTAAACCTCTAC

EcoRI (2212)

2201 AAATGTGGTATGGAATTCATAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGC

SapI (2394)

2301 ATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGAGGTTTAAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTGCTT

SspI (2451) **SwaI (2465)**

2401 CATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGATAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTT

2501 TTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAG
 2601 CAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACA
 141 • N R T Y K L P I L E E I T T K V L K G N M E I L V
 SacI (2726)
 2701 AAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGA
 114 F C D P A Y D S I L E R C M G C P S V V R I S R D V E D S Y P H R V
 StuI (2890)
 2801 CAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAAT
 81 A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I Y A E I
 2901 GTGGACAGCAGAGATGATCTCCCAGTCTGGTCTGATGGCCGCCCGACATGGTGTCTGTCTCATAGAGCATGGTGTCTCTCAGTGGCGACC
 48 H V A S I I E G T K T R I A A G V H K N D E Y L M T I K E T A V
 BbsI (3036)
 XmnI (3032) AseI (3098)
 3001 TCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGAT
 14 E V L E L D Q Q S I N F T K M
 SacI (3155)
 3101 TAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCA
 SpeI (3253)
 3201 TTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAACTCCATTGACGTCAATGGGGTGGAGACTGG
 SnaBI (3381)
 3301 AAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAA
 NdeI (3486)
 3401 GTAGGAAAGTCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTT
 3501 GATGTAAGTCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGA
 PacI (3672) SdaI (3664) BspLU11I (3682)
 3601 CGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCC
 3701 AGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG
 3801 GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGTCCCTCGTGCCTCTCTGTTCGACCCTGCCGTTACCGGATACCTG
 ApaLI (3996)
 3901 TCCGCTTTCTCCCTTCGGAAGCGTGGCGTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGC
 4001 ACGAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCAC
 4101 TGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATC
 4201 TGCCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTGTTTGCAAGC
 4301 AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTT
 EagI (4432)
 PacI (4412) SmaI (4421) NotI (4431)
 4401 GGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAA
 4501 CATACGCTCTCCATCAAACAAACGAAACAAACAACTAGCAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA