



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACCGCGCCGCCCTACCTGAGGGC

PvuII (239) 301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

Bsu36I (291)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGTTGCTCAACTCTACGCTTTGTTTCGTTT

NgoMIV (441)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTTCATCATGACATTTGCTGAGGACAAGACCTATAAGTATATCCG

AgeI (552) **BspHI (560)**
13▶ D N H S K F C C V D V L E I L P Y L S C L T A S D Q D R L R A S Y
1▶ M T F A E D K T Y K Y I R

BstAPI (611) 601 AGACAACCACAGCAAGTTTTGCTGTGTTGACGTTCTGGAGATCTGCCTTACCTGTCTCGCTCACAGCTAGTGACCAGGATCGACTGCGGGTCTCCTAC

XcmI (747) 701 AGGCAGATCGGGAACCGGACACTCTGGGACTCTCAATAATCTCCAGCGCCGGCTGGCTGGTGGAGGCTTTCATCCGGGCACTGCGAGATCTGTG

BglII (791) 47▶ R Q I G N R D T L W G L F N N L Q R R P G W V E V F I R A L Q I C

XhoI (827) 801 AGCTGCCTGGGCTGGCTGATCAAGTACTCGAGTTTATCAGAGCTACCTGCCTCCGGGACCTCACTCCGCTCCCTAGAGCCACTGCAGTTACCAGACTT

EcoO109I (856) **BsrBI (867)** 80▶ E L P G L A D Q V T R V Y Q S Y L P P G T S L R S L E P L Q L P D F

NcoI (954) 901 TCCTGCTGCGGTTTCTGGACCCTCTGCATTTGCCCCAGGTCAACATCCCTGACCATGGCTTACGAGAGACCAAGTTGCCCAAGCCTGTCCAGGAC

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

EcoRI (1026) 1001 ACCCAGCCACCAGAGTCCCAGTAGAGAATTCCAGGCAACTCTCCAGACCAACTCCGGGGCCGTCGCGAGGATGTCTGGTGGCTCTTTGATACCCCTCTC

NruI (1064) 147▶ T Q P P E S P V E N S E Q L L Q T N S G A V A R M S G G S L I P S

BstAPI (1177) 1101 CTAACCAGCAGGCTCTCAGCCCTCAGCCCTCCAGAGAGCATCAAGAGCAAGAACCAGAAGTGGTGGCGCCACGCAGCAAATGTTGCCTCTGTTCCCAT

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

PshAI (1211) 1201 AGCAACCTATGGACCTGTGTCTCAACCGTTTCTCCAGCCCTCCACGTACTGCCCTGAGGACAAACCTTGTCTGGGGTACAGTATCAGCCCTA

Bsu36I (1257) 213▶ A T Y G P V S P T V S F Q P L P R T A L R T N L L S G V T V S A L

BstEII (1357) 1301 TCTGCTGATACCTTTTGTCTCCTCGTCCACTGGATCAGCTTTTGC AAAGGAGCTGGTACCAGGCCAAAGCTGCCACCTGTTTCAGTACTACACTCA

ScaI (1387) 247▶ S A D T S L S S S S T G S A F A K G A G D Q A K A A T C F S T T L

1401 CCAATTCTGTGACTACCAGCTCAGTGCCTTCTCCAGATTGGTCCCAGTAAAACCATGTCTTCAAGTTGCCCTCAGTTCAAAGTCCACTGCTGCGAT

280▶ T N S V T T S S V P S P R L V P V K T M S S K L P L S S K S T A A M

MscI (1592) 1501 GACGTCTACTGTGCTACCAATACAGGCCATCAAAATTACCCAGCAACTCAGTGTATGCGGGCACAGTGCCATCCAGAGTGCTGTAGTGTGGCCAAA

313▶ T S T V L T N T A P S K L P S N S V Y A G T V P S R V P A S V A K

1601 GCACCTGCCAACACAATACCACCTGAGAGGAACAGCAAGCAAGGAGACCCCGAGGTCAGCAACCAAAGTCACTGGAGGCAACCAGACTG

347▶ A P A N T I P P E R N S K Q A K E T P E G P A T K V T T G G N Q T

1701 GACCAAATAGCAGTATCAGGAGCTTGCCTGACTCTGGACCAGAGATGAGCAAGCCAGGTGTCTGGTATCCAGTTGGACGAGCCATTCTCAGCCTGCTGT

380▶ G P N S S I R S L H S G P E M S K P G V L V S Q L D E P F S A C S V

NcoI (1845) 1801 GGACCTTGCCATTAGCCCTAGCAGCTCCTGGTCTCAGAACCAACCATGGTCCAGAGGAGAATGAGTATTCGTCCTTTAGAATCCAGGTAGACGAAAGC

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

1901 CCCAGTGTGATCTATTAGGAAGCCCTGAGCCACTAGCCACCCAGCAGCCCAAGAAGAGGAAGAACATTGTGCCAGTTCAATGCCCTGGGCTAAGTGGC

447▶ P S A D L G S P E P L A T Q Q P Q E E E E H C A S S M P W A K W

ApaLI (2012) 2001 TTGGGGCCACCAGTGCCTCTTGGCTGTATTCTGGCAGTGATGCTGTACCGTAGTAGCGCCTGGCCAGTGAAGTCTAGCTAGCCAGACATGATAAGATA

XcmI (2009) 480▶ L G A T S A L L A V F L A V M L Y R S R R L A Q •

NheI (2074) 2101 CATTGATGAGTTTGGACAACCACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGC

HpaI (2212) **MfeI (2223)** 2201 TGCAATAAACAAGTTAAACAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAAT

EcoRI (2308) 2301 GTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCA

2401 GGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGTTTGAAGCTAGCTCTTCATT
SapI (2490)

2501 TCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTTA
SspI (2547) **SwaI (2561)**

2601 TTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAG
EcoO109I (2622)

2701 AAAGCGAGCTTCTAGCTTTAGTTCTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGC
SacI (2822) **BstXI (2851)**

2801 AGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGC
113 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 A
StuI (2986)

2901 CACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGG
80 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 H

3001 ACAGCAGAGATGATCTCCCAGTCTTGGTCTGTAGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCA
46 V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E T A V E V
XmnI (3128) **AseI (3194)**

3101 CCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAAT
13 L E L D Q Q S I N F T K M

3201 TGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTG
SacI (3251)

3301 CGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAAT
SpeI (3349)

3401 CCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAG
SnaBI (3477)

3501 GAAAGTCCATAAGTTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCCTGATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTATG
NdeI (3582)

3601 TACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTC

3701 AATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAGGCCAGCA
SdaI (3760) **PacI (3768)** **BspLU11I (3778)**

3801 AAAGGCCAGGAACCGTAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG
BspLU11I (3778)

3901 CGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCCTGGAAGTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCG

4001 CTTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGA
ApaLI (4092)

4101 ACCCCCCGTTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT

4201 AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCG

4301 CTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCA

4401 GATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTC

4501 ATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATA
EagI (4528) **PacI (4508)** **SwaI (4517)** **NotI (4527)**

4601 CGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGACGGTGCCAGAACATTTCTCTATCGAA