



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

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTGAGGGC

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552)
NcoI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGGAGCATTTTTAGACAAGCCAAAGTGGAAAAGCA

SphI (644)

601 TAATGCCAGGGGAGGGTAATGGGTTGCGATATGGGCTAAGCAGCATGCAAGGCTGGCGTGTGAAATGGAGGATGCACATACGGCTGTGATCGGTTTG

13▶ N A Q G Q G N G L R Y G L S S M Q G W R V E M E D A H T A V I G L

SphI (744)

701 CCAAGTGGACTTGAATCGTGGTCACTTTGCTGTGTATGATGGGCATGCTGGTTCTCAGGTTGCCAAATACTGCTGTGAGCATTGTAGATCACATCA

47▶ P S G L E S W S F F A V Y D G H A G S Q V A K Y C C E H L L D H I

PstI (824)

801 CCAATAACCAGGATTTTAAAGGGTCTGCAGGAGCACCTTCTGTGAAAATGTAAGAATGGAATCAGAACAGGTTTTCTGGAGATTGATGAACACATGAG

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

PvuII (944)

901 AGTTATGTCAGAGAAGAAACATGGTGCAGATAGAAGTGGGTCAACAGCTGTAGGTGCTTAATTTCTCCCAACATACTTATTTTATTAACTGTGGAGAC

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

EcoRI (1082)

1001 TCAAGAGTTTACTTTGTAGGAACAGGAAAGTTCACTTCTTACACAAGATCACAAACCAAGTAATCCGCTGGAGAAAAGAACGAATTCAGAATGCAGGTG

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

XmnI (1078)

Bsp120I (1145)

1101 GCTCTGAATGATTACAGCGTGTGAATGGCTCTCTGGCTGTATCGAGGCGCCTTGGGGATTTTGATTACAAATGTGTCCATGGAAAAGTCCCTACTGAGCA

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

BglIII (1237)

1201 GCTTGTCTCACCAGAGCCTGAAGTCCATGATATTGAAAGATCTGAAGAAGATGATCAGTTCATTATCCTTGCATGTGATGGTATCTGGGATGTTATGGGA

213▶ L V S P E P E V H D I E R S E E D D Q F I I L A C D G I W D V M G

SapI (1303)

1301 AATGAAGAGCTCTGTGATTTTGAAGATCCAGACTTGAAGTCACTGATGACCTTGAGAAAATTTGCAATGAAGTAGTCGACACTGTTTGTATAAGGGAA

247▶ N E E L C D F V R S R L E V T D D L E K V C N E V V D T C L Y K G

BsaBI (1419)

1401 GTCGAGACAACATGAGTGTGATTTTGTCTGTTTTCCAAATGCACCCAAAGTATCGCCAGAAGCAGTGAAGAAGGAGGAGGTTGGACAAGTACCTGGA

280▶ S R D N M S V I L I C F P N A P K V S P E A V K K E A E L D K Y L E

Tth111I (1546) **FspI (1562)**

1501 ATGCAGAGTAGAAGAAATCATAAAGAAGCAGGGGAAGGCGTCCCCGACTTAGTCCATGTGATGCGCACATTAGCGAGTGAAGAATCCCCAGCCTCCCA

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

1601 CCAGGGGGTGAATTGGCAAGCAAGAGGAATGTTATTGAAGCCGTTTACAATAGACTGAATCCTTACAAAAATGACGACACTGACTCTACATCAACAGATG

347▶ P G G E L A S K R N V I E A V Y N R L N P Y K N D D T D S T S T D

MscI (1735)

NheI (1729)

1701 ATATGTGGTAAAAGTCTCATCTAGCCATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAGAAA

380▶ D M W •

HpaI (1867) **MfeI (1878)**

1801 ATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAAATTGCATTATTTATGTTT

EcoRI (1963)

1901 CAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCC

2001 AAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCT

SapI (2145)

2101 TTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTAGCTCTTCACTTTTATGTTTTAAATGCACTGACTCCACATTCCTTTTTAGT

2201 **SspI (2202)** SwaI (2216) AAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAG

2301 TTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTTGAGGGGATG
141 • N R T Y K L P I

2401 AGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGG
131 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 C M G C P

BstXI (2506)

2501 GGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCC
98 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 S V A S G

StuI (2641)

2601 AATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCG
65 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 R I A A G

BbsI (2787) XmnI (2783)

2701 ACATGGTGTCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGG
31 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 T K M

AseI (2849)

2801 CCTCCTATAGTGAGTGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCA
2901 CTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTG

SpeI (3004)

3001 ATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAA

SnaBI (3132)

3101 AACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGTACTGGGCATAATGCCAGGGGGCC

NdeI (3237)

3201 ATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCTCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACG
3301 TCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGTTGGGCGGTACGCCAGCGGGCCATTACC

PacI (3423) **PstI (3416)** **SdaI (3415)** **BspLU11I (3433)**

3401 GTAAGTTATGTAACGCTGCAGGTTAAITAAAGACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCA
3501 TAGGCTCCGCCCCCTGACGAGCATCACA AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATAACAGGCGTTTCCCCTGGA
3601 AGCTCCCTCGTGCCTCTCTGTTCGACCCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCT

ApaLI (3747)

3701 GTAGGTATCTCAGTTCGGTGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCG
3801 TCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCC
3901 TTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTT
4001 GATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTT

EagI (4183) **PacI (4163)** **SwaI (4172)** **NotI (4182)**

4101 TTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAAATAT
4201 CTTTATTTTACATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAATA
4301 GGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTATCGAA