



PvuI (7) **SgfI (6)** **MfeI (82)** **EcoNI (96)**
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) **Bsu36I (291)**
Psp1406I (203) **PvuII (239)** **EcoNI (287)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BbrPI (565) **AgeI (552)** **SphI (560)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAGCATGCACGTGCGCTCAITGCGAGTGCGGCGCCGCACAG

1 M H V R S L R A A A P H S

XhoI (675) **ApaLI (670)** **SgrAI (688)**
601 CTTCTGGGCTCTGGGACCCCTGTTCTGCTGCGCTCCGCCCTGGCCGACTTCAGCCTGGACAACGAGGTGCATCTGAGCTTCATCCACCGCGCCTC

13 F V A L W A P L F L L R S A L A D F S L D N E V H S S F I H R R L

BsrBI (709)
701 CGCAGCCAGGAGCGGGGAGATGCAGCGGAGATCCTCTCCATTTTGGGCTTGGCCACCGCCGCGCCGACCTCCAGGGCAAGCACAACCTCGGCAC

47 R S Q E R R E M Q R E I L S I L G L P H R P R P H L Q G K H N S A

NcoI (827) **XcmI (800)** **BsrGI (818)** **BstXI (827)** **BbsI (889)**
801 CCATGTTTCATGCTGGACCTGTACAACGCCATGGCGTGAAGAGGGCGGGCCCGCGCCAGGGCTTCTCTACCCCTACAAGGCCGCTTCAGTAC

80 P M F M L D L Y N A M A V E E G G G P G G Q G F S Y P Y K A V F S T

BspHI (959) **Tth111I (952)**
901 CCAGGGCCCCCTCTGGCCAGCCTGCAAGATAGCCATTTCTCACCGACGCCGACATGGTCATGAGCTTCGTCAACCTCGTGAACATGACAAGGAATTC

113 Q G P P L A S L Q D S H F L T D A D M V M S F V N L V E H D K E F

BspEI (1082)
1001 TTCCACCCAGCTACCACCATCGAGAGTTCGGTTTGTCTTTCCAAGATCCCAGAAGGGGAAGTGTACGGCAGCCGAATTCGGATCTACAAGGACT

147 F H P R Y H H R E F R F D L S K I P E G E A V T A A E F R I Y K D

BspEI (1130)
1101 ACATCCGGGAACGCTTCGACAATGAGACGTTCCGGATCAGCGTTTATCAGGTGCTCCAGGAGCACTTGGGCGGGAATCGGATCTCTTCTGCTCGACAG

180 Y I R E R F D N E T F R I S V Y Q V L Q E H L G R E S D L F L L D S

DraIII (1261) **SacII (1276)** **PstI (1294)**
1201 CCGTACCCTCTGGGCTCGGAGGAGGGCTGGCTGGTGTGATCAGCCACCAGCAACCACTGGTGGTCAATCCGCGGCACAACCTGGGCGCTGCAG

213 R T L W A S E E G W L V F D I T A T S N H W V V N P R H N L G L Q

1301 CTCTCGTGGAGACGCTGGATGGGAGAGCATCAACCCAAAGTTGGCGGGCTGATTGGGCGGCAGGGCCCCAGAACCAAGCAGCCCTTCATGGTGGCTT

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

BsrBI (1467)
1401 TCTTCAAGGCCACGGAGGTCCACTTCCGAGCATCCGGTCCACGGGAGCAAACAGCGCAGCCAGAACCCTCAAGACGCCCAAGAACCAGGAAGCCCT

280 F F K A T E V H F R S I R S T G S K Q R S Q N R S K T P K N Q E A L

StuI (1544)
1501 GCGGATGGCCAACGTGGCAGAGAACAGCAGCAGCGACCAGAGGCGAGCCTGTAAAGACAGAGCTGTATGTCAGCTTCGAGACCTGGGCTGGCAGGAC

313 R M A N V A E N S S S D Q R Q A C K K H E L Y V S F R D L G W Q D

1601 TGGATCATCGCGCTGAAGGCTACGCCCTACTACTGTGAGGGGAGTGTGCCTTCCCTGAACTCCTACATGAACGCCACCAACCAGCCATCGTGC

347 W I I A P E G Y A A Y Y C E G E C A F P L N S Y M N A T N H A I V

PshAI (1701)
1701 AGACGCTGGTCCACTTCATCAACCCGAAACGGTGCCCAAGCCCTGCTGTGCGCCACGCAGCTCAATGCCATCTCCGCTCTACTTTCGATGACAGCTC

380 Q T L V H F I N P E T V P K P C C A P T Q L N A I S V L Y F D D S S

NheI (1879)
1801 CAACGTCATCCTGAAGAAATACAGAAACATGGTGGTCCGGCCTGTGGCTGCCACTAGCTCCTCCGAGAATTCAGACCCGCTAGTGGCCAGACATGATA

413 N V I L K K Y R N M V V R A C G C H •

1901 AGATACATTGATGAGTTTGGACAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTAA

HpaI (2017) **MfeI (2028)**
2001 TAAGTGCATAAAACAAGTTAAACAACAACAATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTA

2101 CAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGG

SapI (2295)
2201 CATCAGGGCTGTTGCCAATGTGCATTAGCTGTTGACGCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTCCCAAGTTTGAAGTACTCT

2301 TCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTT
SspI (2352) SwaI (2366)

2401 TTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAATAGAAATTGGACA

2501 GCAAGAAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCAC
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

2601 AAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCGACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTG
SacI (2627) BstXI (2656)
 115 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

2701 ACAGCCACAATGGTGTCAAAGTCCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAA
81 V 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

2801 TGTGGACAGCAGAGATGATCTCCCAGTCTGGTCTGATGGCCGCCGACATGGTCTTGTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGAC
48 H 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

BbsI (2937) XmnI (2933) AseI (2999)

2901 CTCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGA
15 E V L E L D Q Q S I N F T K M

SacI (3056)

3001 TTAATTGTCAAACACGCTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCC

SpeI (3154)

3101 ATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTG

SnaBI (3282)

3201 GAAATCCCCTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCA

NdeI (3387)

3301 AGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACT

3401 TGATGTACTGCCAAGTGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTG

PacI (3573) PstI (3566) SdaI (3565) BspLU11I (3583)

3501 ACGTCAATGGGCGGGGTCTGTTGGGCGGTGACCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAITAAAGAACATGTGAGCAAAAGGC
3601 CAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA AAAATCGACGCTCAAGTCAGA

3701 GGTGGCGAAACCCGACAGGACTATAAAGATAACAGCGCTTTCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCGACCCTGCCGCTTACCGGATACCT

ApaLI (3897)

3801 GTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTG

3901 CACGAACCCCGTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCA

4001 CTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT

4101 CTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAG

4201 CAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATT

EagI (4333) PacI (4313) SwaI (4322) NotI (4332)

4301 TGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAAATATCTTTATTTTACATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTA

4401 ACATACGCTCTCCATCAAAAACAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA