



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCAGCGGGTTGAGTCGCGTTCGCGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMI (441) **NaeI (441)**
401 GGGCCTTTGTCGGCGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGCTCAACTCTACGCTTTTGTTTCGTTT

SphI (560)
AgeI (552)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTACAGTGCCTACTCCAACCTGCATCCAGCCATCCACGGCC

BsrBI (609) 1► M P Y S N L H P A I P R P
BstEII (604) **MscI (641)** **BamHI (672)**
601 CAGAGGTACCAGCTCAAATATGTAGCCCTCATCTTTCTGGTGGCCAGCCTGATGATCCTTTGGGTGGCAAAGGATCCACCAAATCACACTCTGAAGTAC

13► R G H R S K Y V A L I F L V A S L M I L W V A K D P P N H T L K Y

Asp718 (788) **Acc65I (788)**
701 CTAGCACTTACCTAGCCTCGCACGAACCTGGACTACTGTTGAAAACTCTGCTGTCTGGTGAAGAGCTGTCCATGTCCAGTCCAGTACCAGGGCA

47► L A L H L A S H E L G L L K N L C C L A E E L C H V Q S R Y Q G

BssHIII (816) **XcmI (836)**
801 GCTACTGGAAGGCTGTGCGCGCTGCTGGGATGCCCATCCACTGTATGGCTATGATTCTACTATCGTCTTATTCTATTCTCCAAAACACTGCTGA

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

SphI (950) **PstI (992)**
901 CATATACTCAGTTGGATGTTTGGCCTTCTGGTCTCTATAAGTCCATAAGCATGCTCCTGGCCTTCCAGAGCTTACTCCAGCGGAAGTCTCTGCAGTC

113► I Y L S W M F G L L V L Y K S L S M L L G L Q S L T P A E V S A V

BamHI (1091)
1001 TGTGAAGAAAAGAGTTAAATGTTGCCACGGGCTGGCCTGTGCTACTACATTGGGTACTTCCGGTTGATCTTACCAGGGCTCCAGGCCCGGATCCGAA

147► C E E K K L N V A H G L A W S Y Y I G Y L R L I L P G L Q A R I R

BsrGI (1151)
BpuAI (1145) **BbsI (1145)**
1101 TGTTCAATCAGTACATAACAACATGCTCAGTGGTGACGGGAGCCGAAGCTGTACATCCTCTTTCCATTGGAGCTGTGGGGTGCCTGACAACCTGAGTGT

180► M F N Q L H N N M L S G A G S R R L Y I L F P L D C G V P D N L S V

1201 AGTTGACCCCAACATTGATTCCGAGATATGCTGCCAGCAAACATCGACCGTGGCTGCATCAAGAAATCGGGTTTATTCCAACAGCGTCTACGAGATT

213► V D P N I R F R D M L P Q Q N I D R A G I K N R V Y S N S V Y E I

1301 CTGGAGAACGGACAGCCAGCAGGCGTCTGTATCCTGGATACGCCACCCCTTGCAGACCTGTTTGCCATGTCCAGGATGCCAAAGCTGGCTTACAGTC

247► L E N G Q P A G V C I L E Y A T P L Q T L F A M S Q D A K A G F S

1401 GGGAGGATCGGCTTGAGCAGGCTAAACTCTTCCGCGACACTTGAGGAAATCCTGGAAGATGTCGCCGAGTCTCGAAATAACTGCCGCCTCATTGTCTA

280► R E D R L E Q A K L F C R T L E E I L E D V P E S R N N C R L I V Y

BstEII (1578) **XcmI (1595)**
1501 CCAAGAACCACAGACGGAAACAGTTTCTCACTGTCTCAGGAGGTGCTCCGGCACCATTGTCAGGAAGAAAAGGAGGAGTTACCATGAATGCCCCCATG

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

BamHI (1696)
1601 ACCTCAGTGGCACCTCCTCCCTCGTACTGTCCCAAGCAAGACTCCTCATCAGTGGTATGGATCAGCCTCTCCACTCCGCACTGACCTCATCGGAT

347► T S V A P P P S V L S Q E P R L L I S G M D Q P L P L R T D L I G

NdeI (1736) **NheI (1793)** **MscI (1799)**
1701 CCTATCCCTATGATGTGCCAGACTATGCTGGCTATCCATATGATGTTCTCTGATTATGCTGGATACCCTTATGATGTCCAGACTATGCCTAAAGCTAGCT

380► S Y P Y D V P D Y A G Y P Y D V P D Y A G Y P Y D V P D Y A •

1801 GGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCAACTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTT

HpaI (1931) **MfeI (1942)**
1901 ATTTGTAACCATTATAAGTGCATAAACAAGTTAACAACAACATTCATTCTTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTAAAGC

EcoRI (2027)
2001 AAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAAACCTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGAT

2101 GAATAAGGCATAGGCATCAGGGCTGTGCAATGTGCATTAGCTGTTTGACGCTCACCTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGG

SspI (2266) **SwaI (2280)**
2201 TTTGAACTAGCTCTTCATTTCTTTATGTTTAAATGCAGTGCCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAA

EcoO109I (2341)
2301 TGAAAAATAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCAATAATCCCCAGTTTAGTGTGGACTTAGGGAACAAAGAACCTTTA

2401 ATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTGATGTTCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTC

141◀ • N R T Y K L P I L E E I T T K V L K G N

SacI (2541) **Ecl136II (2541)** **BstXI (2570)**
2501 ATCTCAATGAGCACAAGCAGTCCAGGAGCATAGTCCAGAGTACTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGCCACCTCATCAG

119◀ 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 D V E D S

2601 AGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCC
86 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 V T V R G

StuI (2705)

2701 AATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGCTGATGGCCGCCGACATGGTCTTGTCTCATAGAGCATGGTGATC
53 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 Y L M T I

BspHI (2855)
BpuAI (2851)
BbsI (2851)
XmnI (2847)

2801 TTCTCAGTGGCGACCTCCACCAGTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATA
19 K E T A V E V L E L D Q Q S I N F T K M

SacI (2970)
Ecl136II (2970)

2901 TACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCACCCTGA

AseI (2913)

SpeI (3068)

3001 CACGCTACCGCCATTGCGTCAATGGGCGGAGTTGTACGACATTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGCTCAAT

SnaBI (3196)

3101 GGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACC

3201 TAGATGTACTGCAAAGTAGGAAAGTCCATAAGGTGATGACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTG

NdeI (3301)

3301 GCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAAC

PacI (3487)
PstI (3480)
SdaI (3479)
SbfI (3479)
PciI (3497)
BspLU11I (3497)

3401 ATACGTCATTATTGACGTCATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACAA
3501 TGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCTTGTGGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCG

3601 ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAAGCTCCCTCGTGGCTCTCTGTTCCGACCCTGCCG

3701 CTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCCA

ApaLI (3811)

3801 AGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGTGGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAGACTTATCGCC

3901 ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCAGGATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA

4001 ACAGTATTTGGTATCTCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCCTGGTAGCGGTGGTT

4101 TTTTTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAAC

EagI (4247)
PacI (4227) SwaI (4236) **NotI (4246)**

4201 ACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGGTTTTTTGT

4301 GTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATT

4401 TCTCTATCGAA