



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

PvuII (239) 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

Bsu36I (291)
NgoMIV (441) 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspHI (560)** 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCATCATGAGCCTCCAGCTCCGCAGCTCCGCCGATCCCCAG

1► M S L Q L R S S A R I P S
601 CGTTCCATCTGCCATTGCGGATGGCGCGCTGGCATTCTGTTGCTGTTACGCTGCCGAGCATCTAGCTGAAGCTGCCCTTCTCAGTCATA

13► G S I S P F M R M A P L A F L L L F T L P Q H L A E A A P S S V I

AseI (745) 701 GCCGCAACGGAGTGC GTTGTGTTTGTCTTAACGTAAC TCCAAAATTAATCCCAAATGATCGCTAATTTGGAGGTGATCCCTGCAGTCCACAGTGCC

47► A A T E L R C V C L T V T P K I N P K L I A N L E V I P A G P Q C

PstI (782) **SdaI (781)**
BamHI (849) 801 CTACGGTGAAGTCATAGCTAACTGAAAAACGAGAAGGAGTCTGTCTGGATCCAGAAGCTCCTGTGATAAAGAAAATCATTGAGAAAATATTGGGCAG

80► P T V E V I A K L K N Q K E V C L D P E A P V I K K I I Q K I L G S

SspI (888)
MscI (970) 901 TGCAAAAAAGAAAGCTAAGCGGAATGCACTCGCAGTGGAAAGAACGGCCAGTGTTCATAGAAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAG

113► D K K K A K R N A L A V E R T A S V Q •

1001 TTTGGACAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTGAATAAAC

HpaI (1102) **MfeI (1113)** 1101 AAGTTAACAAACAATTGCATTCATTTTATGTTTCAGGTTACGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGA

EcoRI (1198) 1201 ATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTG

SapI (1380) 1301 CCAATGTGCATTAGCTGTTG CAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGTTTGAAGTCTTTCATTTCTTTATGTT

SspI (1437) **SwaI (1451)** 1401 TTAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAA

EcoO109I (1512) 1501 TCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCT

1601 TCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGC

—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 F C D P A

SacI (1712) **BstXI (1741)** 1701 ATAGTCAGAGATGAGCTCTG CACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTG

110◀ 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 V I T

StuI (1876) 1801 TCAAAGTCTTCTGCCGTTGCTCAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGA

76◀ 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 V A S I

1901 TGATCTCCCAGTCTTGGTCTGTAGTGGCCGCCGACATGGTGCTTGTGCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACAGCTCCAG

43◀ 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 L E L

BbsI (2022) **XmnI (2018)** 2001 ATCTGCTGAGAGATGTTGAAGTCTTCATGTTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACA

10◀ D Q Q S I N F T K M ◀

AseI (2084) 2101 GCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGG

SacI (2141) 2201 GCGGAGTTGTTACGACATTTTGGAAAAGTCCCGTTGATTTACTAGTCAAACAACCTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGT

SpeI (2239)

2301 CAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCA
SnaBI (2367)

2401 TAAGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAG
NdeI (2472)

2501 TGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGG

2601 GGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAITAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG
PstI (2651) SdaI (2650)PacI (2658) **BspLU11I (2668)**

2701 AACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGA
←

2801 CAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCC

2901 TTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTT
ApaLI (2982)

3001 CAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTA

3101 GCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA

3201 GCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGC

3301 AGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTT
PacI (3398)

3401 AATTAACATTTAAATCAGCGGCCCAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCAT
EagI (3418)
Swal (3407) **NotI (3417)**

3501 CAAAACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAAGTGCCAGAGTCCAGAACATTTCTCTATCGAA