



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

1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **Bsu36I (291)**

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTGCCTGTTGCGCCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **BstEII (555)** **PvuII (583)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTACCATTGGTCACTGGAAGGTCTGCCAGCTGTGCCTAGCACT
1▶ M V T G R S A Q L C L A L

601 GCTGTTTCTGCTCTTGTGATGTCATTCTGACAGCCACTGAGAAATCTGACTGACCTGGACCCACCATTGGATTAGAATTTACAGGAGAGAAAGTGACC
 13▶ L F M S L D V I L T A T E K S V L T L D P P W I R I F T G E K V T

Acc65I (760) **BamHI (749)** **Asp718I (760)**

701 CTTTCTGCTATGGGAACAATCACCTTCAAATGAACTCTACTACTAAATGGATCCACAATGGTACCGTCTCTGAGGTGAACTCTTACATTTGGTCATTG
 47▶ L S C Y G N N H L Q M N S T T K W I H N G T V S E V N S S H L V I

NdeI (831)

801 TGAGTGCCACCGTTCAAGACAGTGGAAAATACATATGTCAGAAGCAAGGATTGTTAAGAGTAAACCTGTGTACTTGAATGTAACGCAAGATTGGCTGCT
 80▶ V S A T V Q D S G K Y I C Q K Q G L F K S K P V Y L N V T Q D W L L

BamHI (934)

901 CCTCAGACATCTGCTGACATGATCTTAGTCCATGGATCCTTTGACATCAGATGCCATGGCTGGAAGAACTGGAATGTCCGCAAGGTGATCTACTACAGG
 113▶ L Q T S A D M I L V H G S F D I R C H G W K N W N V R K V I Y Y R
 1001 AATGACCATGCTTTCAACTACAGTTATGAGAGCCCGTCTCCATTAGAGGCCACACTGAATGACAGTGGCACCTACCACTGCAAGGGCTATCTTAGGC
 147▶ N D H A F N Y S Y E S P V S I R E A T L N D S G T Y H C K G Y L R

HindIII (1142)

1101 AGGTGGAAATATGAATCTGACAAATTCAGAAATGCTGTAGTAAAAGCTTACAAATGCAAGTATTATTGGCTACAACAAATTTCCATTGTTGGTGGCGAT
 180▶ Q V E Y E S D K F R I A V V K A Y K C K Y Y W L Q L I F P L L V A I

BbsI (1269)

1201 TCTGTTTGTGTGGACACGGGTTATTGCTCTCAACCGAAGAACAGTTCAAATCAGTCTTGGAGATTGAGAAGACTGGAAAATACAAGAAAGTTGAAACC
 213▶ L F A V D T G L L L S T E E Q F K S V L E I Q K T G K Y K K V E T

MscI (1358)

1301 GAACCTCTAACCTAGATACATATAGGAACAAATGTCATTGCTGAAGAAGCAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACC
 247▶ E L L T •

HpaI (1490)

1401 ACAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

MfeI (1501)
EcoRI (1586)

1501 ACAATTGCATTCATTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATAC
▶

1601 AGCATAGCAAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATT
◀

1701 AGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACCTG

SspI (1825) **SwaI (1839)**

1801 ACCTCCCACATTCCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCA

EcoO109I (1900)
141◀ • N

1901 AGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGT

2001 TCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAAGGAGCATAGTCAGAGAT
 139▶ 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 Y D S I

SacI (2100)
BstXI (2129)

2101 GAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCT
 106▶ 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 D F D K

StuI (2264)

2201 TGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAG
 72▶ 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 I E G T

2301 TCTTGGTCTGATGGCCGCCCGACATGGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGA
 39▶ 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 D Q Q S

BspHI (2414)
 BbsI (2410)
XmnI (2406)

2401 **GATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCG**
 6 I N F T K M

AseI (2472)

2501 **TCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTA**

SacI (2529)

2601 **CGACATTTTGAAAAGTCCCCTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTAT**

SpeI (2627)

2700 **CCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGGAAAGTCCATAAGGTCATGT**

SnaBI (2755)

2800 **ACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTAAGTGGGCAGTTTA**

NdeI (2860)

2900 **CCGTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGGCGGGGTCGTTGGGC**

PstI (3039)
SdaI (3038) **PacI (3046)** **BspLU11I (3056)**

3000 **GGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA**

3098 **AAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT**

3198 **AAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAG**

ApaLI (3370)

3298 **CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGAC**

3398 **CGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGA**

3498 **GGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC**

3598 **CTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAA**

PacI (3786) **Swal (3795)**

3698 **GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACAT**

EagI (3806)
NotI (3805)

3798 **TTAAATCAGCGGCCCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAA**
 3898 **ACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA**