



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGACAGTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTGCCTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BspHI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCATCATGAAGTCTCCGCGGCAGCCCTCGCTGTCATCCTCAT
 601 TGCTACTGCCCTCTGCGCTCCTGCATCTGCCTCCCATATTCCTCGGACACCACACCTGCTGCTTTGCCTACATTGCCCGCCACTGCCCGTGGCCAC
 13▶ A T A L C A P A S A S P Y S S D T T P C C F A Y I A R P L P R A H

XcmI (787)

701 ATCAAGGAGTATTTCTACACCAGTGGCAAGTGCTCAACCCAGCAGTGTCTTTGTACCCGAAAGAACCGCCAAGTGTGTGCCAACCCAGAGAAGAAAT
 47▶ I K E Y F Y T S G K C S N P A V V F V T R K N R Q V C A N P E K K

MscI (867)

801 GGGTTCGGGAGTACATCAACTCTTTGGAGATGAGCTAGGATGGAGAGTCTTGAACCTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTT
 80▶ W V R E Y I N S L E M S •

HpaI (999)

901 GGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAG

MfeI (1010)
EcoRI (1095)

1001 TTAACAACAACAATTGCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATT
 1101 CTAATAACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCA

SapI (1277)

1201 ATGTGCATTAGCTGTTTGACGCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCTTATTTATGTTTTA

SspI (1334)
Swal (1348)

1301 AATGACTGACCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGATCC

EcoO109I (1409)

1401 AGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCT

1501 AGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATA
 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 Y

SacI (1609)
BstXI (1638)

1601 GTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCA
 109▶ 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 D

StuI (1773)

1701 AAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGA
 75▶ 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 I

1801 TCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATC
 42▶ 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 D

BbsI (1919)
XmnI (1915)
AseI (1981)

1901 CTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAAGTATATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGG
 9▶ Q Q S I N F T K M

SacI (2038)

2001 TGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCG

SpeI (2136)

2101 GAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAACTCCATTGACGTCATGGGGTGGAGACTTGGAAATCCCGTGAGTCAA

SnaBI (2264)

2201 ACCGCTATCCAGCCATTGATGTAAGTCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGGAAAGTCCATAA

NdeI (2369)

2301 GGTGATGTAAGTGGGCAATGCCAGGCGGGCCATTTACCGTCAATGAGGCGGCTACTTGGCATATGATACACTTGTGACTGCAAGTGG

2401 GCAGTTTACCGTAAATACTCCACCATTGACGTCATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCATGGGGGGGGT

PacI (2555)

PstI (2548)
SdaI (2547) BspLU11I (2565)

2501 CGTTGGGCGGTCAGCCAGGCGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAA**TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGAAC**

2601 **CGTAAAAAGGCCGCGTTGCTGGCGTTTTCCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG**

2701 **GACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTC**

ApaLI (2879)

2801 **GGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAG**

2901 **CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA**

3001 **GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCC**

3101 **AGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTGCAAGCAGCAGATTACGCGCAGA**

PacI (3295)

3201 **AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAAT**

EagI (3315)

SwaI (3304) NotI (3314)

3301 **TAACATTTAAATCAGCGGCCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTTGGTGAATCGTAACTAACATACGCTCTCCATCAA**

3401 **AACAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA**