



PvuI (7)
SgfI (6)
 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAAGTGGCGCGGGTAAACTGGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) **PvuII (239)** **Bsu36I (291)**
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCGCCCTACCTGAGGGCC
 301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

AgeI (552) **BspLU11I (560)**
 501 TCTGTTCTGCCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTCAACATGTCAACAGACACAGGTGTTCCCTTCCTTCATATGA
 1▶ M S T D T G V S L P S Y E

BstBI (623) **BstAPI (676)**
 601 GGAAGATCAGGGATCAAACCTCATTGAAAAGCTAAAGAGGCACCATTTCGTACCCGTTGGAATAGCGGGTTTTGCAGCAATTGTTGCATATGGATTATAT
 13▶ E D Q G S K L I R K A K E A P F V P V G I A G F A A I V A Y G L Y

SapI (705)
 701 AAAGTGAAGAGCAGGGGAAATACTAAAATGTCATTTCATCTGATCCACATGCGTGTGGCAGCCCAAGGCTTTGTTGTAGGAGCAATGACTGTTGGTATGG
 47▶ K L K S R G N T K M S I H L I H M R V A A Q G F V V G A M T V G M

NheI (844)
EcoRI (817) **Bsu36I (838)** **MseI (850)**
 801 GCTATTCATGTATCGGGAATCTGGGCAAAACCTAAGCCTTAGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACTAG
 80▶ G Y S M Y R E F W A K P K P •

HpaI (982)
 901 AATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGC

EcoRI (1078)
 1001 ATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAATACAGCATAGC
 1101 AAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTTGCCAATGTGCATTAGCTGTTT

SapI (1260)
 1201 GCAGCCTCACCTCTTTTCATGGAGTTTAAAGATAGTGTATTTTCCCAAGTTTGAAGCTAGCTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCCA

SspI (1317) **SwaI (1331)** **EcoO109I (1392)**
 1301 CATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTT
 1401 CATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTG
 141▶ • N R T

SacI (1592)
 1501 TACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTC
 136▶ 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 L E R

BstXI (1621)
 1601 TGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTT
 103▶ 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 Q G N

StuI (1756)
 1701 GCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTC
 70▶ 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 K T

XmnI (1898)
 1801 CTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGA
 36▶ 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 I N F

BbsI (1902) **AseI (1964)**
 1901 AGGTCTTCATGGTGGCCCTCTATAGTGTGATTATACTATGCGGATATACTATGCGGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGC
 3▶ T K M

SacI (2021)
 2001 TATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTT

SpeI (2119)
 2101 TGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCCA

SnaBI (2247)
 2201 TTGATGTACTGCCAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCTACTGGGCAT

2301 AATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATA

2401 CTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCTGTTGGGCGGTGAGCCA

PacI (2538)

PstI (2531)

SdaI (2530)

BspLU11I (2548)

2501 GCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAAITAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTT

2601 GCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAG

2701 GCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTT

ApaLI (2862)

2801 CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACCGCTGCGCCTT

2901 ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC

3001 GGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAA

3101 GAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGA

EagI (3298)

PacI (3278) SwaI (3287) NotI (3297)

3201 AGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCG

3301 GCCGCAATAAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAA

3401 CAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA