



PvuI (7)
SgfI (6)
MfeI (82)

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

AgeI (552) NcoI (560)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCCTCACCGTTGACCCGCTTTCTGTCGCTGAACCT

601 GCTGCTGCTGGGTGAGTCGATTATCCTGGGAGTGGAGAAGCTAAGCCACAGGCACCCGAACCTCCGAATCTTCCAAGAAAATGGACGCCGAACCTGGT

130 ▶ L L L G E S I I L G S G E A K P Q A P E L R I F P K K M D A E L G

SapI (756)

701 CAGAAGTGGACCTGGTATGTGAAGTGTGGGTCGTTTCGCAAGGATGCTCTTGGCTCTCCAGAACTCCAGCTCCAAACTCCCCAGCCACCTTCG

470 ▶ Q K V D L V C E V L G S V S Q G C S W L F Q N S S S K L P Q P T F

EcoRI (849)

801 TTGTCTATATGGCTTCATCCACAACAAGATAACGTGGGACGAGAAGCTGAATTCGTGAACTGTTTTCTGCCATGAGGGACACGAATAATAAGTACGT

800 ▶ V V Y M A S S H N K I T W D E K L N S S K L F S A M R D T N N K Y V

XmnI (909)

901 TCTCACCTGAACAAGTTCAGCAAGGAAAACGAAGGCTACTATTTCTGCTCAGTCATCAGCAACTCGGTGATGTACTTCAGTTCTGTCGTGCCAGTCCTT

1130 ▶ L T L N K F S K E N E G Y Y F C S V I S N S V M Y F S S V V P V L

ApaI (1051)

1001 CAGAAAGTGAACCTACTACTACCAAGCCAGTGTGCGAACTCCCTCACCTGTGCACCTACCGGACATCTCAGCCCGAGACCAGAAGATTGTGCGG

1470 ▶ Q K V N S T T T K P V L R T P S P V H P T G T S Q P Q R P E D C R

1101 CCCGTGGCTCAGTGAAGGGGACCGGATTGGACTTCGCCTGTGATATTTACATCTGGGCACCCCTTGGCCGGAATCTGCGTGGCCCTTCTGCTGCTTGTAT

1800 ▶ P R G S V K G T G L D F A C D I Y I W A P L A G I C V A L L L S L I

1201 CATCACTCTCATCTGCTACCACAGGAGCCGAAAGCGTGTTCGAAATGTCACAGGCCGCTAGTCAGACAGGAAGGCAAGCCAGACCTTCAGAGAAAATT

2130 ▶ I T L I C Y H R S R K R V C K C P R P L V R Q E G K P R P S E K I

MscI (1329)

NheI (1323)

1301 GTGTAAAATGGCACCGCCAGGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTT

2470 ▶ V •

HpaI (1461) MfeI (1472)

1401 TATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTATGTTTCAGGTT

EcoRI (1557)

1501 CAGGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCA

1601 AGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATG

SapI (1739) **SspI (1796)**

1701 GAGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATAGTAAAAATA

SwaI (1810) **EcoO109I (1871)**

1801 TTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGT

1901 AGTTGGACTTAGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGGATGAGTTCC

1410 ▶ • N R T Y K L P I L E

SacI (2071)

2001 TCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGA

1290 ▶ 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 C M G C P S V

BstXI (2100)

2101 CCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGC

960 ▶ 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 S V A S G I A

StuI (2235)

2201 AATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGCATGG

630 ▶ 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 R I A A G V H

BbsI (2381)
XmnI (2377)

2301 TGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCC
 29 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 T K M ←

AseI (2443)

2401 TATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAAC
 SacI (2500) SpeI (2598)

2501 GAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTAC

2601 TAGTCAAACAAACTCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGC
 ←

SnaBI (2726)

2701 ATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGTCAATGTACTGGGCATAATGCCAGGCGGGCCATTAC

NdeI (2831)

2801 CGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGTTTACCGTAAATACTCCACCCATTGACGTCAATG

2901 GAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCTGGTGGCGGTGAGCCAGGCGGGCCATTACCGTAAGT

PacI (3017)

PstI (3010)
SdaI (3009) BspLU11I (3027)

3001 TATGTAACGCCTGCAGGTTAAITAAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCT
 ←

3101 CCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCC

3201 CTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAGGT

ApaLI (3341)

3301 ATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA

3401 GTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAG

3501 TGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCG

3601 GCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC

EagI (3777)
PacI (3757) SmaI (3766) NotI (3776)

3701 GGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTAT

3801 TTTCATTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACATAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGT

3901 CCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA