



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

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555)

KasI (535)
AgeI (552)
NcoI (560)
BsrBI (574)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTTACCTGAGATCACCGGTCACCATGGCTCCCTCGCCGCTCGCGTGGCTGCTGCGCCTGGC

601 CGCGTTCTTCATTTGTGTACTCTGCTGCCGGTCCAGCACCTGGCATGACGAAATGCGAAATCATGTGCGCAAGATGACCTCACGAATCCCAGTGGCT

139▶ A F F H L C T L L P G Q H L G M T K C E I M C D K M T S R I P V A

BstXI (746)

701 TTGTCATCCGCTATCAGCTAAACCAGGAGTCTCGCGCAAGCTGCCATTGTCCTGGAGACGACACAGCAGCAGCGTTCTGTGCTGACCCGAAGGAGA

47▶ L L I R Y Q L N Q E S C G K R A I V L E T T Q H R R F C A D P K E

801 AATGGGTCCAAGACGCCATGAAGCATCTGGATCACCAGGCTGCTGCCCTACTAAAAATGGTGGCAAGTTTGAGAAGCGGGTGGCAATGTGACACCTGG

80▶ K W V Q D A M K H L D H Q A A A L T K N G G K F E K R V D N V T P G

901 GATCACCTTGGCCACTAGGGGACTGTCCCATCTGCCCTGACAAAGCCTGAATCCGCCACATTGGAAGACCTTGTGTTGAACTGACTACTATTTCCAG

113▶ I T L A T R G L S P S A L T K P E S A T L E D L A L E L T T I S Q

NcoI (1013)

BstAPI (1075)

1001 GAGGCCAGGGGACCATGGGACTTCCCAAGAGCCACCGCAGCAGTGACCGGATCATCTCTCAACTTCCGAGGACAGGATGCAGGGCTTACGGCTA

147▶ E A R G T M G T S Q E P P A A V T G S S L S T S E A Q D A G L T A

1101 AGCCTCAGAGCATTGGAAGTTTTGAGGCGGCTGACATCTCCACCACGTTTGGCCGAGTCTGCTGTCTACCAATCTGGATCTAGCTCCTGGGCTGAGGA

180▶ K P Q S I G S F E A A D I S T T V W P S P A V Y Q S G S S S W A E E

Bsu36I (1237)

1201 AAAAGCTACTGAGTCCCCCTCCACTACAGCCCATCTCCTCAGGTGTCCACTACTTCACTTCAACCCAGAGGAAAATGTTGGGTCCGAAGGCCAACCC

213▶ K A T E S P S T T A P S P Q V S T T S P S T P E E N V G S E G Q P

NcoI (1300)

PshAI (1318)

1301 CCATGGGTCCAGGGACAGGACCTCAGTCCAGAGAAGTCTCTAGGGTCTGAGGAGATAAACCCAGTTTACTACTGATAATTTCCAGGAGAGGGGGCTGGCA

247▶ P W V Q G Q D L S P E K S L G S E E I N P V H T D N F Q E R G P G

1401 ACACAGTCCACCCCTCAGTGGCTCCCATCTCCTCTGAAGAGACCCCGCCAGAGCTGGTGGCCTCGGGCAGCCAGGCTCCTAAGATAGAGGAACCCAT

280▶ N T V H P S V A P I S S E E T P S P E L V A S G S Q A P K I E E P I

PstI (1508)

1501 CCATGCCACTGCAGATCCCAGAAACTGAGTGTGCTTATCACTCCTGTCCCCGACACCCAGGCAGCCACAAGGAGGCAGGCAGTGGGGCTACTGGCTTTC

313▶ H A T A D P Q K L S V L I T P V P D T Q A A T R R R Q A V G L L A F

AvrII (1617)

StuI (1689)

1601 CTTGGTCTTCTTTTCTGCTAGGGGTGGCCATGTTTGTACCAGAGCCTTACGGGCTGTCCCGCAAAATGGCGGGGAAATGGTAGAAGGCCTCCGCT

347▶ L G L L F C L G V A M F A Y Q S L Q G C P R K M A G E M V E G L R

NheI (1753)

1701 ACGTCCCCGTAGCTGTGGCAGTAACTCATACGTCCTGGTGCAGTGTGAGCTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAC

380▶ Y V P R S C G S N S Y V L V P V •

HpaI (1891)

1801 CACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAAC

MfeI (1902)
EcoRI (1987)

1901 AACCAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAAATA

2001 CAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCAT

SapI (2169)

2101 TAGCTGTTTGCAGCCTCACCTTCTTTTATGAGTAAAGATATAGTGTATTTCCCAAGTTTGAAGTACTTCTTCTTATGTTTAAATGCAT

SspI (2226)
SwaI (2240)

2201 GACCTCCACATTCCTTTTTAGTAAAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTC

2301 AAGGCCCTTCATAATATCCCCAGTTTGTAGTGTGACTTAGGGAACAAGGAACCTTAAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAG

141▶ •

2401 TTCCTGGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGA

139▶ 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 D S I

SacI (2501) BstXI (2530)
 2501 TGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTT
 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 (2665)
 2601 CTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCA
 73 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

2701 GTCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAG
 39 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 Q Q S

BspHI (2815) XmnI (2807) AseI (2873)
 2801 AGATGTTGAAGGCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGC
 6 I N F T K M

SacI (2930)
 2901 GTCTCCAGCTTATCTGACGGTCTACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTT

SpeI (3028)
 3001 ACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTAT

SnaBI (3156)
 3101 CCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGT

NdeI (3261)
 3201 ACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTA
 3301 CCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGCTGTTGGGC

PacI (3447) PstI (3440) SdaI (3439) BspLU11I (3457)
 3401 GGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAA
 3501 GGCCCGTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA
 3601 AGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCG

ApaLI (3771)
 3701 TGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCG
 3801 CTGCGCTTATCCGTAACATATCGTCTTGTGATCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG
 3901 TATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT
 4001 TCGGAAAAAGAGTTGGTAGTCTTGTATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGG

PacI (4187) SmaI (4196)
 4101 ATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTT

EagI (4207) NotI (4206)
 4201 AAATCAGCGGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAAC
 4301 GAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTCAAGTGCAGGTGCCAGAACATTTCTATCGAA