



PvuI (7)
SgfI (6)
EcoNI (96)

1 GGATCTGCGATCGCTCCGGTCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGTTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCCGGGGTAA

Psp1406I (203)
PvuII (239)

121 ACTGGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTTCGCAACGGGTTTGGCCCGCAACAAC

HindIII (245)
Bsu36I (291)
EcoNI (287)

241 AGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCCGCCATCCAGCCGGTTGAGTCGCGTTCTGCCCTCCCGCTGTGGTGCCTCCTGAACCTG

NgoMIV (441)

361 CGTCCGCCCTAGTAAAGTTAAAGCTCAGGTCGAGACCGGGCTTTGTCCGGCTCCCTTGGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGCTCAAC

BspLU11I (560)

481 TCTACGCTTTTGTTCGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGTCAACATGTATGTGGTTCAGCAGCCACAGCCCTTCTGCT

1 M Y V W V Q Q P T A L L L

XcmI (687)
NcoI (696)

601 GCTGGGACTCACACTGGAGTTACAGCAAGGAGGCTCAACTGTGTTAAACATACCTACCCAGTGGTACAAGTGTGTCGTGAGTGCAGCCAGGCATGGTATGGTGGCCGCTGTGA

13 L G L T L G V T A R R L N C V K H T Y P S G H K C C R E C Q P G H G M V S R C D

BsrGI (799)
BstXI (813)

721 TCATACCAGGATACTCTATGTATCCATGTGAGACTGGCTTCTACAATGAAGCTGTCAATATGATACCTGCAAGCAGTGTACACAGTGAACCATCGAAGTGGAAAGTGAACCTCAAGCA

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

PstI (867)
HindIII (913)

841 GAATTGCACACCTACTCAGGATACTGTCTGAGATGTAGACCAGGCACCCAACTCGGCAGGACAGCGGCTACAAGCTTGGCGTTGACTGTTCCTGCCCTCTGGCCACTTTTCTCC

93 N C T P T Q D T V C R C R P G T Q P R Q D S G Y K L G V D C V P C P P G H F S P

XcmI (1028)
Tth111I (1042)

961 AGGCAACAACCAGGCTGCAAGCCCTGGACCAATTGTACCTTATCTGGAAAGCAGACCCGCCACCCAGCAGTGCAGCTTGGACGAGTCTGTGAGGACAGAAGCCCTCTGGCCACT

133 G N N Q A C K P W T N C T L S G K Q T R H P A S D S L D A V C E D R S L L A T L

Bsp120I (1188)
Bsu36I (1183)

1081 GCTCTGGGAGACCCAGCCCTACATTAGGCAACCACTGTCCAATCCACCACAGTCTGGCCAGGACTTCTGAGTTGCCCTCTCCACCACCTTGGTACTCTGAGGGCCCTGCATT

173 L W E T Q R P T F R P T T V Q S T T V W P R T S E L P S P P T L V T P E G P A F

AvrII (1209)
BspEI (1268)

1201 TGCTGTTCTCCTAGGCTGGCCCTGGCCCTGTGCTCCCTGACTGTCTGTGGCCTTGTACCTGCTCCGGAAGCTTGGAGATTGCCTAACACTCCCAAACCTTGTGGGGAACAG

213 A V L L G L G L G L L A P L T V L L A L Y L L R K A W R L P N T P K P C W G N S

BglII (1373)
NheI (1409)

1321 CTTAGGACCCGATCCAGGAGGAACACAGACGCACACTTACTCTGGCCAAAGATCTGAGCATTAGTACAGGAGTGGATTTTATGGGGCTAGCTGCAGACATGATAAGATACATTG

253 F R T P I Q E E H T D A H F T L A K I •

HpaI (1547)

1441 ATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAGAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAAC

EcoRI (1643)

1561 ATTGCATTCATTTATGTTTCAGTTCAGGGGGAGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACTCC

1681 AAATCAAGCCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTGGCAATGTGCATTAGCTGTTGCAGCCTCACCTCTTTCATGGAGTTAAGATATA

SapI (1825)
SspI (1882)
SwaI (1896)

1801 GTGTATTTCCAAAGTTTGAACCTAGCTCTTCAATTTCTTATGTTTTAAATGCAGTGCCTCCACATTCCTTTTATGAAAATATTAGAAAATATTAAATACATCATTGCAATGAA

1921 AATAAATGTTTTTATTAGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTAGTAGTTGGACTTAGGGAACAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGC

SacI (2157)

2041 GAGCTTCTAGCTTTAGTCTGGTGTACTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAG

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 D S I L

BstXI (2186)

2161 CTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACC

105 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 Q G N S V A S G

2281 AATGGCAATGGCTTACAGCAGACAGTGCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGCTCCTC

65 I A I A E A C V T V R G I Y A E I H V A S I E G T K T R I A A G V H H K N D E

BbsI (2467)
XmnI (2463)

2401 ATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCACTGGTGGCCCTCTATAGTGTGATTATACTACTGCCGATATACT

25 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 (2529)
SacI (2586)

2521 ATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACAGAGCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTGCGTCA

SpeI (2684)

2641 ATGGGGCGGAGTTGTACGACATTTTGGAAAGTCCCGTGTATTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGGAGTCAAACCGCTATCCAC

SnaBI (2812)

2761 GCCCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAGGTCATGACTGGGCATAATGCCAGCGGGCC

NdeI (2917)

2881 ATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTG

PacI (3103)

PstI (3096)

SdaI (3095) BspLU11I (3113)

3001 GCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTG

3121 AGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCTTGTGGCGTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGTGGCGAAA

3241 CCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGC

ApaLI (3427)

3361 GCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTCGCTCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCCTGCGCCTTATCCGGTAACTATCG

3481 TCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA

3601 CGGCTACACTAGAAGAACAGTATTGGTATCTGCCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCCTGGTAGCGGTGTTTTTT

3721 TGTTCGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTGATCTTTCTACGGGCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGC

EagI (3863)

PacI (3843) SmaI (3852) **NotI (3862)**

3841 TAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAA

3961 CAAAACAACTAGCAAATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA