



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560)
BstEII (555)
KasI (535) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCACATGGCCTCTAAATCTTGGCTGAATTTTTAGTCTTCTCT
AgeI (552) 1 M A S K S W L N F L V F L
601 CTGTGGATCAGCAATAGGTTTTTTTTATGTTCTCAACTCTTGGATTTTTGTTGCGAGAAGAGGCTGCCATTACAGCTTACAGCTTCCACAATGACCTT
13 C G S A I G F F L C S Q L L S I L L R E E A A I Q P N M L H N D P

Tth111I (725)
701 CATGCAAGCATTGAGATGACAATGGACACAGTCACTCAAAGGACAGATGAACTTCAATGCAGATTCAGCCAACATAAAGATGAGAACATAGACGTTG
47 H A R H S D D N G H S H L K G Q M N F N A D S S Q H K D E N I D V

XbaI (858) 801 CTGAGAACCTCTATCAGAAAAGTTAAATCTTTGTTGGGTTATGACAAGTCTCAAATCTAGAGAAAAAGGCCAAGCATGTCAAAGCTACGTGGGCCCA
80 A E N L Y Q K V K I L C W V M T S P Q N L E K K A K H V K A T W A Q
901 GCGTTGTAATAAAGTGTATTTATGAGTTCGGAAGAAAATCAAGACTTCCCTACTGTGGGATTGAAAACCAAAGGAGGAGCAACTATATTGAAAA
113 R C N K V L F M S S E E N Q D F P T V G L K T K E G R E Q L Y W K

HindIII (1007) 1001 ACAATTAAGCTTTCCAGTATGTACATGACCATTATTTAGAAGATGCTGACTGGTTTATGAAAGCAGATGACGACACATACGTCATTGTGGACAACCTGA
147 T I K A F Q Y V H D H Y L E D A D W F M K A D D D T Y V I V D N L
BsrGI (1020)
BsrBI (1190)

1101 GATGGCTTCTATCAAAGTATAACCTGAACAACCCATTTACTTTGGCGAAGATTTAAGCCCTATGTGAAGCAGGGATACATGAGCGGAGGAGCGGGCTA
180 R W L L S K Y N P E Q P I Y F G R R F K P Y V K Q G Y M S G G A G Y
NsiI (1235) 1201 TGTCTAAGCAAGGAAGCCTTGAAGATTTGTTAATGATTTAAACAGAAAAGGTGACACATAGTTCTCCATCGAAGACTTAGCTCTGGGAGGTGC
213 V L S K E A L R R F V N A F K T E K C T H S S S I E D L A L G R C
1301 ATGGAAATTATAAATGTAGAAGCTGGAGATTCCAGAGATACCATTGGGAAAGAAACCTTCCATCCATTGTACCAGAACCCTTAATCAAAGTTATC
247 M E I I N V E A G D S R D T I G K E T F H P F V P E H H L I K G Y

XcmI (1402) 1401 TACCAAAAACATTTTGGTACTGGAATTACAACCTATTATCCTCCATAGAGGGTCTGGATGCTGTTCTGATATTGCAGTTTCTTTTCACTATGTTGATGG
280 L P K T F W Y W N Y N Y Y P P I E G P G C C S D I A V S F H Y V D G
EcoO109I (1449)
NdeI (1544) 1501 GACAACCTATGATGAATTAGAATACCTCGTTTATCATCTTCGTCATATGTTTATTTATAGATATCAACCTGCCTTACCTGAGAATATACTGAAAGAA
313 T T M Y E L E Y L V Y H L R P Y G Y L Y R Y Q P A L P E N I L K E
EcoRV (1562)
MscI (1693)

AseI (1600) 1601 ATTAATCAAGTAAACAGAAAGGAAGATACAAAAATAAAATTAGGCAACCCCTGAAAGCAGAACATAAGTGGTCTACATTGCACTGAAGCTAGCTGGCCAG
347 I N Q V N R K E D T K I K L G N P •
NheI (1687)
1701 ACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGT

HpaI (1825) 1801 AACCATTAAGCTGCAATAAACAAAGTTAAACAACAACATTCATTCTTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAA
MfeI (1836)

EcoRI (1921) 1901 AACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAA
2001 GGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAA

SspI (2160) 2101 CTAGCTCTTCATTTCTTTATGTTTTAAATGCAGCTGACCTCCACATTCCTTTTTAGTAAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAA
SwaI (2174)

EcoO109I (2235) 2201 TAAATGTTTTTTATTAGGCGAATCCAGATGCTCAAGGCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAA
2301 ATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTTCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCA
141 • N R T Y K L P I L E E I T T K V L K G N M E
SacI (2435) 2401 ATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGG
117 I L V F C D P A Y 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
BstXI (2464)

2501 GGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTA
 84 H R V A V I T D 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
 2601 GGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTGTCCTCATAGAGCATGGTGATCTTCTCA
 51 A E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E

BspHI (2749)

2701 GTGGGCACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTAT
 17 T A V E V L E L D Q Q S I N F T K M

XmnI (2741)

AseI (2807)

SacI (2864)

2801 GCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCC

SpeI (2962)

2901 TACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCATTGACGTCAATGGGGTG

SnaBI (3090)

3001 GAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATG

NdeI (3195)

3101 TACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATAT

3201 GATACACTTGATGTACTGCCAAGTGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT

PacI (3381)

PstI (3374)

SdaI (3373)

BspLU11I (3391)

3301 CATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAG

3401 CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTTCTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTC

3501 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACC

3601 GGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGG

ApaLI (3705)

3701 GCTGTGTGCACGAACCCCCGTTAGCCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCCGTAAGACACGACTTATCGCCACTGGC

3801 AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA

3901 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG

4001 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTA

EagI (4141)

PacI (4121)

SwaI (4130)

NotI (4140)

4101 AGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAAATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAAT

4201 CGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAAGTGCCAGGTCAGAACATTTCTCTA

4301 TCGAA