



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

MscI (563)
BstEII (555)
AgeI (552) **NcoI (560)**
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCCATGGCCAGGCTGGCGTTGTCTCTGTGCCAGCCACTG
1 M A R L A L S P V P S H W
Acc65I (665)
AgeI (662)
601 GATGGTGGCGTTGCTGCTGCTCAGCAGCTGAGCCAGTACCAGCAGCCAGATCGGAGGACCGGTACCGAATCCCAAAGGTAGTGCTTGTTCGCGG
13 M V A L L L L L S A A E P V P A A R S E D R Y R N P K G S A C S R
701 ATCTGGCAGAGCCACGTTTCATAGCCAGAAACGGGCTTACGCGTAAAATGCACTGCTACATGAACAGCGCCTCCGGCAATGTGAGCTGGCTCTGGA
47 I W Q S P R F I A R K R G F T V K M H C Y M N S A S G N V S W L W
801 AGCAGGAGATGGACGAGAATCCCGAGCAGTGAAGCTGAAAAGGGCCGATGGAAGAGTCCGAGAACGAATCTCTGCCACCCTCACCATCCAAGGCAT
80 K Q E M D E N P Q Q L K L E K G R M E E S Q N E S L A T L T I Q G I
901 CCGTTTTGAGGACAATGGCATCTACTTCTGCGCAGCAGAAGTGCAACAACCTCGAGGTCTACCAGGGCTGCGGCACAGAGCTGCGAGTCATGGGATTC
113 R F E D N G I Y F C Q Q K C N N T S E V Y Q G C G T E L R V M G F

BspHI [m] (1049)
1001 AGCACCTTGGCACAGCTGAAGCAGAGGAACACGCTGAAGGATGGTATCATGATCCAGACGCTGCTGATCATCCTTTCATCATCGTGCCTATCTTCC
147 S T L A Q L K Q R N T L K D G I I M I Q T L L I I L F I I V P I F

EcoO109I (1154)
1101 TGCTGCTGGACAAGGATGACAGCAAGGCTGGCATGGAGGAAGATCACACCTACGAGGGCTGGACATTGACCAGACAGCCACCTATGAGGACATAGTGAC
180 L L L D K D D S K A G M E E D H T Y E G L D I D Q T A T Y E D I V T

MscI (1263)
NheI (1257)
1201 GCTGCGGACAGGGGAAGTGAAGTGGTCTGTAGGTGAGCACCCAGGCCAGGAGTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGAC
213 L R T G E V K W S V G E H P G Q E

HpaI (1395)
1301 AAACCACAAC TAGAATGCAGTGA AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAA

MfeI (1406) **EcoRI (1491)**
1401 CAACAACAATTGCATTCATTTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAA
1501 AATACAGCATAGCAAACTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGT

SapI (1673)
1601 GCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAC TAGCTCTTCATTTCTTTATGTTTTAAATG

SspI (1730) **SwaI (1744)**
1701 CACTGACCTCCCACATTCCTTTTTAGTAAAATATTCAGAAAATTTAAATACATCATTGCAATGAAAATAATGTTTTTTATTAGGCAGAAATCCAGAT

EcoO109I (1805)
1801 GCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCT

1901 TTAGTTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCA
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

SacI (2005) **BstXI (2034)**
2001 GAGATGAGCTCTCGACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGT
107 S I 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

StuI (2169)
2101 CCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTC
74 K 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
2201 CCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGC
41 G 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

BbsI (2315)
XmnI (2311) **AseI (2377)**
 2301 TGAGAGATGTTGAAGGTCCTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGA
 7 Q S I N F T K M

SacI (2434)
 2401 TGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGCTCAATGGGGCGGAGT

SpeI (2532)
 2501 TGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCG

SnaBI (2660)
 2601 CTATCCACGCCCATTTGATGTAAGTCCAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGGAAAGTCCCATAAAGTCC

NdeI (2765)
 2701 ATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAG
 2801 TTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTTCGTT

Pacl (2951)
PstI (2944)
SdaI (2943) **BspLU11I (2961)**
 2901 GGGCGTCCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTA
 3001 AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT
 3101 ATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGA

ApaLI (3275)
 3201 AGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCG
 3301 ACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT
 3401 GAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT
 3501 ACCTTCGAAAAAGAGTTGGTAGCTCTTATCCGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAA

Pacl (3691)
 3601 AAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAAC

EagI (3711)
SwaI (3700) **NotI (3710)**
 3701 ATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACA
 3801 AAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA