



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) PvuII (239) **Bsu36I (291)**
EcoNI (287)
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGGCC
301 GCCATCCACGCGGTTGAGTGCCTGTTGCGCCCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535) **BstEII (555)** **AgeI (552)** NcoI (560) NcoI (596)
501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCACCATGGCATCTACTTCGTATGACTATTGCAGAGTGCCCAT
1 M A S T S Y D Y C R V P M

BbsI (601) **Eco47III (614)** **EcoRI (641)**
601 GGAAGACGGGGATAAGCGCTGTAAGCTTCTGCTGGGATAGGAATTCTGGTGCTCCTGATCATCGTGATTCTGGGGGTGCCCTTGATTATCTTACCATC
13 E D G D K R C K L L L G I G I L V L L I I V I L G V P L I I F T I

StuI (713)
701 AAGGCCAACAGCGAGGCCTGCCGGACGGCCTTCGGGACAGTGGAGTGTGCAATGTACCCATCTCTGCAACAAGAGCTGACCGAGGCCGAGAAGG
47 K A N S E A C R D G L R A V M E C R N V T H L L Q Q E L T E A Q K

DraIII (838)
801 GCTTTCAGGATGTGGAGGCCAGGCCACCTGCAACACACTGTGATGGCCCTAATGGCTTCCCTGGATGCAGAGAAGGCCAAGGACAAAAGAAAGT
80 G F Q D V E A Q A A T C N H T V M A L M A S L D A E K A Q G Q K K V

MluI (947)
901 GGAGGAGCTTGAGGGAGAGATCACTACATTAACCATAAGCTTCCAGGACGCTGTGCAGAGGTGGAGCGACTGAGAAGAGAAAACAGGCTTAAAGCGTG
113 E E L E G E I T T L N H K L Q D A S A E V E R L R R E N Q V L S V

ScaI (1016) **KasI (1053)** **PvuII (1060)** **Eco47III (1087)**
1001 AGAATCGCGGACAAGAAGTACTACCCAGCTCCAGGACTCCAGCTCCGCTGCGGGCGCCAGCTGCTGATTGTGCTGCTGGGCTCAGCGCTCTGCTGC
147 R I A D K K Y Y P S S Q D S S S A A A P Q L L I V L L G L S A L L

BstXI (1109) **NheI (1133)** **MscI (1139)**
1101 AGTGAGATCCCAGGAAGCTGGCACATCTTGAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAA
180 Q •

HpaI (1271) **MfeI (1282)**
1201 AAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCATTTTAT

EcoRI (1367)
1301 GTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACTTTAAC
1401 CTCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGAGCCTCACC

SapI (1549)
1501 TTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTCATTCTTTATGTTTAAATGCACTGACCTCCACATTCCTTTT

SspI (1606) **SwaI (1620)** **EcoO109I (1681)**
1601 TAGTAAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCC
1701 CCAGTTTGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGG
141 • N R T Y K L P

BstXI (1910) **SacI (1881)**
1801 GATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCA
133 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 E R C M G

StuI (2045)
1901 CAGGGGTCACCCTGATGGATCTGCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAG
99 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

XmnI (2187)
2001 ACCCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCG
66 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 T K T R I A A

BbsI (2191)
2101 CCCGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATG
33 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 I N F T K M

AseI (2253)
2201 GTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGG

SacI (2310)
2301 TTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC

2401 **SpeI (2408)**
GTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTG

2501 **SnaBI (2536)**
CCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCC

2601 **NdeI (2641)**
GGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGAGTTTACCGTAAATACTCCACCCATT

2701
GACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATT

2801 **SdaI (2819)** **PacI (2827)** **BspLU11I (2837)**
TACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTT

2901
TCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTCCCC

3001
TGGAAGCTCCCTCGTGCCTCTCTGTCCGACCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCA

3101 **ApaLI (3151)**
CGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACT

3201
ATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGA

3301
GTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC

3401
TCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGA

3501 **EagI (3587)**
PacI (3567) **SwaI (3576)** **NotI (3586)**
TCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAA

3601
ATATCTTTATTTTATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAACTAGCAA

3701
AATAGGCTGTCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA