



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

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555)
AgeI (552)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGGCGCGCGGACGCCATCCTGGATGCGCTGGA
1 M G R A R D A I L D A L E

XcmI (698)
NcoI (698)
SacII (679)
601 GAACCTGACCGCCGAGGAGCTCAAGAAGTTCAAGCTGAAGCTGCTGTCGGTGCCGCTGCGGAGGGCTACGGGCGCATCCCGGGGGCGCGCTGCTGTCC
13 N L T A E E L K K F K L K L L S V P L R E G Y G R I P R G A L L S

SdaI (792)
701 ATGGACGCTTGGACCTCACCGACAAGCTGGTCAGCTTCTACCTGGAGACCTACGGCGCGAGCTCACCGCTAACGTGCTGCGGACATGGGCGCTGCAGG
47 M D A L D L T D K L V S F Y L E T Y G A E L T A N V L R D M G L Q

BstXI (831) **BamHI (857)** **StuI (891)**
801 AGATGGCCGGGACGCTGCAGGCGCCACGACCGAGGCTTGGAGCCGCGCCAGCTGGGATCCAGGCCCTCCTCAGTCGGCAGCCAAGCCAGGCTGCA
80 E M A G Q L Q A A T H Q G S G A A P A G I Q A P P Q S A A K P G L H

NruI (929) **Psp1406I (943)**
901 CTTTATAGACCAGCACCGGCTGCGCTTATCGCGAGGGTCACAAACGTTGAGTGGCTGCTGGATGCTGTGTACGGGAAGTCTGACGGATGAGCAGTAC
113 F I D Q H R A A L I A R V T N V E W L L D A L Y G K V L T D E Q Y

SapI (1044) **XmnI (1041)** **XcmI (1060)**
1001 CAGGCAGTGCGGGCGAGCCACCAACCAAGCATGCGGAAGCTTTCAGTTTACACACCGCCTGGAAGTGGACCTGCAAGGACTTGTCTCTCCAGG
147 Q A V R A E P T N P S K M R K L F S F T P A W N W T C K D L L L Q

Bsu36I (1101) **BsrBI (1138)** **MscI (1182)**
NheI (1176)
1101 CCCTAAGGGAGTCCAGTCTACCTGGTGGAGGACCTGGAGCGGAGCTGAGGCTCCTCCAGCAACACTCCGGTCCGCTAGCTGGCCAGACATGATAAGA
180 A L R E S Q S Y L V E D L E R S •

1201 TACATTGATGAGTTGGACAACCACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAA

HpaI (1314) **MfeI (1325)**
1301 GCTGCAATAAACAAGTTAAACAACAATTCATTTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAA

EcoRI (1410)
1401 ATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCAT

SapI (1592)
1501 CAGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTTTCA

SspI (1649) **SwaI (1663)**
1601 TTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAAATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTT

1701 TATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCA

1801 AGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGGGGGATGAGTTCCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAA
1 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

BstXI (1953)
1901 GCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACA
114 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 H R V

StuI (2088)
2001 GCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGT
80 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 A E I H

2101 GGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCCGACATGGTCTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTC
47 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 T A V E

BbsI (2234)
XmnI (2230) **AseI (2296)**
2201 CACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTA
14 V L E L D Q Q S I N F T K M

2301 ATTGTCAAACAGCGTGGATGGCTCTCCAGCTTACTGACGGTCACTAAACAGACTGCTTATATAGACCTCCACCGTACACGCCCTACCGCCATT

SpeI (2451)
2401 TCGTCAATGGGCGGAGTTGTTACGACATTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAA

2501 ATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGT **SnaBI (2579)**

2601 AGGAAAGTCCATAAAGTCAATGTACTGGGCATAATGCCAGGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGA **NdeI (2684)**

2701 TGTACTGCCAAGTGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACG

2801 TCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAG **SdaI (2862) PacI (2870) BspLU11I (2880)**

2901 CAAAAGGCCAGGAACCGTAAAAAGGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGT

3001 GCGAAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTC

3101 CGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCAC **ApaLI (3194)**

3201 GAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG

3301 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG

3401 CGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAG

3501 CAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACACTCACGTTAAGGGATTTTGG

3601 **EagI (3630)**
NotI (3629)
TCATGGCTAGTTAATTAACATTTAAATC **AGCGGCCGA**ATAAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACA

3701 TACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA