



125

PvuI (7)
SgfI (6) 1 GGATCTGGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82) **EcoNI (96)**
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACACGGCCCGCCGCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGTCTTTGTTTCGTTT

KasI (535) **AgeI (552)** **BstEII (555)**
501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTACCATTGAAACTGATCTCAATTCCCAGGACAGAAAGGACCT
1 M E T D L N S Q D R K D L

XcmI (648)
601 GGACAAGTTTATTAATTTTTGTCCTCAAGACTGTCCAAGTGATTGTCCAGGCTCGGCTTGGTAAAAGATTGCACTGTTTCATCATCTTCTCCAACG
13 D K F I K F F A L K T V Q V I V Q A R L G E K I C T R S S S S P T
701 GGTTCAGATTGGTCAACTTAGCAATCAAAGACATCCCAGAGGTTACACATGAAGCAAAGAAGGCACTGGCAGGACAGCTGCCTGCAGTCGGGAGGTC
47 G S D W F N L A I K D I P E V T H E A K K A L A G Q L P A V G A R S
801 TGTGTGTGGAGATTTACCTAAGACTTCTGAGGGAGATTCCATGGAGCTGAAAATAGGTGTCTTGAATGAATGAAAAGTGTGATAAAGAAATCAAAGT
80 M C V E I S L K T S E G D S M E L E I W C L E M N E K C D K E I K V

BsrGI (911)
901 TTCCTACACGGTGTACAACAGACTGTCATTGCTGCTGAAGTCCCTTCTTGTATAACTAGGGTGACACCAGCCTATAGGCTCTCCAGGAAACAAGGGCAT
113 S Y T V Y N R L S L L L K S L L A I T R V T P A Y R L S R K Q G H
1001 GAATATGTCATATTATACAGGATATATTTGGAGAAGTTCAGCTGAGTGGCTTAGGAGAAGGCTTCCAGACAGTTCGTGTTGGGACAGTGGGACCCCTG
147 E Y V I L Y R I Y F G E V Q L S G L G E G F Q T V R V G T V G T P
1101 TGGGACCATCACCTTTCTTGTGCTTACAGAATTAAGTGGCATTATGCTTACCAGCAATTTGAGAGGACCCACCTATCATGGGATTATTATTGA
180 V G T I T L S C A Y R I N L A F M S T R Q F E R T P P I M G I I I D

DraIII (1201)
1201 TCACCTTTGTGGACCGTCCCTATCCAGCTCCTCTCCATGCACCCCTGCAATTACAGAAGTGTGGTGGAGACTGGAGTAATATACCCGTCTGTAGAA
213 H F V D R P Y P S S S P M H P C N Y R T A G E D T G V I Y P S V E

Asp718I (1377) **Acc65I (1377)** **XcmI (1395)**
1301 GACTCTCAAGAAGTGTGTACCACCTCTTTTTCCACCTCCACCATCCAGCTGATGGTTCCTGGGAAGGAGTGGGGTACCCCTTGTCTCCAAACACG
247 D S Q E V C T T S F S T S P P S Q L M V P G K E G G V P L A P N Q

Asp718I (1408) **Acc65I (1408)**
1401 CTGTCCATGGTACCAGGCTGACAGGAGACTGGCAACCTGCACCCCTTCTGACAGAACCCACTGTGCTGCCACACCTCCAGTAGTGAGGATACTGA
280 P V H G T Q A D Q E R L A T C T P S D R T H C A A T P S S S E D T E
1501 AACCGTATCAAACAGCAGTGAGGGACGGGCTCCCTCAGGATGCTTGGAGACCATCTTTGTCGAAAAGTGGGGGCTTTGTCAACAAACCCATTAAC
313 T V S N S S E G R A S P H D V L E T I F V R K V G A F V N K P I N

BstEII (1602) **BsaBI (1666)**
1601 CAGGTGACCTGACGAGTTTGGATATACCTTTGCCATGTTTGTCCCAAGAATTTGGAGCTGGAGGATACCGATCCAATGGTGAATCCTCCAGATTCCC
347 Q V T L T S L D I P F A M F A P K N L E L E D T D P M V N P P D S
1701 CAGAGACTGAATCTCCTCAGGGCAGCTGCACTCAGATGGCTCCAGCGGGGAGCAGTGGCAATACCCATGATGACTTTGTTATGATAGACTTTAA
380 P E T E S P L Q G S L H S D G S S G S G N T H D D F V M I D F K
1801 ACCAGCTTTTCTAAAGATGACATCTTCCGATGGACCTGGGACCTTCTATCGGGAGTTTTCAGAACCACCTCAGTCAGCAGCCTCCATAGATATT
413 P A F S K D D I L P M D L G C T F Y R E F Q N P P Q L S S L S I D I
1901 GGAGCACAGTCCATGGCTGAAGACTTGGACTCATTACCAGAGAAGCTGGCTGTGCATGAGAAGTGTCCGCGAGTTTGTGCTTTGTGAAACCCCTGC
447 G A Q S M A E D L D S L P E K L A V H E K N V R E F D A F V E T L

MscI (2013) **NheI (2007)**
2001 AGTAAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGT
480 Q •

HpaI (2145) **MfeI (2156)**
2101 GATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGG

EcoRI (2241)
2201 AGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACCTTAACTCCAAATCAAGCCTCTACTTGAATC
2301 CTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTAAGATATAGT

SspI (2480) **SwaI (2494)**
2401 GTATTTTCCCAAGGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAA
2501 ATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAA
2601 CAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTTCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGA
141 • N R T Y K L P I L E E I T T K V

2701 CCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCT
124 L K G N M E 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
2801 GTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAG
91 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 I A I A E A C

2901 ACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTGCTCCTCAT
57 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 G V H H K N D E Y

3001 AGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAGTCGTATT
24 L M T I K E T A V E V L E L D Q Q S I N F T K M

3101 ATACTATGCCGATATACTATGCCGATGATTAATTGTCAA AACAGCGTGGATGGCGTCTCCAGC T TATCTGACGGTCACTAAACGAGCTCTGCTTATATA

3201 GACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACT
3300 CCCATTGACGTCAATGGGTGGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA CTGCAAAAACCGCATCATCATGGTAATA

3400 GCGATGACTAATACGTAGATGTA CTGCAAGTAGGAAAGTCCCATAAAGTCACTGTA CTGCGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAA

3500 TAGGGGGCGTACTTGGCATATGATACACTTGATGTA CTGCAAGTGGGCGAGTTACCGTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGG

3600 CGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGC

3699 AGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGAC

3798 GAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTC

3898 CTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGT

3998 GTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA

4098 AGACAGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACT

4198 ACGGTACTACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCGATTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCAC

4298 CGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCT

4398 CAGTGAACGAAAACCTCACGTAAAGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCT

4498 GTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGAAGT

4598 GCAGGTGCCAGAACATTTCTCTATCGAA