



PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

AgeI (552) **NcoI (568)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGTAGGAGGGCCACCATGGCTGAAGTGAGGGGGTCCAGCGAGTG
1 M A E V R G V Q R V
XmnI (695)

601 CTGTTTGGAGACTGGCTATTGGGGGAGGTGAGCAGCGGCCAGTACGAGGGGCTGCAGTGGCTGAACGAGGCTCGCACAGTCTTCCGCGTACCCTGGAAGC
11 L F G D W L L G E V S S G Q Y E G L Q W L N E A R T V F R V P W K

BglII (736) **DraIII (775)** **HpaI (786)**
701 ATTTCCGTCGTAGGGATCTGGATGAAGAAGATGCACAGATCTTCAAGGCTGGCTGTGGCCCGAGGGAGGTGCCACCTAGTGGAGTTAACCTGCCACC
44 H F G R R D L D E E D A Q I F K A W A V A R G R W P P S G V N L P P

ApaLI (859)
801 CCCAGAGGCTGAGGCTGCTGAGCGAAGAGAGCGAAGAGGCTGGAAGACCAACTCCGCTGTGCACTCCACAGCACAGGGCGTTTTATCTTGCGCCAAGAC
77 P E A E A A E R R E R R G W K T N F R C A L H S T G R F I L R Q D

BamHI (908) **Bsp120I (965)**
901 AATTCAGGGGATCCAGTTGATCCGATAAGGTGTACGAACTTAGCCGGGAGCTTGATCTACTGTGGCCAGCCACGGAAAATAGGGAAGAAGTGAGCC
111 N S G D P V D P H K V Y E L S R E L G S T V G P A T E N R E E V S

DraIII (1018)
1001 TCAGCAATGCTCTGCCACACAGGGTGTGTCGCCAGGATCATTCTGGCAAGAGAAAATGCTGGGCTCCAAACCCCAAGCCCTCTGCTTTCTAGTGATGC
144 L S N A L P T Q G V S P G S F L A R E N A G L Q T P S P L L S S D A

Tth111I (1161)
1101 CGGGGACCTCTTGCTTACAGTCTGTCAGTACAGCCACATACTGGAATCCGAGTCTGGGGCAGACCCCGTCCACCACAGGCTCCTGGCCAGGAGCAAGAC
177 G D L L L Q V L Q Y S H I L E S E S G A D P V P P Q A P G Q E Q D

1201 CGTGTTCAGGAAACCCATGACAGCATGGCAGGTGGAAGCTGTCCCCAGTCCAGGCCCTCAACAGCCAGCTCTCACCAGGCGCAGCCTTGGGTTCTGG
211 R V Y E E P Y A A W Q V E A V P S P R P Q Q P A L T E R S L G F L

BsrGI (1312) **BsrGI (1369)** **NcoI (1378)**
1301 ATGTGACCATCATGTACAAGGCCGCACAGTGTACTAGGCAGTGGTGGGGCACCCAGATGCGTGTTCCTGTACAGCCCCATGGCCAGCAGTAAGAAC
244 D V T I M Y K G R T V L Q A V V G H P R C V F L Y S P M A P A V R T

1401 TTCAGAGCCCCAGCCGGTATCTTCCAGTCCCTGCTGAGCTCCAGATCAGAAGCAGCTGCACTACACAGAGACGCTTCTCCAGCATGTGTCTCCCGC
277 S E P Q P V I F P S P A E L P D Q K Q L H Y T E T L L Q H V S P G

Bsp120I (1531)
1501 CTTAGCTGGAGCTTCGAGGACCGTCACTGTGGGCCCTGCGTATGGGCAAGTGC AAGGTGACTGGGAGGTAGGCAGCCCTATGGGCACTACCGGCCCT
311 L Q L E L R G P S L W A L R M G K C K V Y W E V G S P M G T T G P

1601 CCACCCACCCAGCTGTGGAGCGCAACCGCCACACCCCATCTTCACTTACGACTTTCTCCGAGAAGTGGAGGAGTTTCGGGCTCGGAGCGCGCA
344 S T P P Q L L E R N R H T P I F D F S T F F R E L E E F R A R R Q

BstEII (1702) **BstXI (1717)** **NcoI (1794)**
1701 AGGGTCACACACTACACCATCTACCTGGGTTTTGGGCAAGACTTGTGACGAGGGAGGCCAAGGAGAAGACCCTGATCCTGGTGAAGCTGGAGCCATGG
377 G S P H Y T I Y L G F G Q D L S A G R P K E K T L I L V K L E P W

1801 GTATGCAAGGCATACCTGGAGGGCGTGCAGCGTGGGTTGTCTCCCTGGACAGCAGCAGTCTCGGCTTGTCTGTAGCACCAACAGTCTCTACG
411 V C K A Y L E G V Q R E G V S S L D S S S L G L C L S S T N S L Y

PshAI (1923) **NheI (1975)**
1901 AAGACATCGAACCTTCTCATGGACCTGGGTGAGTGGCCTTGTACTCAGAATCCCACTCCCAATAAATAGTTAGCTAGCTGGCCAGACATGATAAGAT
444 E D I E H F L M D L G Q W P •

2001 ACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAG

HpaI (2113) **MfeI (2124)**
2101 CTGCAATAAACAAGTTAAACAACAACATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAA

EcoRI (2209)
2201 TGTGGTATGGAATTCTAAATAACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGCATAGGCATC

SapI (2391)
2301 AGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTTCCCAAGGTTTGAAC TAGCTCTTCAT

SspI (2448) **SwaI (2462)**
2401 TTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAAATGTTTTTT

2501 ATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAA

2601 GAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAG
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

2701 CAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAG
113 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 A
2801 CCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTG
80 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
2901 GACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCC
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

BstXI (2752)

3001 ACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATACTATGCCGATGATTA
13 V L E L D Q Q S I N F T K M
3101 TTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATT

XmnI (3029) AseI (3095)

3201 GCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTGATTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAA
SpeI (3250)

3301 TCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTA
SnaBI (3378)

3401 GGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGAT
NdeI (3483)

3501 GTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGT

PacI (3669)

3601 CAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGC
SdaI (3661) BspLU11I (3679)

3701 AAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGCGCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG
BspLU11I (3679)

3801 GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCC

ApaLI (3993)

3901 GCCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCAAGCTGGGCTGTGTGCAGC
ApaLI (3993)

4001 AACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG
ApaLI (3993)

4101 TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAGTATTTGGTATCTGC
ApaLI (3993)

4201 GCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGTGCAAGCAGC
ApaLI (3993)

4301 AGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGTCTGACGCTCAGTGAACGAAAACTCACGTTAAGGGATTTTGGT
EagI (4429)

4401 CATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACAT
PacI (4409) SmaI (4418) NotI (4428)

4501 ACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA