



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

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCC
HindIII (245)
Bsu36I (291)
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

NgoMIV (441)
501 TCTGTTCTGCGCGCTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTGAGCATGCAACCAGACATGTCTTGAATGTATTAAAGATGAA
AgeI (552) **SphI (560)** **BspLU11I (572)**
1► M Q P D M S L N V I K M K

XcmI (602)
601 ATCCAGTGACTTCTGGAGAGTGCAGAAGTGGACAGCGGAGGCTTTGGGAAGGTGTCTGTGTTCACAGAACCCAGGACTCATGATCATGAAAAA
13► S S D F L E S A E L D S G G F G K V S L C F H R T Q G L M I M K T

Bsp120I (709)
BsrGI (701)
701 GTGTACAAGGGGCCAACTGCATTGAGCACAACGAGGCCCTCTGGAGAGGCGAAGATGATGAACAGACTGAGACACAGCCGGTGGTGAAGCTCCTGG
47► V Y K G P N C I E H N E A L L E E A K M M N R L R H S R V V K L L

BbrPI (865)
801 GCGTCATCATAGAGGAAGGAAGTACTCCCTGGTGATGGAGTACATGGAGAAGGGCAACCTGATGCACGTGCTGAAAGCCGAGATGAGTACTCCGCTTTC
80► G V I I E E G K Y S L V M E Y M E K G N L M H V L K A E M S T P L S
901 TGTAAGGAAGGATAATTTGGAAATCATTGAAGGAATGTGCTACTTACATGAAAAAGCGTGATACACAAGGACCTGAAGCCTGAAAAATCCTTGT
113► V K G R I I L E I I E G M C Y L H G K G V I H K D L K P E N I L V
1001 GATAATGACTTCCACATTAAGATCGCAGACCTCGGCCCTGGCCTCTTAAGATGTGGAGCAAAGTGAATAATGAAGAGCACAATGAGCTGAGGGAAGTGG
147► D N D F H I K I A D L G L A S F K M W S K L N N E E H N E L R E V

BsrGI (1193)
1101 ACGGCACCCTAAGAAGAAATGGCGGCACCTCTACTACATGGCGCCGAGCACCTGAATGACGTCAACGCAAAGCCACAGAGAAGTCGGATGTGTACAG
180► D G T A K K N G G T L Y Y M A P E H L N D V N A K P T E K S D V Y S
1201 CTTTGTGTAGTACTCTGGCGATATTTGCAAATAAGGAGCCATATGAAAATGCTATCTGTGAGCAGCAGTTGATAATGTGCATAAAATCTGGGAACAGG
213► F A V V L W A I F A N K E P Y E N A I C E Q Q L I M C I K S G N R

BspEI (1374) **EagI (1384)**
1301 CCAGATGTGGATGACATCACTGAGTACTGCCAAGAGAAATTATCAGTCTCATGAAGCTCTGTGGGAAGCGAATCCGGGAAGCTCGGCCGACATTTCTGT
247► P D V D D I T E Y C P R E I I S L M K L C W E A N P E A R P T F P

StuI (1417)
1401 GCATTGAAGAAAAATTTAGGCCCTTTTATTTAAGTCAATTAGAAGAAAGTGTAGAAGAGGACGTGAAGAGTTTAAAGAAAGAGTATTCAAACGAAAATGC
280► G I E E K F R P F Y L S Q L E E S V E E D V K S L K K E Y S N E N A
1501 AGTTGTGAAGAGAATGCAGTCTCTTCACTTGTGTGGCAGTACCTTCAAGCCGGTCAAATTCAGCCACAGAACAGCCTGGTTCAGTGCACAGTTCC
313► V V K R M Q S L Q L D C V A V P S S R S N S A T E Q P G S L H S S

PstI (1681)
1601 CAGGGACTTGGGATGGGTCTGTGGAGGAGTCTGGTTTGTCTCTTCCCTGGAGCACCAAGAAGAGAATGAGCCAGCCTGCAGAGTAACTCCAAG
347► Q G L G M G P V E E S W F A P S L E H P Q E E N E P S L Q S K L Q

XcmI (1757)
1701 ACGAAGCCAACCTACCATCTTTATGGCAGCCGATGGACAGGACAGCAAAACAGCAGCCAGACAGAATGTGGCTTACAACAGAGAGGAGGAAAGGAGACG
380► D E A N Y H L Y G S R M D R Q T K Q Q P R Q N V A Y N R E E E R R R
1801 CAGGGTCTCCCATGACCTTTTGCACAGCAAAGACCTTACGAGAATTTTCCAGAATACAGAGGGAAAAGGCACTGCTTATTCCAGTGCAGCCAGTCATGGT
413► R V S H D P F A Q Q R P Y E N F Q N T E G K G T A Y S S A A S H G

ApaLI (1906) **Bsu36I (1916)** **BamHI (1998)**
1901 AATGCAGTGCACCAGCCCTCAGGGCTCACCAGCCAACCTCAAGTACTGTATCAGAACAATGGATTATATAGCTCACATGGCTTTGGAACAAGACCACTGG
447► N A V H Q P S G L T S Q P Q V L Y Q N N G L Y S S H G F G T R P L
2001 ATCCAGGAACAGCAGGTCAGAGTTTGGTACAGGCAATTCAGTCAATATGCCTAGTCTGCATAATATCCAGTGCCTGAGACCAACTATCTAGGAAA
480► D P G T A G P R V W Y R P I P S H M P S L H N I P V P E T N Y L G N
2101 TACACCCACCATGCCATTCAGTCTTCCACCAACAGATGAATCTATAAAATATACCATATAACAATAGTACTGGCATTGAGATTGGAGCCTACAATTAT
513► T P T M P F S S L P P T D E S I K Y T I Y N S T G I Q I G A Y N Y

SpeI (2299)
2201 ATGGAGATTGGTGGGACGAGTTCATCACTACTAGACAGCACAATAACGAATTCAAAGAAGAGCCAGCTGCTAAGTACCAAGCTATCTTTGATAATACCA
547► M E I G G T S S S L L D S T N T N F K E E P A A K Y Q A I F D N T
2301 CTAGTCTGACGGATAAACACCTGGACCAATCAGGGAAAATCTGGGAAAGCACTGGAAAACTGTGCCGTAAGTGGGCTTACACAGTCTCAGATTGA
580► T S L T D K H L D P I R E N L L G K H W K N C A R K L G F T Q S Q I D
2401 TGAAATGACCATGACTATGAGCAGATGGACTGAAAGAAAAGTTTACCAGATGCTCAAAAGTGGGTGATGAGGGAAGGCATAAAGGAGCAGCAGGTG
613► E I D H D Y E R D G L K E K V Y Q M L Q K W V M R E G I K G A T V
2501 GGGAAAGCTGGCCAGGCGCTCCACAGTGTCCAGGATCGACCTTCTGAGCAGCTTATTTACGTCAGCCAGAATAACCCTGGATGGGCTACGGCAGCT
647► G K L A Q A L H Q C S R I D L L S S L I Y V S Q N •

MscI (2624)
NheI (2618)

2601 GAAGTGGACGCCTCACTTGTAGCTGGCCAGACATGATAAGATAACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTT

HpaI (2756) MfeI (2767)

2701 GTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAATTGCATTCATTTTATGTTTCAGGTTCCAGGG

EcoRI (2852)

2801 GGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCT

2901 CTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTTCATGGAGTT

SspI (3091)

3001 TAAGATATAGTGATTTTTCCAAGGTTTGAAGTACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCCTTTTGTAGTAAAATATTCAG

SwaI (3105)

3101 AAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTG

3201 GACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAAT

SacI (3366)

3301 GGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACC

128 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 C P S V V

3401 CTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGG

94 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 G I A I A

StuI (3530)

3501 CTTGAGCAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTT

61 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 G V H H K

BbsI (3676)
XmnI (3672)

3601 GTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGCTTCATGGTGGCCCTCTATAG

28 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 (3738) **SacI (3795)**

3701 TGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCTACTAACAGAGCT

SpeI (3893)

3801 CTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCT

3901 AAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGTATCCACGCCATTGATGTAAGTCCAAAACCGCATCAT

SnaBI (4021)

4001 CATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCA

4101 TTGACGTCAATAGGGGGCTACTTGGCATATGATACTTGTACTGACTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAG

4201 TCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGT

PacI (4312)
PstI (4305)
SdaI (4304) **BspLU11I (4322)**

4301 AACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCC

4401 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGT

4501 GCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACTGTCCGCTTTCTCCCTTCCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTC

ApaLI (4636)

4601 AGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGACGAAACCCCGTTCAGCCCAGCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCA

4701 ACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTG

4801 GCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA

4901 CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGT

EagI (5072)
PacI (5052) SwaI (5061) NotI (5071)

5001 CTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAAATATCTTTATTTTCA

5101 TTACATCTGTGTGTTGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCA

5201 GTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA