



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAGGCC
HindIII (245)
301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

SphI (560)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACAGATGCAGAGCACAGCAATTACCTGTGGCACACAGATGA
AgeI (552) 1► M Q S T A N Y L W H T D D
BsrGI (629) 601 CCTGTGGGCGAGGGGCCACTGCCAGTGTGTACAAGGCCGCAACAAGAAATCCGGAGAGCTGGTTGCTGTGAAGGCTTCAACACTACCAGCTACCTG
13► L L G Q G A T A S V Y K A R N K K S G E L V A V K V F N T T S Y L
BspEI (652) 701 CGGCCCGCAGGTTGAGTGTGAGGGAGTTGAGTCTCGGGAAGCTGAACCACCAGAATCATGTCAAGCTCTTTCGGTGGAGGAGACGGGCGGAAGCC
47► R P R E V Q V R E F E V L R K L N H Q N I V K L F A V E E T G G S
XmnI (672)
801 GGCAGAAGTACTGGTGTGAGTACTGCTCCAGTGGGAGCCTGCTGAGTGTGCTGGAGAGCCCTGAGAATGCCTTTGGGCTGCTGAGGATGAGTTCCT
80► R Q K V L V M E Y C S S G S L L S V L E S P E N A F G L P E D E F L
NruI (960)
901 GGTGGTGTGCGTGTGTGGTGGCCGGCATGAACCACCTGCGGAGAACGGCATTGTGCATCGCGACATCAAGCCGGGAACATCATGCGCCTCGTAGGG
113► V V L R C V V A G M N H L R E N G I V H R D I K P G N I M R L V G
XmaI (1043)
1001 GAGGAGGGCAGAGCATCTACAAGCTGACAGACTTCGGCGCTGCCGGAGCTGGATGATGATGAGAAGTTCGCTCGGTCTATGGGACTGAGGAGTACC
147► E E G Q S I Y K L T D F G A A R E L D D D E K F V S V Y G T E E Y

BsrBI (1117) 1101 TGCATCCCCGACATGTATGAGCGGGCGGTTCGAAAGCCCCAGCAAAAAGCGTTTGGGGTGACTGTGGATCTCTGGAGCATTGGAGTGACCTTGATCCA
BspLU11I (1109) 180► L H P D M Y E R A V L R K P Q Q K A F G V T V D L W S I G V T L Y H
BstBI (1130) 1201 TGCAGCCACTGGCAGCCTGCCCTTCATCCCTTTGGTGGGCCACGGCGGAACAAGGAGATCATGTACCGGATCACACGGAGAAGCCGGCTGGGGCATT
213► A A T G S L P F I P F G G P R R N K E I M Y R I T T E K P A G A I
Bsp120I (1324)
1301 GCAGGTGCCAGAGGGGAGAACGGGCCCTGGAGTGGAGCTACACCCTCCCATCACCTGCCAGCTGCTACTGGGGCTGCAGAGCCAGCTGGTGCCCA
247► A G A Q R R E N G P L E W S Y T L P I T C Q L S L G L Q S Q L V P
BstXI (1406)
1401 TCCTGGCCAAACATCTGGAGGTGGAGCAGGCCAAGTGTGGGGCTTCGACCAGTTCTTTCGGGAGACCAGTGACATCCTGCAGCGAGTTGTCGTCATGT
MscI (1403) 280► I L A N I L E V E Q A K C W G F D Q F F A E T S D I L Q R V V V H V
1501 CTTCTCCCTGTCCAGGCACTGTCACACATCTATATCCATGCCACAAACACGATAGCCATTTTCCAGGAGCCGTGCACAAGCAGACCAGTGTGGCC
313► F S L S Q A V L H H I Y I H A H N T I A I F Q E A V H K Q T S V A
BstEII (1627) 1601 CCCCAGACACCAGGAGTACCTCTTTGAGGGTACCTCTGTCTCGAGCCAGCGTCTCAGCACAGCACATCGCCACACGACGGCAAGCAGCCCTGA
347► P R H Q E Y L F E G H L C V L E P S V S A Q H I A H T T A S S P L
XhoI (1642)
SandI (1739)
1701 CCCTCTCAGCACAGCCATCCCTAAGGGGTGGCCTTCAGGGACCCTGCTCTGGACGTCCCAAGTTCGTCGCCAAAGTGACCTGCAGCGGATTACAA
380► T L F S T A I P K G L A F R D P A L D V P K F V P K V D L Q A D Y N

XcmI (1805) 1801 CACTGCCAAGGGCTGTTGGGCGCCGGTACCAGGCCCTGCGGCTGGCACGGGCCCTGCTGGATGGGAGGAGCTAATGTTTCGGGGCTGCACTGGGTC
413► T A K G V L G A G Y Q A L R L A R A L L D G Q E L M F R G L H W V
Bsp120I (1850) 1901 ATGGAGGTGCTCCAGGCCACATGCAGACGGACTCTGAAAGTGGCAAGGACATCCCTCCTACCTCAGCAGCAGCCTGGAACTGAGAGGTTACGACGG
447► M E V L Q A T C R R T L E V A R T G S S L L Y L S S S L G T E R F S S
2001 TGGCTGGAAGCCTGAGATCCAGGAAGTGAAGCGGCTGCAGAACTGAGTCCAGGCTGCGGACTCTAGCGGAGTCTCCTCAGATGCTCCAAAATAT
480► V A G T P E I Q E L K A A A E L R S R L R T L A E V L S R C S Q N I
2101 CACGGAGACCCAGGAGAGCTGAGCAGCTGAACCGGGAGCTGGTGAAGAGCCGGATCAGGTACATGAGGACAGAAGCATCCAGCAGATTCAAGTGTGT
513► T E T Q E S L S S L N R E L V K S R D Q V H E D R S I Q Q I Q C C
2201 TTGGACAAGATGAACCTCATCAAAACAGTTCAAGAAGTCTAGGATGAGGCGGGCTGGCTATAACGAGGAGCAGATTCAAAAGCTGGATAAGGTGA
547► L D K M N F I Y K Q F K K S R M R P G L G Y N E E Q I H K L D K V
2301 ATTCAGTCATTTAGCCAAAAGACTCCTGCAGGTGTTCCAGGAGGAGTGCCTGCAGAAGTATCAAGCGTCTTGTAGTACACACAGGCAAGAGGATGAGGGT
580► N F S H L A K R L L Q V F Q E E C V Q K Y Q A S L V T H G K R M R V
2401 GGTGCACGAGACCAGGAACACCTGCGCCTGGTTGGCTGTTCTGTGGCTGCCTGTAACACAGAAGCCAGGGGTCCAGGAGAGTCTCAGCAAGCTCCTG
613► V H E T R N H L R L V G C S V A A C N T E A Q G V Q E S L S K L L
StuI (2546)
2501 GAAGAGCTATCTACCAGCTCCTCAGGACCGAGCAAAGGGGGCTCAGGCCTCGCCGCTCCCATAGCTCCTTACCCAGCCCTACACGAAAGGACCTGC
647► E E L S H Q L L Q D R A K G A Q A S P P P I A P Y P S P T R K D L
2601 TTCTCCACATGCAAGAGCTGTCGAGGGGATGAAGCTGCTGGCATCTGACCTCCTGGACAACAACCGCATCATCGAACGGCTAAATAGAGTCCCAGCACC
680► L L H M Q E L C E G M K L L A S D L L D N N R I I E R L N R V P A P

MscI (2726)

2701 TCCTGATGTCTGAGCTCCATGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACACTAGAATGCAGTGAAAAAATGCTTTAT
713▶ P D V •

HpaI (2858) MfeI (2869)

2801 TTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAG

EcoRI (2954)

2901 GGGGAGGTGTGGGAGTTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGC

3001 CTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAG

SspI (3193)

3101 TTTAAGATATAGTGATTTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAATATTC

SwaI (3207)

3201 AGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGT

3301 TGGACTTAGGGAACAAAGGAACCTTTAATAGAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCA
141▶ • N R T Y K L P I L E E

BstXI (3497)

3401 ATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCA
128▶ 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 C P S V V

3501 CCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAAT
95▶ 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

StuI (3632)

3601 GGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTGGTCTGATGGCCGCCCGACATGGTGC
62▶ 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 G V H H

XmnI (3774)

3701 TTGTTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTAT
28▶ 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 (3840)

3801 AGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAG

SpeI (3995)

3901 CTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTTGATTTACTAG
4001 TCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGACTGCCAAAACCGCATC

SnaBI (4123)

4101 ATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGACTGGGCATAATGCCAGGCGGGCATTACCGT

NdeI (4228)

4201 CATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAA

4301 AGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTGGGCGGTGAGCCAGGCGGGCATTACCGTAAAGTTAT

PacI (4414) BspLU11I (4424)

4401 GTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCG
4501 CCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACAGGCGTTTTCCCTGGAAGCTCCCTC
4601 GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATC
4701 TCAGTTCCGGTGTAGTTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTC
4801 CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGG
4901 TGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCA
5001 AACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG

EagI (5174)

5101 GTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTT
5201 CATTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCC
5301 CAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA