



100

PvuI (7)
SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) HindIII (245) **Bsu36I (291)**
PvuII (239) EcoNI (287)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGGCC
301 GCCATCCACGCGGTTGAGTGCAGTTCGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NcoI (560)
BstEII (555)
AgeI (552)
KasI (535)
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGACGCAGCTACTCTGACCTACGACTCTCCGGTT
1 M D A A T L T Y D T L R F

XmnI (610) **BglIII (683)**
601 TGCTGAGTTTGAAGATTTTCTGAGACCTCAGAGCCGTTGGATACTGGGTAGAAAATACAGCATTTTACAGAAAAGACGAGATCTTGCTGATGTG
13 A E F E D F P E T S E P V W I L G R K Y S I F T E K D E I L S D V
XbaI (703) **SphI (782)**
701 GCATCTAGACTTTGGTTTACATACAGAAAACTTTCCAGCCATTGGGGGACAGGCCACCTCGGACACAGGCTGGGGCTGCATGCTGCGGTGTGGAC
47 A S R L W F T Y R K N F P A I G G T G P T S D T G W G C M L R C G

NcoI (827)
AvrII (834)
801 AGATGATCTTTGCCAAGCCTGGTGTGCCGGCACCTAGGCCGAGATTGGAGTGGACACAAAGGAAGAGGCAGCAGACTACTTCCAGCGTCTCAA
80 Q M I F A Q A L V C R H L G R D W R W T Q R K R Q P D S Y F S V L N

Bsp120I (991)
901 CGCATTTCGACAGGAAGGACAGTTACTACTCCATTCCAGATAGCGCAAATGGGAGTTGGCGAAGGCAAGTCCATAGGCCAGTGGTACGGGCCAAC
113 A F I D R K D S Y Y S I H Q I A Q M G V G E G K S I G Q W Y G P N

HindIII (1021)
1001 ACTGTCGCCAGGTCTGAGAAGCTTGTCTTTCGATACGTGGAGCTCCTTGGCGGTCACATTGCAATGGACAACACTGTTGTGATGGAGGAAATCA
147 T V A Q V L K K L A V F D T W S S L A V H I A M D N T V V M E E I

KasI (1132) **BstEII (1194)**
1101 GAAGTTGTGAGGACAGCGTTCCCTGTGCAAGCGCCACTGCGTTTCTGCAAGTCCGACCGGCACTGCAACCGATTCCCTGCCGGAGCTGAGGTCAC
180 R R L C R T S V P C A G A T A F P A D S D R H C N G F P A G A E V T

NcoI (1213) **StuI (1271)**
1201 CAACAGGCCGTCGCATGGAGACCCCTGGTACTTCTCATTCCCTGCGCTGGGGCTCACGGACATCAACGAGGCTACGTGGAGACGCTGAAGCACTGC
213 N R P S P W R P L V L L I P L R L G L T D I N E A Y V E T L K H C

BspHI (1301)
1301 TTCATGATGCCCCAGTCCCTGGGCGTCATCGGAGGGAAGCCAAACAGCGCCACTACTTCATCGGCTACGTTGGTGGAGGCTCATCTACCTGGACCCCC
247 F M M P Q S L G V I G G K P N S A H Y F I G Y V G E E L I Y L D P
1401 ACACCACGACGACCGCTGGAGCCACTGATGGCTGCTTCCCGGACGAGGCTTCCACTGCCAGCACCCGCGTGGCGCATGAGCATCGCGGAGCT
280 H T T Q P A V E P T D G C F I P D E S F H C Q H P P C R M S I A E L

BstXI (1508)
1501 TGACCCGTCATGCTGTGGGTTTTCTGTAAGACTGAAGATGACTTCAATGATTGGTGCCAGCAAGTCAAAAAGCTGTCTGCTTGGAGGTGCCCTG
313 D P S I A V G F F C K T E D D F N D W C Q Q V K K L S L L G G A L

XcmI (1601)
1601 CCCATGTTGAGCTGGTGGAGCAAGCAGCCTTCCATCTGGCCTGCCCGACGCTCCTGAACCTGTCCCTAGATTCTTCTGATGTAGAGCGACTGAAAAGAT
347 P M F E L V E Q Q P S H L A C P D V L N L S L D S S D V E R L E R

MscI (1759) **NheI (1753)**
1701 TCTTCGACTCAGAAGATGAAGACTTTGAAATCCTGTCCCTTTGAAAATCCTGGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAC
380 F F D S E D E D F E I L S L •

HpaI (1891)
1801 CACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAAC

MfeI (1902) **EcoRI (1987)**
1901 AACCAATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATA
2001 CAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCAT
2101 TAGCTGTTTGCAGCCTCACCTTCTTTCATGAGTAAAGATATAGTGTATTTTCCCAAGGTTTGAAGTACTGCTTCTCATTCTTTATGTTTTAAATGCACT

SspI (2226) **SwaI (2240)**
2201 GACCTCCCACATTCCTTTTATGTAATAATTCAGAAAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTC
2301 AAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTAAATAGAAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAG
141 •

2401 TTCCTGGTACTTGGAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCATTCACTCAATGAGCAAAAGCAGTCAGGAGCATAGTCAGAGA
139 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 C D P A Y D S I

BstXI (2530)

2501 TGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCTT
106 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 V I T D F D K

StuI (2665)

2601 CTGCCCCTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCA
73 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 V A S I I E G

2701 GTCTTGGTCTGATGGCCGCCGACATGGTGTCTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAG
39 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 V L E L D Q Q S

BspHI (2815)

XmnI (2807) AseI (2873)

2801 AGATGTTGAAGGTCCTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGC
6 I N F T K M

2901 GTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTCGTCATGCGGCGGAGTTGTT

SpeI (3028)

3001 ACGACATTTTGGAAAGTCCCCTTGTATTACTAGTCAAAACAACTCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTA

SnaBI (3156)

3100 TCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATG

NdeI (3261)

3200 TACTGGGCATAATGCCAGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGCCATATGATACACTTGTACTGCCAAGTGGGCAGTTT

3300 ACCGTAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGTCTGGG

SdaI (3439) PacI (3447) BspLU11I (3457)

3400 CGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAA
6 I N F T K M

3498 AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTA

3598 TAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAA

ApaLI (3771)

3698 GCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGA
3798 CCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG
3898 AGGTATGTAGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA
3998 CCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTCAAGCAGCAGATTACGCGCAGAAAAAA

PacI (4187) SwaI (4196)

4098 AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACA

EagI (4207)
NotI (4206)

4198 TTTAAATC AGCGGCCGAATAAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAA
4298 AACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA