



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGTGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)** **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACC

NgoMIV (441) **NaeI (441)**
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

KasI (535) **AgeI (552)** **NcoI (560)** **NotI (586)**
BsrBI (584) **BsrBI (579)** **EagI (587)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCCACATGGAGTCCGAATCGGAGAGCGGAGCGCCGCTGACAC
1 M E S E S E S G A A A D T
BamHI (660)

601 CCCGCTCTGGAGACTCTGAGCTTTCACGGAGATGAAGAGATCATTGAGGTGGTAGAGCTGGATCCAGGCCCGCCGGACCCGGATGATCTGGCCAGGAG
13 P P L E T L S F H G D E E I I E V V E L D P G P P D P D D L A Q E
701 ATGGAAGACGTGGACTTTGAGGAAGAGGAAGAAGAAGAGGGCAATGACGAGGGCTGGTCTTGAACCCAGGAAGGGTGGTGGTAGCATGGAGG
47 M E D V D F E E E E E E E G N D E G W V L E P Q E G V G S M E
801 GCCCGATGATAGTGAAGTACCTTTGCATTGCACCTCAGCGTGTGTCTGTGTGAGACCCAAAACACACCTTGGCAGTGACAGGGGGCGA
80 G P D D S E V T F A L H S A S V F C V S L D P K T N T L A V T G G E

StuI (908)
901 AGACGACAAGGCTTCTGTGGAGGCTCGGTGATGGAGAGCTGCTCTTGTGAGTGTGCAGGCCACAAGACTCTGTGACATGCGCTGGTTTCAGTCACGAT
113 D D K A F V W R L G D G E L L F E C A G H K D S V T C A G F S H D
1001 TCCACCCTAGTGGCCACAGGGGACATGAGTGGTCTTTGAAAGTATGGCAGGTAGACACCAAGGAAGAAGTCTGGTCTTTGAAGCAGGAGACCTGGAGT
147 S T L V A T G D M S G L L K V W Q V D T K E E V W S F E A G D L E
1101 GGATGGAGTGGCACCCCTCGGGCTCCTGTCTGTGGCGGGCACAGCCGATGGCAACACTTGGATGTGGAAGGTCCCGAATGGTACTGTAAGACCTTTCA
180 W M E W H P R A P V L L A G T A D G N T W M W K V P N G D C K T F Q

Asp718I (1273) **Acc65I (1273)**
1201 GGGCCCCAACTGCCTGCAACCTGTGGCCGCTCCTCCCTGATGGGAAGAGAGCTGTGGTAGGTATGAAGATGGTACCATCAGGATCTGGGACCTCAAG
213 G P N C P A T C G R V L P D G K R A V V G Y E D G T I R I W D L K
1301 CAAGGAAACCCATCCATGTAATAAAGGACTGAGGGTCAAGGGCCCTCTGACCTGTGTAGCCACCAACCAGGATGGCAGTCTGATCCTGACTGGCT
247 Q G N P I H V L K G T E G H Q G P L T C V A T N Q D G S L I L T G

XcmI (1433)
1401 CTGTAGACTGCCAGGCCAAGCTGGTGCAGTGCACCACTGGCAAGTGGTGGTGTGTTTGTGAGTGTGCAGGCTGAGACAGTGCCTCCAGCCAGCTGGGAGAGGG
280 S V D C Q A K L V S A T T G K V V G V F R P E T V A S Q P S L G E G

PstI (1539)
1501 GGAGGAGAGTGAAGTCTAACTCCGTGGAGTCTTGGGCTTCTGCAGTGTATGCCTCTGGCCGCTGTTGGCTATCTGGACGGAACCTTGGCCATCTATGAC
313 E E S E S N S V E S L G F C S V M P L A A V G Y L D G T L A I Y D

BsrGI (1682)
1601 CTGTCTACGAGACACTCCGGCACCATGTGAGCACCAGTCCGGCATTGTTTGTGAGTGTGTTGGGAGGCTGGCACTGCTGTGGTACACCTGTAGCCTGG
347 L S T Q T L R H Q C Q H Q S G I V Q L L W E A G T A V V Y T C S L
1701 ATGGTGTGTACGCTCTGGGATGCCCGGACTGGCCGCTGCTTACTGACTACCGGGCCACACTGCTGAGATCCTGGACTTTGCCCTCAGCAAAGATGC
380 D G V V R L W D A R T G R L L T D Y R G H T A E I L D F A L S K D A

HpaI (1865) **NheI (1895)**
1801 TTCCTGGTGGTACCACATCAGGAGACCACAAGCAAAAGTATTTTGTGTCAGAGACCTGACCGTTAACAGCTGTAGCCTCTGGCATGGTGTGCTAG
413 S L V V T T S G D H K A K V F C V Q R P D R •
1901 CTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCT

HpaI (2033) **MfeI (2044)**
2001 TTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTCTTTATGTTTCAGGTTTCAGGGGAGGTGGGAGTTTTTTAAA

EcoRI (2129)
2101 GCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAAATACAGCATAGCAAACCTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGG
2201 ATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTAAGATATAGTGTATTTCCCAA

SspI (2368) **SwaI (2382)**
2301 GGTTTGAAGTACTCTTCTTCTTTATGTTTTAAATGCAGCTGACCTCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGC
2401 AATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTT
2501 TAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCAT
141 • N R T Y K L P I L E E I T T K V L K G N

SacI (2643)
2601 TCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGTGAAGTCTTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATC
120 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 D V E D

2701 AGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTG
87 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 V T V R
StuI (2807)

2801 CCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCGACATGGTCTTGTTCCTCATAGAGCATGGTGA
53 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 L M T I
BspHI (2957)

2901 TCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAGTCTATTATACTATGCCGA
20 K E T A V E V L E L D Q Q S I N F T K M
XmnI (2949)

3001 TATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCCACC
AseI (3015) SacI (3072)

3100 GTACACGCCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGT
SpeI (3170)

3199 CAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAA

SnaBI (3298)

3299 TACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTGATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTA

NdeI (3403)

3399 CTTGGCATATGATACACTTGATGACTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGG

PstI (3582)
SdaI (3581) PacI (3589)

3499 GAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCCTG C A G G T T A A T T A

BspLU11I (3599)

3597 AGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAA
AGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAA

3697 AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACC

3797 CTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCC

ApaLI (3913)

3897 GCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGTGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAAGACACGACTT

3997 ATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACT

4097 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCCTGGTAGCG

4197 GTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGA

PacI (4329) SwaI (4338) EagI (4349)
NotI (4348)

4297 AAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGGTT
AAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGGTT

4397 TTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAG

4497 AACATTTCTCTATCGAA