



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BspLU11I (560)
AgeI (552) 501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCAACATGTCCAAAGAACCTCTATTCTCTGGCTGATGATTGA
1 M S K E P L I L W L M I E

PshAI (618) 601 GTTTTGGTGGCTTACCTGACACCAGTCACTTCAGAGACTGTTGTGACGGAGGTTTTGGGTACCGGGTGACTTTGCCCTGTCTGTAATCATCTGGTCT
13 F W W L Y L T P V T S E T V V T E V L G H R V T L P C L Y S S W S **DraIII (661)**
BstEII (658) 701 CACAACAGCAACAGCATGTGCTGGGGAAAGACCAGTGCCCTACTCCGTTGCAAGGAGGCGCTCATCCGACTGATGGAATGAGGGTGACCTCAAGAA
47 H N S N S M C W G K D Q C P Y S G C K E A L I R T D G M R V T S R **BstEII (786)**
801 AGTCAGCAAAATATAGACTTCAGGGGACTATCCCGAGAGGTGATGTCTCTTACCATCTTAAACCCAGTGAAGTACAGCGGTGTGTAAGTCTGCGC
80 K S A K Y R L Q G T I P R G D V S L T I L N P S E S D S G V Y C C R
901 CATAGAAGTGCCTGGCTGGTTCAACGATGTAAGATAAACGTGCGCCTGAATCTACAGAGAGCCTCAACAACCACGCACAGAACGCAACCACCACACA
113 I E V P G W F N D V K I N V R L N L Q R A S T T T H R T A T T T T

PvuII (1052) 1001 CGCAGAACAACAACAAGCCACCACCACCAGCAAAATGACAACAACCCAGCTGCATTCCAACAACAGTCGTGACCACACCCGATCTCACAACCG
147 R R T T T T S P T T T R Q M T T T P A A L P T T V V T T P D L T T

BbrPI (1146) 1101 GAACACCACTCCAGATGACAACCATTGCCGTCTTCAACAGCAAAACACGTGCCTTCACTAACCCTCCGAGGAGCCACAGGTCCTTCT
180 G T P L Q M T T I A V F T T A N T C L S L T P S T L P E E A T G L L **BspEI (1176)**

Bsp120I (1222) 1201 GACTCCCAGCCTTCTAAGGAAGGCCCATCTCACTGCAGAACTGCTCCACAGTATTCTGGAGTAGTCTGAGTCTACTTCTGCTGAC
213 T P E P S K E G P I L T A E S E T V L P S D S W S S A E S T S A D **Tth1111**
EcoO109I (1221) **PstI (1235)**

BbrPI (1354) 1301 ACTGTCTGTGACATCCAAAGAGTCCAAAGTTGGGATCTCCCATCAACATCCACAGTGTCAATGTGGAAAACGAGTGATTCTGTGCTTCTCCTCAGC
247 T V L L T S K E S K V W D L P S T S H V S M W K T S D S V S S P Q
1401 CTGGAGCATCTGATACAGCAGTTCTGAGCAGAAACAAACAAACAGGACAGATGGAAATACCCATGCAATGAAGAATGAAATGCCCATCTC
280 P G A S D T A V P E Q N K T T K T G Q M D G I P M S M K N E M P I S

BsaBI (1509) 1501 CCAACTACTGATGATCATCGCCCTCCTGGGATTTGTGCTCTTCGCATTGTTTGTGGCGTTTCTCCTGAGAGGGAAACTCATGGAACCTATTGTTCCG
313 Q L L M I I A P S L G F V L F A L F V A F L L R G K L M E T Y C S
1601 CAGAAACACACAAGGCTAGACTACATTGGAGATAGTAAAAATGCTCAATGACGTGCAGCATGGAAGGGAAGACGAAGACGGCCTTTTACCCTCTAAC
347 Q K H T R L D Y I G D S K N V L N D V Q H G R E D E D G L F T L •

MscI (1735) 1701 AACGCAGTAGCATGTTAGATTGAGGATGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGCAGTAAAAAAA
NheI (1729)

HpaI (1867) **MfeI (1878)** 1801 ATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCTTTATGTTT

EcoRI (1963) 1901 CAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCC
2001 AAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCT

SapI (2145) 2101 TTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTCTTTCATTCTTTATGTTTTAAATGCACTGACCTCCACATCCCTTTTATG

SspI (2202) **SwaI (2216)** 2201 AAAATATTGAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAG
2301 TTTAGTAGTTGACTTAGGGAACAAAGGAACCTTAAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTGATTCTGGTGTACTTGGGGGATG
141 • N R T Y K L P I **EcoO109I (2277)**
SacI (2477) 2401 AGTTCCTCAATGGTGGTTTTGACAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTTCGCACATGCCACAGG
131 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 L E R C M G C P

BstXI (2506)
2501 GGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCC
98 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 Q G N S V A S G

StuI (2641)
2601 AATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCG
65 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 T K T R I A A G

XmnI (2783)
2701 ACATGGTCTTGTGTCTCATAGAGCATGGTATCTTCTCAGTGGGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGG
31 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 I N F T K M

AseI (2849)
2801 CCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCA

SacI (2906)
2901 CTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTG

SpeI (3004)
3001 ATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAA

SnaBI (3132)
3101 AACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGGCATAATGCCAGGCGGGCC

NdeI (3237)
3201 ATTTACCGTCATTGACGTCAATAGGGGCGTACTTGGCATATGATACACTTGATGTAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACG
3301 TCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTACC

PacI (3423)
PstI (3416)
SdaI (3415)
BspLU11I (3433)
3401 GTAAGTTATGTAACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAGGCCGCTTGTGGCGTTTTTCCA
3501 TAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTTCCCTGGA
3601 AGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCT

ApaLI (3747)
3701 GTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAACTATCG
3801 TCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTC
3901 TTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGGAGTTGGTAGCTCTT
4001 GATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTT

EagI (4183)
PacI (4163) **Swal (4172)** **NotI (4182)**
4101 TTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATAT

4201 CTTTATTTTTCATTACATCTGTGTGTTGTTTTTTGTGTAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATA
4301 GGCTGTCCCAGTCAAGTGCAGGTGCCAGAACATTTCTATCGAA