



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

MfeI (82)
101 GAGAAGGTGGCCGGGGTAAACTGGGAAAGTGTGCTGTACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACCATATAAGTGCAGTAGTCGCC

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

301 GCCATCCACGCGGTTGAGTCGCGTCTGCGCCCTCCCGCTGTGGTGCTCCTGAAGTCCGCTCCGCTTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMI (441)
NaeI (441)
401 GGGCCTTTGTCGGCGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTTCTGTTT

BstEII (555)
AgeI (552)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTCCACATGGAGGAGTCCGAACCCGAACGGAAGCGGCTCGCAC
1 M E E S E P E R K R A R T

BsrBI (624) **NgoMI (686)**
601 CGACGAGGTGCCTCCGGAGGAAGCCGCTCCGAGGCGGAAGATGAGGACGACGAGGACTACGTGCCCTATGTGCCGTTACGGCAGCGCCGGCAGCTACTG
13 D E V P A G G S R S E A E D E D E D E D Y V P Y V P L R Q R R Q L L

NaeI (686)
701 CTCGAGAAGCTGCTGCAGCGAAGACGCAAGGGAGCTGCGGAGGAAGACGACGAGCGGTAGTGAACCCCGGGAGATGAGGACGACATCCCGCTAG
47 L Q K L L Q R R R K G A A E E E Q Q D S G S E P R G D E D D I P L

SmaI (770)
801 GCCCTCAGTCCAACGCTCAGCCTCTGGATCAGCACCAGCACCTTAAGAGAAGGCTGAAGCGCGCAAAGAGTCTGCCAAGGAGAAGCAGCTGAAGGAAGA
80 G P Q S N V S L L D Q H Q H L K E K A E A R K E S A K E K Q L K E E

BssHII (859)
901 AGAGAAGATCCTGGAGAGTGTGCCGAGGGCCGAGCATTGATGTGAGTGAAGGAGATGGCTAAGGGCATTACGTATGATGACCCCATCAAACACGCTGG
113 E K I L E S V A E G R A L M S V K E M A K G I T Y D D P I K T S W

SnaBI (969)
1001 ACTCCACCCGTTATGTTCTGAGCATGTCTGAAGAGCGACATGAGCGCGTCCGGAAGAAATACCACATCTGGTGGAGGGAGACGGTATCCACACCACCA
147 T P P R Y V L S M S E E R H E R V R K K Y H I L V E G D G I P P P

StuI (1143)
1101 TCAAGAGCTTCAAGGAATGAAGTTTCTGCAGCCATCTGAGAGGCTGAAGAAGAAAGGCATTACCACCCAACACCCATTAGATCCAGGGCATCCC
180 I K S F K E M K F P A A I L R G L K K K G I H H P T P I Q I Q G I P

BsaBI (1224)
1201 CACCATTCTATCTGCGCCGTGACATGATAGGCATCGCTTTCACGGGTTGAGGCAAGACACTGTTGTTGACGTTGCCGTCATCATGTTCTGCTGGAACAA
213 T I L S G R D M I G I A F T G S G K T L V F T L P V I M F C L E Q

BstEII (1307) **Bsp120I (1330)** **ScaI (1394)**
1301 GAGAAGGTTACCTTCTCAAAGCGCGAGGGGCCATGGAATCATCATCTGCCCTCGGGGAGCTGGCCCGGACACCCATGGCATCTGGAGTACT
247 E K R L P F S K R E G P Y G L I I C P S R E L A R Q T H G I L E Y

1401 ACTGCGCCTGCTGAGGAGGACAGCTCACCCTCTGCGCTGCGCCCTCTGATTGGGGCATGTCCTGAAAGAGCAGATGGAGACCATCCGACACCG
280 Y C R L L Q E D S S P L L R C A L C I G G M S V K E Q M E T I R H G

SmaI (1521)
1501 TGTACACATGATGGTGGCCACCCCGGGCCCTCATGGATTTGCTGCAGAAGAAGTGGTGCAGCCTAGACATCTGTCGCTACTGTCGCTGGCCCTGGACGAGGCT
313 V H M M V A T P G R L M D L L Q K K M V S L D I C R Y L A L D E A

BsrGI (1500) **MscI (1514)** **PshAI (1567)**
1601 GACCGCATGATCGACATGGGCTTCGAGGGTGCATCCGTACCATCTTCTCTACTTCAAGGGCCAGCGACAGACCTGCTTTCAGTGCCACCATGCCGA
347 D R M I D M G F E G D I R T I F S Y F K G Q R Q T L L F S A T M P

BssHII (1758)
1701 AGAAGATTCAGAACCTTGTAAAGAGTGCCTTGTAAAGCCTGTGACCATCAATGTGGGGCGCGTGGGGCTGCCAGCCTGGATGTATCCAGGAGGTAGA
380 K K I Q N F A K S A L V K P V T I N V G R A G A A S L D V I Q E V E

XhoI (1834)
1801 ATATGTGAAGGAGGAGGCAAGATGGTGTACCTGCTGAGTGCCTGCAGAAACACCCCGCCTGACTCATCTTTCAGAGAAGAAGGACGACGTGGAC
413 Y V K E E A K M V Y L L E C L Q K T P P P V L I F A E K K A D V D

1901 GCCATCCACGAGTACCTGCTGCTCAAGGGGTTGAGGCCGTAGCCATCCATGGGGCAAAGACAGGAGGAACGGACTAAGGCCATCGAGGATTCGGG
447 A I H E Y L L L K G V E A V A I H G G K D Q E E R T K A I E A F R

2001 AGGGCAAGAAGGATGCTCTAGTACGACAGAGTTCGCTCAAGGGCCTGGACTTCCTGCCATCCAGCACGTCAATTATGACATGCCAGAGGAGAT
480 E G K K D V L V A T D V A S K G L D F P A I Q H V I N Y D M P E E I

BsrGI (2109)
2101 TGAGAATATGTACACCGGATTGGCCGACCGGGGCTCGGGAACACAGGCATCGCCACTCCTTTCATCAACAAAGCGTGTGATGAGTCACTGCTGATG
513 E N Y V H R I G R T G R S G N T G I A T T F I N K A C D E S V L M

Eco47III (2208)
2201 GACCTCAAAGCGCTGCTGCTAGAAGCAAGCAGAAGGTGCCGCCGCTGCTGAGGTGCTGATTGCGGGGATGAGTCCATGCTGGACATTGGAGGAGGC
547 D L K A L L L E A K Q K V P P V L Q V L H C G D E S M L D I G G E

XhoI (2353)
2301 GCGGCTGTGCTTCTGCGGGGCTGGGTCATCGGATCACTGACTGCCCAAACCTGAGGCTATGAGACCAAGCAGGTGAGCAACATCGGTGCGCAAGGA
580 R G C A F C G G L G H R I T D C P K L E A M Q T K Q V S N I G R K D

BamHI (2428) **NdeI (2468)**
2401 CTACCTGGCCACAGCTCCATGGACTTCGGATCCTATCCCTATGATGTCCAGACTATGCTGGCTATCCATATGATGTTCTGATTATGCTGGATACCTT
613 Y L A H S S M D F G S Y P Y D V P D Y A G Y P Y D V P D Y A G Y P

MscI (2531)
NheI (2525)
2501 TATGATGTCCAGACTATGCCTAAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTGGACAACCAACAATGAGTGCAGTGAATAAATGC
647 Y D V P D Y A •

HpaI (2663) **MfeI (2674)**
2601 TTTATTTGTAAAATTTGTGATGCTATTGCTTTATTTGTAACATTATAAGTGCATAAACAAGTTAACAACAACAATGCAATTTATGTTTCAGG

2701 **EcoRI (2759)**
 TTCAGGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATCTAAAAATACAGCATAGCAAACCTTTAACCTCCAAT

2801 CAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCA

2901 **SspI (2998)**
 TGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAAGCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAA

3001 **SwaI (3012)**
 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTA

3101 GTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTT
 141 • N R T Y K L P I L E

3201 **SacI (3273)**
 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCT
 130 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 S

3301 **Ecl136II (3273)**
 GACCACCCTGATGGATCTGTCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG
 97 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 I

3401 **StuI (3437)**
 GCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACAT
 63 A I A E A C V T V R G I Y A E I H V A S I I E G U T K T R I A A G V H

3501 **XmnI (3579)**
 GGTGCTTGTTCCTCATAGAGCATGGTATCTTCTAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTATGATGGCCCT
 30 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

3601 **AseI (3645)**
 CCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACGCTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAA

3701 **SacI (3702)**
 ACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTT

3801 **SpeI (3800)**
 ACTAGTCAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACC

3901 **SnaBI (3928)**
 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTT

4001 **NdeI (4033)**
 ACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAA

4101 TGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTATTATTGACGTCAATGGGGGGGGTCTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAA

4201 **PacI (4219)**
SdaI (4211)
SbfI (4211)
PciI (4229)
BspLU11I (4229)
 GTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGAAAAGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGG

4301 CTCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCT

4401 CCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTCGGAAGCGTGGCGTTTCTCATAGCTCACGCTGTAG

4501 **ApaLI (4543)**
 GTATCTCAGTTCGGTGTAGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTT

4601 GAGTCAACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGA

4701 AGTGGTGGCCTAACTACGGCTACACTAGAAGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATC

4801 CGGCAACAAACCACCGCTGGTAGCGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT

4901 **EagI (4979)**
PacI (4959) **SwaI (4968)** **NotI (4978)**
 ACGGGGTCTGACGCTCAGTGGAAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTT

5001 ATTTTCATTACATCTGTGTGTTGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAACTAGCAAATAGGCT

5101 GTCCCCAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA