



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAAGTGGCGGGGTAAGTGGAAAGTGTGTCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC **PvuII (239)** **Bsu36I (291)**

301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

NcoI (560)
501 TCTGTTTGGCGCGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTACCATTGGAGCGGAAGAGTGGGAGTGGCCGGCGCTCCCGCA **AgeI (552)** 1► M E R K R W E C P A L P Q

601 GGGCTGGGAGAGGAAGAAGTGCCAGAAAGTCCGGGCTGTCCGGCCAGCAGGGATGCTTTTACTATAGCCGAGCGGGAAGAAGTCCGACAGCAAG **NgoMIV (643)**
13► G W E R E E V P R R S G L S A G H R D V F Y Y S P S G K K F R S K

BssHII (709)
701 CCGCAGCTGGCGCGTACCTGGGCGGCTCCATGGACCTGAGCACCTTCGACTTCCGCACGGGCAAGATGCTGATGAGCAAGATGAACAAGAGCCGCCAGC **PvuII (703)** **NcoI (728)**
47► P Q L A R Y L G G S M D L S T F D F R T G K M L M S K M N K S R Q

801 GCGTGCCTACGACTCCTCAACAGGTCAGGGCAAGCCGACCTGAACACGGCGCTGCCCGTGCAGACGGCGTCCATCTTCAAGCAGCCGGTGAC **Tth111I (870)**
80► R V R Y D S S N Q V K G K P D L N T A L P V R Q T A S I F K Q P V T
901 CAAGATTACCAACCACCCAGCAACAAGTCAAGAGCGACCCGAGAAGGCGGTGGACAGCCCGCCAGCTCTTCTGGGAGAAGAAGCTGAGCGGCCGT
113► K I T N H P S N K V K S D P Q K A V D Q P R Q L F W E K K L S G L

PstI (1054)
1001 AACGCCTTCGACATTGCTGAGGAGCTGGTCAAGACCATGGACCTCCCAAGGGCTGCAGGGGTGGACCTGGCTGCACGGATGAGACGCTGCTGTCGG **SdaI (1053)**
147► N A F D I A E E L V K T M D L P K G L Q G V G P G C T D E T L L S
1101 CCATCGCCAGCGCCTGCACACTAGCACCATGCCATCAGGGACAGCTCTCGGCCGCGTGGAGAAGAACCCTGGGCTATGGCTCAACACCACGCGCC
180► A I A S A L H T S T M P I T G Q L S A A V E K N P G V W L N T T Q P

1201 CCTGTGCAAAGCCTTCATGGTGACCGACGAGGACATCAGGAAGCAGGAAGAGCTGGTGCAGCAGGTGCGGAAGCGGCTGGAGGAGCGCTGATGGCCGAC **BstAPI (1257)**
213► L C K A F M V T D E D I R K Q E E L V Q Q V R K R L E E A L M A D

1301 ATGCTGGCGCACGTGGAGGAGCTGGCCCGTACGGGGAGGCGCCGCTGGACAAGCCCTGCGCTGAGGACGACGACGAGGAAGACGAGGAGGAGGAGG **BbrPI (1309)** **StuI (1352)** **BbsI (1378)**
247► M L A H V E E L A R D G E A P L D K A C A E D D D E E D E E E E

MscI (1451)
1401 AGGAGCCCGACCCGACCCGGAGATGGAGCACGTCTAGGCGAGTGTCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAAC **NheI (1445)**
280► E E P D P D P E M E H V •

1501 GAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAATTTG **HpaI (1583)** **MfeI (1594)**

1601 CATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCAAAATACAGCATAG **EcoRI (1679)**

1701 CAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTT

1801 TGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCAGTACCTCCC

1901 ACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCT **SspI (1918)** **SwaI (1932)**

2001 TCATAATATCCCCAGTTTAGTGTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGT **SacI (2193)**
141► • N R T

2101 GACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAAGCAGTACAGGAGCATAGTACAGATGAGCTCT **BstXI (2222)**
137► 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 L E

2201 CTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGT **StuI (2357)**
103► 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 Q G N

2301 TGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGT **SacI (2193)**
70► 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 T K T

2401 CCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTG **SacI (2193)**
37► 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 I N

BbsI (2503) AseI (2565)
2501 **AAGGTC**TT**CATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAA**AAACAGCGTGGATGGCGTCTCCAG
3 F T K M

SacI (2622)
2601 **CTT**ATCTGACGGT**CTCA**TAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATT

SpeI (2720)
2701 TTGGAAAGTCCCCTTGATTT**ACTAGT**CAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCC

SnaBI (2848)
2801 ATTGATG**TA**CTGCCAAAACCGCAT**CAT**CATGGTAATAGCGATGACTAATACGTAGATG**TA**CTGCCAAGTAGGAAAGTCCATAAGGTCATG**TA**CTGGGCA

NdeI (2953)
2901 TAATGCCAGGGCGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTT**GA**TG**TA**CTGCCAAGTGGGCAGTTTACCGTAAAT

3001 ACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT**CA**TATTGACGTCAATGGGGGGGGTCTGGGGCGGT**CA**GC

PstI (3132) SdaI (3131) PacI (3139) BspLU11I (3149)
3101 AGGCGGGCCATTTACCGTAA**GT**TATGTAACGCCTGCAGGTTAA**T**TAAGAA**CA**TGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGT

3201 TGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCA

3301 GGGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTT

ApaLI (3463)
3401 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTT**CG**CTCAAGCTGGGCTGTGTGCACGAACCCCGCTT**CA**GCCCGACCGCTGCGCCT

3501 TATCCGGTAACTATCGTCTT**GAG**TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGG

3601 CGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAA

3701 AGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAG

PacI (3879) SwaI (3888) NotI (3898)
3801 AAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAA**AA**CTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGC

3901 GGGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAA

4001 ACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA