



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACGCGCCCGCCGCCCTACCTGAGGGCC **HindIII (245)** **Bsu36I (291)**
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCCTCCCGCCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)** **NaeI (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCACCATTGGAGAGGCTGGTGATCAGGATGCCCTTCTCTCATCT **XcmI (560)** **NcoI (560)**
1 M E R L V I R M P F S H L
KasI (535) **AgeI (552)**
601 GTCTACCTACAGCCTGGTTTGGTTCATGGCAGCAGTGGTGTGTGCACAGCACAAAGTGAAGTGGTGACCAGGATGAAAGAGAGCAGCTGTACACAACT **ApaI (642)** **BsrGI (689)**
13▶ S T Y S L V W V M A A V V L C T A Q V Q V V T Q D E R E Q L Y T T
701 GCTTCCTTAAAATGCTCTCTGCAAAATGCCAGGAAGCCCTATTGTGACATGGCAGAAAAAGAAAGTGTAAAGCCAGAAAAACATGGTCACCTTCAGCG **NcoI (804)**
47▶ A S L K C S L Q N A Q E A L I V T W Q K K K A V S P E N M V T F S
801 AGAACCATGGGGTGGTATCCAGCCTGCCTATAAGGACAAGATAAACATTACCAGCTGGGACTCCAAAACCTCAACCATCACCTTCTGGAATATCACCT **BspLU11I (917)** **BglIII (950)** **BsrGI (981)**
901 GGAGGATGAAGGGTGTACATGTGTCTCTTCAATACCTTTGGTTTTGGGAAGATCTCAGGAACGGCCTGCCTCACCGTATGTACAGCCCATAGTATCC **NcoI (1064)** **EcoO109I (1079)**
113▶ E D E G C Y M C L F N T F G F G K I S G T A C L T V Y V Q P I V S
1001 CTTCACTACAAATCTCTGAAGACCACCTAAATATCACTTGTCTGCCACTGCCCGCCAGCCCATGGTCTTCTGGAAGGTCCTCGGTCAGGGATTG **Tth11II (1113)** **Tth11II (1134)**
147▶ L H Y K F S E D H L N I T C S A T A R P A P M V F W K V P R S G I
1101 AAAATAGTACAGTACTGTCTCACCCAAATGGGACCAGCTGTGTACCAGCATCCTCCATATCAAAGACCCTAAGAATCAGGTGGGGAAGGAGGTGAT **NheI (1399)**
180▶ E N S T V T L S H P N G T T S V T S I L H I K D P K N Q V G K E V I
1201 CTGCCAGGTGCTGCACCTGGGACTGTGACCGACTTTAAGCAAACCGTCAACAAAGGCTATTGGTTTTAGTTCCGCTATTGCTAAGCATTGTTTCTG **MscI (1405)**
213▶ C Q V L H L G T V T D F K Q T V N K G Y W F S V P L L L S I V S L
1301 GTAATCTTCTCGTCTCAATCTCAATCTTACTGTACTGAAACGTACCAGGATCAGGACCGAGAGCCCTAAATAAGTACACAGCACCTGAAAGTGAG **HpaI (1537)** **MfeI (1548)**
247▶ V I L L V L I S I L L Y W K R H R N Q D R E P •
1401 CTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAGTGAAGTGAAGGATGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTAT

1501 TGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAAACAATTGCATTCATTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTTTT **EcoRI (1633)**
1601 TAAAGCAAGTAAACCTCTACAAATGTGGTATGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTTACTTGAATCCTTTTCTG **SacI (2147)** **BstXI (2176)**
1701 AGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATAGTGATTTTC

1801 CCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATAGTAAATATTCAGAAATAATTTAAATACATCA **SspI (1872)** **SwaI (1886)**

1901 TTGCAATGAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAA **EcoO109I (1947)**
2001 CCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTG **N R T Y K L P I L E E I T T K V L K**
2101 CCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCGCACATGCCACAGGGGTGACCCCTGATGGATCTGTCCACCT **SacI (2147)** **BstXI (2176)**
121▶ 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 V V R I S R D V E
2201 CATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGC **StuI (2311)**
88▶ D 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
2301 CCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAGAGCATG **BspHI (2461)**
55▶ R 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
2401 GTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATG **XmnI (2453)**
21▶ T I K E T A V E V L E L D Q Q S I N F T K M

2501 **AseI (2519)** **SacI (2576)**
CCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGACCTCCC

2601 **SpeI (2674)**
ACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCATTGA

2700
CGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGAC

SnaBI (2802)
2800 TAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGC

NdeI (2907)
2900 GTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTA

PstI (3086)
SdaI (3085)**PacI (3093)**
3000 TGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA

BspLU11I (3103)
3098 TTAAGAACATGTGAGCAAAGGCCAGAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCA

3198 CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCG

3298 ACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCG

ApaLI (3417)
3398 TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGA

3498 CTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC

3598 ACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTA

3698 GCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAA

EagI (3853)
PacI (3833) **SwaI (3842)** **NotI (3852)**
3798 CGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTG

3898 GTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGC

3998 CAGAACATTTCTCTATCGAA