



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

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

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTACCCATGGAGGAGAGTGTGTCGTACGGCCCTCAGTGTGTGGT **NcoI (560)** **AgeI (552)** **BsiWI (576)**
1 M E E S V V R P S V F V V
XmaI (668)
601 GGATGGACAGACCACATCCCATTACAGAGGCTGGGACGAAGCCACCGGAGACAGTCTGTCAGTGTGGCCCGGTGGGTCTGGTCTCTTGTGTGCTG **SdaI (787)**
13 D G Q T D I P F T R L G R S H R R Q S C S V A R V G L G L L L L

701 ATGGGGGCTGGGCTGGCCGTCCAAGGCTGGTCTCCTCCTGCAGTGCACCTGGCGTCTAGGAGAGATGGTACCCGCTGCCTGACGGACCTGCAGGCTCCT **SmaI (1034)**
47 M G A G L A V Q G W F L L Q L H W R L G E M V T R L P D G P A G S
801 GGGAGCAGCTGATACAAGAGCGAAGGTCTCAGGAGTCAACCCAGCAGCGCATCTCACAGGGGCAACTCCAGCTTGACCGGCAGCGGGGGCCGCTGTT **Bsu36I (927)** **Bsp120I (953)** **XcmI (995)**
80 W E Q L I Q E R R S H E V N P A A H L T G A N S S L T G S G G P L L
901 ATGGGAGACTCAGCTGGGCTGGCCTTCTGAGGGGCTCAGTACCACGATGGGCGCCTTGTGGTACCAAAGCTGGTACTACTACATCTACTCCAAG **MscI (1034)**
113 W E T Q L G L A F L R G L S Y H D G A L V V T K A G Y Y Y I Y S K
1001 GTGCAGCTGGGCGGTGTGGGCTGCCCGTGGCCAGCACCATCACCCAGGCCTTACAAAGCGCACACCCGCTACCCGAGGAGCTGGAGCTGT **XmaI (1142)**
147 V Q L G G V G C P L G L A S T I T H G L Y K R T P R Y P E E L E L
1101 TGGTCAGCCAGCAGTCCCTGCGGACGGGCCACCAGCAGTCCCGGCTGGTGGGACAGCAGCTTCTGGGTGGTGTGGTACACCTGGAGGCTGGGA **Acc65I (1249)**
180 L V S Q Q S P C G R A T S S S R V W W D S S F L G G V V H L E A G E
1201 GGAGTGGTGTCCGTGTGCTGGATGAACGCTGGTTCGACTGCGTGTGGTACCCGCTTACTTCCGGGCTTTCATGGTGTGAAGGAAGGAGCGTGGT **MscI (1327)**
213 E V V V R V L D E R L V R L R D G T R S Y F G A F M V •

1301 GCATTGGACATGGGTCTGACAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACAAGTGAATGCAGTGAAAAAATGCTTTA **PshAI (1306)** **NheI (1321)**

1401 TTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCTTTATGTTTCAGGTTCA **HpaI (1459)** **MfeI (1470)**

1501 GGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAG **EcoRI (1555)**
1601 CCTCTACTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGA

1701 GTTTAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTCTTCAATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTGTAGAAAATATT **SapI (1737)** **SspI (1794)**

1801 CAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAG **Swal (1808)**
1901 TTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCTCT **SacI (2069)** **BstXI (2098)**
141 • N R T Y K L P I L E E
2001 AATGGTGGTTTTGACCAGCTTGCCATTCACTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGTGACC **SacI (2069)** **BstXI (2098)**
129 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 V
2101 ACCCTGATGGATCTGCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAA **StuI (2233)**
95 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 A I
2201 TGGCTTACGACAGCAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTG **StuI (2233)**
62 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 V H H
BbsI (2379)
2301 CTTGTTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTTTCATGGTGGCCCTCCTA **XmnI (2375)**
29 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

2401 TAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGA **AseI (2441)** **SacI (2498)**

2501 GCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTA

2601 GTCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCAT

SnaBI (2724)

2701 CATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGGGGCCATTTACCG

NdeI (2829)

2801 TCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGA

2901 AAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTA

SdaI (3007) PacI (3015) **BspLU11I (3025)**

3001 TGTAACGCCTGCAGGTTAATTAAAGACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCC

3101 GCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCTGGAAGCTCCCT

3201 CGTGCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT

ApaLI (3339)

3301 CTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT

3401 CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG

3501 GTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC

3601 AAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG

EagI (3775)
PacI (3755) SmaI (3764) **NotI (3774)**

3701 GGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTT

3801 TCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCC

3901 CCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA