



PvuI (7)
SgfI (6) 1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA MfeI (82)

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTCCGCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC PvuII (239) Bsu36I (291)

301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCAACTCTACGCTTTTGTTCGTTT NgoMIV (441)

NcoI (560)
BstEII (555)
AgeI (552) 501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTACCATTGGGAAAAATCAGCAGTCTTCCAACCAATTATTTAA BstEII (555) AgeI (552) 1 M G K I S S L P T Q L F K

601 GTGCTGCTTTTGTGATTTCTGAAGTGAAGATGCACACCATGTCCTCTCGCATCTCTTACCTGGCGCTGTGCTCCTCACCTTCCAGCTCTGCC 13 C C F C D F L K V K M H T M S S S H L F Y L A L C L L T F T S S A

701 ACGGCTGGACCGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTTTCAGTTCTGTGTGGAGACAGGGGCTTTTATTCAACAAGCCACAGGGTATG SapI (742) 47 T A G P E T L C G A E L V D A L Q F V C G D R G F Y F N K P T G Y

801 GCTCCAGCAGTCGGAGGGCGCTCAGACAGGCATCGTGGATGAGTGTCTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGATTGCGCACCCCTCAA BspEI (851) FspI (886) 80 G S S S R R A P Q T G I V D E C C F R S C D L R R L E M Y C A P L K

901 GCCTGCCAAGTCAGCTCGCTCTGTCGTGCCGAGCCACACCACATGCCAAGACCCAGAAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCA 113 P A K S A R S V R A Q R H T D M P K T Q K E V H L K N A S R G S A

MscI (1067)
Bsu36I (1033) 1001 GGAAACAAGAACTACAGGATGTAGGAAGACCCTCTGAGGAGTGAAGAGTGACATGCCACCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTT MscI (1067) Bsu36I (1033) 147 G N K N Y R M •

1101 GGACAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAG HpaI (1199)

MfeI (1210) 1201 TTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTACAGGGGAGGTGTGGAGGTTTTTAAAGCAAGTAAACCTTACAAATGTGGTATGGAATT MfeI (1210) EcoRI (1295)

1301 CTAATAACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCA

1401 ATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGGTTTGAAGTACTGCTTCTTATTTATGTTTTA SapI (1477)

1501 AATGCACTGACCTCCACATTCCCTTTTATGAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCC SspI (1534) SwaI (1548)

1601 AGATGCTCAAGGCCCTTCATAATATCCCCAGTTTGTAGTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCT EcoO109I (1609)

1701 AGCTTTAGTTCTGGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATA 141 • N R T 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

1801 GTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGCA SacI (1809) BstXI (1838) 109 D S I L E 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

1901 AAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCCAGCAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGA StuI (1973) 75 F D K Q G N 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

2001 TCTCCCAGTCTGGTCCCTGATGGCCGCCCGACATGGTGTCTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACAGCTCCAGATC 42 E G T K T 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

2101 CTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCTATAGTGAAGTATTATATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCG XmnI (2115) AseI (2181) 9 Q Q S I N F T K M

2201 TGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTCGTCATGGGGCG SacI (2238)

2301 GAGTTGTTACGACATTTTGAAGTCCCGTTGATTTACTAGTCAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAA SpeI (2336)

2401 ACCGCTATCCACGCCATTGATGTAAGTCCGCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAA SnaBI (2464)

NdeI (2569)

2501 GGTCATG TACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATG TACTGCCAAGTGG

2601 GCAGTTTACC GTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGCGGGGGT

PacI (2755)

PstI (2748)
SdaI (2747)

BspLU11I (2765)

2701 CGTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAAC

2801 CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG

2901 GACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTC

ApaLI (3079)

3001 GGG AAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCAG

3101 CCCGACCGCTGCGCTTATCCGTAAC TATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA

3201 GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGCCTAACTACGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCC

3301 AGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGA

PacI (3495)

3401 AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAAC TACGTTAAGGGATTTTGGTCATGGCTAGTTAAT

EagI (3515)

SwaI (3504) NotI (3514)

3501 TAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAAC TAACATACGCTCTCCATCAA

3601 AACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA