



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**
101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCTGTACTGGTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTCGCAACGGGTTTGGCCGACAGTGAAGCTTCAGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
HindIII (245)
PvuII (239) 301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
Bsu36I (291)

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCCGCTTGTCTCAACTCTACGCTTTTGTTCGTTT
NgoMIV (441)

501 TCTGTTTGTCCGCGCTTACAGATCCAAGCTGTGACCGGCGCCTACCTGAGATCACCGGTAGGAGGCCATCATGAGTGATTCTAAGGAAATGGGGAAGAGG
AgeI (552) **BspHI (568)**
1 M S D S K E M G K R
XcmI (671) **DraIII (698)**

601 CAGCTTCGCCCTCTGGATGAGGAACTGTGACATCCAGCCACACCAGGCACTCCATCAAAGGCTTTGGCTTCCAAACAAATTCTGGATTCAGTAGCTTCA
11 Q L R P L D E E L L T S S H T R H S I K G F G F Q T N S G F S S F

701 CAGGGTGCCTGGTCCACAGTCAAGTCCCCTTGGCACTGACGGTCTTCTCTAGCTGTTTGTCTGTGCTGCTGGTTGCATCCTTGTCAAAGTCTACAA
44 T G C L V H S Q V P L A L Q V L F L A V C S V L L V V I L V K V Y K

801 AATACCCAGTTCTCAGGAAGAAAACAATCAGATGAATGTCTACCAAGAAGTACCCAGTTGAAGGCTGGCGTAGATCGACTGTGCCGCTCCTGCCCTGG
77 I P S S Q E E N N Q M N V Y Q E L T Q L K A G V D R L C R S C P W

901 GACTGGACGCACTTCCAAGGAAGCTGTTACTTCTCTGTGGCCGAGAAGTCTGGAATGATTCTGCCACTGCCTGCCACAATGTGGGGGCTCAACTTG
111 D W T H F Q G S C Y F F S V A Q K S W N D S A T A C H N V G A Q L

1001 TGGTCATCAAGAGTGTGAAGAGCAGAACCTTCTACAACAACTTCTAAGAAGAGAGGCTACACTTGGATGGGCTCATTGACATGAGCAAGGAGTCTAC
144 V V I K S D E E Q N F L Q Q T S K K R G Y T W M G L I D M S K E S T

1101 ATGGTACTGGGTAGATGGTTACCTCTGACTCTCAGTTTCATGAAGTATTGGAGTAAAGGAGAACCTAACACCTGGGAGAGGAAGACTGTGCAGAGTTC
177 W Y W V D G S P L T L S F M K Y W S K G E P N N L G E E D C A E F

1201 AGAGATGACGGCTGGAATGACACCAAATGACTAACAAGAAATCTGGATCTGCAAAAAGCTTCAACTTCTGCCCCTAGCAAGTGTAGGCCAACTCCCT
211 R D D G W N D T K C T N K K F W I C K K L S T S C P S K •

MscI (1331)
1301 CCACCATCTCCACAGTCCCAAAACCGTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAAC TAGAATGCAGTGAAAAAATGC

1401 TTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCTTTATGTTTCAGG
HpaI (1463) **MfeI (1474)**

1501 TTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTCAAATACAGCATAGCAAACTTTAACCTCCAAT
EcoRI (1559)

1601 CAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCA

1701 TGGAGTTTAAAGATATAGTGTATTTTCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCAGTACCTCCACATTCCCTTTTATAGTAAAA
SspI (1798)

1801 TATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTA
SwaI (1812) **EcoO109I (1873)**

1901 GTAGTTGGACTTAGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTT
141 • N R T Y K L P I L E

2001 CCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTCTGCACATGCCACAGGGGCT
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
BstXI (2102)

2101 GACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATG
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

2201 GCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCCCCGACAT
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 T K T R I A A G V H
StuI (2237)

2301 GGTGCTTGTTCCTCATAGAGCATGGTGTCTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCT
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
BbsI (2383) **XmnI (2379)**

2401 CCTATAGTGAAGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAA
AseI (2445)

SacI (2502)
2501 ACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAAGTCCC GTTGATTT

SpeI (2600)
2601 ACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACC

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SnaBI (2728)
2701 GCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA CTGCCAAGTAGGAAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTT

NdeI (2833)
2801 ACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACTTGTACTGCAAGTGGGCAGTTTACC GTAAATACTCCACCCATTGACGTCAA

2901 TGGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGT CATTATTGACGTCAATGGGGGGGGTCTTTGGCGGTTCAGCCAGGCGGGCCATTTACC GTAA

PacI (3019)
PstI (3012)
SdaI (3011) BspLU11I (3029)
3001 GTTATGTAACGCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGG

3101 CTCCGCCCCCTGACGAGCATC AAAAAATCGACGCTCAAGT CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCT

3201 CCCTCGTGCCTCTCTGTTCGACCCCTGCCGCTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG

ApaLI (3343)
3301 GTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTT CAGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTT

3401 GAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGATTCTTGA

3501 AGTGGTGGCCTAACTACGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTTTGATC

3601 CGGCAACAACACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCT

PacI (3759) SwaI (3768) EagI (3779) NotI (3778)
3701 ACGGGGTCTGACGCTCAGTGGAACGAAAAC TACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTT

3801 ATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCT

3901 GTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA