



PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
MfeI (82)
101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC
PvuII (239)
Bsu36I (291)
301 GCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAATGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCGCTGACCTGCTTCTCAACTCTACGCTTTGTTTCGTTT

AgeI (552) **BspHI (560)**
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTATCATGAAGACATTGCCTGCCATGCTTGGAACTGGAAATT
1 M K T L P A M L G T G K L

NcoI (645) **BsrGI (666)**
601 ATTTTGGTCTTCTTCTTAATCCATATCTGGACATCTGGAACATCCATGGGAAAGAATCATGTGATGTACAGCTTTATATAAAGAGACAATCTGAACAC
13 F W V F F L I P Y L D I W N I H G K E S C D V Q L Y I K R Q S E H

StuI (757) **BspLU11I (793)**
701 TCCATCTTAGCAGGAGATCCCTTGAAGTAGAATGCCCTGTGAAATACTGTGCTAACAGGCCCTCATGTGACTTGGTGAAGCTCAATGGAACAACATGTG
47 S I L A G D P F E L E C P V K Y C A N R P H V T W C K L N G T T C
801 TAAAACCTGAAGATAGACAAACAAGTTGGAAGGAGAGAAGAACATTTCAATTTTCTACATTTTGAACCAAGTCTTCTAATGACAATGGGTGATA
80 V K L E D R Q T S W K E E K N I S F F I L H F E P V L P N D N G S Y

XcmI (992)
901 CCCTGTTCTGCAATTTTTCAGTCTAATCTCATTGAAAGCCACTCAACAACCTTTTATGTGACAGATGAAAAAGTGCCTCAGAACGACCCTCCAAGGAC
113 R C S A N F Q S N L I E S H S T T L Y V T D V K S A S E R P S K D
1001 GAAATGGCAAGCAGACCTGGCTCCTGTATAGTTACTTCCTTTGGGGGATTGCCTACTACTACTACCTGTTTCTGCCTGTTCTGCTGCTGCTGAGAA
147 E M A S R P W L L Y S L L P L G L P L L I T T C F C L F C C L R
1101 GGCACCAAGGAAAGCAAAATGAACTCTGTGACAGCAGGAAGGGAAATTAACCTGGTTGATGCTCACCTTAAGAGTGAAGCAAGCAAGCACCAG
180 R H Q G K Q N E L S D T A G R E I N L V D A H L K S E Q T E A S T R

ScaI (1212)
1201 GCAAAATCCCAAGTACTGCTATCAGAACTGGAATTTATGATAATGACCCTGACCTTTGTTTCAGGATGCAGGAAGGGTCTGAAGTTTATTCTAATCCA
213 Q N S Q V L L S E T G I Y D N D P D L C F R M Q E G S E V Y S N P

XcmI (1344)
1301 TGCTGGAAGAAAACAAACCAGGCATTGTTTATGCTTCCCTGAACCTTGTCTATTGGACIGAACTCAAGACTGGCAAGAAATGAAAAAGCACCACAA
247 C L E E N K P G I V Y A S L N H S V I G L N S R L A R N V K E A P

NdeI (1413) **NheI (1459)**
NsiI (1406) **BstXI (1456)** **MscI (1465)**
1401 CAGAATATGCATCCATATGTGTGAGGAGTTAAGTCTGTTTCTGACTCCAACAGGGACCAGCTAGTGGCCAGACATGATAAGATACATTGATGAGTTGG
280 T E Y A S I C V R S •

HpaI (1597)
1501 ACAAACCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTT

MfeI (1608) **EcoRI (1693)**
1601 AACAAACAAC AATTGCATTCATTTATGTTTCAGGTT CAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCT
1701 AAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTGAAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAAT

SapI (1875)
1801 GTGCATTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTCTTTCATTTCTTTATGTTTTAAA

SspI (1932) **SwaI (1946)**
1901 TGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAAATCCAG

EcoO109I (2007)
2001 ATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAG

SacI (2207) **BstXI (2236)**
2101 CTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGT
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 D
2201 CAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAA
108 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 F

StuI (2371)
2301 GTCCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATC
75 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

2401 TCCCCAGTCTTGGTCCTGATGGCCGCCCGACATGGTGCTTGTGTCCTCATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCT
41 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 Q
XmnI (2513) AseI (2579)

2501 GCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTG
8 Q S I N F T K M
Sacl (2636)

2601 GATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTCGCTCAATGGGGCGGA

2701 GTTGTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAAC
SpeI (2734)

2801 CGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGG
SnaBI (2862)

2901 TCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCAATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGC
NdeI (2967)

3001 AGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCCG

3101 TTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACAATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCG
PacI (3153) PstI (3146) SdaI (3145) BspLU11I (3163)

3201 TAAAAAGCGCGCTTGTGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA

3301 CTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGG

3401 GAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCC
ApaI (3477)

3501 CGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA

3601 GCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAG

3701 TTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAA

3801 AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTA
PacI (3893)

3901 ACATTTAAATCAGCGGCCCAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAA
EagI (3913) SwaI (3902) NotI (3912)

4001 CAAAACGAAACAAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA