



PvuI (7)
SgfI (6) **MfeI (82)**
1 GGATCTGGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) **HindIII (245)**
PvuII (239) **Bsu36I (291)**
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTGCAGTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
NaeI (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCAACTCTACGTCTTTGTTTCGTTT

NcoI (560)
KasI (535) **BstEII (555)** **BstEII (571)** **SacII (586)**
501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACTCTGAGATCACCGGTACCATTGGGCAAGGGTGACCTAACCAAGCCGCGGGGCAAAAT
1 M G K G D P N K P R G K M

BsiWI (605)
601 GTCCTCGTACGCCTTCTTCGTGCAGACCTGCCGCGAGGAGCACAAGAAGAAGCATCCCGACTCGTCGGTGAACCTCGCCGAGTTCCTCAAGAAATGCTCC
13 S S Y A F F V Q T C R E E H K K K H P D S S V N F A E F S K K C S

Tth111I (711)
BbsI (708) **MscI (749)**
701 GAGAGATGGAAGACCATGTCTGCAAAGGAAAAGTCCAAGTTTGAAGATTTGGCCAAGAGCGCAAAGCTGTTATGACAGGGAGATGAAGAACTATGTTC
47 E R W K T M S A K E K S K F E D L A K S D K A R Y D R E M K N Y V

PshAI (851)
801 CTCCCAAAGGGGATAAGAAAGGAAAAGAAAAAGACCCCAATGTCCGAAGAGACCAACCGTCTGCCTTCTCCTGTTTTGCTCTGAAAATCGCCCAAAGAT
80 P P K G D K K G K K K D P N A P K R P P S A F F L F C S E N R P K I

StuI (915)
901 CAAAATTGAACACCCAGGCTGTCTATTGGAGATACTGCGAAGAACTGGGTGAGATGTGGTCTGAGCAATCTGCCAAAGATAAACACCGTATGAGCAG
113 K I E H P G L S I G D T A K K L G E M W S E Q S A K D K Q P Y E Q

EcoO109I (1080)
1001 AAAGCAGCTAAACTAAAGGAGAAGTATGAAAAGGATATTGCTGCATACCGTGCCAAGGGCAAAAGTGAAGCAGGAAAGAAGGGTCTGGTAGGCCAACAG
147 K A A K L K E K Y E K D I A A Y R A K G K S E A G K K G P G R P T

1101 GCTCAAAGAAGAAGAACCAAGAGATGAGGAGGAGGAAGAAGAGGAGGAAGATGACGAGGAAGAAGAGGAGGATGAAGAATAAGTGGC
180 G S K K K N E P E D E E E E E E E E D D E E E E E D E E •

MscI (1220)
NheI (1214)
1201 TGTCTAAAGTGTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGA

HpaI (1352) **MfeI (1363)**
1301 AATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACACAACAATTGCATTATTTATGTTTCAGGTTTCAGGGGAG

EcoRI (1448)
1401 GTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTAC
1501 TTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAG

SspI (1687)
1601 ATATAGTGTATTTTCCCAAGTTTGAACCTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAAT

SwaI (1701) **EcoO109I (1762)**
1701 AATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACT
1801 TAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTGGTACTTGAGGGGATGAGTTCCTCAATGGTG
141 • N R T Y K L P I L E E I T

SacI (1962) **BstXI (1991)**
1901 GTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCCCTGA
126 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 V R I

2001 TGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTC
93 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 A E

StuI (2126)
2101 AGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTTGTG
60 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 K N

BspHI (2276)
BbsI (2272)
XmnI (2268)
2201 TCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGATGGCCCTCTATAGTGAG
26 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

AseI (2334) **SacI (2391)**
2301 TCGTATTACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAGCTCTG

2400 CTTATATAGACCTCCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCC GTT GATTTA **SpeI (2489)**
2499 AACAAACTCCCATTGACGTC AATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCA
SnaBI (2617)
2599 TGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATT
NdeI (2722)
2699 GACGTC AATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTC AATGGAAAGTC
2799 CCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTC AATGGGCGGGGTCGTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAA
PstI (2901)
SdaI (2900) **Pacl (2908)** **BspLU11I (2918)**
2899 CGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCC
2997 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGT
3097 GCGCTCTCTGTTCGGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTC
ApaLI (3232)
3197 AGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCA
3297 ACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG
3397 GCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA
3497 CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGT
EagI (3668)
Pacl (3648) **SwaI (3657)** **NotI (3667)**
3597 CTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTCA
3697 TTACATCTGTGTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCA
3797 GTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA