



PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGTGGCGCGGGTAAACTGGAAAGTGTGTCGTGTAAGTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC

Psp1406I (203)
HindIII (245) **Bsu36I (291)**

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACAGCGCCCGCCGCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535)
NcoI (560) **BstEII (555)**

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTACCATGGCTAGGCTCTGTGCTTTCCTCATGATCCTGGTAAT
1 M A R L C A F L M I L V M

EcoO109I (670)

601 GATGAGCTACTACTGGTCAGCCTGTTCTCTAGGATGTGACCTGCCTCACACTTATAACCTCGGAACAAGAGGGCCTTACAGTCTGGAAGAAATGAGA
 13 M S Y Y W S A C S L G C D L P H T Y N L G N K R A L T V L E E M R
 701 AGACTCCCCCTCTTTCCTGCTGAAGGACAGGAAGGATTTGGATTCCCTTGGAGAAGGTGGATAACCAACAGATCCAGAAGGCTCAAGCCATCCTTG
 47 R L P P L S C L K D R K D F G F P L E K V D N Q Q I Q K A Q A I L

BglII (807)
XmnI (828)

801 TGCTAAGAGATCTTACCCAGCAGATTTTGAACCTCTTACATCAAAGACTTGTCTGCTACTTGGAAATGCAACTCTCTAGACTCATTCTGCAATGACCT
 80 V L R D L T Q Q I L N L F T S K D L S A T W N A T L L D S F C N D L
 901 CCATCAGCAGCTCAATGATCTCAAAGCCTGTGTGATGCAGGAACCTCCTCTGACCCAGGAAGACTCCCTGCTGGCTGTGAGGACATACTCCACAGGATC
 113 H Q Q L N D L K A C V M Q E P P L T Q E D S L L A V R T Y F H R I

BstXI (1085)

1001 ACTGTGTACTTGAGAAAAGAAACACAGCCTCTGTGCCTGGGAGGTGATCAGAGCAGAAGTCTGGAGAGCCCTCTTCTCAACCAACTTGTGGCAA
 147 T V Y L R K K K H S L C A W E V I R A E V W R A L S S S T N L L A

MscI (1138)
NheI (1132)

1101 GACTGAGTGAGGAGAAGGAGTGAGTCTGAGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAA
 180 R L S E E K E •

HpaI (1270) **MfeI (1281)**

1201 AAAATGCTTATTGTGAAATTTGTGATGCTATTGCTTTATTGTAAACCATTATAAGCTGCAATAAACCAAGTTAACAAACAATTGCATTCTTTTATG

EcoRI (1366)

1301 TTTAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACC
 1401 TCCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCT

SapI (1548)

1501 TCTTTCATGGAGTTTAAGATATAGTGTATTTTCCCAAGTTTGAACCTAGCTCTTCTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTT

SspI (1605)
Swal (1619) **EcoO109I (1680)**

1601 AGTAAAATATTTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCC
 1701 CAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGG
141 • N R T Y K L P

SacI (1880)

1801 ATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCAC
 132 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 S I L E R C M G C

BstXI (1909)

1901 AGGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGA
 99 P S 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

StuI (2044)

2001 CCCAATGGCAATGGCTTTCAGCACAGACAGTGCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAAGTCTTGGTCTGATGGCCGCC
 66 G I 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

XmnI (2186)

2101 CCGACATGGTCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCTCATGG
 32 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 Q S I N F T K M

AseI (2252)

2201 TGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGT

SacI (2309)

2301 TCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCG

SpeI (2407)

2401 TTGATTTACTAGTCAAAACAACTCCCATTTGACGTCATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTATCCACGCCCATTTGATGTACTGC

2501 CAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGG
SnaBI (2535)

2601 GCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTG
NdeI (2640)

2701 ACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTT

2801 ACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGGAAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT
PstI (2819) **SdaI (2818)** **BspLU11I (2836)** **PacI (2826)**

2901 CCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCT
←

3001 GGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCATAGCTCAC

3101 GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTA
ApaLI (3150)

3201 TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG

3301 TTCTTGAAGTGGTGGCCTAACTACGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT

3401 CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGGTTTCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGAT

3501 CTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAA
EagI (3586) **PacI (3566)** **SwaI (3575)** **NotI (3585)**

3601 TATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAA

3701 ATAGGCTGTCCCAGTGCAAGTGCAAGTGCCAGAACATTTCTCTATCGAA