



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

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC
 301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTGTTTCGTTT

BspLU11I (560)

501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGCGCTACCTGAGATCACCGGTCAACATGTGCTTCCCGAAGGTCCTCTCTGATGACATGAAGAA
AgeI (552)
M C F P K V L S D D M K K

601 GCTGAAGGCCGAATG CACCAGGCCATAGAAAGATTTTATGATAAAATGCAAAATGCAGAATCAGGACGTGGACAGGTGATGTCGAGCCTGGCAGAGCTG
 13▶ L K A R M H Q A I E R F Y D K M Q N A E S G R G Q V M S S L A E L
 701 GAGGACGACTTCAAAGAGGGCTACCTGGAGACAGTGGCGGCTTATTATGAGGAGCAGCACCCAGAGCTCACTCTCTACTTGAAAAAGAAAGAGATGGAT
 47▶ E D D F K E G Y L E T V A A Y Y E E Q H P E L T P L L E K E R D G

BspHI (884)

801 TACGGTGCAGGCAACAGATCCCTGTCCCGGATGTTGAGGATCCCGCAACCGAGGAGCCTGGGGAGAGCTTTGTGCAAGGTCATGAGATGGTTCCA
 80▶ L R C R G N R S P V P D V E D P A T E E P G E S F C D K V M R W F Q

BamHI (840)
Tth111I (877)

901 GGCCATGCTGCAGCGGCTGCAGACCTGGTGGCACGGGTTCTGGCCTGGGTGAAGGAGAAGGTGGTGGCCTGGTCCATGCAGTGCAGGCCCTCTGGAAA
 113▶ A M L Q R L Q T W W H G V L A W V K E K V V A L V H A V Q A L W K

XmnI (996)

1001 CAGTTCAGAGTTTCTGCTGCTCTCTGTGAGAGCTCTTATGCTCTTTCCAGTCTACGGAGCCCCACGGGGGACAAGGAGGAGCTGACACCCAGA
 147▶ Q F Q S F C C S L S E L F M S S F Q S Y G A P R G D K E E L T P Q

SapI (1032)

1101 AGTGTCTGAACCCCAATCCTCAAATGAAGATACTGACACCACCTTTGCCGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCA
 180▶ K C S E P Q S S K •

MscI (1157)

1201 CAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

HpaI (1289)

1301 CAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACA

MfeI (1300)
EcoRI (1385)

1401 GCATAGCAAAACTTAACTCCAATCAAGCCTCTACTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTTTGCCAATGTGCATTA

SapI (1567)

1501 GCTGTTTGAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGTTTGAAGTACTCTTCTTCTTATGTTTAAATGCACTGA

SspI (1624)
Swal (1638)

1601 CCTCCACATTCCCTTTTGTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAA

1701 GGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTAAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTT

1+1+1 • N

1801 CCTGGTGTACTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCTTGCATTCACTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATG
 139▶ 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 S I

BstXI (1928)

1901 AGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCT
 105▶ 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 D K Q

StuI (2063)

2001 GCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGT
 72▶ 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 E G T

2101 CTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTCTCTATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAG
 39▶ 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 Q S

BspHI (2213)

BbsI (2209)
XmnI (2205)
AseI (2271)

2201 ATGTTGAAGGTCTTCATGATGGCCCTCTATAGTGAAGTCTTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGT
 5▶ I N F T K M

2301 CTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTAC

SpeI (2426)

2401 GACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCC

2501 ACGCCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTAC
SnaBI (2554)

2601 TGGGCATAATGCCAGGCGGGCCATTTACCCTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACC
NdeI (2659)

2701 GTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGG

2801 TCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGGTTAA**TAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGG**
SdaI (2837) **PacI (2845)** **BspLU11I (2855)**

2901 **CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG**

3001 **ATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG**

3101 **GCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCT**
ApaLI (3169)

3201 **GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA**

3301 **TGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC**

3401 **GGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGAT**

3501 **CTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA**
PacI (3585) **SwaI (3594)**

EagI (3605)
NotI (3604)

3601 **ATCAGCGCCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAAACAAAACGA**

3701 AACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA