



PvuI (7)
SgfI (6)
MfeI (82)

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGACAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGGTAAGTGGAAAGTGATGTCTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACAGCGCCCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCGGGTTGAGTCGCGTTCTGCCGCCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

KasI (535)
AgeI (552)
SphI (560)

501 TCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGCGGCTACCTGAGATCACCGGTCAGCATGCCCTCAACGTGAACCTTCAACAACAGGAACATGA

601 CCTCGACTACGACTCCGTACAGCCCTATTTTCATCTGCGACGAGGAAGAGAATTTCTATCACCAGCAACAGCAGAGCGAGCTGCAGCCGCCCGCCAGT

13▶ L D Y D S V Q P Y F I C D E E E N F Y H Q Q Q Q S E L Q P P A P S

EcoRV (703)

701 GAGGATATCTGGAAGAAATTCGAGCTGCTTCCACCCCGCCCTGTCCCGAGCCGCGCTCCGGGCTGCTCTCCATCCTATGTTGCGGTGCTACGT

47▶ E D I W K K F E L L P T P P L S P S R R S G L C S P S Y V A V A T

BbsI (814)

801 CCTTCTCCCAAGGGAAGACGATGACGGCGCGGTGGCAACTTCTCCACCGCCGATCAGCTGGAGATGATGACCGAGTTACTTGGAGGAGACATGGTGAA

80▶ S F S P R E D D D G G G G N F S T A D Q L E M M T E L L G G D M V N

901 CCAGAGCTTCATCTGCGATCCTGACGACGAGACCTTCATCAAGAACATCATCATCCAGACTGTATGTGGAGCGGTTTCTCAGCCGCTGCCAAGCTGGTC

113▶ Q S F I C D P D D E T F I K N I I I Q D C M W S G F S A A A K L V

BssHIII (1027)
SacII (1059)
SdaI (1095)

1001 TCGGAGAAGCTGGCTCCTACCAGGCTGCGCGCAAAGACAGCACCAGCCTGAGCCCGCCCGGGCACAGCGTCTGCTCCACCTCCAGCCTGTACCTGC

147▶ S E K L A S Y Q A A R K D S T S L S P A R G H S V C S T S S L Y L

1101 AGGACCTCACCGCCGCGCGTCCGAGTGCAATTGACCCCTCAGTGGTCTTTCCCTACCCGCTCAACGACAGCAGCTCGCCCAAATCCTGTACTCGTCCGA

180▶ Q D L T A A A S E C I D P S V V F P Y P L N D S S S P K S C T S S D

1201 TTCCACGGCTTCTCCTCCTCGACTCGTGTCTCCGAGCTCCTCCACGGGCGAGCCCTGAGCCCTAGTGTGCATGAGGAGACACCGCC

213▶ S T A F S P S S D S L L S E S S P R A S P E P L V L H E E T P P

1301 ACCACCAGCAGCAGCTCTGAAGAAGAGCAAGAAGATGAGGAAGAAATGATGTGGTGTCTGTGGAGAAGAGGCAAACCCCTGCCAAGAGTCCGAGTCCG

247▶ T T S S D S E E E Q E D E E E I D V V S V E K R Q T P A K R S E S

1401 GCTCATCTCCATCCCGAGGCCACAGCAAACCTCCGACAGCCACTGGTCTCAAGAGGTGCCACGTCTCCACTCACCAGCACAACACTACGCCGACCC

280▶ G S S P S R G H S K P P H S P L V L K R C H V S T H Q H N Y A A P P

1501 CTCCACAAGGAAGACTATCCAGCTGCCAAGAGGGCAAGTTGGACAGTGGCAGGGTCTGAAGCAGATCAGCAACAACCGCAAGTGTCCAGCCCGAGG

313▶ S T R K D Y P A A K R A K L D S G R V L K Q I S N N R K C S S P R

1601 TCCTCAGACACGGAGGAAACGACAAGAGGCGGACACACAACGCTTTGGAACGTCAGAGGAGGAACGAGCTGAAGCGCAGCTTTTTTGCCTGCGTGACC

347▶ S S D T E E N D K R R T H N V L E R Q R R N E L K R S F F A L R D

1701 AGATCCCTGAATTGGAAAACAACGAAAAGGCCCAAGGTAGTATCTCAAAAAAGCCACCCCTACATCCTGTCCATTCAAGCAGACGAGCACAAGCT

380▶ Q I P E L E N N E K A P K V V I L K K A T A Y I L S I Q A D E H K L

BstBI (1862)
XhoI (1892)

1801 CACCTCTGAAAAGACTTTATGAGGAAACGACGAGAACAGTTGAAACACAACCTCGAACAGCTTGGAACTCTGGTGCATAAACTGACCTAACTCGAGGA

413▶ T S E K D L L R K R R E Q L K H K L E Q L R N S G A •

MscI (1915)

NheI (1909)

1901 GGAGCTGGAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTT

HpaI (2047)
MfeI (2058)

2001 GTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCAATTTATGTTTCAGGTTTCAGGGGAGGTGTG

EcoRI (2143)

2101 GGAGGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTTCTAAAATACAGCATAGCAAACTTTAACTCCAAATCAAGCCTCTACTTGAA

2201 TCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAGATATA

SspI (2382)
SwaI (2396)

2301 GTGTATTTTCCCAAGGTTTGAACAGTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAAATATTCAGAAATAATTT

2401 AAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGG

2501 AACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGGGGATGAGTTCCTCAATGGTGGTTTT

141▶ • N R T Y K L P I L E E I T T K

SacI (2657)
BstXI (2686)

2601 GACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGAT

125▶ 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 S

2701 CTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCAC

91▶ 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 A C

StuI (2821)

2801 AGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTCTC

58▶ 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 D E

2901 ATAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGCTTCATGATGGCCCTCTATAGTGAGTCGTA
 25 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 ← **BspHI (2971)**
 BbsI (2967)

3001 TTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTATATCTGACGGTTCCTAAACGAGCTCTGCTTATA
 ← **AseI (3029)** SacI (3086)

3101 TAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAAC
 ← **SpeI (3184)**

3201 TCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGTTAAT

3301 AGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTAAGTGGGCATAATGCCAGGGGGCCATTACCGTCATTGACGTCA
 ← **SnaBI (3312)**

3401 ATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCAAGTGGGCGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTG
 ← **NdeI (3417)**

3501 GCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTG
 ← **SdaI (3595)**

3601 AGGTTAATTAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGAGC
 ← **PacI (3603) BspLU11I (3613)**

3701 AGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAAGCTCCCTCGTGGCTCTCC

3801 TGTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTG

3901 TAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA
 ← **ApaLI (3927)**

4001 GACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA

4101 CGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACC

4201 GCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTC

4301 AGTGGAAACGAAACTCACGTAAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTG
 ← **PacI (4343) SwaI (4352) NotI (4362) EagI (4363)**

4401 TGTGTTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTG

4501 CAGGTGCCAGAACATTTCTATCGAA