



PvuI (7)
SgfI (6)

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)
Psp1406I (203)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGGC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

PvuII (239)
Bsu36I (291)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

NgoMIV (441)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTCAACATGTCTGGTTTGTGGCCACTCTCCGGCCTGGCCC

601 TCTCCCGTCCGCTGGCTCTTTCTGTTGCTGCTCGGCCAGCTCGGTCCTCGGCATCTCCTTCCATCTGCCGTGAACTCTCGCAAGTGTCTCCGAGAG

13▶ L P S A W L F L L L L G P S S V L G I S F H L P V N S R K C L R E

701 GAGATCCACAAGGACCTGCTGGTACGGGCGCCTACGAGATCACCGACCAGTCTGGGGCGCTGGCGGCTGCGCACCACCTCAAGATCACAGATTCTG

47▶ E I H K D L L V T G A Y E I T D Q S G G A G G L R T H L K I T D S

801 CTGGCCATATTCTGTATGCCAAAGAGGATGCAACCAAGGGGAAGTTTGCCTTTACCACGGAAGACTATGACATGTTTGAAGTGTGTTTGGAGCAAGGG

80▶ A G H I L Y A K E D A T K G K F A F T T E D Y D M F E V C F E S K G

901 AACAGGGCGGATACCTGACCAACTCGTGATTCTAGACATGAAGCATGGAGTAGAGGCGAAAAATTATGAAGAGATTGCAAAAGTCGAGAACTCAAACCA

113▶ T G R I P D Q L V I L D M K H G V E A K N Y E E I A K V E K L K P

1001 CTGGAGGTGGAGTTACGACGGCTCGAGGACCTTCCGAGTCCATTGTTAATGACTTTGCCTACATGAAGAAGCGGAAGAGGAGATGAGGGACACTAATG

147▶ L E V E L R R L E D L S E S I V N D F A Y M K K R E E E M R D T N

1101 AGTCCACGAACACCCGGTCTGTACTTTCAGCATCTTTCCATGTTCTGCCTATTGGACTAGCCACCTGGCAGGTCTTCTACCTGCGTCGCTTCTCAA

180▶ E S T N T R V L Y F S I F S M F C L I G L A T W Q V F Y L R R F F K

1201 GGCCAAGAAGTTGATAGAGTAATGAGGCTCAGTGTCTGTCCCTAGAGCCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAC

213▶ A K K L I E • •

AgeI (552)
FspI (770)

1301 ACAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACA

MfeI (1401)
EcoRI (1486)

1401 ACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATAC

1501 AGCATAGCAAACTTTAACTCCAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATT

SapI (1668)

1601 AGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTCCCAAGTTTGAACCTAGCTCTTCACTTTATGTTTAAATGCACTG

SspI (1725)

1701 ACCTCCCACATCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCA

1801 AGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGT

1901 TCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGAT

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

2001 GAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCCAATGGTGTCAAAGTCTCTC

106▶ 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

2101 TGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCG

72▶ 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 E G T

2201 TCTTGGTCTGATGGCCGCCGACATGGTGTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCCCTGCTGAGA

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

2301 GATGTTGAAGTCTTCTCATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCG

6▶ I N F T K M

XmnI (2306)
AseI (2372)

2401 TCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTA

SacI (2429)

2501 CGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATC

SpeI (2527)

2601 CACGCCCATTTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTA

SnaBI (2655)

2701 CTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTAC

NdeI (2760)

2801 CGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTTTGGGGC

2901 GTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAAAGCCAGCAAAAAGCCAGGAACCGTAAAAAG

PacI (2946)
PstI (2939)
SdaI (2938)

3001 GCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAA

3101 GATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCCTTCTCCCTTCGGGAAGCGT

3201 GCGCCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTTCAGCCCGACCGC

ApaLI (3270)

3301 TCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGT

3401 ATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCCTCTGCTGAAGCCAGTTACCTT

3501 CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGA

3601 TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTA

PacI (3686) SmaI (3695)

3701 AATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACG

EagI (3706)
NotI (3705)

3801 AAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA