



PvuI (7) SgfI (6) MfeI (82) EcoNI (96)
1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGTCTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) Bsu36I (291)
Psp1406I (203) PvuII (239) EcoNI (287)
201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555) AgeI (552) NcoI (560) NgoMIV (578)
501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTACCATGGCCCTCCACCTGCCGCTCCTCAGTGTGCACT

601 GGCTCTGCTGCTGCTGCTGGCCACCAACCAGGCTACAGGGGCTGTGTGGCCAGTGAAGTGCCTGTCAGTGCCTGAACACCCTACCAAGGGTTGAT

133 V L L L L L A T N H Q A T G A V V A S E L R C Q C L N T L P R V D

PshAI (753)
701 TTTGAGACCATCCAGAGCTTGACGGTGACGCCCCAGGACCCACTGCACCCAGACAGAAGTCATAGCCACTCTCAAGGATGGTCAAGAAGTTTGCCTCA

473 F E T I Q S L T V T P P G P H C T Q T E V I A T L K D G Q E V C L

BsrBI (846) BsaBI (822) SapI (843) PvuII (858) NheI (872)
801 ACCCCCAAGGCCAGGCTTTCAGATAATCATCAAGAAGATACTGAAGAGCGGCAAGTCCAGCTGAGCCGGGAGCTAGCTGGCCAGACATGATAAGATACA

803 N P Q G P R L Q I I I K K I L K S G K S S •

901 TTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTG

HpaI (1010) MfeI (1021)
1001 CAATAAACAAGTTAAACAACAACATTCATTCTTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGT

EcoRI (1106)
1101 GGTATGAATTCTAAATACAGCATAGCAAACTTTAACCTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGG

SapI (1288)
1201 GGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAACAGCTCTTCATTTT

SspI (1345) SwaI (1359)
1301 TTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATT

1401 AGGCAGAATCCAGATGCTCAAGGCCCTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAAATTTGACAGCAAGAA

1501 AGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAG

141 • N 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

SacI (1620) BstXI (1649)
1601 TCAGGAGCATAGTCAGAGATGAGCTCTGTCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCA

112 D P A Y D S I 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

StuI (1784)
1701 CAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGAC

79 I T D F D K 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

1801 AGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTGTGTTGCTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACC

46 A S I I E G T 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

BbsI (1930) XmnI (1926) AseI (1992)
1901 AGCTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAAGTCTGATTATACTATGCGGATATACTATGCCGATGATTAATTG

12 L E L D Q Q S I N F T K M

SacI (2049)
2001 TCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTGCG

SpeI (2147)
2101 TCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTTGACGTCAATGGGGTGGAGACTTGAAATCC

SnaBI (2275)
2201 CCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAGTAGGA

NdeI (2380)

2301 AAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTA

2401 CTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAA

Pacl (2566)

PstI (2559)

SdaI (2558)

BspLU11I (2576)

2501 TGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAAATAAGAACATGTGAGCAAAAGGCCAGCAAA

2601 AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG

2701 AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCC

ApaLI (2890)

2801 TTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAAC

2901 CCCCCTTCAGCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA

3001 CAGGATTAGCAGAGCGAGGTATGTAGGCGGTCTACAGAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCT

3101 CTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGA

3201 TTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCAT

EagI (3326)

Pacl (3306) SwaI (3315) **NotI (3325)**

3301 GGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACG

3401 CTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA