



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

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTGTGTCTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245)

Psp1406I (203)
PvuII (239)
Bsu36I (291)

201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGCC

301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTCTCAACTCTACGCTTTTGTTCGTTT

BstEII (555) BstAPI (565)
SapI (598)

AgeI (552) NcoI (560)
SdaI (591)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCATCTTCTGCAGAGCTGGACTTCAACCTGCAGGC

601 TCTTCTGGAGCAGCTCAGCCAGGATGAGTTGAGCAAGTTCAAGTCTCTGATCAGAACAATCTCCCTGGAAAGGAGCTACAGACCGTCCCCGACAGAG

13▶ L L E Q L S Q D E L S K F K S L I R T I S L G K E L Q T V P Q T E

701 GTAGACAAGGCTAATGGGAAGCAACTGGTAGAAATCTCACCAGCCACTCCTGCAGCTACTGGCAGGGATGGCAGCCATCCAGGCTTTGAAAAGATGA

47▶ V D K A N G K Q L V E I F T S H S C S Y W A G M A A I Q V F E K M

DraIII (832)
NheI (856)
MscI (862)

801 ATCAAACGCATCTGTCTGGGAGAGCTGATGAACACTGTGTGATGCCCCACCTTAAGCTAGTGGCCAGACATGATAAGATACATTGATGAGTTTGGACA

80▶ N Q T H L S G R A D E H C V M P P P •

901 AACCAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAAGTTAAC

MfeI (1005)
EcoRI (1090)

1001 AACACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATCTAAA

1101 ATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTG

SapI (1272)

1201 CATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCAAGGTTTGAAGTCTTTCATTTCTTTATGTTTAAATGC

SspI (1329)
SwaI (1343)

1301 ACTGACCTCCCACATTCCCTTTTATGAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATG

EcoO109I (1404)

1401 CTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTT

1501 TAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAG

140◀ • 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 D P A Y D S

SacI (1604)
BstXI (1633)

1601 AGATGAGCTCTCTGCACATGCCACAGGGGTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTC

107◀ 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 I T D F D

StuI (1768)

1701 CTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCC

74◀ 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 A S I I E

1801 CCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCT

40◀ 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 L E L D Q Q

BbsI (1914)
AseI (1976)

XmnI (1910)

1901 GAGAGATGTTGAAGGTTCTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGAT

7◀ S I N F T K M

SacI (2033)

2001 GGCGTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTT

SpeI (2131)

2101 GTTACGACATTTTGGAAAGTCCCCTGATTACTAGTCAAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGC

SnaBI (2259)

2201 TATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAAGGTCA

NdeI (2364)

2301 TG TACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGT

2401 TTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGT TACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTG

SdaI (2542)PacI (2550) **BspLU11I (2560)**

2501 GGCGGT CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACG CCTGCAGGTTAATTAAGA ACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAA

2601 AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATC AAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTA

2701 TAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA

ApaLI (2874)

2801 GCGTGGCGCTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTT CAGCCCGA

2901 CCGCTGCGCCTTATCCGTAAC TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG

3001 AGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA

3101 CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAA

PacI (3290) SwaI (3299)

3201 AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAAC TACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACA

EagI (3310)

NotI (3309)

3301 TTTAAATCAGCGGCGCAATAAAAATATCTTTATTTTCATTACATCTGTGTGGTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAA

3401 AACGAAACAAAACAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA